



Full wwPDB EM Validation Report ⓘ

Dec 12, 2022 – 12:10 pm GMT

PDB ID : 6YWX
EMDB ID : EMD-10978
Title : The structure of the mitoribosome from *Neurospora crassa* with tRNA bound to the E-site
Authors : Amunts, A.; Itoh, Y.; Naschberger, A.
Deposited on : 2020-04-30
Resolution : 3.10 Å(reported)

This is a Full wwPDB EM Validation 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:

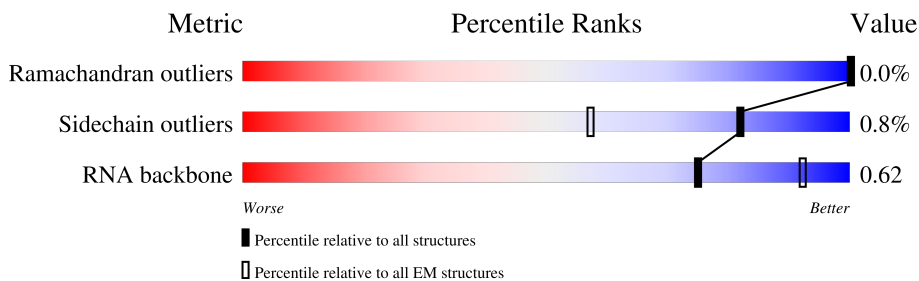
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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.



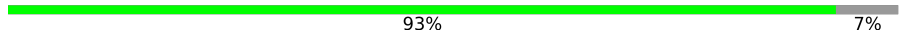
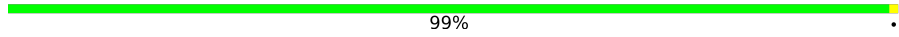



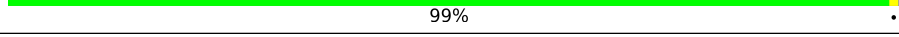


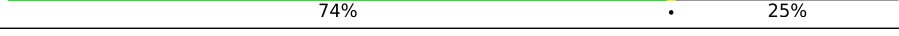

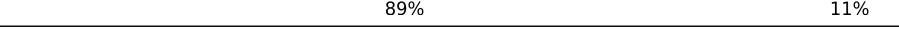
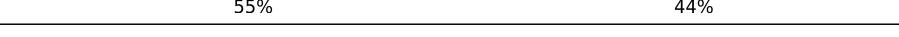

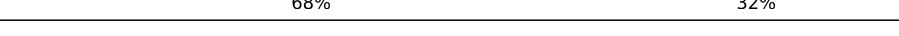


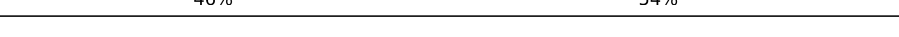

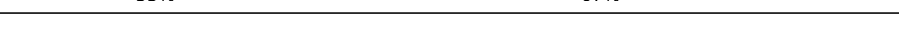






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	3464	
2	B	383	
3	C	384	
4	D	325	
5	E	352	
6	F	255	
7	G	300	
8	f	347	


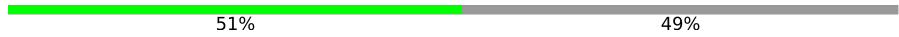

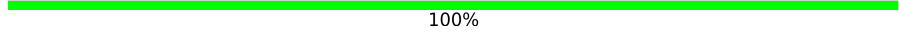



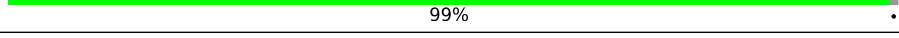
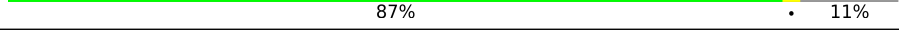
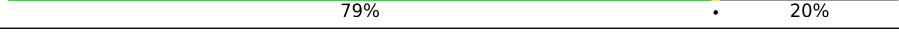
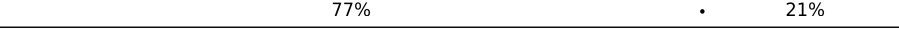

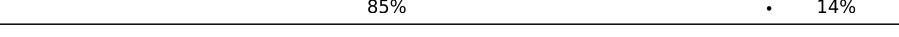
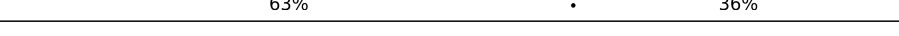
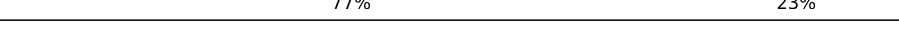
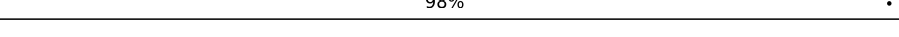

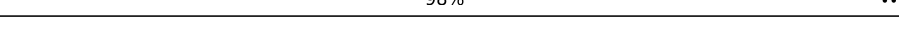
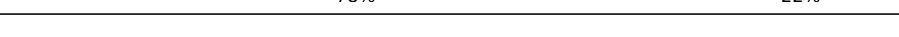

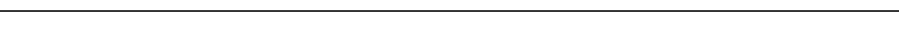

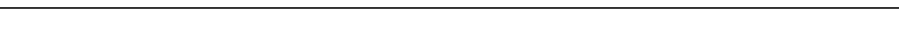


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Mol	Chain	Length	Quality of chain
9	g	158	 93% 7%
10	H	183	 99%
11	I	131	 91% 9%
12	J	312	 76% 22%
13	K	249	 67% 33%
14	L	193	 99%
15	M	258	 74% 25%
16	N	217	 61% 39%
17	O	364	 74% 25%
18	P	228	 78% 21%
19	Q	396	 89% 11%
20	R	447	 55% 44%
21	S	274	 65% 35%
22	T	263	 68% 32%
23	U	161	 85% 14%
24	V	219	 26% 74%
25	W	129	 46% 54%
26	X	59	 81% 19%
27	Y	140	 33% 67%
28	0	124	 36% 63%
29	1	449	 80% 18%
30	2	370	 33% 67%
31	3	103	 90% 8%
32	4	138	 98%
33	5	439	 79% 20%


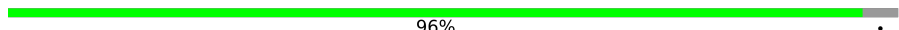








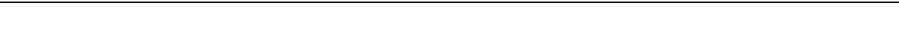

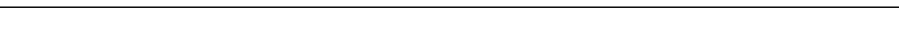
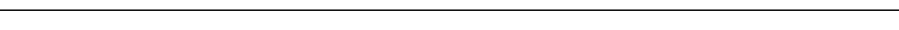











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Mol	Chain	Length	Quality of chain
34	6	368	 73% 26%
35	7	165	 51% 49%
36	8	443	 74% 25%
37	h	98	 100%
38	i	218	 57% 43%
39	9	267	 76% 23%
40	a	225	 72% 28%
41	b	162	 99%
42	c	110	 87% 11%
43	d	292	 79% 20%
44	AA	470	 77% 21%
45	BB	428	 67% 32%
46	CC	508	 85% 14%
47	DD	453	 63% 36%
48	EE	477	 77% 23%
49	FF	117	 98%
50	GG	309	 70% 30%
51	HH	161	 98%
52	II	315	 78% 22%
53	JJ	268	 69% 30%
54	KK	376	 33% 67%
55	LL	174	 74% 26%
56	MM	119	 99%
57	NN	113	 99%
58	OO	320	 86% 14%

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Mol	Chain	Length	Quality of chain
59	PP	107	 92% 8%
60	QQ	165	 96% .
61	RR	256	 52% 48%
62	SS	91	 89% 11%
63	TT	236	 37% 63%
64	UU	253	 86% 14%
65	VV	316	 83% 17%
66	WW	396	 89% 11%
67	XX	469	 86% . 13%
68	YY	108	 92% 8%
69	ZZ	382	 81% . 18%
70	11	90	 98% .
71	22	344	 10% 90%
72	33	236	 81% 18%
73	44	310	 84% 16%
73	55	310	 74% . 25%
74	66	348	 81% . 19%
75	77	414	 43% 57%
76	88	508	 91% . 8%
77	00	95	 51% 49%
77	99	95	 37% . 62%
78	aa	1864	 66% 11% 23%
79	bb	61	 82% 18%
80	e	303	 49% 50%
81	j	201	 96% . .

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 390774 atoms, of which 173664 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 RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	A	2838	90895	27142	30363	10859	19693	2838	0	0

- Molecule 2 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	B	317	4996	1537	2523	502	419	15	0	0

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	C	307	4757	1468	2421	447	413	8	0	0

- Molecule 4 is a protein called 60S ribosomal protein L4, variant.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	D	254	4068	1280	2040	372	371	5	0	0

- Molecule 5 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	E	309	4910	1558	2461	436	443	12	0	0

- Molecule 6 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	F	201	3253	1022	1645	290	288	8	0	0

- Molecule 7 is a protein called RIBOSOMAL_L9 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
7	G	74	1245	390	627	121	104	3	0	0

- Molecule 8 is a protein called uL10m.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
8	f	245	3801	1202	1925	325	346	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
9	g	147	2257	700	1154	203	196	4	0	0

- Molecule 10 is a protein called Ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
10	H	183	2885	899	1459	268	251	8	0	0

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
11	I	119	1898	564	985	182	159	8	0	0

- Molecule 12 is a protein called 50S ribosomal subunit protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
12	J	243	3827	1198	1939	346	343	1	0	0

- Molecule 13 is a protein called 60S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
13	K	168	2751	850	1401	263	231	6	0	0

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace	
14	L	192	Total	C	H	N	O	S	0	0
			3135	960	1590	294	285	6		

- Molecule 15 is a protein called Mitochondrial ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
15	M	194	Total	C	H	N	O	S	0	0
			3164	981	1628	292	253	10		

- Molecule 16 is a protein called Aconitate hydratase.

Mol	Chain	Residues	Atoms					AltConf	Trace	
16	N	133	Total	C	H	N	O	S	0	0
			2176	673	1120	195	182	6		

- Molecule 17 is a protein called Mitochondrial large ribosomal subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace	
17	O	272	Total	C	H	N	O	S	0	0
			4532	1392	2323	424	387	6		

- Molecule 18 is a protein called Mitochondrial ribosomal protein subunit L23.

Mol	Chain	Residues	Atoms					AltConf	Trace	
18	P	180	Total	C	H	N	O	S	0	0
			2975	953	1494	270	254	4		

- Molecule 19 is a protein called KOW domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
19	Q	353	Total	C	H	N	O	S	0	0
			5829	1786	2961	547	524	11		

- Molecule 20 is a protein called bL27m.

Mol	Chain	Residues	Atoms					AltConf	Trace	
20	R	249	Total	C	H	N	O	S	0	0
			4195	1283	2149	412	347	4		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
21	S	179	2979	937	1507	281	252	2	0	0

- Molecule 22 is a protein called 54S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
22	T	180	2950	937	1453	279	278	3	0	0

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
23	U	138	2263	698	1164	213	185	3	0	0

- Molecule 24 is a protein called bL31m.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
24	V	56	921	291	462	85	82	1	0	0

- Molecule 25 is a protein called Mitochondrial ribosomal protein subunit L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
25	W	59	949	282	489	98	72	8	0	0

- Molecule 26 is a protein called bL33m.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
26	X	48	836	263	433	71	65	4	0	0

- Molecule 27 is a protein called Related to ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
27	Y	46	777	224	412	84	56	1	0	0

- Molecule 28 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
28	0	46	797	240	409	86	58	4	0	0

- Molecule 29 is a protein called Mitochondrial large ribosomal subunit YmL35.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
29	1	367	6014	1899	3029	547	531	8	0	0

- Molecule 30 is a protein called mL40.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
30	2	123	2101	660	1055	211	171	4	0	0

- Molecule 31 is a protein called mL41.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
31	3	95	1536	489	773	135	137	2	0	0

- Molecule 32 is a protein called Mitochondrial ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
32	4	137	2139	671	1087	192	183	6	0	0

- Molecule 33 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
33	5	350	5429	1740	2710	477	493	9	0	0

- Molecule 34 is a protein called 50S ribosomal subunit L30.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
34	6	273	4474	1418	2248	399	401	8	0	0

- Molecule 35 is a protein called mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
35	7	84	1383	431	709	130	113	0	0

- Molecule 36 is a protein called mL50.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
36	8	331	5374	1683	2714	480	489	8	0	0

- Molecule 37 is a protein called Mitochondrial ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
37	h	98	1577	490	798	139	146	4	0	0

- Molecule 38 is a protein called mL54.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
38	i	124	1999	613	1022	181	178	5	0	0

- Molecule 39 is a protein called RNase III domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
39	9	206	3341	1051	1698	295	290	7	0	0

- Molecule 40 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
40	a	161	2671	837	1340	253	235	6	0	0

- Molecule 41 is a protein called Mitochondrial 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
41	b	161	2693	840	1379	249	221	4	0	0

- Molecule 42 is a protein called 54S ribosomal protein L31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
42	c	98	1700	528	873	162	134	3	0	0

- Molecule 43 is a protein called mL67.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
43	d	235	3797	1180	1909	363	339	6	0	0

- Molecule 44 is a protein called bS1m.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
44	AA	372	5790	1827	2907	507	543	6	0	0

- Molecule 45 is a protein called Mito ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
45	BB	290	4570	1426	2301	423	414	6	0	0

- Molecule 46 is a protein called Ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
46	CC	438	7538	2388	3897	636	612	5	0	0

- Molecule 47 is a protein called Mito ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
47	DD	290	4716	1501	2373	430	401	11	0	0

- Molecule 48 is a protein called 37S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
48	EE	367	5798	1799	2918	526	543	12	0	0

- Molecule 49 is a protein called Mito ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
49	FF	117	1901	591	966	176	165	3	0	0

- Molecule 50 is a protein called Ribosomal_S7 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
50	GG	217	3409	1063	1737	307	296	6	0	0

- Molecule 51 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
51	HH	160	2521	783	1286	226	220	6	0	0

- Molecule 52 is a protein called 37S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
52	II	247	3995	1253	2026	366	345	5	0	0

- Molecule 53 is a protein called 37S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
53	JJ	188	3105	998	1554	273	272	8	0	0

- Molecule 54 is a protein called Mitochondrial ribosomal protein subunit S18.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
54	KK	124	2020	625	1025	195	170	5	0	0

- Molecule 55 is a protein called Mitochondrial 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
55	LL	128	1992	591	1033	198	165	5	0	0

- Molecule 56 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
56	MM	118	1923	586	986	186	161	4	0	0

- Molecule 57 is a protein called Mitochondrial 40S ribosomal protein MRP2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
57	NN	112	1875	573	961	184	150	7	0	0

- Molecule 58 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
58	OO	276	4428	1361	2230	431	401	5	0	0

- Molecule 59 is a protein called Ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
59	PP	98	1612	510	826	141	135	0	0

- Molecule 60 is a protein called Mitochondrial 37S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
60	QQ	158	2561	789	1314	234	219	5	0	0

- Molecule 61 is a protein called Mito ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
61	RR	134	2169	679	1089	206	190	5	0	0

- Molecule 62 is a protein called Mitochondrial ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
62	SS	81	1325	422	677	118	107	1	0	0

- Molecule 63 is a protein called Mito ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
63	TT	88	1518	470	772	157	119	0	0

- Molecule 64 is a protein called 37S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
64	UU	218	3600	1139	1801	334	319	7	0	0

- Molecule 65 is a protein called mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
65	VV	261	4192	1300	2112	390	387	3	0	0

- Molecule 66 is a protein called mS27.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
66	WW	353	5744	1804	2901	514	515	10	0	0

- Molecule 67 is a protein called Mitochondrial ribosomal protein DAP3.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
67	XX	408	6446	2010	3271	562	587	16	0	0

- Molecule 68 is a protein called mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
68	YY	99	1609	491	823	152	142	1	0	0

- Molecule 69 is a protein called 37S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
69	ZZ	312	5114	1631	2528	450	495	10	0	0

- Molecule 70 is a protein called 37S ribosomal protein mrp10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
70	11	88	1358	417	686	128	121	6	0	0

- Molecule 71 is a protein called DUF1713 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
71	22	33	660	187	359	70	43	1	0	0

- Molecule 72 is a protein called IGR domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
72	33	193	3161	989	1607	295	268	2	0	0

- Molecule 73 is a protein called Fe superoxide dismutase.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
73	44	260	4045	1318	1983	355	378	11	0	0
73	55	232	3652	1195	1794	316	337	10	0	0

- Molecule 74 is a protein called mS45.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
74	66	283	4628	1455	2330	425	414	4	0	0

- Molecule 75 is a protein called mS46.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
75	77	179	2796	893	1396	227	277	3	0	0

- Molecule 76 is a protein called 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
76	88	467	7327	2340	3650	634	691	12	0	0

- Molecule 77 is a protein called IF1.

Mol	Chain	Residues	Atoms				AltConf	Trace	
77	00	48	Total	C	H	N	O	0	0
			823	252	417	77	77		
77	99	36	Total	C	H	N	O	0	0
			639	191	333	59	56		

- Molecule 78 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
78	aa	1435	Total	C	H	N	O	P	0	0
			45981	13712	15373	5486	9975	1435		

- Molecule 79 is a RNA chain called tRNA E-site.

Mol	Chain	Residues	Atoms					AltConf	Trace	
79	bb	61	Total	C	H	N	O	P	0	0
			1957	581	658	233	424	61		

- Molecule 80 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
80	e	150	Total	C	H	N	O	S	0	0
			2435	762	1234	212	220	7		

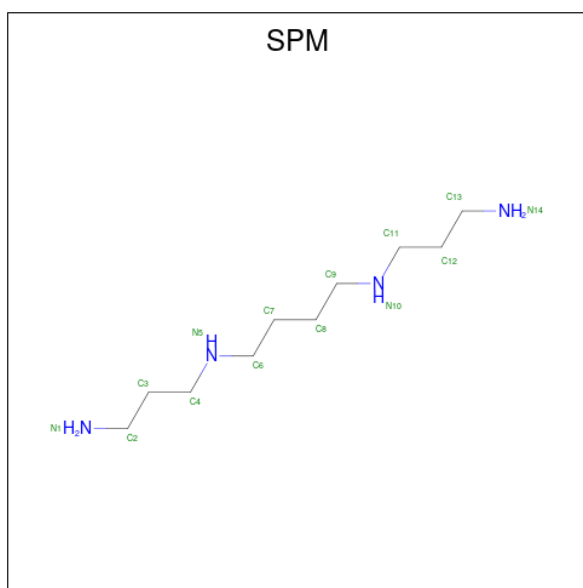
- Molecule 81 is a protein called L51_S25_CI-B8 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
81	j	195	Total	C	H	N	O	S	0	0
			3139	971	1586	290	284	8		

- Molecule 82 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	A	150	Total	Mg	0
			150	150	
82	BB	1	Total	Mg	0
			1	1	
82	XX	1	Total	Mg	0
			1	1	
82	00	1	Total	Mg	0
			1	1	
82	aa	96	Total	Mg	0
			96	96	

- Molecule 83 is SPERMINE (three-letter code: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms			AltConf	
			Total	C	H		N
83	A	1	40	10	26	4	0

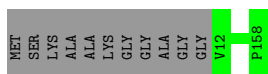
- Molecule 84 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
84	A	28	Total	K	0
			28	28	
84	K	1	Total	K	0
			1	1	
84	2	1	Total	K	0
			1	1	
84	3	1	Total	K	0
			1	1	
84	77	1	Total	K	0
			1	1	
84	88	1	Total	K	0
			1	1	
84	aa	17	Total	K	0
			17	17	

- Molecule 85 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).

- Molecule 9: 60S ribosomal protein L19

Chain g:  93% 7%




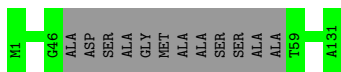
- Molecule 10: Ribosomal protein L13

Chain H:  99%



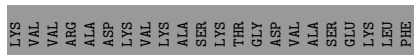
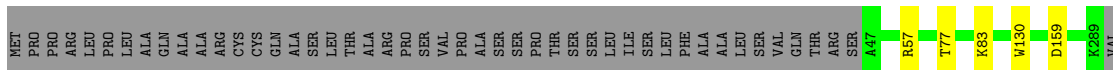
- Molecule 11: 50S ribosomal protein L14

Chain I:  91% 9%



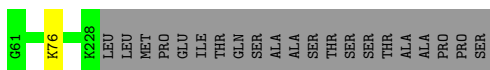
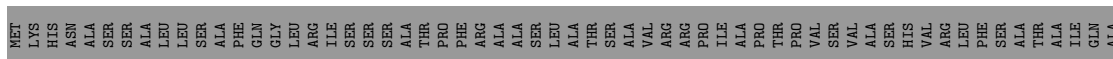
- Molecule 12: 50S ribosomal subunit protein L15

Chain J:  76% 22%



- Molecule 13: 60S ribosomal protein L16

Chain K:  67% 33%



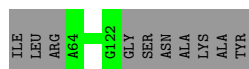
- Molecule 14: 50S ribosomal protein L17

Chain L:  99%

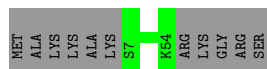
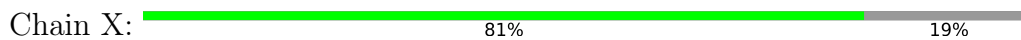


- Molecule 15: Mitochondrial ribosomal protein

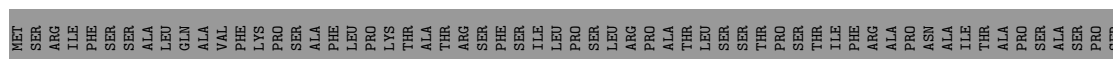
Chain M:  74% 25%



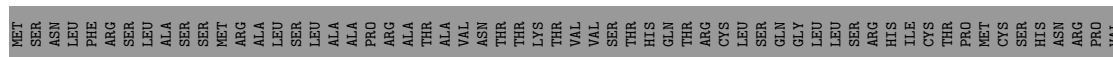
• Molecule 26: bL33m



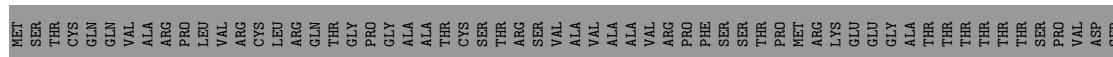
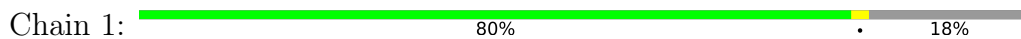
• Molecule 27: Related to ribosomal protein L34, mitochondrial



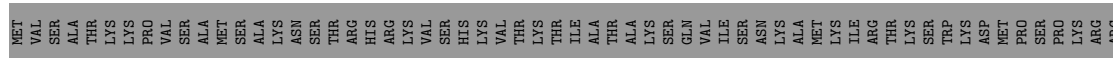
• Molecule 28: Ribosomal protein




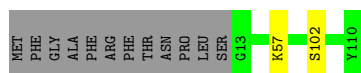
• Molecule 29: Mitochondrial large ribosomal subunit YmL35




• Molecule 30: mL40

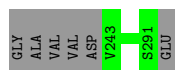
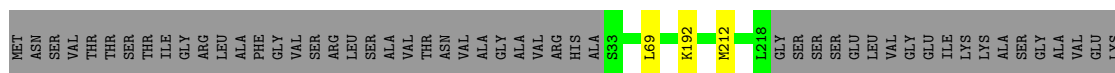


Chain c:  87% 11%




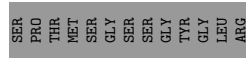
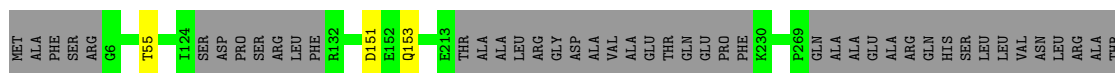
• Molecule 43: mL67

Chain d:  79% 20%



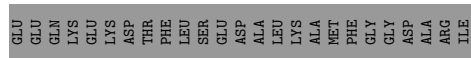
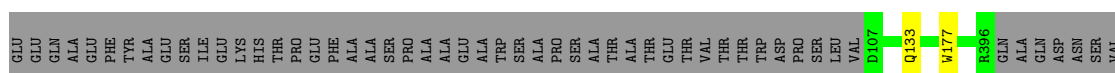
• Molecule 44: bS1m

Chain AA:  77% 21%



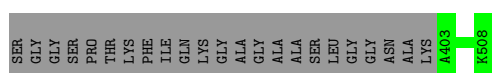
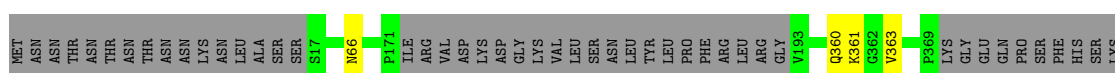
• Molecule 45: Mito ribosomal protein S2

Chain BB:  67% 32%

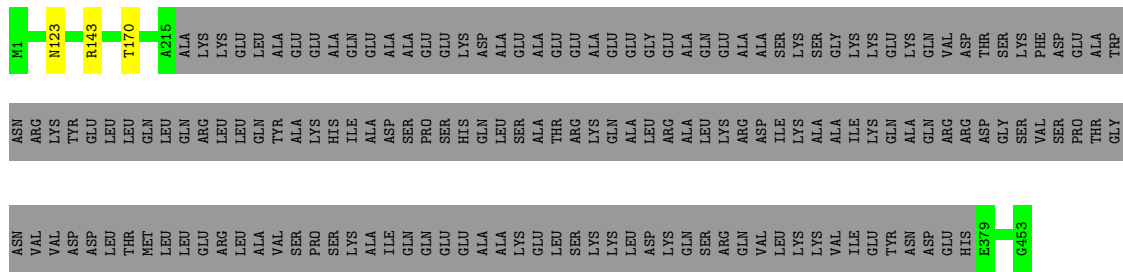


• Molecule 46: Ribosomal protein S5, mitochondrial

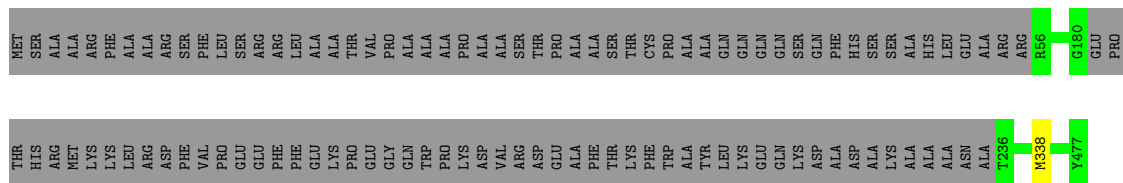
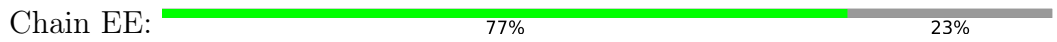
Chain CC:  85% 14%



• Molecule 47: Mito ribosomal protein S4



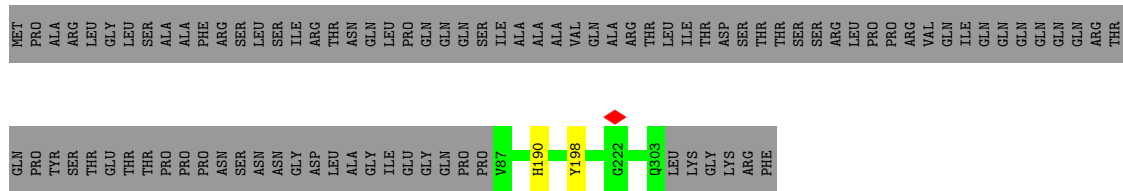
• Molecule 48: 37S ribosomal protein S5



• Molecule 49: Mito ribosomal protein S6



• Molecule 50: Ribosomal_S7 domain-containing protein



• Molecule 51: 40S ribosomal protein S8

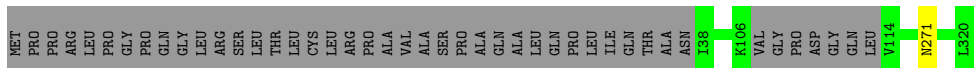
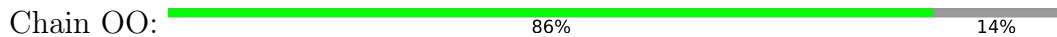


• Molecule 52: 37S ribosomal protein S9, mitochondrial

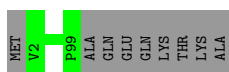




- Molecule 58: Ribosomal protein S15



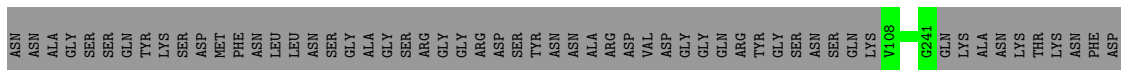
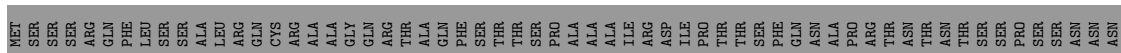
- Molecule 59: Ribosomal protein S16, mitochondrial



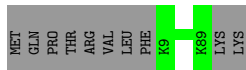
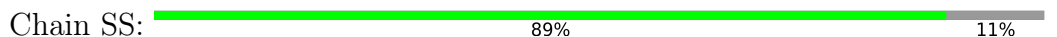
- Molecule 60: Mitochondrial 37S ribosomal protein S17



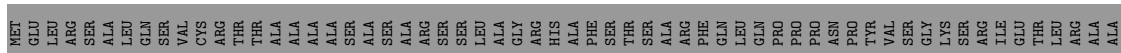
- Molecule 61: Mito ribosomal protein S18




- Molecule 62: Mitochondrial ribosomal protein S19



- Molecule 63: Mito ribosomal protein S21

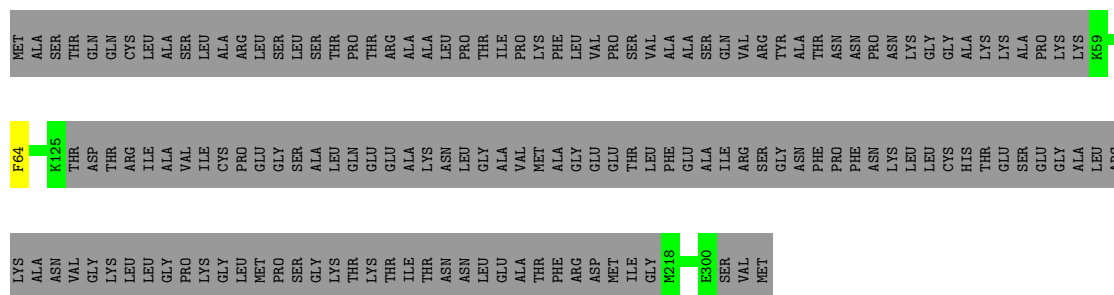


Chain bb:  82% 18%



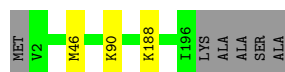
- Molecule 80: 60S ribosomal protein L1

Chain e:  49% 50%



- Molecule 81: L51_S25_CI-B8 domain-containing protein

Chain j:  96%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23802	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	37.985	Depositor
Minimum map value	-23.213	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.342	Depositor
Recommended contour level	0.0295	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, ZN, K, NAD, MG, SPM

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	0.24	0/67790	0.68	0/105564
2	B	0.26	0/2531	0.45	0/3410
3	C	0.27	0/2380	0.46	0/3209
4	D	0.25	0/2072	0.40	0/2794
5	E	0.28	0/2518	0.41	0/3427
6	F	0.25	0/1644	0.41	0/2218
7	G	0.25	0/630	0.46	0/842
8	f	0.24	0/1923	0.40	0/2631
9	g	0.25	0/1126	0.42	0/1525
10	H	0.27	0/1460	0.43	0/1975
11	I	0.26	0/918	0.46	0/1225
12	J	0.26	0/1931	0.43	0/2597
13	K	0.25	0/1376	0.42	0/1842
14	L	0.25	0/1569	0.41	0/2106
15	M	0.25	0/1572	0.42	0/2117
16	N	0.26	0/1077	0.44	0/1452
17	O	0.25	0/2248	0.40	0/3015
18	P	0.26	0/1523	0.40	0/2058
19	Q	0.25	0/2916	0.40	0/3927
20	R	0.25	0/2083	0.42	0/2789
21	S	0.25	0/1510	0.40	0/2042
22	T	0.24	0/1538	0.39	0/2086
23	U	0.25	0/1117	0.43	0/1496
24	V	0.29	0/471	0.43	0/638
25	W	0.25	0/467	0.43	0/616
26	X	0.27	0/411	0.42	0/551
27	Y	0.26	0/368	0.44	0/485
28	0	0.27	0/395	0.46	0/523
29	1	0.27	0/3053	0.42	0/4108
30	2	0.28	0/1074	0.39	0/1449
31	3	0.27	0/783	0.43	0/1056
32	4	0.27	0/1077	0.42	0/1453

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	5	0.26	0/2790	0.40	0/3794
34	6	0.29	0/2274	0.43	0/3062
35	7	0.25	0/686	0.42	0/919
36	8	0.24	0/2714	0.39	0/3657
37	h	0.25	0/791	0.38	0/1065
38	i	0.24	0/990	0.40	0/1324
39	9	0.24	0/1678	0.39	0/2267
40	a	0.25	0/1364	0.41	0/1842
41	b	0.24	0/1348	0.37	0/1816
42	c	0.26	0/846	0.41	0/1134
43	d	0.24	0/1930	0.41	0/2597
44	AA	0.26	0/2948	0.40	0/3995
45	BB	0.26	0/2314	0.41	0/3142
46	CC	0.28	0/3712	0.41	0/4978
47	DD	0.27	0/2409	0.39	0/3255
48	EE	0.26	0/2928	0.41	0/3947
49	FF	0.26	0/952	0.42	0/1285
50	GG	0.26	0/1712	0.40	0/2324
51	HH	0.27	0/1259	0.43	0/1707
52	II	0.26	0/2013	0.40	0/2720
53	JJ	0.28	0/1590	0.41	0/2140
54	KK	0.25	0/1015	0.43	0/1357
55	LL	0.27	0/973	0.44	0/1305
56	MM	0.25	0/950	0.40	0/1274
57	NN	0.27	0/929	0.40	0/1243
58	OO	0.24	0/2242	0.39	0/3016
59	PP	0.29	0/806	0.42	0/1096
60	QQ	0.25	0/1268	0.39	0/1701
61	RR	0.25	0/1105	0.38	0/1491
62	SS	0.27	0/667	0.42	0/902
63	TT	0.25	0/761	0.37	0/1015
64	UU	0.26	0/1845	0.37	0/2491
65	VV	0.25	0/2120	0.38	0/2851
66	WW	0.24	0/2897	0.37	0/3911
67	XX	0.26	0/3234	0.41	0/4374
68	YY	0.26	0/797	0.40	0/1070
69	ZZ	0.26	0/2645	0.39	0/3566
70	11	0.24	0/686	0.38	0/929
71	22	0.24	0/301	0.39	0/388
72	33	0.26	0/1589	0.43	0/2140
73	44	0.24	0/2121	0.38	0/2879
73	55	0.25	0/1912	0.40	0/2600
74	66	0.26	0/2348	0.39	0/3163

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	77	0.28	0/1431	0.39	0/1934
76	88	0.26	0/3760	0.40	0/5085
77	00	0.23	0/409	0.36	0/540
77	99	0.22	0/307	0.32	0/405
78	aa	0.24	0/34270	0.68	0/53383
79	bb	0.12	0/1449	0.65	0/2248
80	e	0.24	0/1223	0.40	0/1645
81	j	0.24	0/1583	0.42	0/2130
All	All	0.25	0/230442	0.56	0/332328

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
2	B	313/383 (82%)	307 (98%)	6 (2%)	0	100	100
3	C	305/384 (79%)	301 (99%)	4 (1%)	0	100	100
4	D	250/325 (77%)	247 (99%)	3 (1%)	0	100	100
5	E	307/352 (87%)	304 (99%)	3 (1%)	0	100	100
6	F	199/255 (78%)	198 (100%)	1 (0%)	0	100	100
7	G	72/300 (24%)	68 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	f	243/347 (70%)	240 (99%)	3 (1%)	0	100	100
9	g	145/158 (92%)	142 (98%)	3 (2%)	0	100	100
10	H	181/183 (99%)	176 (97%)	5 (3%)	0	100	100
11	I	115/131 (88%)	114 (99%)	1 (1%)	0	100	100
12	J	241/312 (77%)	236 (98%)	4 (2%)	1 (0%)	34	69
13	K	166/249 (67%)	166 (100%)	0	0	100	100
14	L	190/193 (98%)	186 (98%)	4 (2%)	0	100	100
15	M	192/258 (74%)	187 (97%)	5 (3%)	0	100	100
16	N	131/217 (60%)	124 (95%)	7 (5%)	0	100	100
17	O	268/364 (74%)	266 (99%)	2 (1%)	0	100	100
18	P	178/228 (78%)	178 (100%)	0	0	100	100
19	Q	351/396 (89%)	350 (100%)	1 (0%)	0	100	100
20	R	245/447 (55%)	241 (98%)	4 (2%)	0	100	100
21	S	175/274 (64%)	173 (99%)	2 (1%)	0	100	100
22	T	178/263 (68%)	177 (99%)	1 (1%)	0	100	100
23	U	134/161 (83%)	133 (99%)	1 (1%)	0	100	100
24	V	54/219 (25%)	54 (100%)	0	0	100	100
25	W	57/129 (44%)	54 (95%)	3 (5%)	0	100	100
26	X	46/59 (78%)	44 (96%)	2 (4%)	0	100	100
27	Y	44/140 (31%)	44 (100%)	0	0	100	100
28	0	44/124 (36%)	44 (100%)	0	0	100	100
29	1	365/449 (81%)	358 (98%)	6 (2%)	1 (0%)	41	73
30	2	121/370 (33%)	120 (99%)	1 (1%)	0	100	100
31	3	93/103 (90%)	90 (97%)	3 (3%)	0	100	100
32	4	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
33	5	346/439 (79%)	344 (99%)	2 (1%)	0	100	100
34	6	267/368 (73%)	267 (100%)	0	0	100	100
35	7	82/165 (50%)	81 (99%)	1 (1%)	0	100	100
36	8	329/443 (74%)	328 (100%)	1 (0%)	0	100	100
37	h	96/98 (98%)	95 (99%)	1 (1%)	0	100	100
38	i	120/218 (55%)	114 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	9	204/267 (76%)	199 (98%)	5 (2%)	0	100	100
40	a	157/225 (70%)	156 (99%)	1 (1%)	0	100	100
41	b	159/162 (98%)	158 (99%)	1 (1%)	0	100	100
42	c	96/110 (87%)	95 (99%)	1 (1%)	0	100	100
43	d	231/292 (79%)	229 (99%)	2 (1%)	0	100	100
44	AA	360/470 (77%)	351 (98%)	9 (2%)	0	100	100
45	BB	288/428 (67%)	279 (97%)	9 (3%)	0	100	100
46	CC	432/508 (85%)	426 (99%)	6 (1%)	0	100	100
47	DD	286/453 (63%)	280 (98%)	6 (2%)	0	100	100
48	EE	363/477 (76%)	352 (97%)	11 (3%)	0	100	100
49	FF	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
50	GG	215/309 (70%)	213 (99%)	2 (1%)	0	100	100
51	HH	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
52	II	245/315 (78%)	239 (98%)	6 (2%)	0	100	100
53	JJ	186/268 (69%)	180 (97%)	6 (3%)	0	100	100
54	KK	122/376 (32%)	118 (97%)	4 (3%)	0	100	100
55	LL	126/174 (72%)	118 (94%)	8 (6%)	0	100	100
56	MM	116/119 (98%)	111 (96%)	5 (4%)	0	100	100
57	NN	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
58	OO	272/320 (85%)	268 (98%)	4 (2%)	0	100	100
59	PP	96/107 (90%)	94 (98%)	2 (2%)	0	100	100
60	QQ	156/165 (94%)	154 (99%)	2 (1%)	0	100	100
61	RR	132/256 (52%)	128 (97%)	4 (3%)	0	100	100
62	SS	79/91 (87%)	77 (98%)	2 (2%)	0	100	100
63	TT	86/236 (36%)	86 (100%)	0	0	100	100
64	UU	216/253 (85%)	212 (98%)	4 (2%)	0	100	100
65	VV	255/316 (81%)	249 (98%)	6 (2%)	0	100	100
66	WW	349/396 (88%)	346 (99%)	3 (1%)	0	100	100
67	XX	404/469 (86%)	396 (98%)	8 (2%)	0	100	100
68	YY	97/108 (90%)	97 (100%)	0	0	100	100
69	ZZ	310/382 (81%)	303 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	11	86/90 (96%)	84 (98%)	2 (2%)	0	100	100
71	22	31/344 (9%)	31 (100%)	0	0	100	100
72	33	191/236 (81%)	182 (95%)	9 (5%)	0	100	100
73	44	258/310 (83%)	254 (98%)	4 (2%)	0	100	100
73	55	228/310 (74%)	223 (98%)	4 (2%)	1 (0%)	34	69
74	66	281/348 (81%)	279 (99%)	2 (1%)	0	100	100
75	77	177/414 (43%)	176 (99%)	1 (1%)	0	100	100
76	88	465/508 (92%)	447 (96%)	18 (4%)	0	100	100
77	00	46/95 (48%)	45 (98%)	1 (2%)	0	100	100
77	99	34/95 (36%)	34 (100%)	0	0	100	100
80	e	146/303 (48%)	141 (97%)	5 (3%)	0	100	100
81	j	193/201 (96%)	188 (97%)	5 (3%)	0	100	100
All	All	15335/21339 (72%)	15058 (98%)	274 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
73	55	200	ALA
12	J	83	LYS
29	1	410	VAL

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	
2	B	259/312 (83%)	257 (99%)	2 (1%)	81	92
3	C	242/303 (80%)	241 (100%)	1 (0%)	91	96
4	D	216/274 (79%)	216 (100%)	0	100	100
5	E	267/296 (90%)	263 (98%)	4 (2%)	65	85
6	F	173/216 (80%)	172 (99%)	1 (1%)	86	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	64/254 (25%)	64 (100%)	0	100	100
8	f	206/287 (72%)	206 (100%)	0	100	100
9	g	120/124 (97%)	120 (100%)	0	100	100
10	H	149/149 (100%)	148 (99%)	1 (1%)	84	93
11	I	100/105 (95%)	100 (100%)	0	100	100
12	J	198/255 (78%)	194 (98%)	4 (2%)	55	80
13	K	142/205 (69%)	141 (99%)	1 (1%)	84	93
14	L	164/165 (99%)	163 (99%)	1 (1%)	86	94
15	M	164/209 (78%)	162 (99%)	2 (1%)	71	88
16	N	119/188 (63%)	119 (100%)	0	100	100
17	O	235/315 (75%)	233 (99%)	2 (1%)	78	91
18	P	158/196 (81%)	156 (99%)	2 (1%)	69	87
19	Q	312/347 (90%)	311 (100%)	1 (0%)	92	96
20	R	212/359 (59%)	210 (99%)	2 (1%)	78	91
21	S	159/242 (66%)	159 (100%)	0	100	100
22	T	161/224 (72%)	161 (100%)	0	100	100
23	U	118/138 (86%)	117 (99%)	1 (1%)	81	92
24	V	52/170 (31%)	52 (100%)	0	100	100
25	W	50/102 (49%)	50 (100%)	0	100	100
26	X	46/54 (85%)	46 (100%)	0	100	100
27	Y	38/116 (33%)	38 (100%)	0	100	100
28	0	41/108 (38%)	40 (98%)	1 (2%)	49	76
29	1	316/384 (82%)	310 (98%)	6 (2%)	57	81
30	2	109/317 (34%)	107 (98%)	2 (2%)	59	82
31	3	83/91 (91%)	81 (98%)	2 (2%)	49	76
32	4	113/114 (99%)	111 (98%)	2 (2%)	59	82
33	5	279/351 (80%)	277 (99%)	2 (1%)	84	93
34	6	238/310 (77%)	234 (98%)	4 (2%)	60	83
35	7	69/136 (51%)	69 (100%)	0	100	100
36	8	285/378 (75%)	283 (99%)	2 (1%)	84	93
37	h	88/88 (100%)	88 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	i	101/162 (62%)	101 (100%)	0	100	100
39	9	176/225 (78%)	173 (98%)	3 (2%)	60	83
40	a	146/196 (74%)	146 (100%)	0	100	100
41	b	141/141 (100%)	141 (100%)	0	100	100
42	c	86/96 (90%)	84 (98%)	2 (2%)	50	77
43	d	201/243 (83%)	198 (98%)	3 (2%)	65	85
44	AA	314/393 (80%)	305 (97%)	9 (3%)	42	72
45	BB	237/347 (68%)	235 (99%)	2 (1%)	81	92
46	CC	405/461 (88%)	401 (99%)	4 (1%)	76	90
47	DD	242/377 (64%)	239 (99%)	3 (1%)	71	88
48	EE	308/392 (79%)	307 (100%)	1 (0%)	92	96
49	FF	99/99 (100%)	97 (98%)	2 (2%)	55	80
50	GG	181/260 (70%)	179 (99%)	2 (1%)	73	89
51	HH	134/135 (99%)	132 (98%)	2 (2%)	65	85
52	II	206/263 (78%)	205 (100%)	1 (0%)	88	94
53	JJ	166/227 (73%)	164 (99%)	2 (1%)	71	88
54	KK	108/324 (33%)	108 (100%)	0	100	100
55	LL	103/142 (72%)	103 (100%)	0	100	100
56	MM	98/99 (99%)	98 (100%)	0	100	100
57	NN	96/97 (99%)	96 (100%)	0	100	100
58	OO	230/265 (87%)	229 (100%)	1 (0%)	91	96
59	PP	85/92 (92%)	85 (100%)	0	100	100
60	QQ	132/138 (96%)	132 (100%)	0	100	100
61	RR	118/218 (54%)	118 (100%)	0	100	100
62	SS	70/80 (88%)	70 (100%)	0	100	100
63	TT	75/191 (39%)	75 (100%)	0	100	100
64	UU	187/218 (86%)	187 (100%)	0	100	100
65	VV	224/268 (84%)	224 (100%)	0	100	100
66	WW	300/333 (90%)	300 (100%)	0	100	100
67	XX	345/391 (88%)	340 (99%)	5 (1%)	67	86
68	YY	83/89 (93%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	ZZ	278/328 (85%)	275 (99%)	3 (1%)	73	89
70	11	73/75 (97%)	73 (100%)	0	100	100
71	22	33/293 (11%)	33 (100%)	0	100	100
72	33	163/195 (84%)	162 (99%)	1 (1%)	86	94
73	44	215/250 (86%)	215 (100%)	0	100	100
73	55	195/250 (78%)	192 (98%)	3 (2%)	65	85
74	66	245/303 (81%)	243 (99%)	2 (1%)	81	92
75	77	153/304 (50%)	152 (99%)	1 (1%)	84	93
76	88	388/419 (93%)	382 (98%)	6 (2%)	65	85
77	00	43/78 (55%)	43 (100%)	0	100	100
77	99	34/78 (44%)	33 (97%)	1 (3%)	42	72
80	e	134/256 (52%)	133 (99%)	1 (1%)	84	93
81	j	168/171 (98%)	165 (98%)	3 (2%)	59	82
All	All	13264/17844 (74%)	13155 (99%)	109 (1%)	82	92

All (109) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	109	HIS
2	B	298	HIS
3	C	160	GLU
5	E	194	ILE
5	E	239	ASN
5	E	246	GLN
5	E	268	ARG
6	F	100	MET
10	H	2	SER
12	J	57	ARG
12	J	77	THR
12	J	130	TRP
12	J	159	ASP
13	K	76	LYS
14	L	8	TYR
15	M	84	LYS
15	M	203	ARG
17	O	43	TRP
17	O	352	ASP

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Mol	Chain	Res	Type
18	P	53	PHE
18	P	88	ASP
19	Q	198	ARG
20	R	75	ARG
20	R	190	VAL
23	U	68	LEU
28	0	106	TYR
29	1	211	ILE
29	1	271	ARG
29	1	402	ARG
29	1	405	ILE
29	1	409	GLU
29	1	430	GLU
30	2	265	ARG
30	2	325	ARG
31	3	31	ARG
31	3	41	TYR
32	4	91	GLU
32	4	123	SER
33	5	289	GLU
33	5	419	LEU
34	6	181	ARG
34	6	311	LEU
34	6	334	ASN
34	6	349	LEU
36	8	218	ASN
36	8	322	TRP
39	9	72	ARG
39	9	123	LEU
39	9	220	MET
42	c	57	LYS
42	c	102	SER
43	d	69	LEU
43	d	192	LYS
43	d	212	MET
44	AA	55	THR
44	AA	151	ASP
44	AA	153	GLN
44	AA	372	LYS
44	AA	385	VAL
44	AA	414	LYS
44	AA	415	GLU

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Mol	Chain	Res	Type
44	AA	419	ASP
44	AA	421	ARG
45	BB	133	GLN
45	BB	177	TRP
46	CC	66	ASN
46	CC	360	GLN
46	CC	361	LYS
46	CC	363	VAL
47	DD	123	ASN
47	DD	143	ARG
47	DD	170	THR
48	EE	338	MET
49	FF	84	ASP
49	FF	92	ASN
50	GG	190	HIS
50	GG	198	TYR
51	HH	31	TYR
51	HH	78	ARG
52	II	216	ASN
53	JJ	121	ILE
53	JJ	122	ARG
58	OO	271	ASN
67	XX	181	VAL
67	XX	182	THR
67	XX	186	LEU
67	XX	218	TYR
67	XX	307	PHE
69	ZZ	93	GLN
69	ZZ	200	TYR
69	ZZ	338	ASP
72	33	119	ASP
73	55	58	ILE
73	55	270	VAL
73	55	273	MET
74	66	331	VAL
74	66	346	LYS
75	77	290	ASN
76	88	68	TYR
76	88	201	PHE
76	88	212	PRO
76	88	255	ARG
76	88	330	GLN

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Mol	Chain	Res	Type
76	88	444	ASN
77	99	67	LYS
80	e	64	PHE
81	j	46	MET
81	j	90	LYS
81	j	188	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
6	F	205	GLN
18	P	142	GLN
29	1	342	ASN
46	CC	58	ASN
46	CC	121	HIS
49	FF	74	HIS
57	NN	23	HIS
74	66	195	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2820/3464 (81%)	370 (13%)	11 (0%)
78	aa	1430/1864 (76%)	201 (14%)	0
79	bb	57/61 (93%)	11 (19%)	0
All	All	4307/5389 (79%)	582 (13%)	11 (0%)

All (582) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	18	A
1	A	19	G
1	A	29	A
1	A	46	U
1	A	47	A
1	A	78	C
1	A	79	A
1	A	90	A
1	A	98	A
1	A	99	U

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Mol	Chain	Res	Type
1	A	104	U
1	A	106	A
1	A	107	U
1	A	118	G
1	A	311	G
1	A	317	A
1	A	319	C
1	A	334	U
1	A	347	U
1	A	348	A
1	A	350	U
1	A	351	A
1	A	353	A
1	A	367	A
1	A	370	A
1	A	376	U
1	A	387	A
1	A	392	A
1	A	393	A
1	A	395	U
1	A	414	U
1	A	419	U
1	A	435	A
1	A	440	A
1	A	441	U
1	A	442	U
1	A	443	A
1	A	462	U
1	A	477	A
1	A	478	U
1	A	486	A
1	A	522	C
1	A	526	G
1	A	527	A
1	A	552	A
1	A	569	G
1	A	583	A
1	A	584	A
1	A	587	A
1	A	599	A
1	A	609	U
1	A	611	A

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Mol	Chain	Res	Type
1	A	639	A
1	A	829	A
1	A	839	A
1	A	840	U
1	A	845	A
1	A	846	A
1	A	849	U
1	A	855	A
1	A	888	U
1	A	910	A
1	A	914	U
1	A	931	U
1	A	948	A
1	A	958	A
1	A	960	C
1	A	967	A
1	A	969	G
1	A	976	C
1	A	977	U
1	A	988	G
1	A	995	U
1	A	1011	A
1	A	1012	U
1	A	1028	U
1	A	1042	G
1	A	1060	G
1	A	1070	A
1	A	1071	G
1	A	1094	A
1	A	1107	U
1	A	1108	U
1	A	1109	U
1	A	1118	C
1	A	1119	A
1	A	1134	A
1	A	1136	A
1	A	1137	U
1	A	1140	U
1	A	1141	A
1	A	1190	A
1	A	1206	G
1	A	1219	A

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Mol	Chain	Res	Type
1	A	1235	A
1	A	1242	G
1	A	1248	G
1	A	1257	U
1	A	1258	U
1	A	1268	U
1	A	1271	A
1	A	1280	A
1	A	1287	A
1	A	1307	G
1	A	1316	A
1	A	1326	A
1	A	1331	A
1	A	1333	G
1	A	1334	A
1	A	1376	A
1	A	1377	U
1	A	1379	U
1	A	1380	A
1	A	1381	A
1	A	1382	C
1	A	1389	A
1	A	1415	A
1	A	1431	A
1	A	1452	G
1	A	1453	A
1	A	1457	G
1	A	1484	A
1	A	1487	U
1	A	1494	U
1	A	1495	A
1	A	1496	U
1	A	1509	A
1	A	1522	U
1	A	1526	A
1	A	1528	U
1	A	1529	G
1	A	1565	A
1	A	1566	A
1	A	1567	A
1	A	1568	A
1	A	1578	G

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Mol	Chain	Res	Type
1	A	1589	A
1	A	1590	A
1	A	1591	A
1	A	1595	U
1	A	1604	G
1	A	1605	U
1	A	1613	C
1	A	1620	U
1	A	1626	U
1	A	1627	A
1	A	1634	G
1	A	1648	U
1	A	1655	A
1	A	1695	A
1	A	1703	A
1	A	1719	A
1	A	1722	A
1	A	1726	A
1	A	1835	U
1	A	1836	A
1	A	1842	A
1	A	1843	A
1	A	1844	U
1	A	1850	A
1	A	1866	A
1	A	1880	U
1	A	1881	G
1	A	1882	A
1	A	1884	U
1	A	1896	C
1	A	1910	G
1	A	1921	A
1	A	1922	C
1	A	1951	A
1	A	1970	A
1	A	1971	A
1	A	1973	A
1	A	1985	U
1	A	1988	A
1	A	1991	A
1	A	1993	U
1	A	2002	A

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Mol	Chain	Res	Type
1	A	2029	C
1	A	2030	A
1	A	2039	A
1	A	2041	A
1	A	2048	A
1	A	2051	A
1	A	2052	U
1	A	2105	A
1	A	2136	A
1	A	2142	G
1	A	2145	C
1	A	2147	U
1	A	2148	A
1	A	2149	G
1	A	2150	C
1	A	2153	G
1	A	2154	A
1	A	2163	A
1	A	2164	G
1	A	2165	G
1	A	2172	A
1	A	2173	A
1	A	2190	U
1	A	2198	U
1	A	2199	G
1	A	2202	U
1	A	2205	A
1	A	2206	U
1	A	2207	G
1	A	2226	U
1	A	2228	U
1	A	2256	A
1	A	2258	A
1	A	2265	C
1	A	2266	A
1	A	2268	A
1	A	2278	C
1	A	2287	A
1	A	2290	C
1	A	2291	G
1	A	2295	A
1	A	2304	G

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Mol	Chain	Res	Type
1	A	2328	G
1	A	2329	A
1	A	2331	U
1	A	2332	A
1	A	2333	C
1	A	2334	G
1	A	2337	U
1	A	2347	U
1	A	2367	A
1	A	2370	A
1	A	2371	G
1	A	2384	C
1	A	2406	U
1	A	2409	U
1	A	2411	A
1	A	2418	A
1	A	2419	A
1	A	2420	U
1	A	2421	U
1	A	2427	A
1	A	2439	A
1	A	2440	G
1	A	2441	A
1	A	2477	A
1	A	2481	G
1	A	2482	U
1	A	2483	G
1	A	2486	U
1	A	2506	G
1	A	2509	U
1	A	2511	C
1	A	2512	A
1	A	2541	A
1	A	2543	C
1	A	2547	A
1	A	2548	U
1	A	2558	A
1	A	2559	G
1	A	2578	C
1	A	2581	G
1	A	2582	G
1	A	2583	G

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Mol	Chain	Res	Type
1	A	2592	A
1	A	2595	A
1	A	2596	A
1	A	2611	A
1	A	2612	U
1	A	2613	U
1	A	2621	A
1	A	2623	U
1	A	2626	U
1	A	2628	C
1	A	2638	A
1	A	2658	A
1	A	2659	G
1	A	2663	U
1	A	2666	G
1	A	2675	A
1	A	2685	A
1	A	2686	U
1	A	2689	G
1	A	2690	G
1	A	2694	G
1	A	2705	U
1	A	2706	C
1	A	2710	U
1	A	2711	U
1	A	2719	U
1	A	2720	U
1	A	2721	U
1	A	2722	U
1	A	2758	U
1	A	2759	U
1	A	2775	U
1	A	2784	U
1	A	2786	A
1	A	2795	U
1	A	2797	C
1	A	2806	U
1	A	2808	A
1	A	2810	A
1	A	2811	A
1	A	2836	G
1	A	2838	C

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Mol	Chain	Res	Type
1	A	2842	G
1	A	2843	G
1	A	2852	A
1	A	2875	U
1	A	2878	U
1	A	2881	G
1	A	2882	A
1	A	2883	A
1	A	2884	A
1	A	2891	G
1	A	2897	G
1	A	2898	A
1	A	2899	U
1	A	2900	A
1	A	2909	A
1	A	2912	U
1	A	2927	A
1	A	2942	U
1	A	2945	G
1	A	2949	C
1	A	2964	G
1	A	2969	A
1	A	2971	C
1	A	2980	U
1	A	2981	G
1	A	3018	A
1	A	3019	A
1	A	3025	C
1	A	3030	G
1	A	3034	G
1	A	3053	C
1	A	3054	A
1	A	3055	G
1	A	3061	U
1	A	3062	U
1	A	3065	U
1	A	3081	U
1	A	3082	U
1	A	3124	G
1	A	3125	G
1	A	3156	U
1	A	3166	U

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Mol	Chain	Res	Type
1	A	3259	A
1	A	3260	C
1	A	3262	A
1	A	3263	U
1	A	3276	G
1	A	3288	A
1	A	3296	A
1	A	3310	A
1	A	3349	A
1	A	3359	A
1	A	3391	A
1	A	3399	A
1	A	3407	U
1	A	3408	A
1	A	3413	A
1	A	3420	A
1	A	3424	A
1	A	3425	U
1	A	3428	U
1	A	3429	A
1	A	3447	A
1	A	3448	A
1	A	3449	U
1	A	3455	U
78	aa	49	U
78	aa	51	G
78	aa	52	A
78	aa	54	G
78	aa	67	G
78	aa	77	A
78	aa	84	U
78	aa	90	U
78	aa	92	C
78	aa	93	U
78	aa	96	A
78	aa	106	A
78	aa	113	G
78	aa	115	U
78	aa	117	A
78	aa	118	A
78	aa	121	U
78	aa	125	C

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Mol	Chain	Res	Type
78	aa	238	C
78	aa	242	A
78	aa	249	G
78	aa	256	A
78	aa	266	A
78	aa	268	A
78	aa	269	A
78	aa	270	U
78	aa	271	A
78	aa	273	U
78	aa	278	C
78	aa	282	U
78	aa	302	U
78	aa	311	U
78	aa	314	C
78	aa	318	A
78	aa	376	A
78	aa	380	G
78	aa	388	U
78	aa	389	C
78	aa	390	A
78	aa	401	G
78	aa	416	G
78	aa	417	C
78	aa	430	U
78	aa	431	A
78	aa	441	G
78	aa	445	A
78	aa	446	A
78	aa	454	A
78	aa	455	G
78	aa	482	A
78	aa	483	A
78	aa	496	A
78	aa	497	U
78	aa	499	G
78	aa	518	U
78	aa	523	C
78	aa	540	A
78	aa	556	G
78	aa	561	A
78	aa	669	C

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Mol	Chain	Res	Type
78	aa	670	G
78	aa	674	A
78	aa	676	U
78	aa	677	U
78	aa	679	U
78	aa	684	U
78	aa	722	A
78	aa	725	U
78	aa	737	U
78	aa	744	C
78	aa	756	G
78	aa	759	A
78	aa	773	A
78	aa	786	A
78	aa	790	A
78	aa	799	A
78	aa	802	G
78	aa	803	G
78	aa	828	A
78	aa	830	U
78	aa	838	A
78	aa	849	A
78	aa	856	U
78	aa	861	A
78	aa	862	A
78	aa	867	G
78	aa	871	U
78	aa	879	A
78	aa	880	G
78	aa	911	G
78	aa	913	C
78	aa	921	G
78	aa	945	A
78	aa	952	G
78	aa	974	A
78	aa	978	A
78	aa	990	U
78	aa	991	A
78	aa	1012	A
78	aa	1014	U
78	aa	1024	C
78	aa	1038	U

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Mol	Chain	Res	Type
78	aa	1039	U
78	aa	1040	A
78	aa	1063	U
78	aa	1064	A
78	aa	1106	A
78	aa	1118	G
78	aa	1119	U
78	aa	1122	C
78	aa	1126	C
78	aa	1127	A
78	aa	1138	A
78	aa	1152	U
78	aa	1158	G
78	aa	1161	C
78	aa	1164	C
78	aa	1167	A
78	aa	1168	A
78	aa	1169	A
78	aa	1184	U
78	aa	1185	G
78	aa	1192	A
78	aa	1345	G
78	aa	1357	U
78	aa	1358	C
78	aa	1385	U
78	aa	1386	U
78	aa	1392	G
78	aa	1417	U
78	aa	1425	A
78	aa	1426	U
78	aa	1437	U
78	aa	1438	U
78	aa	1445	U
78	aa	1446	A
78	aa	1450	A
78	aa	1457	G
78	aa	1475	A
78	aa	1476	A
78	aa	1480	A
78	aa	1481	U
78	aa	1492	A
78	aa	1493	U

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Mol	Chain	Res	Type
78	aa	1504	A
78	aa	1505	U
78	aa	1511	U
78	aa	1518	U
78	aa	1526	A
78	aa	1527	A
78	aa	1529	A
78	aa	1537	G
78	aa	1539	A
78	aa	1553	U
78	aa	1559	A
78	aa	1566	A
78	aa	1579	A
78	aa	1580	A
78	aa	1581	U
78	aa	1582	A
78	aa	1583	U
78	aa	1584	A
78	aa	1585	C
78	aa	1601	A
78	aa	1619	A
78	aa	1620	A
78	aa	1630	A
78	aa	1643	C
78	aa	1647	A
78	aa	1654	G
78	aa	1655	G
78	aa	1658	A
78	aa	1664	C
78	aa	1677	A
78	aa	1680	A
78	aa	1707	G
78	aa	1723	C
78	aa	1724	U
78	aa	1725	U
78	aa	1731	U
78	aa	1735	A
78	aa	1738	U
78	aa	1751	A
78	aa	1753	G
78	aa	1758	G
78	aa	1803	A

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Mol	Chain	Res	Type
78	aa	1805	G
78	aa	1814	C
78	aa	1817	U
78	aa	1818	U
78	aa	1828	G
78	aa	1840	G
78	aa	1841	A
78	aa	1843	U
78	aa	1844	U
78	aa	1847	C
78	aa	1848	A
78	aa	1849	A
78	aa	1853	U
78	aa	1854	G
78	aa	1864	A
79	bb	9	A
79	bb	13	C
79	bb	19	G
79	bb	20	U
79	bb	21	A
79	bb	44	A
79	bb	49	C
79	bb	66	C
79	bb	69	A
79	bb	75	C
79	bb	76	A

All (11) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	442	U
1	A	526	G
1	A	909	A
1	A	1107	U
1	A	1205	A
1	A	2051	A
1	A	2481	G
1	A	2720	U
1	A	2758	U
1	A	2883	A
1	A	3054	A

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 304 ligands modelled in this entry, 301 are monoatomic - leaving 3 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
83	SPM	A	3651	-	13,13,13	0.32	0	12,12,12	0.76	0
85	NAD	E	4301	84	42,48,48	0.75	1 (2%)	50,73,73	1.10	3 (6%)
87	ATP	XX	501	82	26,33,33	3.49	1 (3%)	31,52,52	0.94	1 (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
83	SPM	A	3651	-	-	2/11/11/11	-
85	NAD	E	4301	84	-	7/26/62/62	0/5/5/5
87	ATP	XX	501	82	-	3/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	XX	501	ATP	C2'-C1'	-17.14	1.27	1.53
85	E	4301	NAD	C2N-N1N	-2.39	1.32	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	E	4301	NAD	O4D-C1D-C2D	-4.42	100.47	106.93
87	XX	501	ATP	C3'-C2'-C1'	3.57	106.35	100.98
85	E	4301	NAD	N3A-C2A-N1A	-2.63	124.56	128.68
85	E	4301	NAD	O4B-C1B-C2B	-2.62	103.09	106.93

There are no chirality outliers.

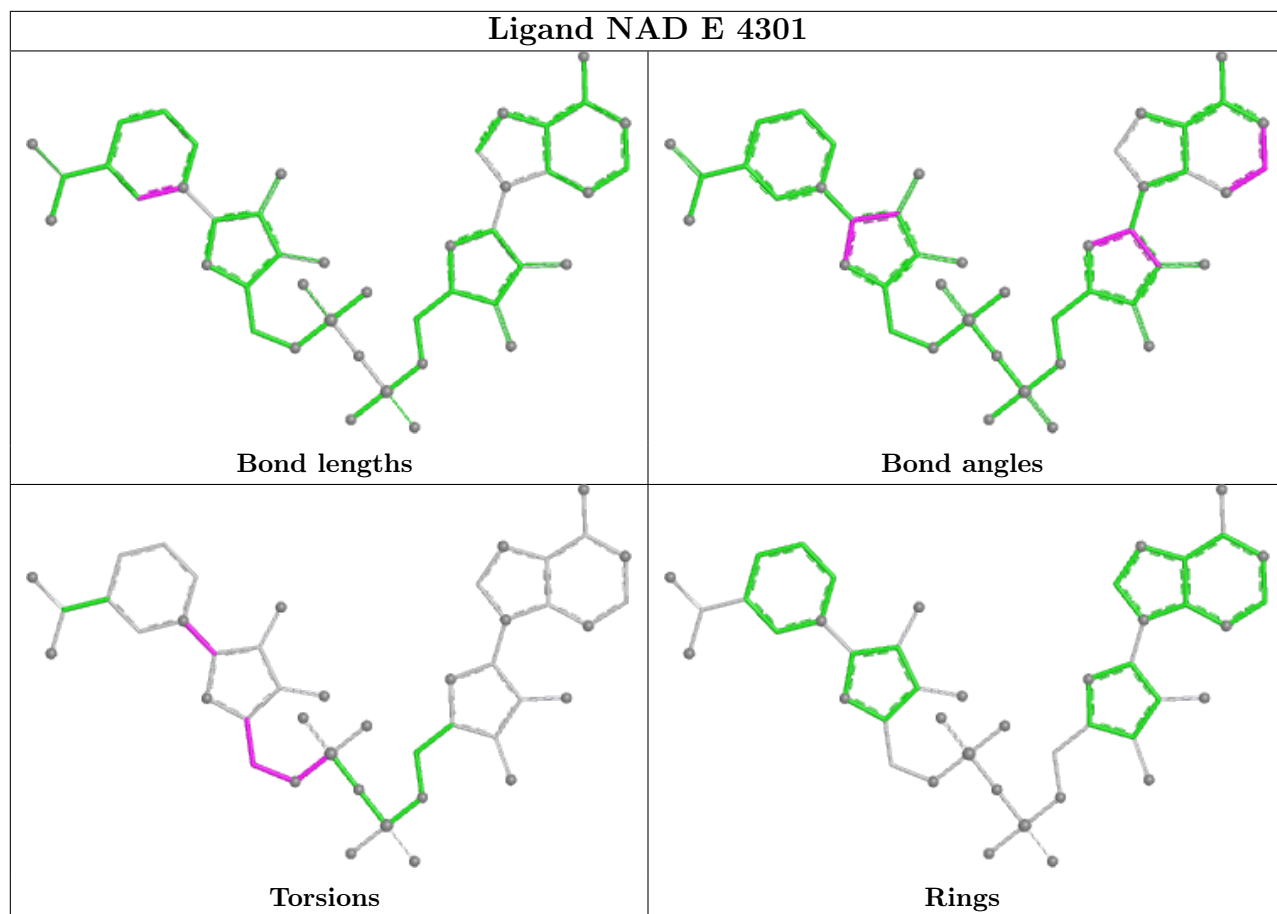
All (12) torsion outliers are listed below:

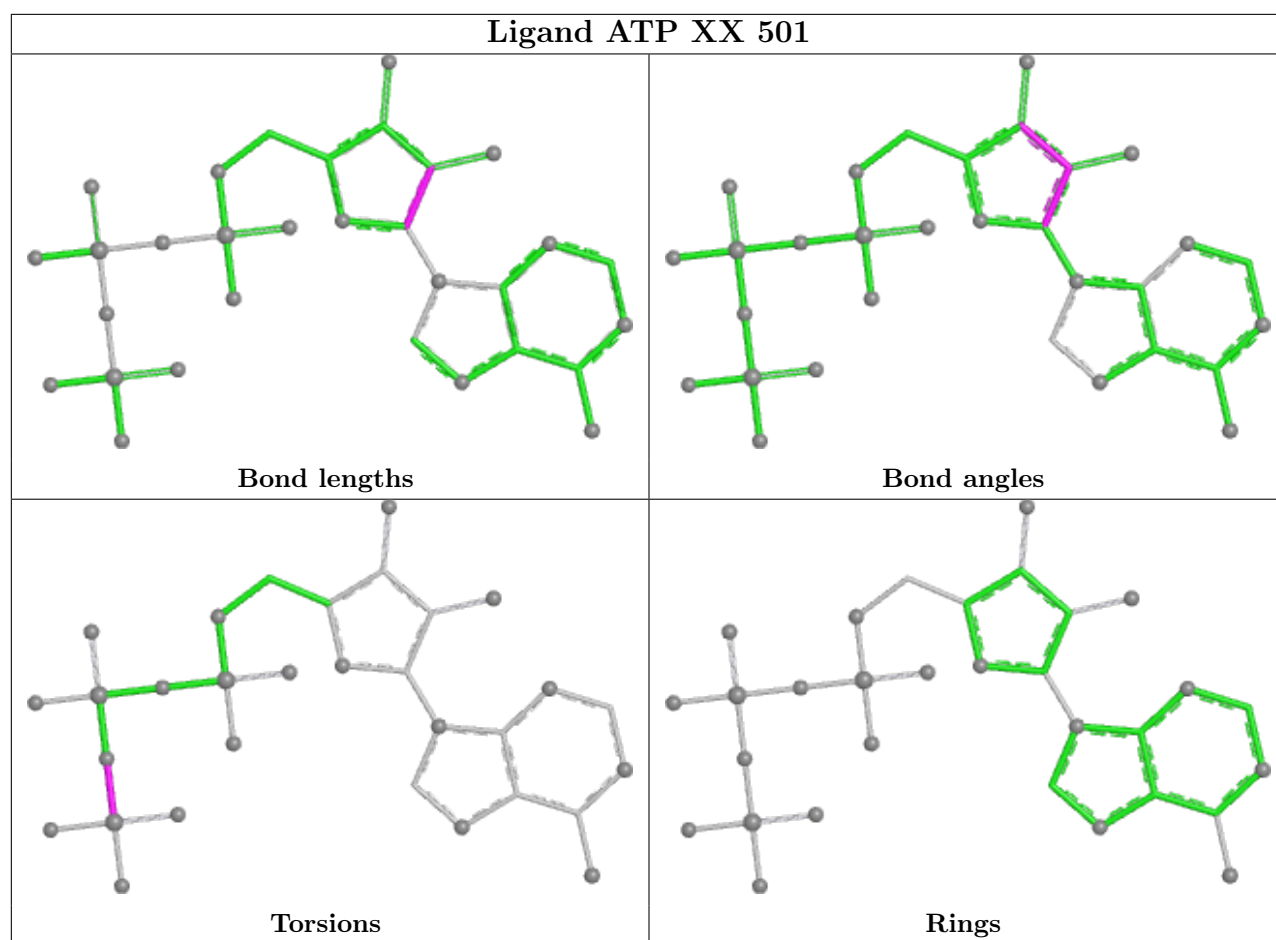
Mol	Chain	Res	Type	Atoms
85	E	4301	NAD	C5D-O5D-PN-O3
87	XX	501	ATP	PB-O3B-PG-O2G
87	XX	501	ATP	PB-O3B-PG-O3G
83	A	3651	SPM	C12-C11-N10-C9
83	A	3651	SPM	N5-C6-C7-C8
85	E	4301	NAD	C4D-C5D-O5D-PN
85	E	4301	NAD	C5D-O5D-PN-O1N
85	E	4301	NAD	C3D-C4D-C5D-O5D
85	E	4301	NAD	C2D-C1D-N1N-C2N
85	E	4301	NAD	C2D-C1D-N1N-C6N
85	E	4301	NAD	O4D-C4D-C5D-O5D
87	XX	501	ATP	PB-O3B-PG-O1G

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
79	bb	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	bb	28:A	O3'	41:G	P	18.21
1	bb	15:A	O3'	18:A	P	8.73
1	bb	46:G	O3'	48:U	P	3.74

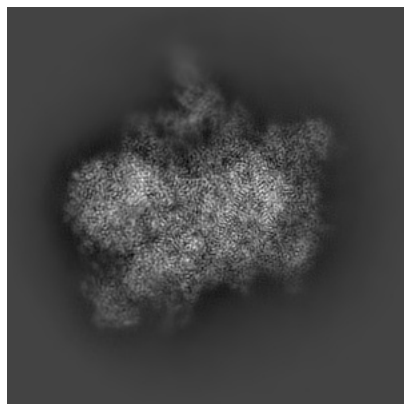
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10978. These allow visual inspection of the internal detail of the map and identification of artifacts.

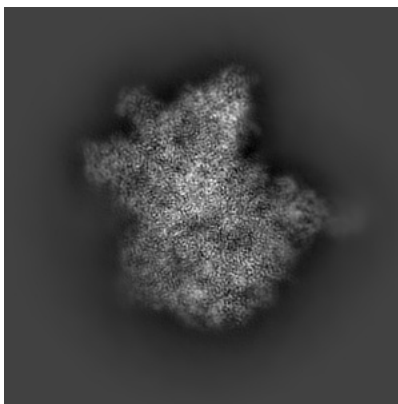
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

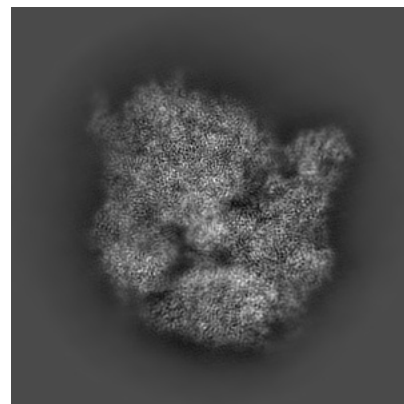
6.1.1 Primary map



X

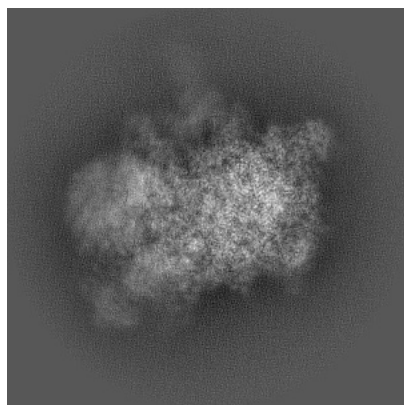


Y

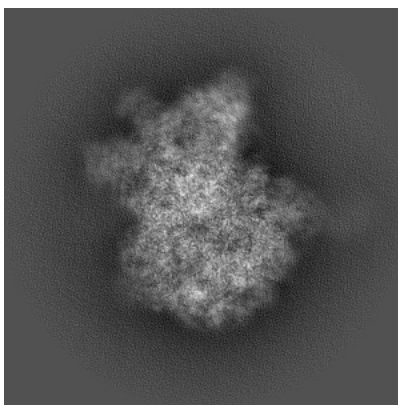


Z

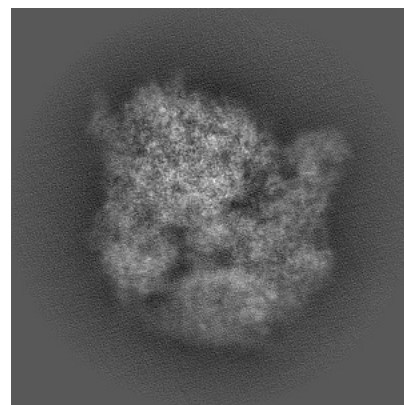
6.1.2 Raw map



X



Y

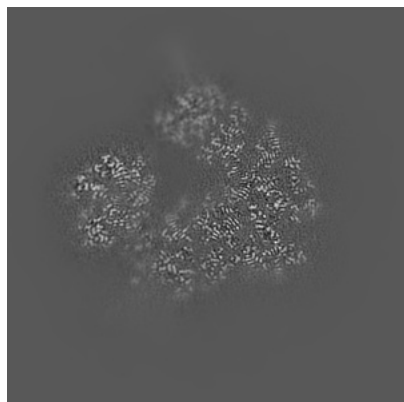


Z

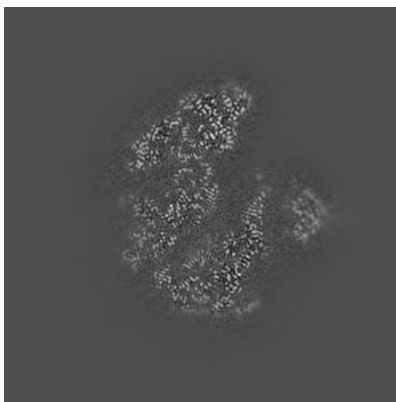
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

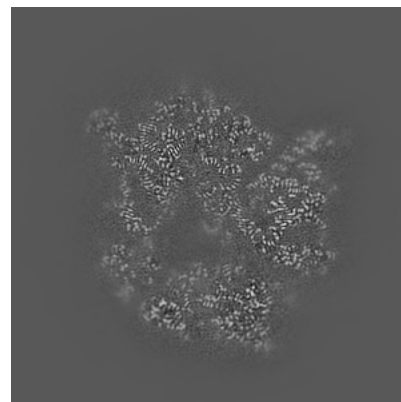
6.2.1 Primary map



X Index: 200

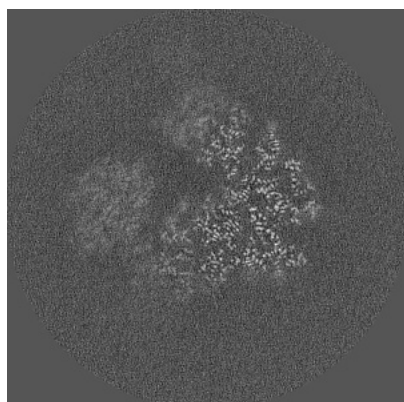


Y Index: 200

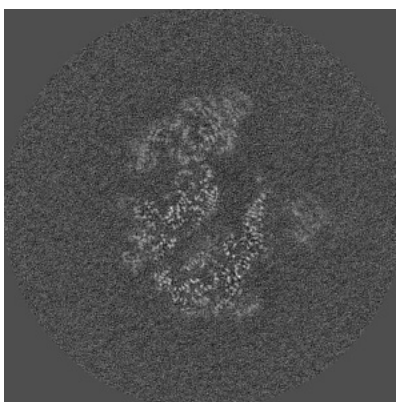


Z Index: 200

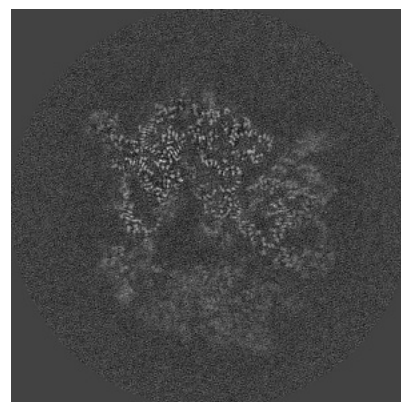
6.2.2 Raw map



X Index: 200



Y Index: 200

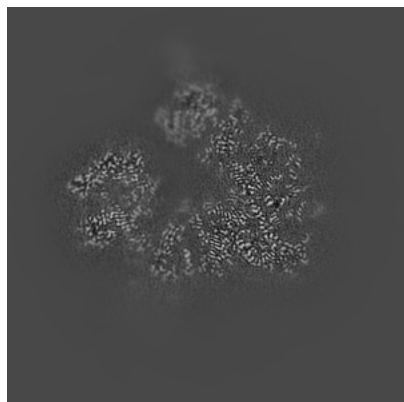


Z Index: 200

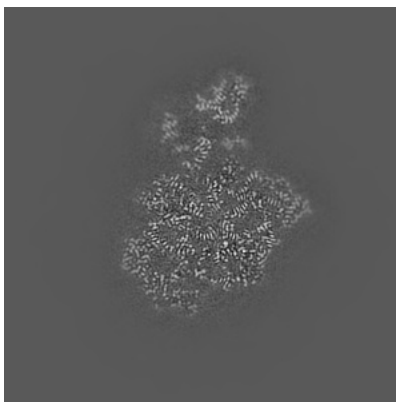
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

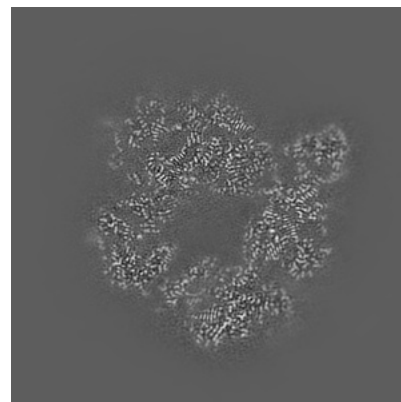
6.3.1 Primary map



X Index: 195

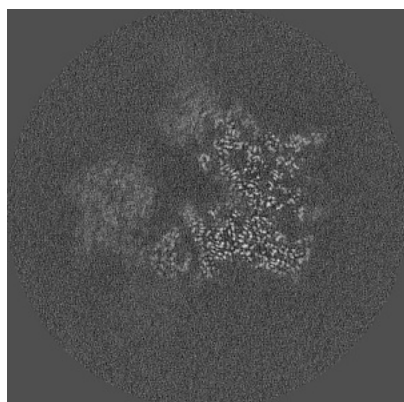


Y Index: 228

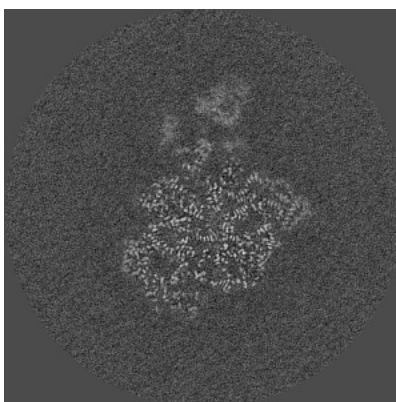


Z Index: 219

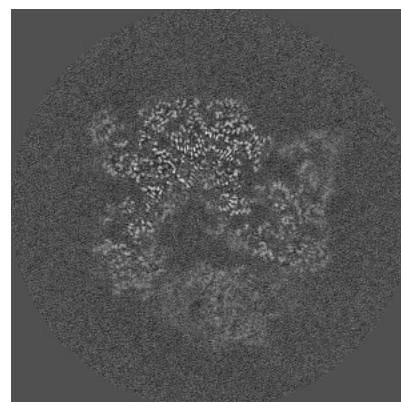
6.3.2 Raw map



X Index: 192



Y Index: 228



Z Index: 207

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

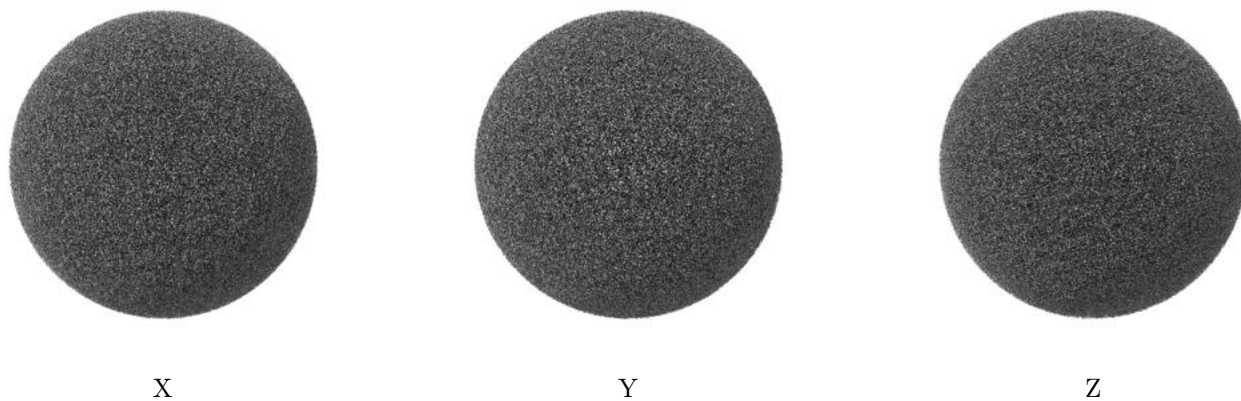
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0295. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

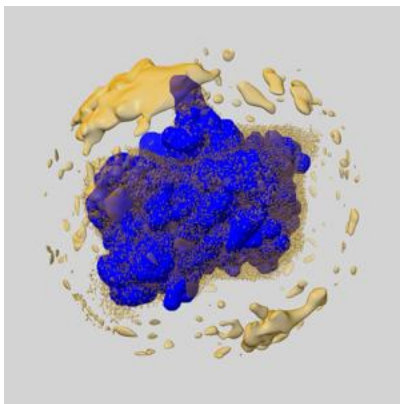
6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

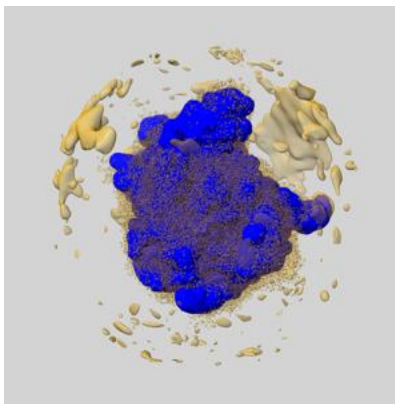
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

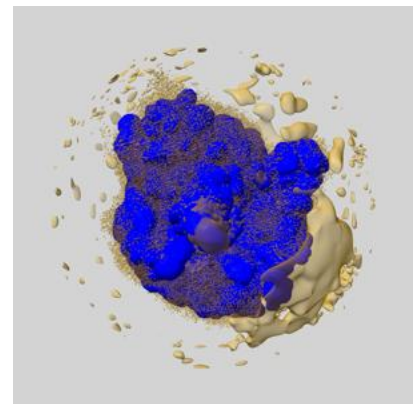
6.5.1 emd_10978_msk_1.map [i](#)



X



Y

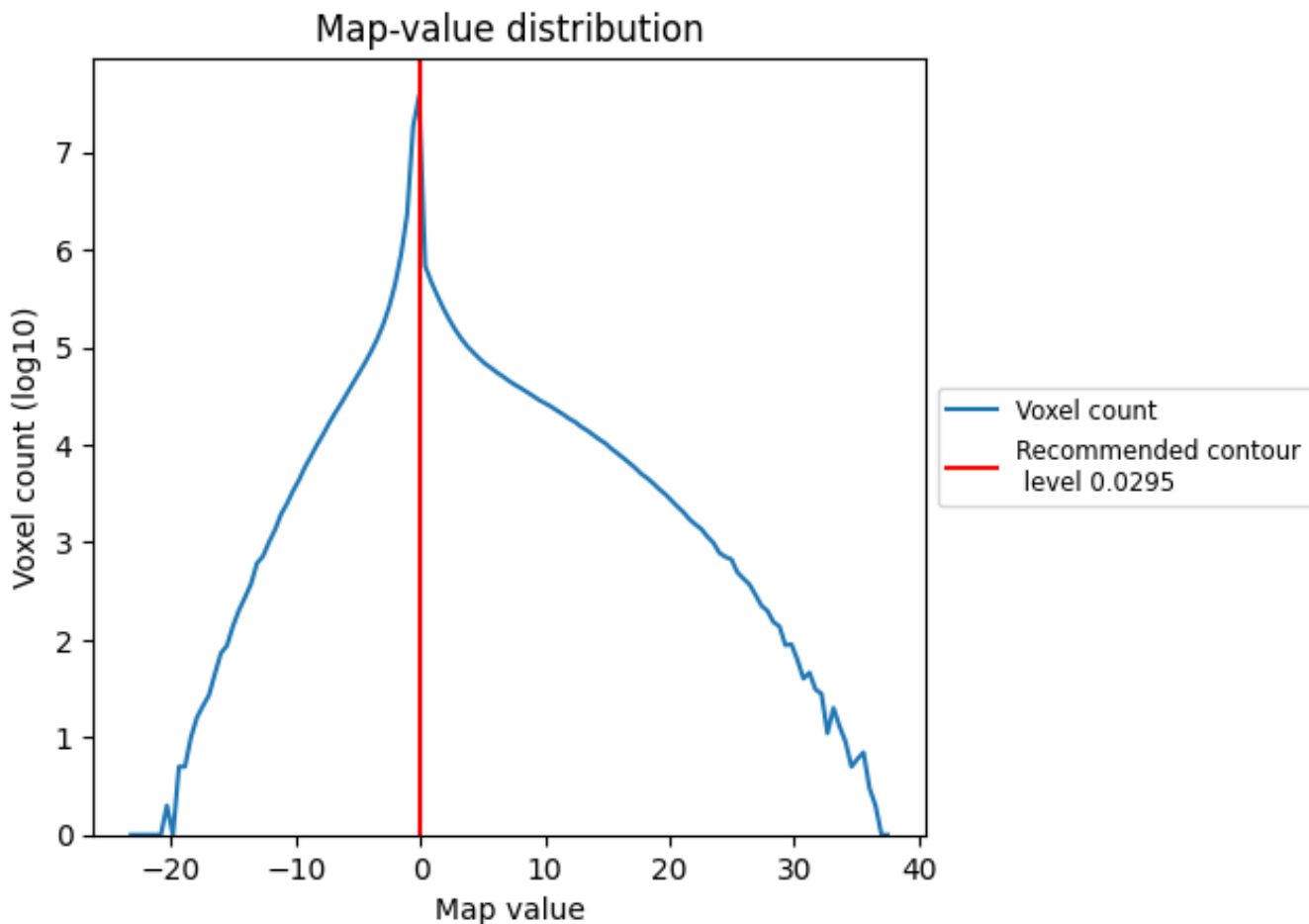


Z

7 Map analysis [i](#)

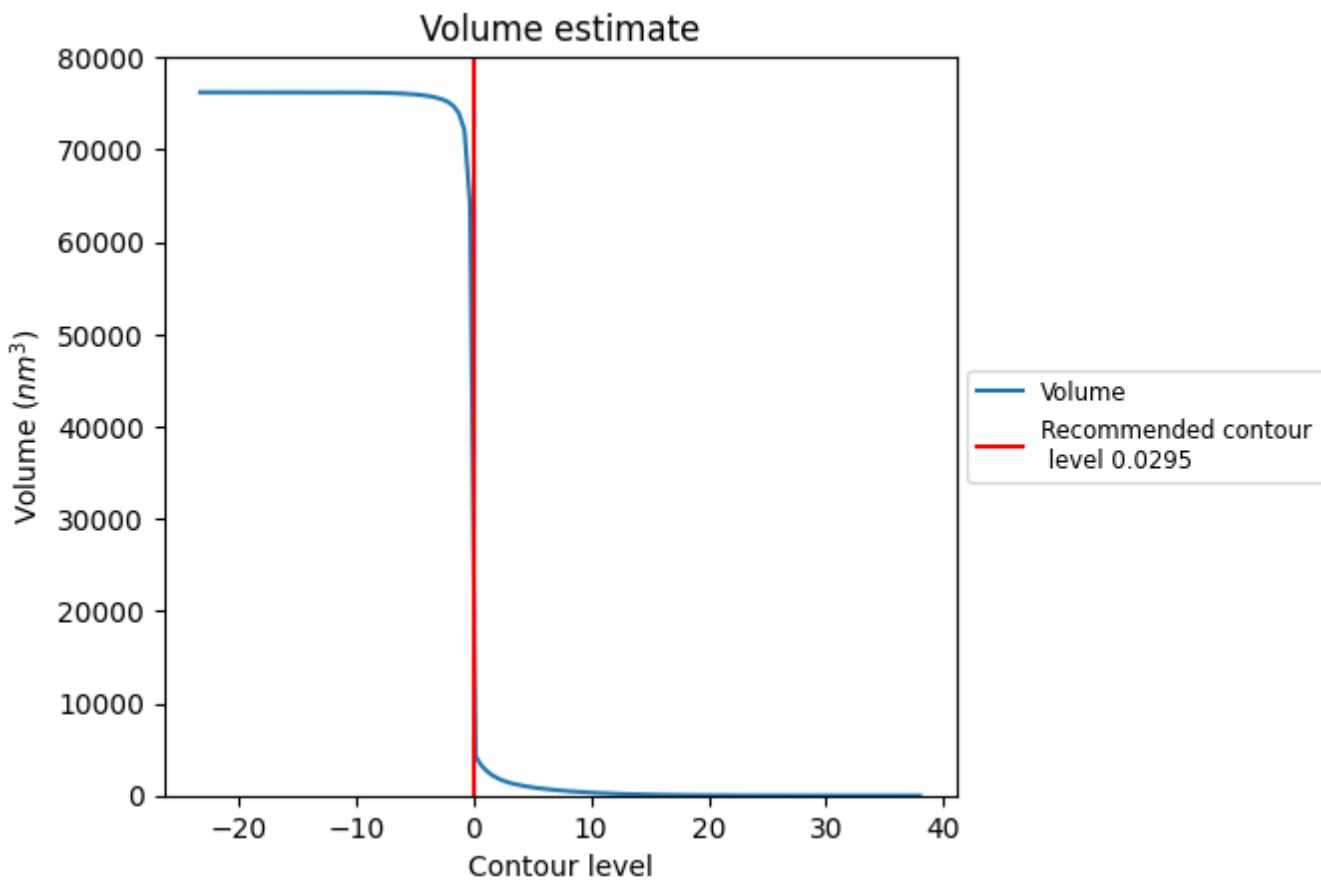
This section contains the results of statistical analysis of the map.

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.

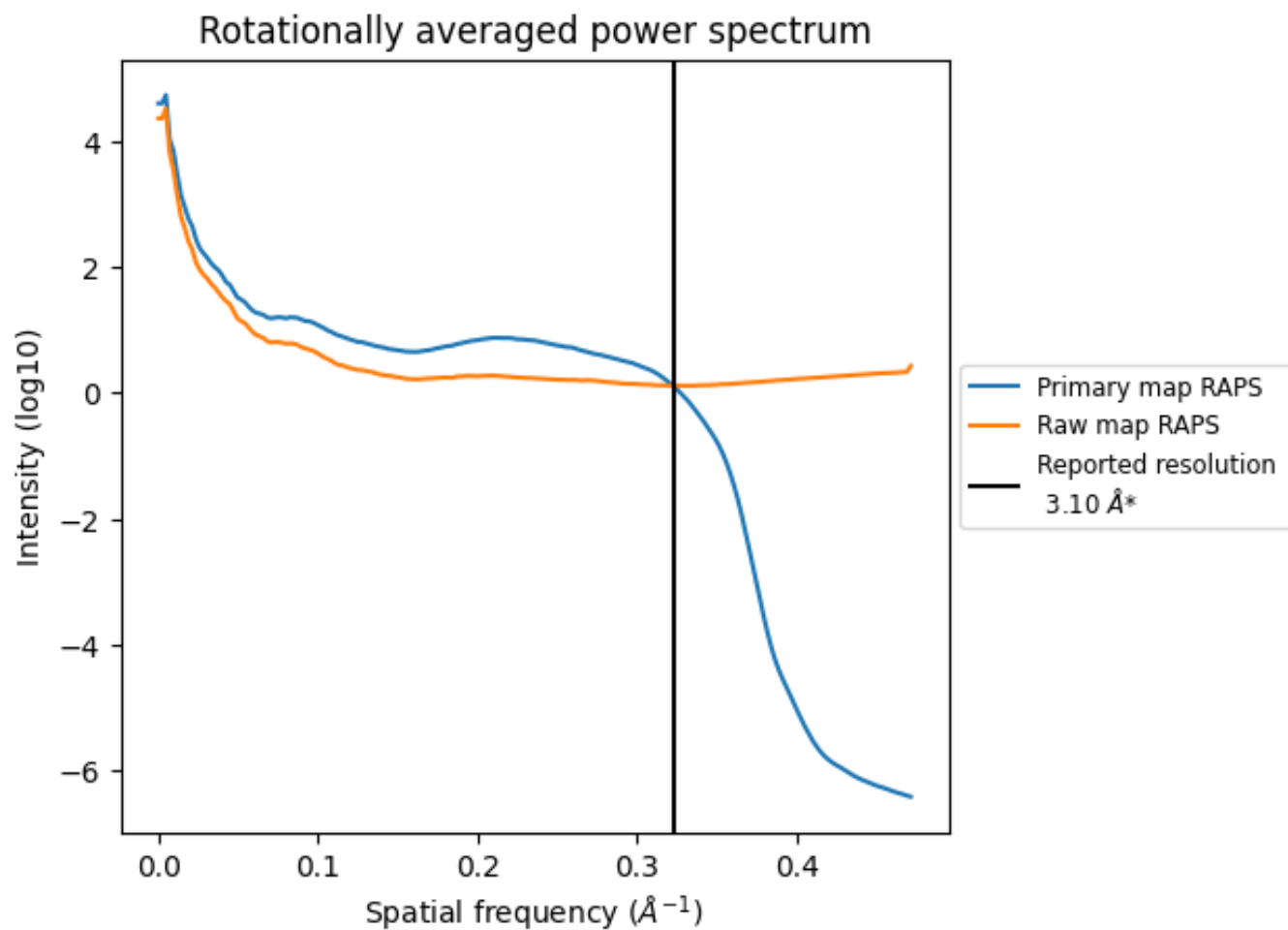
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 27404 nm³; this corresponds to an approximate mass of 24754 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

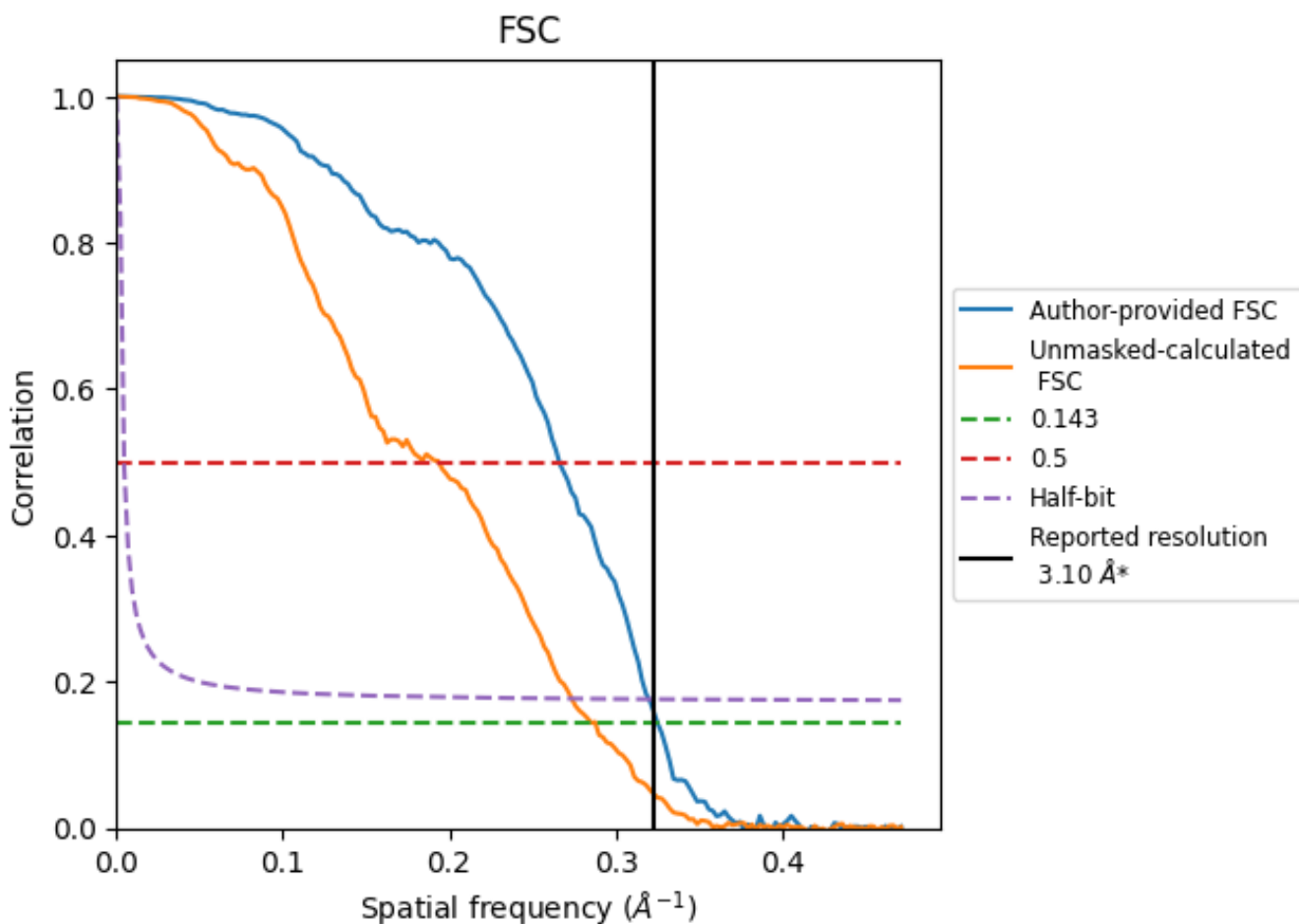


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

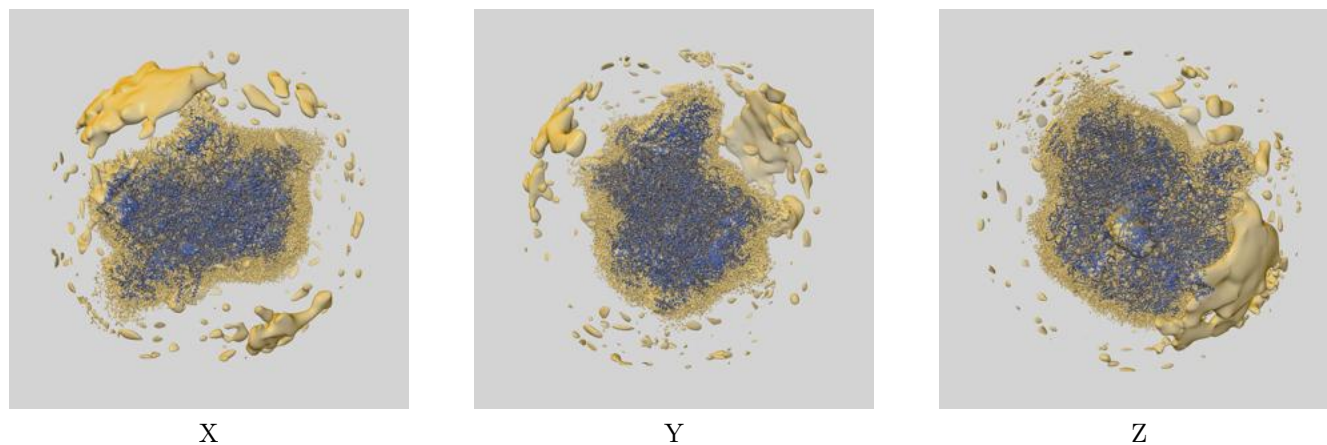
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.07	3.76	3.12
Unmasked-calculated*	3.47	5.16	3.65

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.47 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10978 and PDB model 6YWX. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

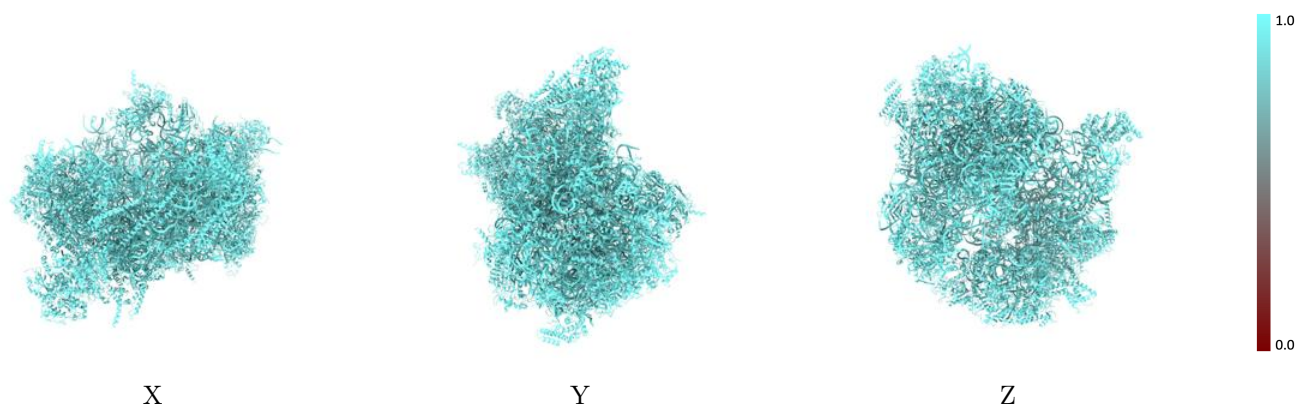


The images above show the 3D surface view of the map at the recommended contour level 0.0295 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

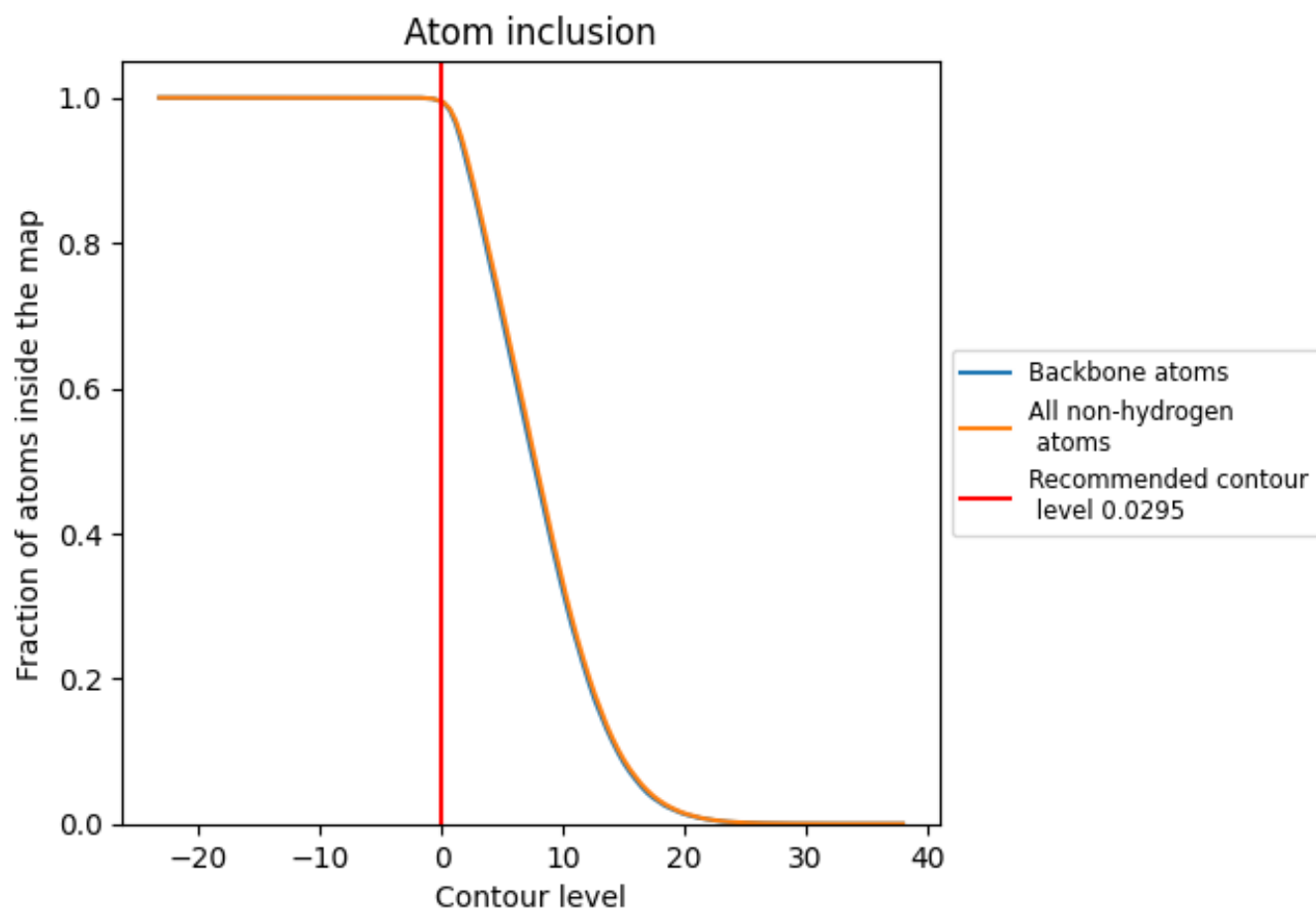
This section was not generated.

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 (0.0295).




































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 100% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)











































The table lists the average atom inclusion at the recommended contour level (0.0295) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	 0.9950
0	 0.9946
00	 0.9850
1	 0.9941
11	 0.9863
2	 0.9830
22	 0.9789
3	 0.9933
33	 0.9874
4	 0.9961
44	 0.9941
5	 0.9909
55	 0.9918
6	 0.9908
66	 0.9911
7	 0.9924
77	 0.9906
8	 0.9942
88	 0.9933
9	 0.9969
99	 0.9933
A	 0.9980
AA	 0.9901
B	 0.9975
BB	 0.9937
C	 0.9934
CC	 0.9891
D	 0.9949
DD	 0.9956
E	 0.9901
EE	 0.9954
F	 0.9923
FF	 0.9934
G	 0.9966
GG	 0.9890










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Chain	Atom inclusion
H	 0.9928
HH	 0.9859
I	 0.9978
II	 0.9932
J	 0.9940
JJ	 0.9934
K	 0.9954
KK	 0.9969
L	 0.9940
LL	 0.9871
M	 0.9953
MM	 0.9934
N	 0.9981
NN	 0.9875
O	 0.9949
OO	 0.9911
P	 0.9889
PP	 0.9935
Q	 0.9953
QQ	 0.9943
R	 0.9959
RR	 0.9952
S	 0.9972
SS	 0.9874
T	 0.9959
TT	 0.9944
U	 0.9944
UU	 0.9902
V	 0.9978
VV	 0.9872
W	 0.9889
WW	 0.9874
X	 0.9948
XX	 0.9905
Y	 0.9885
YY	 0.9842
ZZ	 0.9917
a	 0.9930
aa	 0.9982
b	 0.9945
bb	 0.9684
c	 0.9937

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Chain	Atom inclusion
d	 0.9946
e	 0.9804
f	 0.9919
g	 0.9945
h	 0.9804
i	 0.9864
j	 0.9927