



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:34 PM UTC

PDB ID : 8ANY / pdb_00008any
EMDB ID : EMD-15544
Title : Human mitochondrial ribosome in complex with LRPPRC, SLIRP, A-site, P-site, E-site tRNAs and mRNA
Authors : Singh, V.; Itoh, Y.; Amunts, A.
Deposited on : 2022-08-06
Resolution : 2.85 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : **FAILED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

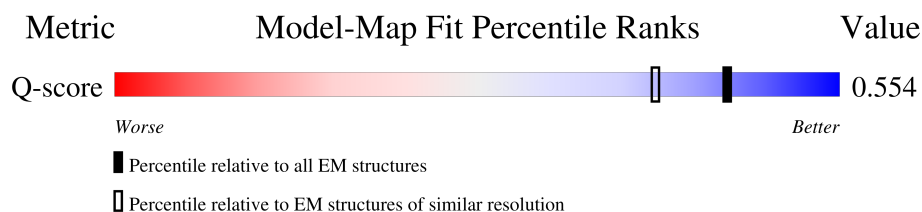
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.85 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	11965 (2.35 - 3.35)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 103 unique types of molecules in this entry. The entry contains 355123 atoms, of which 160326 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 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	AA	954	Total	C	H	N	O	P	0	0
			30565	9088	10305	3647	6571	954		

- Molecule 2 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AB	225	Total	C	H	N	O	S	0	0
			3654	1164	1826	331	323	10		

- Molecule 3 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	AC	132	Total	C	H	N	O	S	0	0
			2179	699	1096	195	185	4		

- Molecule 4 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AD	343	Total	C	H	N	O	S	0	0
			5545	1713	2814	518	487	13		

- Molecule 5 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	AE	122	Total	C	H	N	O	S	0	0
			1976	614	1004	177	177	4		

- Molecule 6 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	AF	208	Total	C	H	N	O	S	0	0
			3503	1104	1778	312	298	11		

- Molecule 7 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	AG	327	Total	C	H	N	O	S	0	0
			5385	1710	2697	477	487	14		

- Molecule 8 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	AH	140	Total	C	H	N	O	S	0	0
			2343	745	1191	194	210	3		

- Molecule 9 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	AI	137	Total	C	H	N	O	S	0	0
			2086	642	1066	192	182	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	184	5F0	ASN	conflict	UNP P82912

- Molecule 10 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	AJ	108	Total	C	H	N	O	S	0	0
			1731	521	892	169	143	6		

- Molecule 11 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AK	101	Total	C	H	N	O	S	0	0
			1751	537	889	179	141	5		

- Molecule 12 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AL	174	Total	C	H	N	O	S	0	0
			2998	925	1545	270	251	7		

- Molecule 13 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AM	119	Total	C	H	N	O	S	0	0
			1914	594	972	185	157	6		

- Molecule 14 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AN	110	Total	C	H	N	O	S	0	0
			1801	562	933	156	147	3		

- Molecule 15 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AO	193	Total	C	H	N	O	S	0	0
			3162	1014	1570	294	277	7		

- Molecule 16 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	AP	97	Total	C	H	N	O	S	0	0
			1590	501	809	134	138	8		

- Molecule 17 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	AQ	86	Total	C	H	N	O	S	0	0
			1504	460	760	150	126	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AQ	50	ARG	CYS	variant	UNP P82921

- Molecule 18 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	AR	295	Total	C	H	N	O	S	0	0
			4845	1533	2436	413	455	8		

- Molecule 19 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	AS	135	Total	C	H	N	O	S	0	0
			2228	716	1117	198	196	1		

- Molecule 20 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	AT	168	Total	C	H	N	O	S	0	0
			2767	877	1396	239	244	11		

- Molecule 21 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	AU	176	Total	C	H	N	O	S	0	0
			2993	916	1505	301	267	4		

- Molecule 22 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	AV	362	Total	C	H	N	O	S	0	0
			5941	1904	2972	495	558	12		

- Molecule 23 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AW	100	Total	C	H	N	O	S	0	0
			1595	498	806	141	146	4		

- Molecule 24 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AX	352	Total	C	H	N	O	S	0	0
			5708	1822	2859	499	517	11		

- Molecule 25 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	AZ	100	Total	C	H	N	O	S	0	0
			1701	534	862	153	148	4		

- Molecule 26 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	A0	215	Total	C	H	N	O	S	0	0
			3589	1130	1802	339	313	5		

- Molecule 27 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	A1	277	Total	C	H	N	O	S	0	0
			4526	1424	2281	382	428	11		

- Molecule 28 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	A2	117	Total	C	H	N	O	S	0	0
			1906	579	971	182	166	8		

- Molecule 29 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	A3	70	Total	C	H	N	O	S	0	0
			1327	401	702	134	89	1		

- Molecule 30 is a RNA chain called A/A-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	Aw	68	Total	C	H	N	O	P	0	0
			2159	646	725	248	472	68		

- Molecule 31 is a RNA chain called P/P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	Ax	70	Total	C	H	N	O	P	0	0
			2232	665	750	260	487	70		

- Molecule 32 is a RNA chain called E/E-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	Ay	70	Total	C	H	N	O	P	0	0
			2235	665	752	261	487	70		

- Molecule 33 is a RNA chain called 16S mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	A	1558	Total	C	H	N	O	P	0	0
			49872	14843	16802	5963	10706	1558		

- Molecule 34 is a RNA chain called mitochondrial tRNAVal.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	B	72	Total	C	H	N	O	P	0	0
			2303	685	779	269	498	72		

- Molecule 35 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	D	238	Total	C	H	N	O	S	0	0
			3787	1157	1928	376	317	9		

- Molecule 36 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	E	305	Total	C	H	N	O	S	0	0
			4830	1545	2424	418	432	11		

- Molecule 37 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	F	252	Total	C	H	N	O	S	0	0
			4106	1305	2075	370	350	6		

- Molecule 38 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	I	212	Total	C	H	N	O	S	0	0
			3489	1088	1794	304	292	11		

- Molecule 39 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	J	175	Total	C	H	N	O	S	0	0
			2739	847	1409	237	244	2		

- Molecule 40 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	K	177	Total	C	H	N	O	S	0	0
			2915	936	1460	259	253	7		

- Molecule 41 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	L	115	Total	C	H	N	O	S	0	0
			1835	559	945	171	155	5		

- Molecule 42 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	M	289	Total	C	H	N	O	S	0	0
			4701	1476	2387	427	405	6		

- Molecule 43 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	N	222	Total	C	H	N	O	S	0	0
			3610	1143	1824	326	307	10		

- Molecule 44 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	O	154	Total	C	H	N	O	S	0	0
			2557	792	1298	241	219	7		

- Molecule 45 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	P	144	Total	C	H	N	O	S	0	0
			2344	733	1171	224	211	5		

- Molecule 46 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	Q	238	Total	C	H	N	O	S	0	0
			4004	1268	2025	352	350	9		

- Molecule 47 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	R	140	Total	C	H	N	O	S	0	0
			2374	732	1220	231	187	4		

- Molecule 48 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	S	161	Total	C	H	N	O	S	0	0
			2662	835	1369	227	227	4		

- Molecule 49 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	T	166	Total	C	H	N	O	S	0	0
			2786	875	1417	254	233	7		

- Molecule 50 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	U	152	Total	C	H	N	O	S	0	0
			2486	788	1235	234	226	3		

- Molecule 51 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	V	205	Total	C	H	N	O	S	0	0
			3367	1068	1691	298	302	8		

- Molecule 52 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	W	116	Total	C	H	N	O	S	0	0
			1847	577	943	171	153	3		

- Molecule 53 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	X	244	Total	C	H	N	O	S	0	0
			4109	1322	2065	352	365	5		

- Molecule 54 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	Y	181	Total	C	H	N	O	S	0	0
			3159	995	1603	298	259	4		

- Molecule 55 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	Z	122	Total	C	H	N	O	S	0	0
			2048	636	1052	186	171	3		

- Molecule 56 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	0	110	Total	C	H	N	O	S	0	0
			1817	554	919	176	162	6		

- Molecule 57 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	1	56	Total	C	H	N	O	S	0	0
			977	296	513	89	77	2		

- Molecule 58 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	2	46	Total	C	H	N	O	S	0	0
			786	233	409	83	60	1		

- Molecule 59 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	3	95	Total	C	H	N	O	S	0	0
			1718	539	886	162	128	3		

- Molecule 60 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	4	38	Total	C	H	N	O	S	0	0
			705	217	363	72	49	4		

- Molecule 61 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	5	394	Total	C	H	N	O	S	0	0
			6432	2073	3222	560	566	11		

- Molecule 62 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	6	354	Total	C	H	N	O	S	0	0
			5802	1881	2854	525	533	9		

- Molecule 63 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	7	294	Total	C	H	N	O	S	0	0
			4796	1529	2406	405	438	18		

- Molecule 64 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	8	157	Total	C	H	N	O	S	0	0
			2698	844	1371	235	246	2		

- Molecule 65 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	9	124	Total	C	H	N	O	S	0	0
			1985	644	988	170	181	2		

- Molecule 66 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	a	100	Total	C	H	N	O	S	0	0
			1659	529	819	152	154	5		

- Molecule 67 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	b	151	Total	C	H	N	O	S	0	0
			2395	744	1199	231	218	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	2	ACE	-	acetylation	UNP Q8N983

- Molecule 68 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	c	286	Total	C	H	N	O	S	0	0
			4624	1470	2325	397	423	9		

- Molecule 69 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	d	241	Total	C	H	N	O	S	0	0
			3971	1273	1986	340	359	13		

- Molecule 70 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	e	238	Total	C	H	N	O	S	0	0
			3853	1222	1922	339	364	6		

- Molecule 71 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	f	157	Total	C	H	N	O	S	0	0
			2529	799	1277	207	242	4		

- Molecule 72 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	g	134	Total	C	H	N	O	S	0	0
			2214	719	1101	193	199	2		

- Molecule 73 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	h	110	Total	C	H	N	O	S	0	0
			1780	568	885	156	168	3		

- Molecule 74 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	i	97	Total	C	H	N	O	S	0	0
			1690	532	862	165	127	4		

- Molecule 75 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	j	94	Total	C	H	N	O	S	0	0
			1492	463	747	144	136	2		

- Molecule 76 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	k	101	Total	C	H	N	O	S	0	0
			1562	479	788	148	142	5		

- Molecule 77 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	l	82	Total	C	H	N	O	S	0	0
			1364	437	676	120	128	3		

- Molecule 78 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	m	92	Total	C	H	N	O	S	0	0
			1554	488	763	159	142	2		

- Molecule 79 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
79	o	94	Total	C	H	N	O	S	0	0
			1608	501	810	165	129	3		

- Molecule 80 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	p	147	Total	C	H	N	O	S	0	0
			2433	748	1228	228	225	4		

- Molecule 81 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
81	q	165	Total	C	H	N	O	S	0	0
			2766	865	1377	270	249	5		

- Molecule 82 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
82	r	162	Total	C	H	N	O	S	0	0
			2677	839	1355	252	223	8		

- Molecule 83 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
83	s	386	Total	C	H	N	O	S	0	0
			6306	2023	3151	559	559	14		

- Molecule 84 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	t	46	Total	C	H	N	O	0	0
			732	228	378	56	70		
84	u	32	Total	C	H	N	O	0	0
			541	168	284	40	49		
84	v	32	Total	C	H	N	O	0	0
			541	168	284	40	49		
84	w	31	Total	C	H	N	O	0	0
			520	159	275	39	47		
84	x	31	Total	C	H	N	O	0	0
			520	159	275	39	47		
84	y	31	Total	C	H	N	O	0	0
			520	159	275	39	47		

- Molecule 85 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
85	H	202	Total	C	H	N	O	S	0	0
			3398	1067	1737	304	286	4		

- Molecule 86 is a protein called 39S ribosomal protein L1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
86	z	252	Total	C	H	N	O	S	0	0
			4107	1304	2080	336	381	6		

- Molecule 87 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
87	AY	221	Total	C	H	N	O	S	0	0
			3622	1159	1787	319	352	5		

- Molecule 88 is a protein called Leucine-rich PPR motif-containing protein, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
88	A5	581	Total	C	H	N	O	S	0	0
			9336	2959	4690	790	871	26		

- Molecule 89 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
89	A4	595	Total	C	H	N	O	S	0	0
			9643	3080	4828	815	892	28		

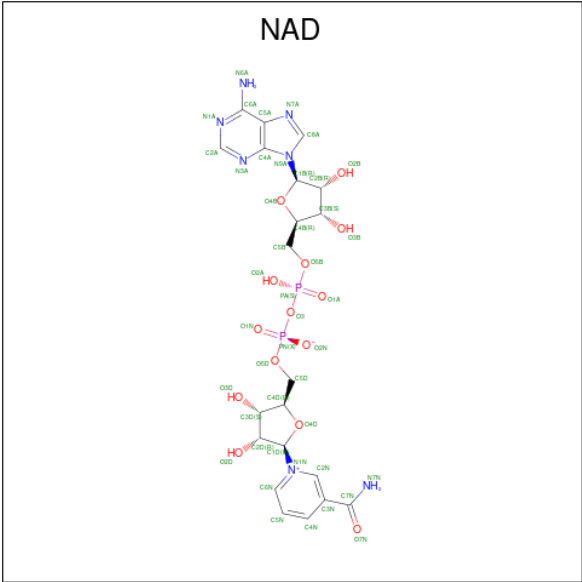
- Molecule 90 is a protein called SRA stem-loop-interacting RNA-binding protein, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
90	A6	74	Total	C	H	N	O	S	0	0
			1197	384	594	115	103	1		

- Molecule 91 is a RNA chain called mRNA.

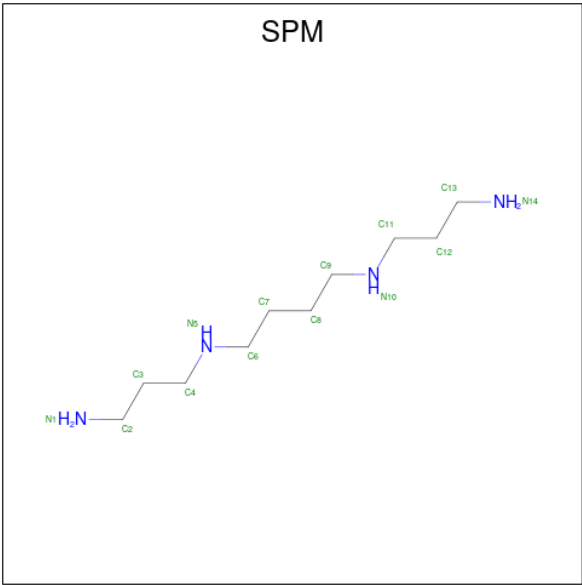
Mol	Chain	Residues	Atoms						AltConf	Trace
91	Az	42	Total	C	H	N	O	P	0	0
			1325	396	445	144	298	42		

- Molecule 92 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



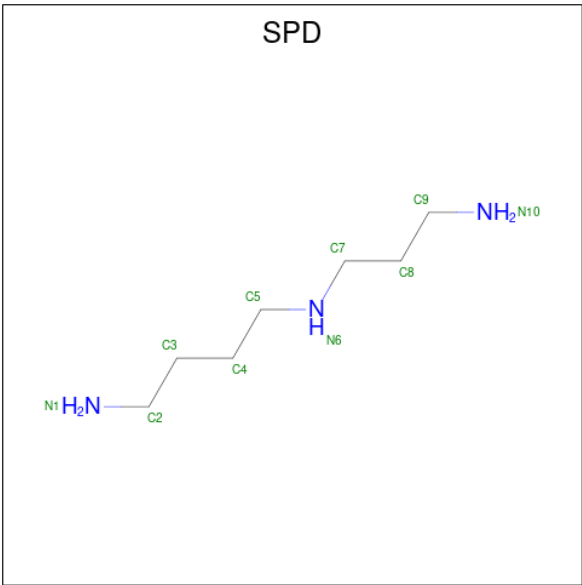
Mol	Chain	Residues	Atoms						AltConf
92	AA	1	Total	C	H	N	O	P	0
			70	21	26	7	14	2	

- Molecule 93 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms				AltConf
93	AA	1	Total	C	H	N	0
			44	10	30	4	

- Molecule 94 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms				AltConf
94	AA	1	Total	C	H	N	0
			32	7	22	3	
94	A	1	Total	C	H	N	0
			32	7	22	3	
94	A	1	Total	C	H	N	0
			32	7	22	3	
94	A	1	Total	C	H	N	0
			32	7	22	3	

- Molecule 95 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
95	AA	62	Total	Mg	0
			62	62	
95	AB	1	Total	Mg	0
			1	1	
95	AX	1	Total	Mg	0
			1	1	
95	A3	1	Total	Mg	0
			1	1	
95	Aw	1	Total	Mg	0
			1	1	
95	A	136	Total	Mg	0
			136	136	
95	D	2	Total	Mg	0
			2	2	
95	E	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
95	g	1	Total 1	Mg 1	0

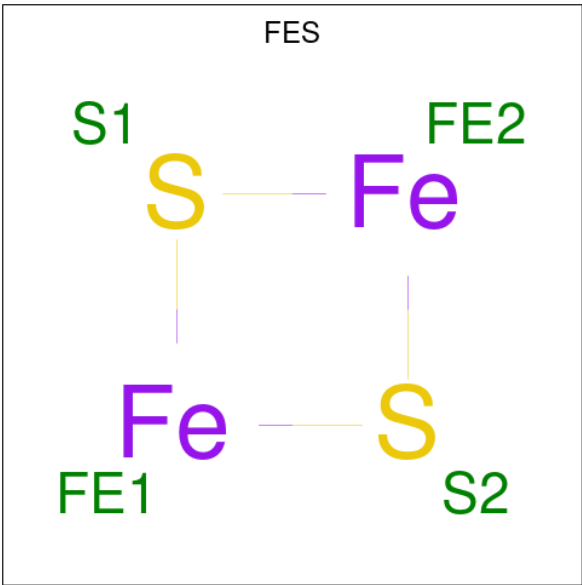
- Molecule 96 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
96	AA	16	Total 16	K 16	0
96	A	28	Total 28	K 28	0
96	D	1	Total 1	K 1	0
96	M	1	Total 1	K 1	0
96	P	1	Total 1	K 1	0
96	i	1	Total 1	K 1	0
96	o	1	Total 1	K 1	0

- Molecule 97 is ZINC ION (CCD ID: ZN) (formula: Zn).

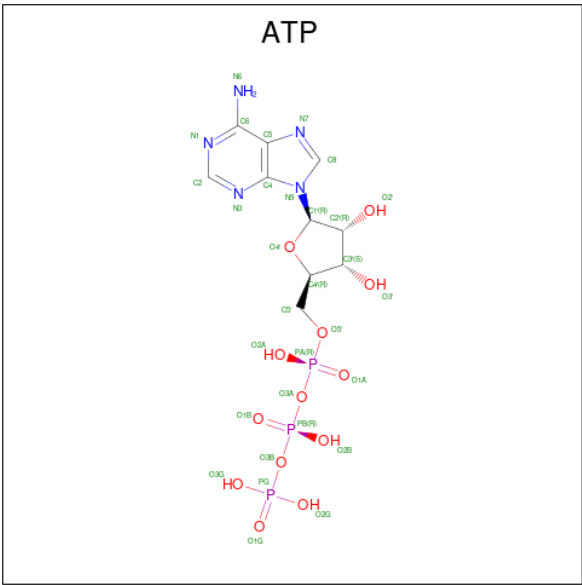
Mol	Chain	Residues	Atoms		AltConf
97	AO	1	Total 1	Zn 1	0
97	0	1	Total 1	Zn 1	0
97	4	1	Total 1	Zn 1	0

- Molecule 98 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



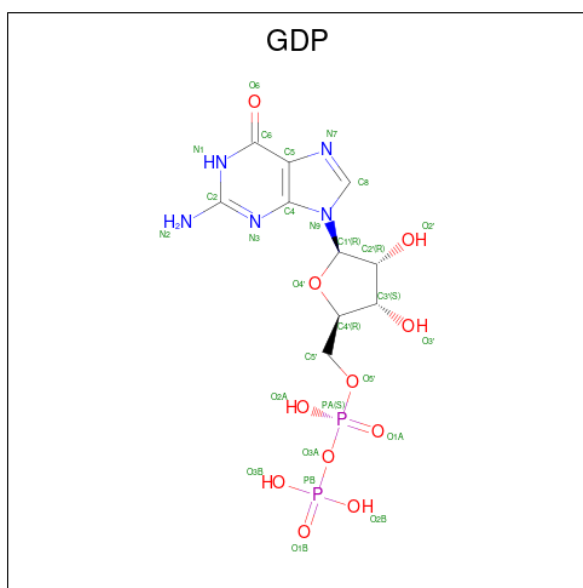
Mol	Chain	Residues	Atoms			AltConf
98	AP	1	Total	Fe	S	0
			4	2	2	
98	AT	1	Total	Fe	S	0
			4	2	2	
98	r	1	Total	Fe	S	0
			4	2	2	

- Molecule 99 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



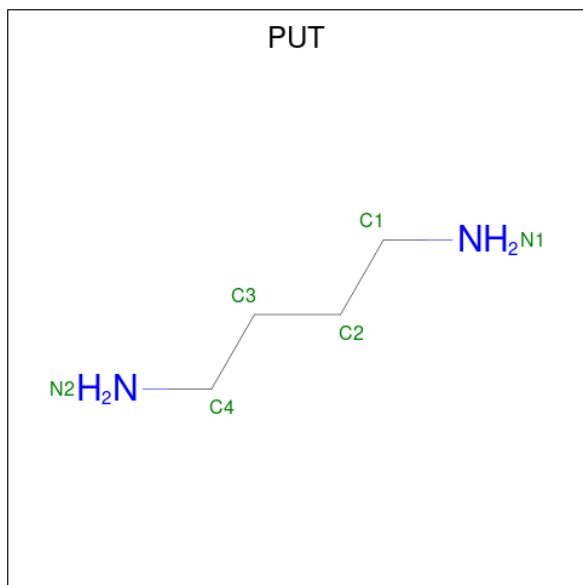
Mol	Chain	Residues	Atoms						AltConf
99	AX	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

- Molecule 100 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



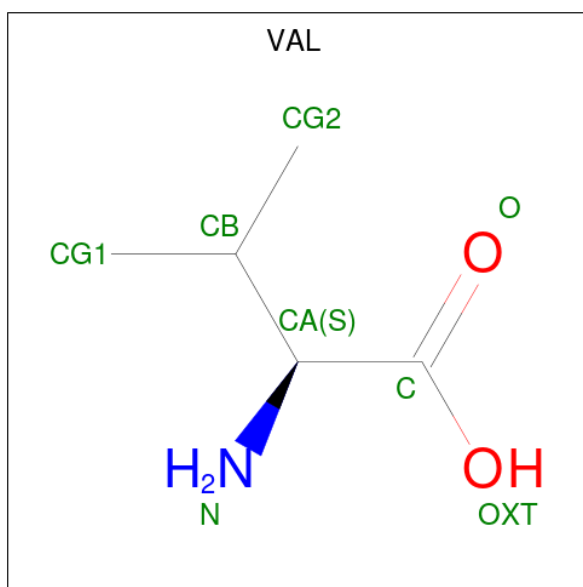
Mol	Chain	Residues	Atoms						AltConf
100	AX	1	Total	C	H	N	O	P	0
			40	10	12	5	11	2	

- Molecule 101 is 1,4-DIAMINOBTANE (CCD ID: PUT) (formula: $C_4H_{12}N_2$).



Mol	Chain	Residues	Atoms				AltConf
101	A	1	Total	C	H	N	0
			20	4	14	2	

- Molecule 102 is VALINE (CCD ID: VAL) (formula: $C_5H_{11}NO_2$).



Mol	Chain	Residues	Atoms					AltConf
102	B	1	Total	C	H	N	O	0
			18	5	11	1	1	

- Molecule 103 is water.

Mol	Chain	Residues	Atoms		AltConf
103	AA	1747	Total	O	0
			1747	1747	
103	AB	60	Total	O	0
			60	60	
103	AC	48	Total	O	0
			48	48	
103	AD	66	Total	O	0
			66	66	
103	AE	20	Total	O	0
			20	20	
103	AF	29	Total	O	0
			29	29	
103	AG	53	Total	O	0
			53	53	
103	AH	46	Total	O	0
			46	46	
103	AI	30	Total	O	0
			30	30	
103	AJ	14	Total	O	0
			14	14	
103	AK	49	Total	O	0
			49	49	

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Mol	Chain	Residues	Atoms		AltConf
103	AL	42	Total 42	O 42	0
103	AM	13	Total 13	O 13	0
103	AN	29	Total 29	O 29	0
103	AO	33	Total 33	O 33	0
103	AP	23	Total 23	O 23	0
103	AQ	52	Total 52	O 52	0
103	AR	9	Total 9	O 9	0
103	AS	18	Total 18	O 18	0
103	AT	26	Total 26	O 26	0
103	AU	4	Total 4	O 4	0
103	AW	9	Total 9	O 9	0
103	AX	44	Total 44	O 44	0
103	AZ	24	Total 24	O 24	0
103	A0	2	Total 2	O 2	0
103	A1	36	Total 36	O 36	0
103	A2	26	Total 26	O 26	0
103	A3	43	Total 43	O 43	0
103	Aw	4	Total 4	O 4	0
103	Ax	8	Total 8	O 8	0
103	Ay	1	Total 1	O 1	0
103	A	2847	Total 2847	O 2847	0

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Mol	Chain	Residues	Atoms		AltConf
103	B	55	Total 55	O 55	0
103	D	68	Total 68	O 68	0
103	E	57	Total 57	O 57	0
103	F	74	Total 74	O 74	0
103	I	21	Total 21	O 21	0
103	K	68	Total 68	O 68	0
103	L	27	Total 27	O 27	0
103	M	46	Total 46	O 46	0
103	N	50	Total 50	O 50	0
103	O	34	Total 34	O 34	0
103	P	69	Total 69	O 69	0
103	Q	26	Total 26	O 26	0
103	R	59	Total 59	O 59	0
103	S	43	Total 43	O 43	0
103	T	47	Total 47	O 47	0
103	U	25	Total 25	O 25	0
103	V	6	Total 6	O 6	0
103	W	49	Total 49	O 49	0
103	X	11	Total 11	O 11	0
103	Y	23	Total 23	O 23	0
103	Z	35	Total 35	O 35	0

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Mol	Chain	Residues	Atoms		AltConf
103	0	27	Total 27	O 27	0
103	1	2	Total 2	O 2	0
103	2	33	Total 33	O 33	0
103	3	43	Total 43	O 43	0
103	4	11	Total 11	O 11	0
103	5	15	Total 15	O 15	0
103	6	69	Total 69	O 69	0
103	7	11	Total 11	O 11	0
103	8	14	Total 14	O 14	0
103	9	16	Total 16	O 16	0
103	a	9	Total 9	O 9	0
103	b	32	Total 32	O 32	0
103	c	16	Total 16	O 16	0
103	d	6	Total 6	O 6	0
103	e	8	Total 8	O 8	0
103	f	18	Total 18	O 18	0
103	g	10	Total 10	O 10	0
103	i	50	Total 50	O 50	0
103	j	21	Total 21	O 21	0
103	l	1	Total 1	O 1	0
103	m	8	Total 8	O 8	0

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Mol	Chain	Residues	Atoms		AltConf
103	o	33	Total 33	O 33	0
103	p	4	Total 4	O 4	0
103	r	35	Total 35	O 35	0
103	s	40	Total 40	O 40	0
103	H	7	Total 7	O 7	0
103	AY	20	Total 20	O 20	0
103	A4	7	Total 7	O 7	0
103	Az	12	Total 12	O 12	0

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	82522	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.335	Depositor
Minimum map value	-0.152	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	531.2, 531.2, 531.2	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83000004, 0.83000004, 0.83000004	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
40	SAC	K	2	40	7,8,9	0.26	0	7,9,11	0.62	0
1	MA6	AA	1584	1	23,26,27	0.30	0	33,38,41	0.59	1 (3%)
17	AYA	AQ	2	17	6,7,8	0.82	0	6,8,10	0.43	0
1	5MC	AA	1488	1	19,22,23	0.32	0	26,32,35	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
33	1MA	A	2617	33	21,25,26	0.75	1 (4%)	30,37,40	0.65	1 (3%)
1	B8T	AA	1486	1,95	19,22,23	0.26	0	25,31,34	0.34	0
76	AYA	k	2	76	6,7,8	0.85	0	6,8,10	0.47	0
9	5F0	AI	184	9	8,8,9	0.56	0	8,9,11	1.10	1 (12%)
1	MA6	AA	1583	1	23,26,27	0.26	0	33,38,41	0.55	1 (3%)
28	AYA	A2	2	28	6,7,8	0.84	0	6,8,10	0.53	0
1	5MU	AA	1076	1	19,22,23	0.60	0	27,32,35	1.22	3 (11%)
34	1MA	B	9	34	21,25,26	0.74	1 (4%)	30,37,40	0.63	1 (3%)
34	PSU	B	39	34	18,21,22	0.75	0	21,30,33	2.77	5 (23%)
50	AYA	U	2	50	6,7,8	0.80	0	6,8,10	0.54	0
33	OMG	A	3040	33,30	23,26,27	0.23	0	32,38,41	0.37	0
34	2MG	B	10	34	23,26,27	0.45	0	33,38,41	0.49	0
33	OMU	A	3039	33,96	19,22,23	0.22	0	25,31,34	0.43	0
33	OMG	A	2815	33,96,31	23,26,27	0.25	0	32,38,41	0.38	0
33	PSU	A	3067	33	18,21,22	0.77	0	21,30,33	2.77	6 (28%)

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
40	SAC	K	2	40	-	0/7/8/10	-
1	MA6	AA	1584	1	-	2/11/29/30	0/3/3/3
17	AYA	AQ	2	17	-	1/5/6/8	-
1	5MC	AA	1488	1	-	0/7/25/26	0/2/2/2
33	1MA	A	2617	33	-	0/7/25/26	0/3/3/3
1	B8T	AA	1486	1,95	-	1/7/27/28	0/2/2/2
76	AYA	k	2	76	-	1/5/6/8	-
9	5F0	AI	184	9	-	0/9/9/10	-
1	MA6	AA	1583	1	-	0/11/29/30	0/3/3/3
28	AYA	A2	2	28	-	0/5/6/8	-
1	5MU	AA	1076	1	-	0/7/25/26	0/2/2/2
34	1MA	B	9	34	-	0/7/25/26	0/3/3/3
34	PSU	B	39	34	-	0/7/25/26	0/2/2/2
50	AYA	U	2	50	-	1/5/6/8	-
33	OMG	A	3040	33,30	-	0/9/27/28	0/3/3/3
34	2MG	B	10	34	-	0/9/27/28	0/3/3/3
33	OMU	A	3039	33,96	-	0/9/27/28	0/2/2/2
33	OMG	A	2815	33,96,31	-	0/9/27/28	0/3/3/3
33	PSU	A	3067	33	-	0/7/25/26	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	A	2617	1MA	C6-N6	3.08	1.35	1.28
34	B	9	1MA	C6-N6	3.05	1.35	1.28

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B	39	PSU	N1-C2-N3	8.63	124.27	115.17
33	A	3067	PSU	N1-C2-N3	8.60	124.24	115.17
34	B	39	PSU	C4-N3-C2	-6.90	116.87	126.37
33	A	3067	PSU	C4-N3-C2	-6.86	116.93	126.37
1	AA	1076	5MU	C4-N3-C2	-4.76	121.11	127.34

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	AQ	2	AYA	O-C-CA-CB
76	k	2	AYA	C-CA-N-CT
1	AA	1584	MA6	C4'-C5'-O5'-P
1	AA	1584	MA6	C5-C6-N6-C9
50	U	2	AYA	C-CA-N-CT

There are no ring outliers.

No monomer is involved in short contacts.

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 271 ligands modelled in this entry, 258 are monoatomic - leaving 13 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
100	GDP	AX	503	-	29,30,30	0.42	0	45,47,47	0.42	0
92	NAD	AA	1701	95	46,48,48	0.40	0	64,73,73	0.40	0
93	SPM	AA	1702	-	13,13,13	0.24	0	12,12,12	0.98	0
98	FES	r	201	82,38	0,4,4	-	-	-		
98	FES	AP	201	16,5	0,4,4	-	-	-		
94	SPD	AA	1703	-	9,9,9	0.23	0	8,8,8	1.33	2 (25%)
94	SPD	A	3301	-	9,9,9	0.21	0	8,8,8	1.23	0
98	FES	AT	201	20,13	0,4,4	-	-	-		
102	VAL	B	101	34	4,6,7	0.55	0	6,7,9	0.77	0
94	SPD	A	3302	-	9,9,9	0.24	0	8,8,8	1.15	0
94	SPD	A	3303	-	9,9,9	0.25	0	8,8,8	1.18	0
101	PUT	A	3304	-	5,5,5	0.22	0	4,4,4	0.48	0
99	ATP	AX	501	95	32,33,33	0.53	0	48,52,52	0.52	0

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
100	GDP	AX	503	-	-	0/16/32/32	0/3/3/3
92	NAD	AA	1701	95	-	0/30/62/62	0/5/5/5
93	SPM	AA	1702	-	-	0/11/11/11	-
98	FES	r	201	82,38	-	-	0/1/1/1
98	FES	AP	201	16,5	-	-	0/1/1/1
94	SPD	AA	1703	-	-	0/7/7/7	-
94	SPD	A	3301	-	-	1/7/7/7	-
102	VAL	B	101	34	-	0/5/6/8	-
98	FES	AT	201	20,13	-	-	0/1/1/1
94	SPD	A	3302	-	-	0/7/7/7	-
94	SPD	A	3303	-	-	2/7/7/7	-
101	PUT	A	3304	-	-	0/3/3/3	-
99	ATP	AX	501	95	-	1/22/38/38	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
94	AA	1703	SPD	C4-C5-N6	-2.31	105.86	112.07
94	AA	1703	SPD	C8-C7-N6	-2.09	106.46	112.07

There are no chirality outliers.

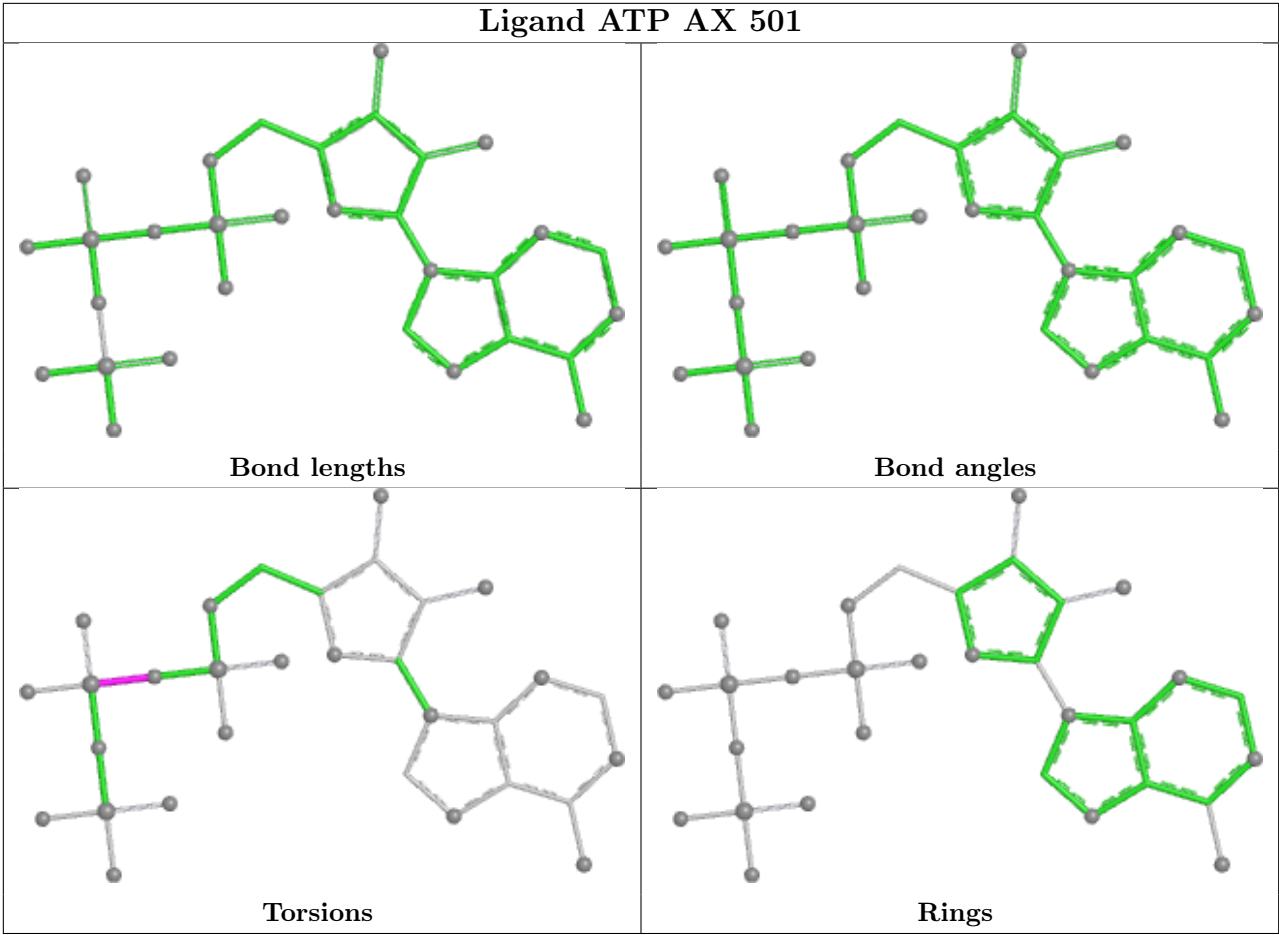
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
94	A	3303	SPD	C4-C5-N6-C7
94	A	3303	SPD	C8-C7-N6-C5
94	A	3301	SPD	N6-C7-C8-C9
99	AX	501	ATP	PA-O3A-PB-O2B

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.



4.7 Other polymers ⓘ

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	Ay	1
31	Ax	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Ay	15:A	O3'	21:A	P	9.63
1	Ax	15:A	O3'	21:A	P	8.88

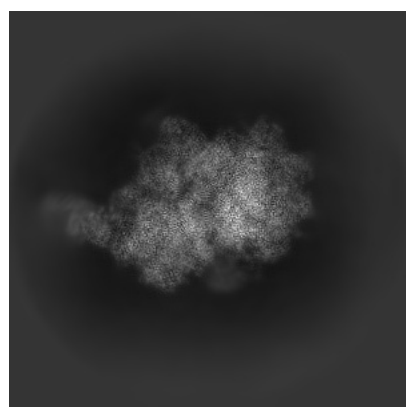
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15544. These allow visual inspection of the internal detail of the map and identification of artifacts.

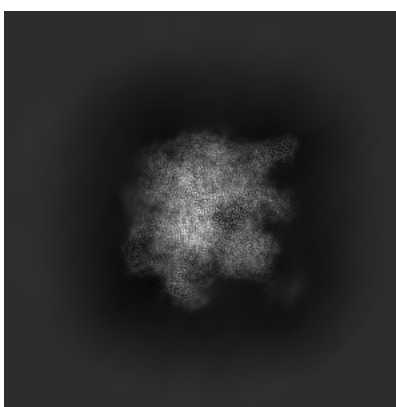
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

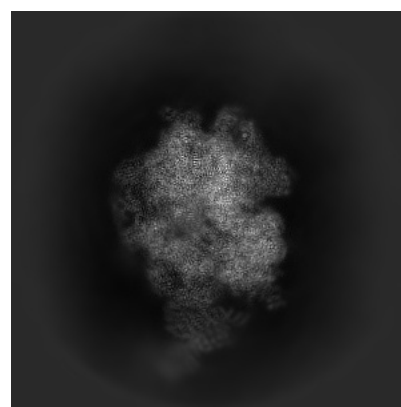
5.1.1 Primary map



X



Y

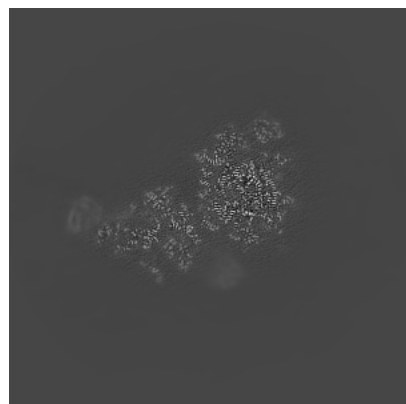


Z

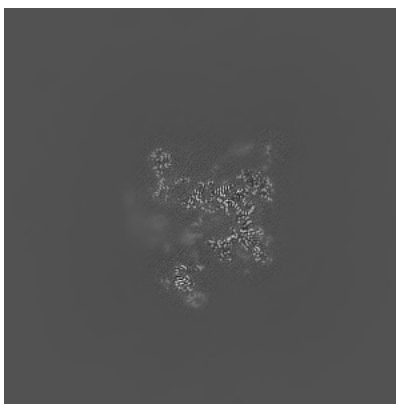
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

5.2.1 Primary map



X Index: 320



Y Index: 320

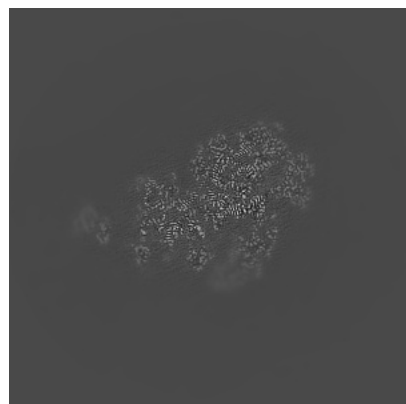


Z Index: 320

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

5.3 Largest variance slices [i](#)

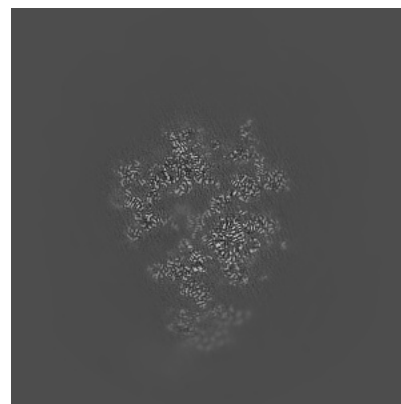
5.3.1 Primary map



X Index: 342



Y Index: 369

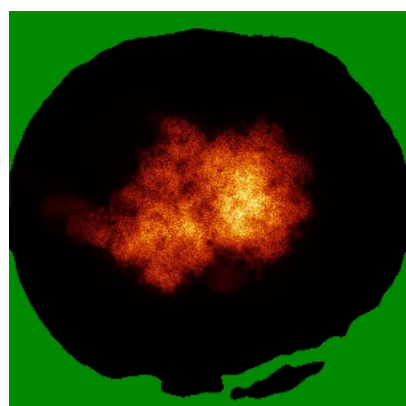


Z Index: 292

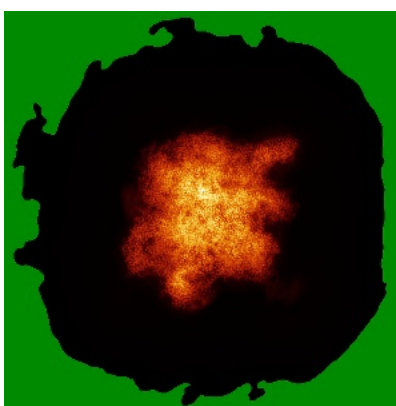
The images above show the largest variance slices of the map in three orthogonal directions.

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

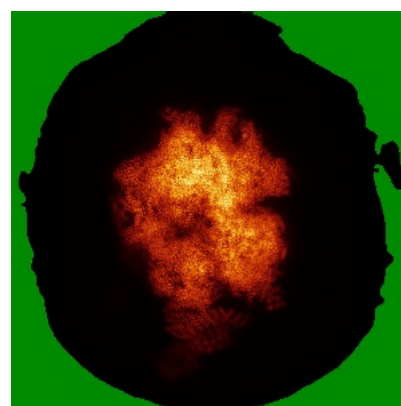
5.4.1 Primary map



X



Y

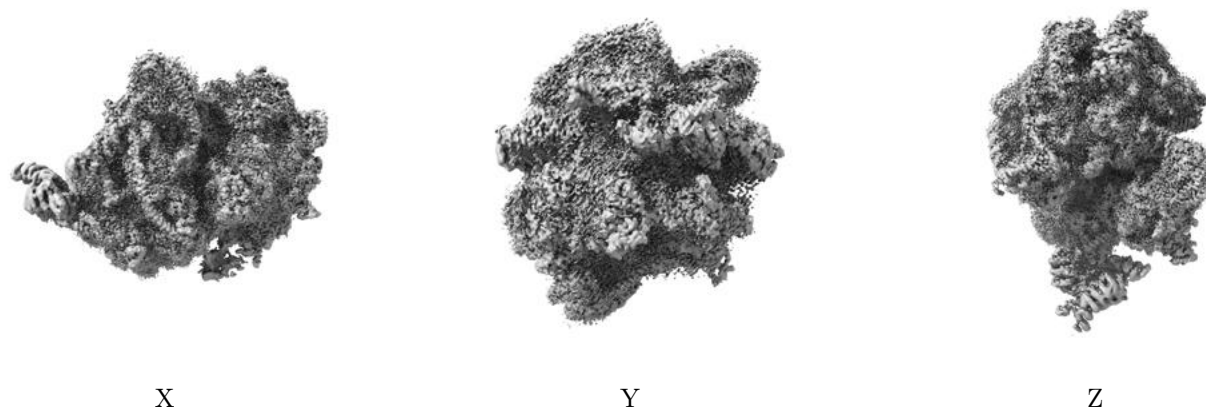


Z

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.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

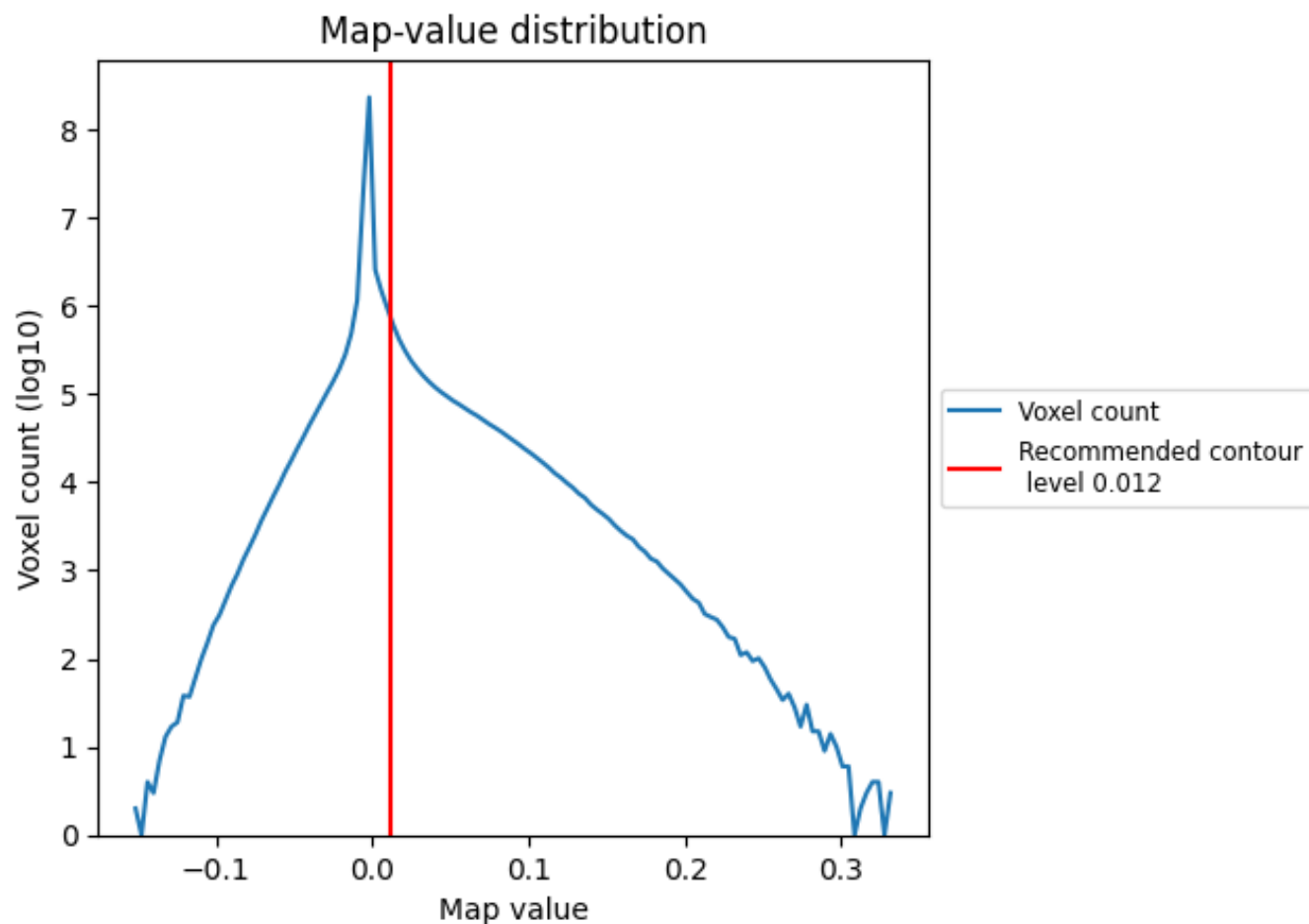
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

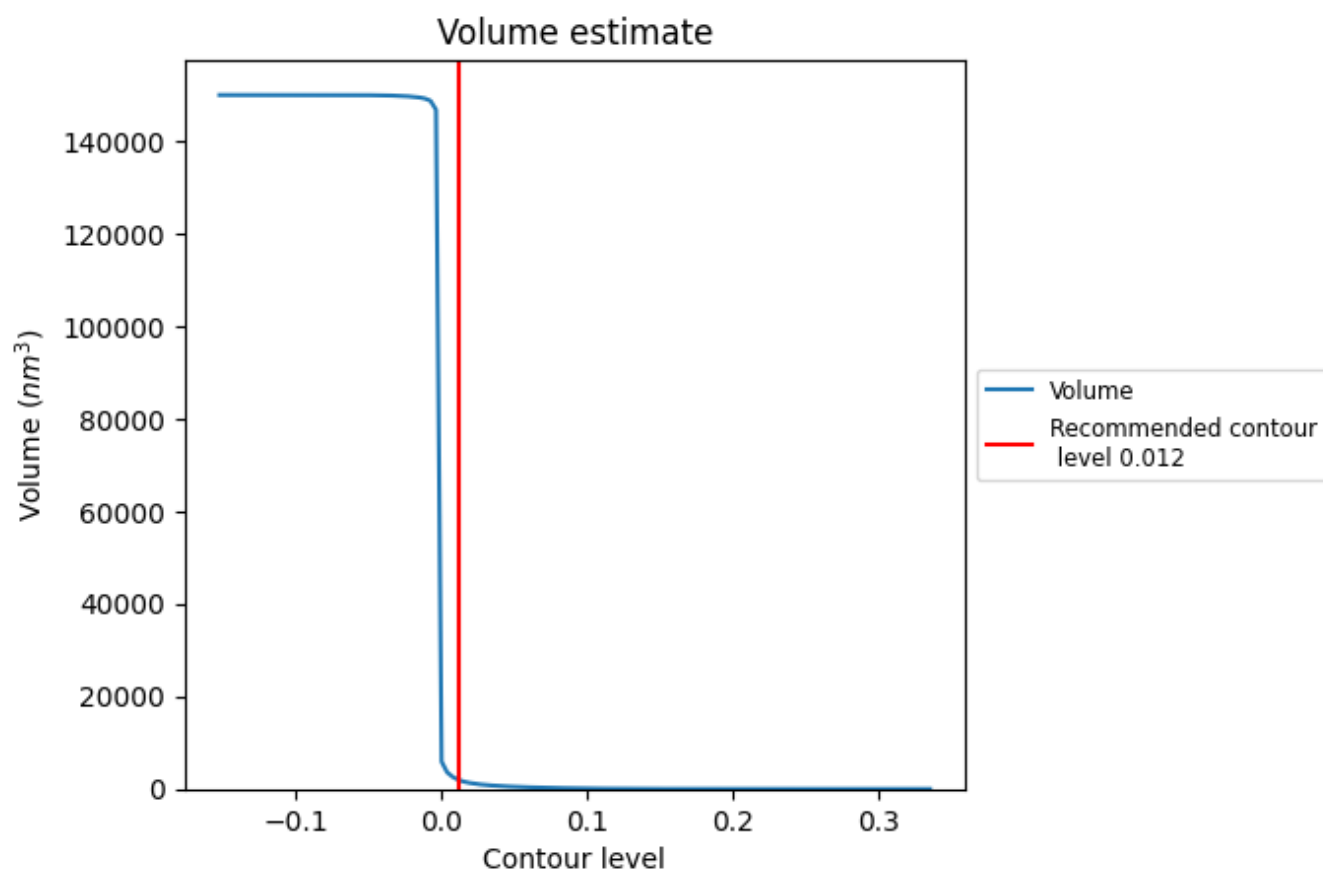
This section contains the results of statistical analysis of the map.

6.1 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.

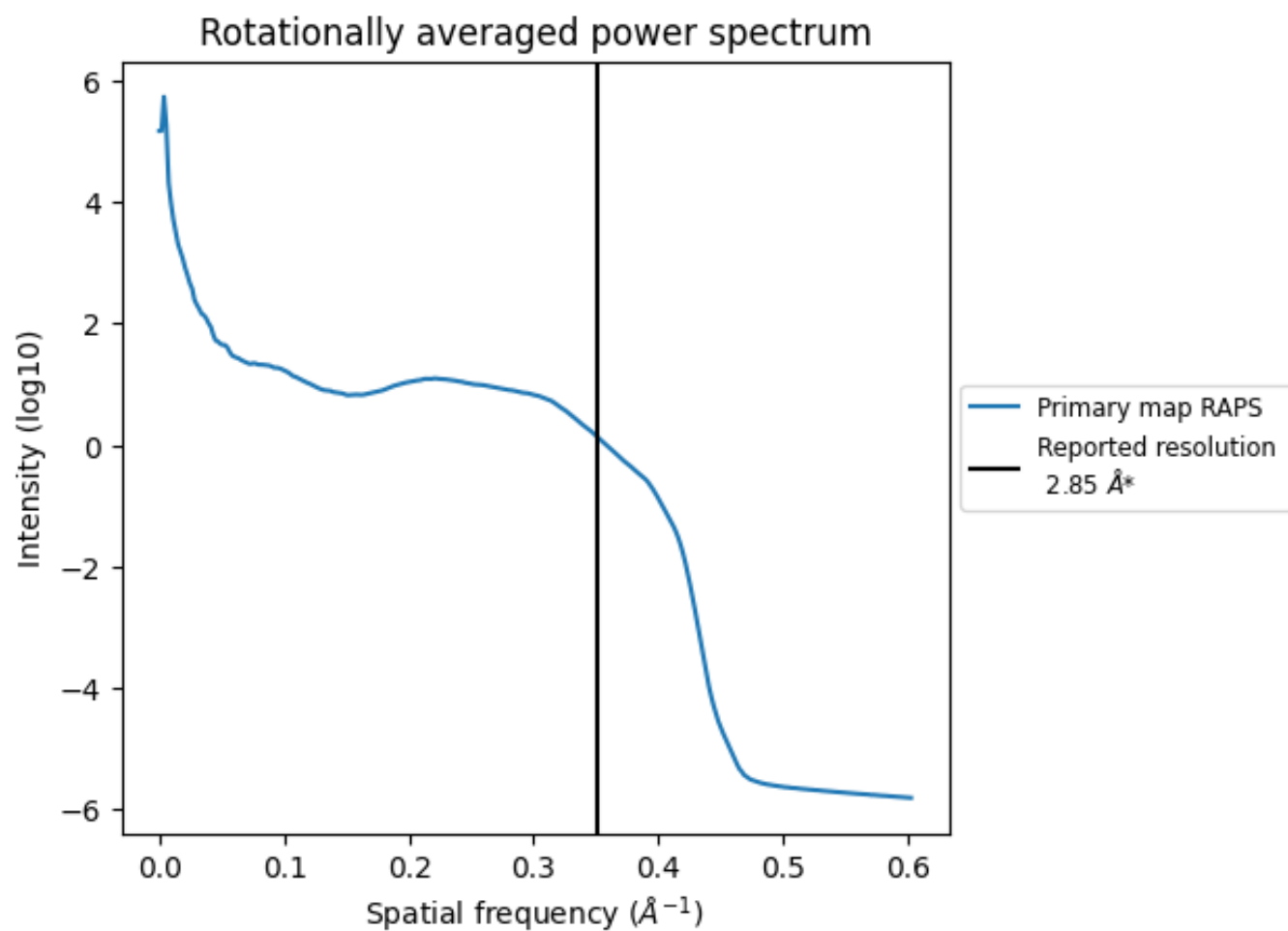
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 1967 nm^3 ; this corresponds to an approximate mass of 1777 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.

6.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.351 Å⁻¹

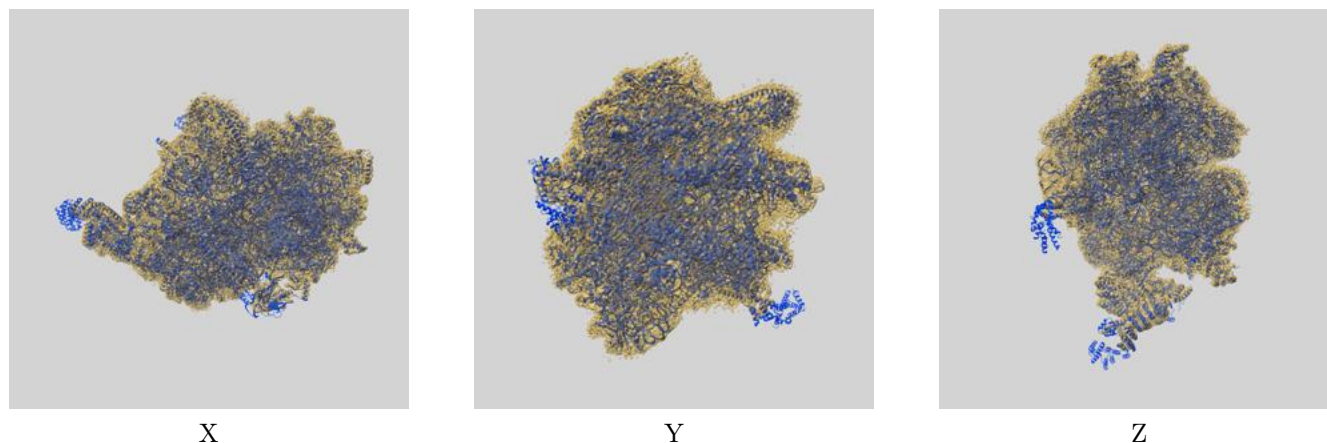
7 Fourier-Shell correlation ⓘ

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

8 Map-model fit [i](#)

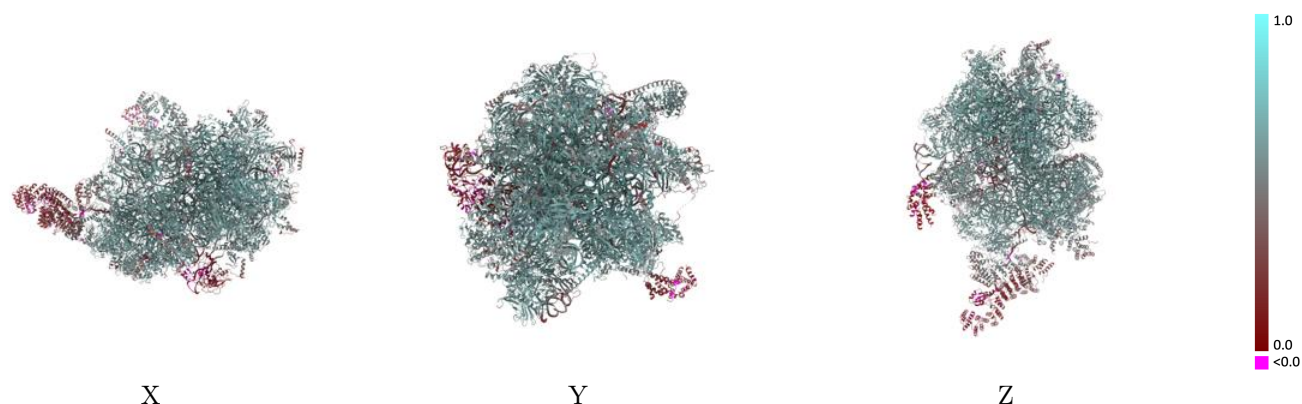
This section contains information regarding the fit between EMDB map EMD-15544 and PDB model 8ANY. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



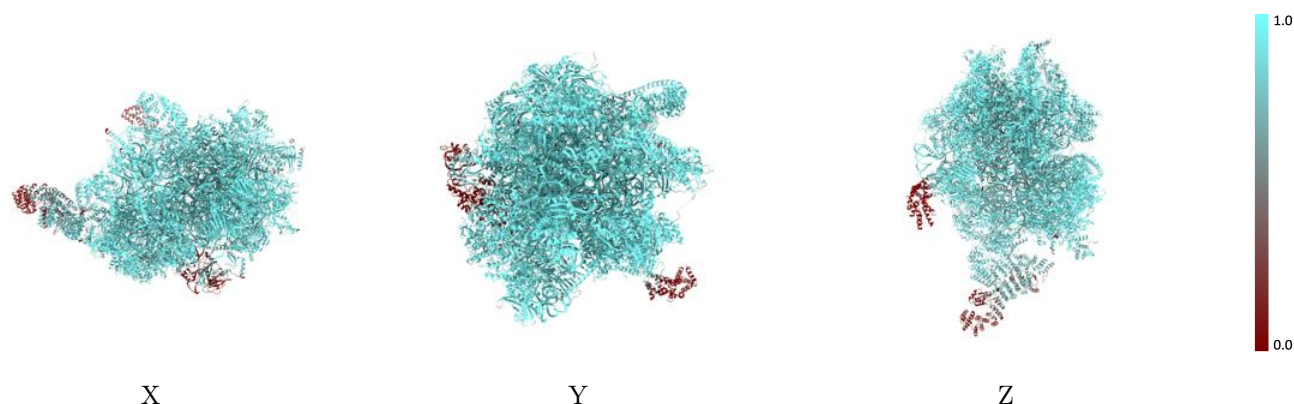
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



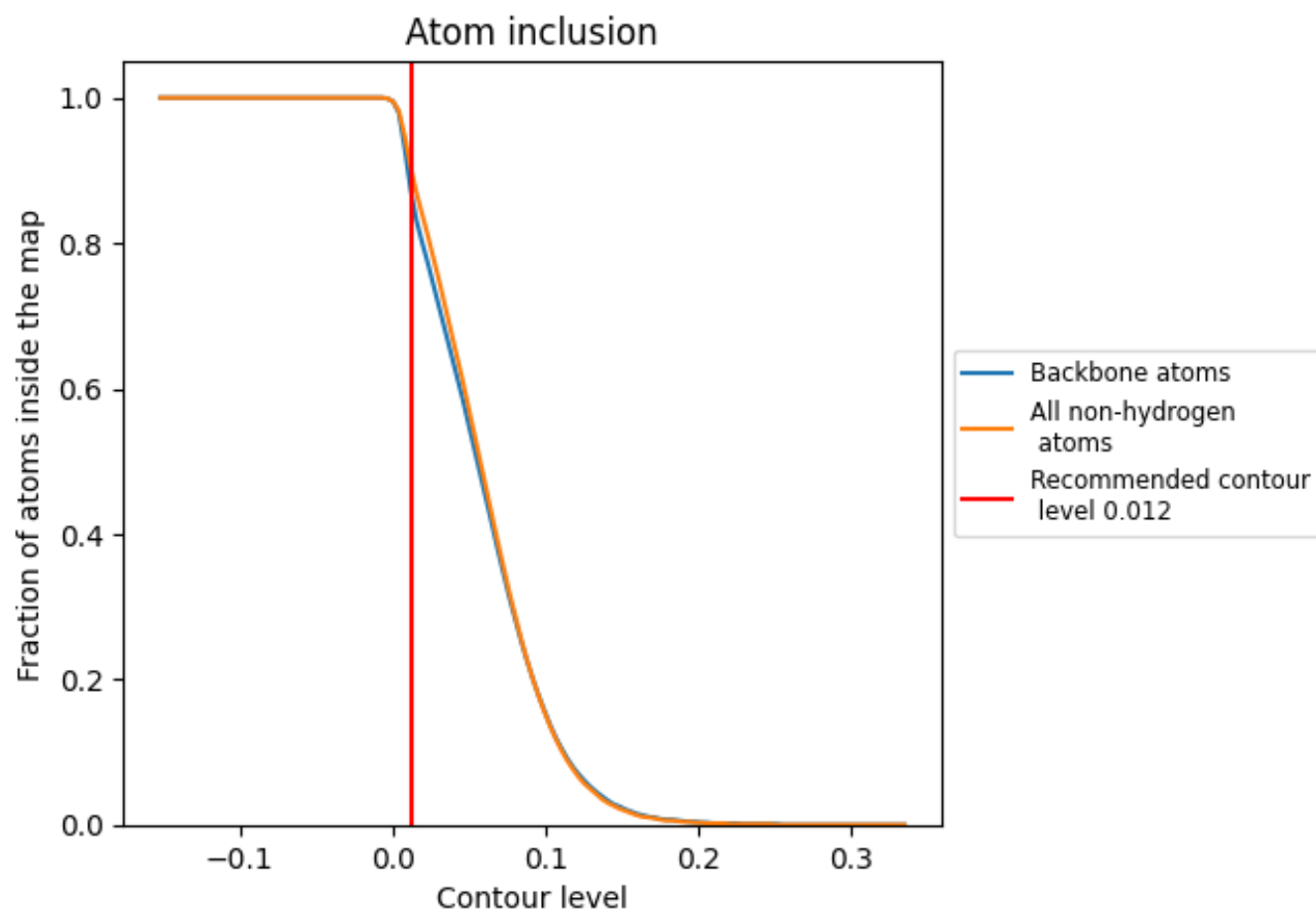
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

8.3 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 (0.012).

8.4 Atom inclusion ⓘ



At the recommended contour level, 87% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9040	 0.5540
0	 0.9620	 0.6050
1	 0.9450	 0.5770
2	 0.9950	 0.6820
3	 0.9910	 0.6710
4	 0.9880	 0.6420
5	 0.9640	 0.5810
6	 0.9650	 0.5940
7	 0.9410	 0.5410
8	 0.8720	 0.4880
9	 0.9310	 0.5690
A	 0.9810	 0.6290
A0	 0.9360	 0.5540
A1	 0.9340	 0.5680
A2	 0.9070	 0.5040
A3	 0.9610	 0.6000
A4	 0.8590	 0.4320
A5	 0.4750	 0.1750
A6	 0.2210	 0.1260
AA	 0.9930	 0.6240
AB	 0.9610	 0.5980
AC	 0.9860	 0.6490
AD	 0.9500	 0.5700
AE	 0.9520	 0.5800
AF	 0.9550	 0.5730
AG	 0.9270	 0.5530
AH	 0.9570	 0.5990
AI	 0.9700	 0.5910
AJ	 0.9570	 0.5740
AK	 0.9890	 0.6560
AL	 0.9240	 0.5440
AM	 0.9290	 0.5770
AN	 0.9590	 0.5930
AO	 0.9510	 0.5610
AP	 0.9620	 0.5930



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Chain	Atom inclusion	Q-score
AQ	 0.9790	 0.6240
AR	 0.9040	 0.4830
AS	 0.9170	 0.5270
AT	 0.9440	 0.5720
AU	 0.9060	 0.5090
AV	 0.9290	 0.5300
AW	 0.9490	 0.5580
AX	 0.9680	 0.5870
AY	 0.7040	 0.4040
AZ	 0.9400	 0.5880
Aw	 0.7730	 0.3380
Ax	 0.9390	 0.4600
Ay	 0.5110	 0.2100
Az	 0.7640	 0.2910
B	 0.9740	 0.5180
D	 0.9830	 0.6350
E	 0.9720	 0.6260
F	 0.9820	 0.6360
H	 0.5850	 0.3310
I	 0.7680	 0.4640
J	 0.8970	 0.4790
K	 0.9760	 0.6420
L	 0.9830	 0.6300
M	 0.9780	 0.6270
N	 0.9660	 0.6120
O	 0.9770	 0.6180
P	 0.9820	 0.6270
Q	 0.9350	 0.5810
R	 0.9810	 0.6560
S	 0.9720	 0.6220
T	 0.9800	 0.6390
U	 0.9160	 0.5650
V	 0.9320	 0.5310
W	 0.9810	 0.6490
X	 0.9460	 0.5770
Y	 0.9710	 0.6130
Z	 0.9630	 0.6260
a	 0.9150	 0.5520
b	 0.9840	 0.6320
c	 0.9440	 0.5700
d	 0.8920	 0.4830
e	 0.8790	 0.4870

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Chain	Atom inclusion	Q-score
f	 0.9100	 0.5390
g	 0.9610	 0.6090
h	 0.9450	 0.5290
i	 0.9890	 0.6640
j	 0.9330	 0.5710
k	 0.9420	 0.5240
l	 0.9220	 0.5190
m	 0.8500	 0.4660
o	 0.9870	 0.6520
p	 0.8840	 0.5060
q	 0.7490	 0.4140
r	 0.9590	 0.5940
s	 0.9620	 0.5980
t	 0.3910	 0.2650
u	 0.3360	 0.2270
v	 0.0000	 0.1330
w	 0.0000	 0.0430
x	 0.0000	 0.0870
y	 0.0000	 0.0560
z	 0.1860	 0.1010