



wwPDB EM Validation Summary Report ⓘ

Dec 10, 2023 – 11:26 pm GMT

PDB ID : 8QSJ
EMDB ID : EMD-17720
Title : Human mitoribosomal large subunit assembly intermediate 2 with GTPBP7
Authors : Ritter, C.; Nguyen, T.G.; Kummer, E.
Deposited on : 2023-10-10
Resolution : 3.00 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:

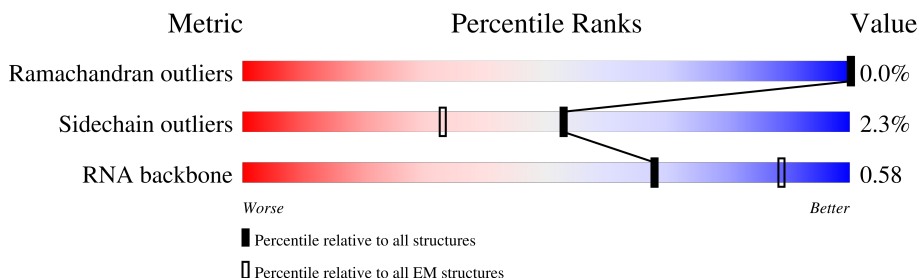
EMDB validation analysis : 0.0.1.dev70
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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 3.00 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.



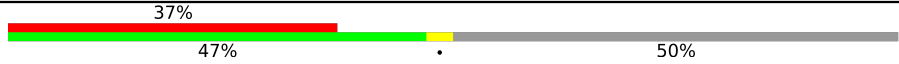







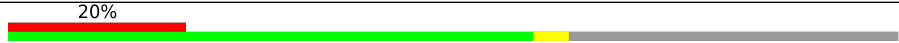

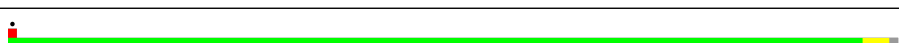


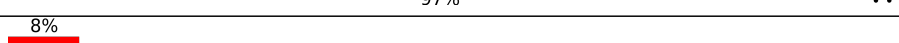
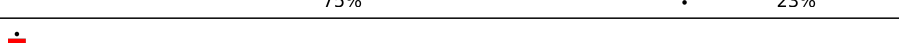
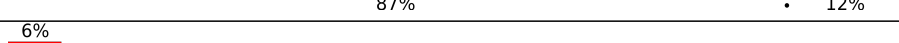
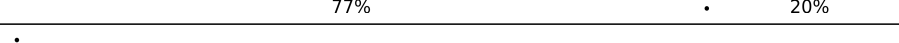
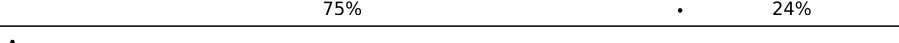
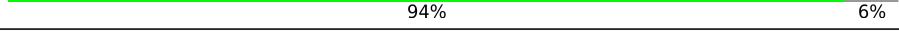


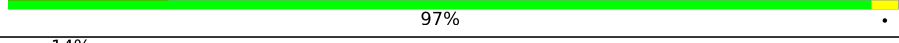
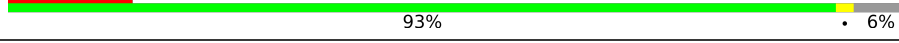

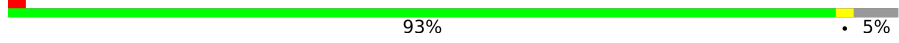
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	0	188	57% (Green), 41% (Grey)
2	1	65	5% (Red), 83% (Green), 15% (Grey)
3	2	92	50% (Green), 50% (Grey)
4	3	188	51% (Green), 49% (Grey)
5	4	103	36% (Green), 64% (Grey)
6	5	423	12% (Red), 92% (Green), 7% (Grey)
7	6	380	5% (Red), 12% (Orange), 92% (Green), 7% (Grey)
8	7	338	5% (Red), 86% (Green), 13% (Grey)

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Mol	Chain	Length	Quality of chain
9	8	206	
10	9	137	
11	A	1603	
12	B	72	
13	D	305	
14	E	348	
15	F	311	
16	H	267	
17	I	261	
18	J	192	
19	K	178	
20	L	145	
21	M	296	
22	N	251	
23	O	175	
24	P	180	
25	Q	292	
26	R	149	
27	S	205	
28	T	206	
29	U	153	
30	V	216	
31	W	148	
32	X	256	
33	Y	250	

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Mol	Chain	Length	Quality of chain
34	Z	161	75% 24%
35	a	142	10% 69% 30%
36	b	215	67% 31%
37	c	332	5% 85% 14%
38	d	306	21% 79% 19%
39	e	279	71% 79% 18%
40	f	212	40% 68% 29%
41	g	166	80% 19%
42	h	158	8% 69% 30%
43	i	128	75% 24%
44	j	123	6% 72% 27%
45	k	112	8% 69% 29%
46	l	138	16% 83%
47	m	128	27% 24% 73%
48	o	102	12% 90% 8%
49	p	206	17% 69% 29%
50	q	222	7% 62% 36%
51	r	196	73% 26%
52	s	439	86% 12%
53	u	234	5% 52% 46%
54	v	70	26% 96%
55	w	156	35% 46% 49%
56	x	384	8% 85% 12%
57	y	381	11% 62% 36%
58	z	334	5% 92% 7%

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 108265 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	110	898	554	176	162	6	0	0

- Molecule 2 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	55	455	290	87	76	2	0	0

- Molecule 3 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	46	377	233	83	60	1	0	0

- Molecule 4 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	95	832	539	162	128	3	0	0

- Molecule 5 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	37	333	212	71	47	3	0	0

- Molecule 6 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	394	3210	2073	560	566	11	0	0

- Molecule 7 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	6	354	2948	1881	525	533	9	0	0

- Molecule 8 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	7	294	2390	1529	405	438	18	0	0

- Molecule 9 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	8	102	860	543	152	163	2	0	0

- Molecule 10 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	9	124	997	644	170	181	2	0	0

- Molecule 11 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	A	1418	30108	13514	5446	9730	1418	0	0

- Molecule 12 is a RNA chain called tRNA-Val.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
12	B	72	1522	683	269	498	72	0	0

- Molecule 13 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	D	240	1872	1165	378	320	9	0	0

- Molecule 14 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	E	305	2406	1545	418	432	11	0	0

- Molecule 15 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	F	252	2031	1305	370	350	6	0	0

- Molecule 16 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	H	97	802	508	155	139	0	0

- Molecule 17 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	I	165	1338	863	242	223	10	0	0

- Molecule 18 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	J	137	1040	665	189	184	2	0	0

- Molecule 19 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	K	177	1455	936	259	253	7	0	0

- Molecule 20 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L	115	890	559	171	155	5	0	0

- Molecule 21 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	M	291	2327	1483	430	408	6	0	0

- Molecule 22 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	N	194	1583	1014	291	269	9	0	0

- Molecule 23 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	O	154	1259	792	241	219	7	0	0

- Molecule 24 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	P	144	1173	733	224	211	5	0	0

- Molecule 25 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Q	221	1843	1179	327	328	9	0	0

- Molecule 26 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	R	140	1154	732	231	187	4	0	0

- Molecule 27 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	S	161	1293	835	227	227	4	0	0

- Molecule 28 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	T	166	1369	875	254	233	7	0	0

- Molecule 29 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	U	152	1251	788	234	226	3	0	0

- Molecule 30 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	V	204	1667	1062	296	301	8	0	0

- Molecule 31 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	W	106	835	536	157	139	3	0	0

- Molecule 32 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	X	244	2044	1322	352	365	5	0	0

- Molecule 33 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Y	181	1556	995	298	259	4	0	0

- Molecule 34 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Z	122	996	636	186	171	3	0	0

- Molecule 35 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	100	Total	C	N	O	S	0	0
			840	529	152	154	5		

- Molecule 36 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b	149	Total	C	N	O	S	0	0
			1189	739	230	217	3		

- Molecule 37 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c	286	Total	C	N	O	S	0	0
			2299	1470	397	423	9		

- Molecule 38 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	249	Total	C	N	O	S	0	0
			2039	1306	352	367	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	228	Total	C	N	O	S	0	0
			1848	1174	326	342	6		

- Molecule 40 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f	150	Total	C	N	O	S	0	0
			1196	764	197	231	4		

- Molecule 41 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g	134	Total	C	N	O	S	0	0
			1113	719	193	199	2		

- Molecule 42 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	h	110	895	568	156	168	3	0	0

- Molecule 43 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	i	97	828	532	165	127	4	0	0

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	j	90	722	449	140	131	2	0	0

- Molecule 45 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	k	80	627	392	116	114	5	0	0

- Molecule 46 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
46	l	23	221	137	52	32	0	0

- Molecule 47 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	m	35	292	187	55	48	2	0	0

- Molecule 48 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	o	94	798	501	165	129	3	0	0

- Molecule 49 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	p	147	1205	748	228	225	4	0	0

- Molecule 50 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	q	141	1177	732	229	211	5	0	0

- Molecule 51 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	r	146	1203	764	232	199	8	0	0

- Molecule 52 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	s	386	3155	2023	559	559	14	0	0

- Molecule 53 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	u	126	1044	671	172	191	10	0	0

- Molecule 54 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
54	v	69	588	372	116	100	0	0

- Molecule 55 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	w	79	638	410	95	128	5	0	0

- Molecule 56 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	x	338	2676	1703	467	489	17	0	0

- Molecule 57 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	y	244	1980	1264	342	362	12	0	0

- Molecule 58 is a protein called Mitochondrial ribosome-associated GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	z	311	2443	1549	445	433	16	0	0

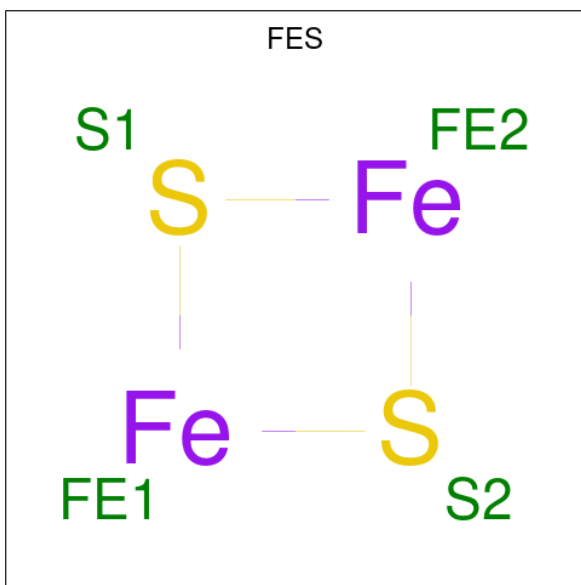
- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
59	0	1	1	1	0
59	4	1	1	1	0

- Molecule 60 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

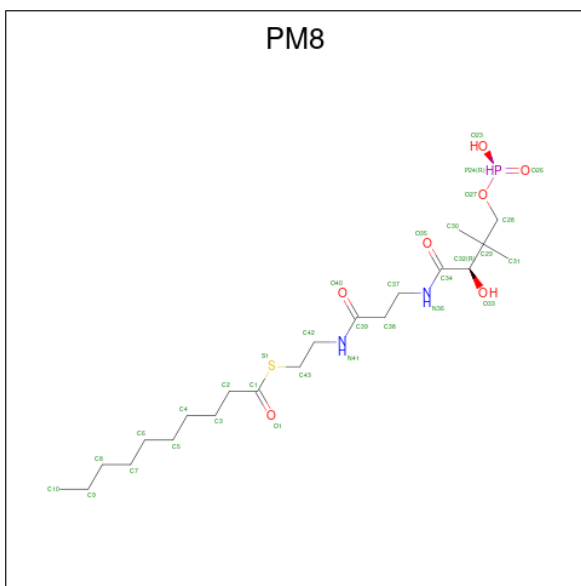
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
60	A	35	35	35	0
60	M	1	1	1	0
60	g	1	1	1	0
60	z	1	1	1	0

- Molecule 61 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
61	r	1	Total	Fe	S	0
			4	2	2	

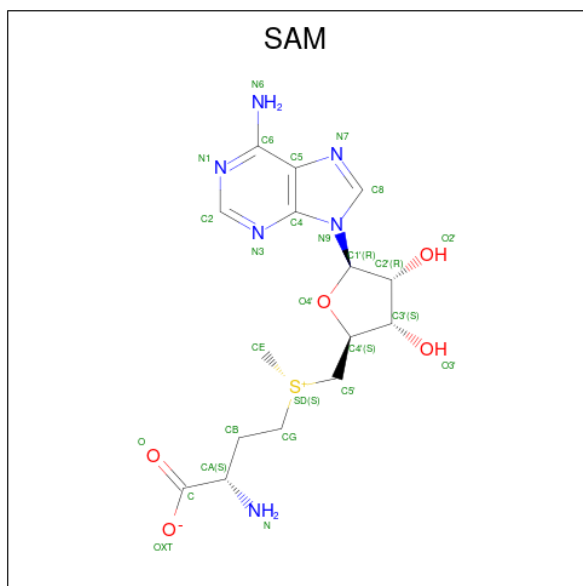
- Molecule 62 is S-(2-{[N-(2-HYDROXY-4-{[HYDROXY(OXIDO)PHOSPHINO]OXY}-3,3-DIMETHYLBUTANOYL)-BETA-ALANYL]AMINO}ETHYL) DECANETHIOATE (three-letter code: PM8) (formula: C₂₁H₄₁N₂O₇PS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf	
62	w	1	Total	C	N	O	P	S	0
			32	21	2	7	1	1	

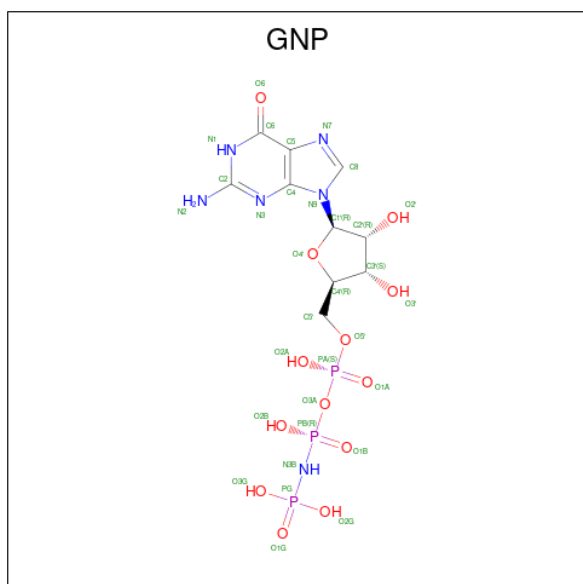
- Molecule 63 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: C₁₅H₂₂N₆O₅S)

(labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
63	x	1	27	15	6	5	1	0

- Molecule 64 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

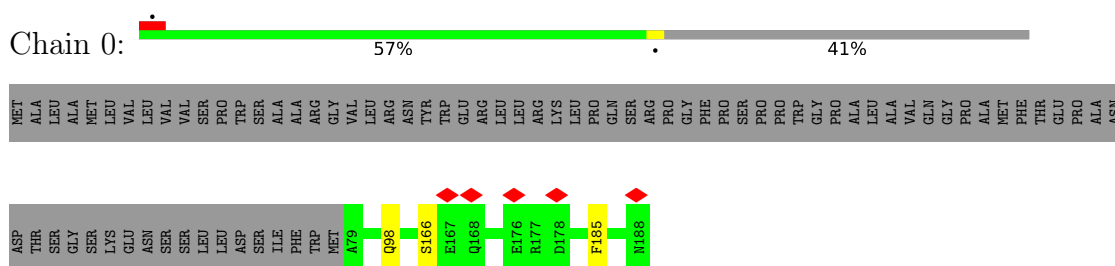


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
64	z	1	32	10	6	13	3	0

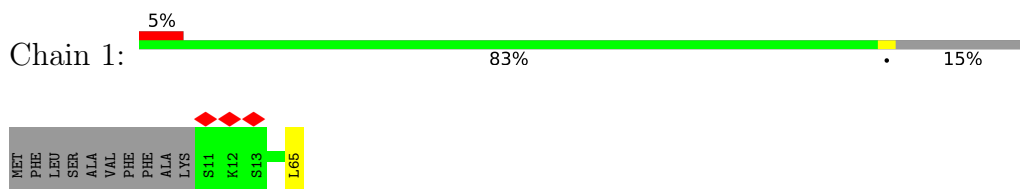
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

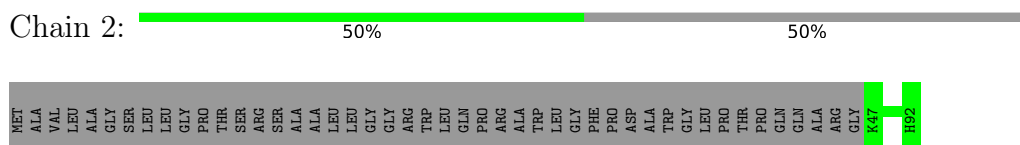
- Molecule 1: 39S ribosomal protein L32, mitochondrial



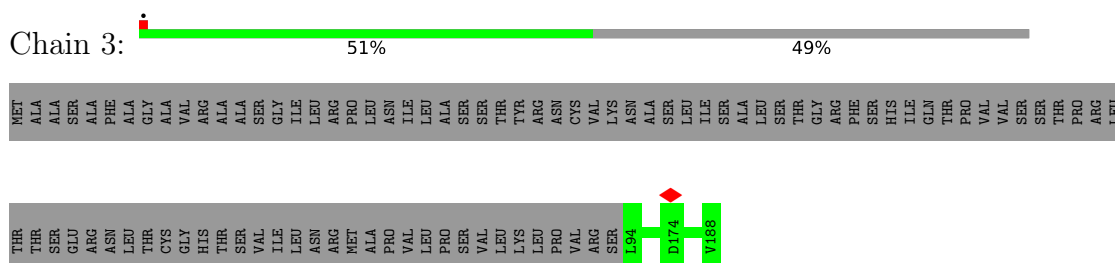
- Molecule 2: 39S ribosomal protein L33, mitochondrial



- Molecule 3: 39S ribosomal protein L34, mitochondrial



- Molecule 4: 39S ribosomal protein L35, mitochondrial



- Molecule 5: 39S ribosomal protein L36, mitochondrial



MET ALA PRO ASN PHE ILE ARG LYS MET VAL ASN PRO LEU LEU TYR SER ARG HIS THR VAL LYS PRO ARG ALA LEU SER PHE LEU PHE GLY SER ILE ARG GLY ALA ALA PRO VAL ALA VAL GLU PRO GLY ALA VAL ARG SER LEU LEU PRO HIS LEU

LEU PRO ALA LEU GLY F66 Q102 MET

- Molecule 6: 39S ribosomal protein L37, mitochondrial

Chain 5: 92% 7%

MET ALA LEU ALA SER GLY PRO ARG ALA ARG ALA CYS LEU LEU GLY SER GLN LEU GLY LEU GLY LEU PHE PHE ALA PRO ARG ARG GLY A30 S41 E42 K63 G51 Y52 K83 D151 C203 E243 F256 D264 C268 V401 A423

- Molecule 7: 39S ribosomal protein L38, mitochondrial

Chain 6: 12% 92% 7%

MET ALA ALA PRO TRP ARG ALA ALA CYS GLU CYS ARG TRP ARG ALA PHE SER THR SER ALA VAL LEU GLY R27 N44 L45 E46 R47 R59 E62 Q63 E64 E80 K81 T82 D83 P84 K85 E86 K87 K96 Q102 M116 V117 E118 E119 E120 R121 R124

S129 D133 R141 D160 G180 E181 D182 D183 G190 Q200 E207 A208 E209 E210 L217 R244 V245 A246 E247 L271 L272 D276 D280 F281 S282 E283 D284 F298 D302 E309 T310 M311 Y380

- Molecule 8: 39S ribosomal protein L39, mitochondrial

Chain 7: 5% 86% 13%

MET GLU ALA LEU MET ALA SER ALA LEU ARG LEU TRP VAL PRO GLY GLN SER ILE THR SER SER ALA SER Q34 L35 L56 S57 F60 R61 D109 S187 K196 E197 V221 E222 A223 K224 E228 I229 F230 E242

Q246 Q290 E326 D327 GLN SER LYS ALA THR GLU CYS THR

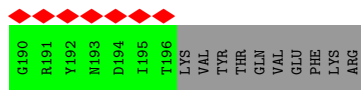
- Molecule 9: 39S ribosomal protein L40, mitochondrial

Chain 8: 37% 47% 50%

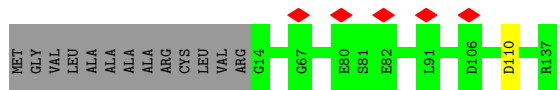
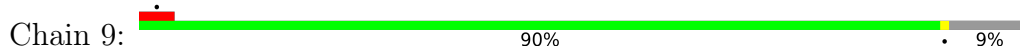
MET THR ALA SER VAL LEU ARG SER ILE SER SER ILE LEU LEU ARG PRO THR SER LEU LEU GLN LEU LEU TRP TRP GLN THR GLN ARG ARG LEU PHE ASP ILE THR PRO LEU LYS ARG SER LEU LEU D96 K97 A98 R99 E100 R101 P102 Q103 V104 E105 L106 T107 F108 E109 E110 R113 R114 A115 L116 L117 K119 K120

ASP GLN ALA LEU ARG SER ILE SER SER ILE LEU LEU ARG PRO THR SER LEU LEU GLN LEU LEU TRP TRP GLN THR GLN ARG ARG LEU PHE ASP ILE THR PRO LEU LYS ARG SER LEU LEU D96 K97 A98 R99 E100 R101 P102 Q103 V104 E105 L106 T107 F108 E109 E110 R113 R114 A115 L116 L117 K119 K120

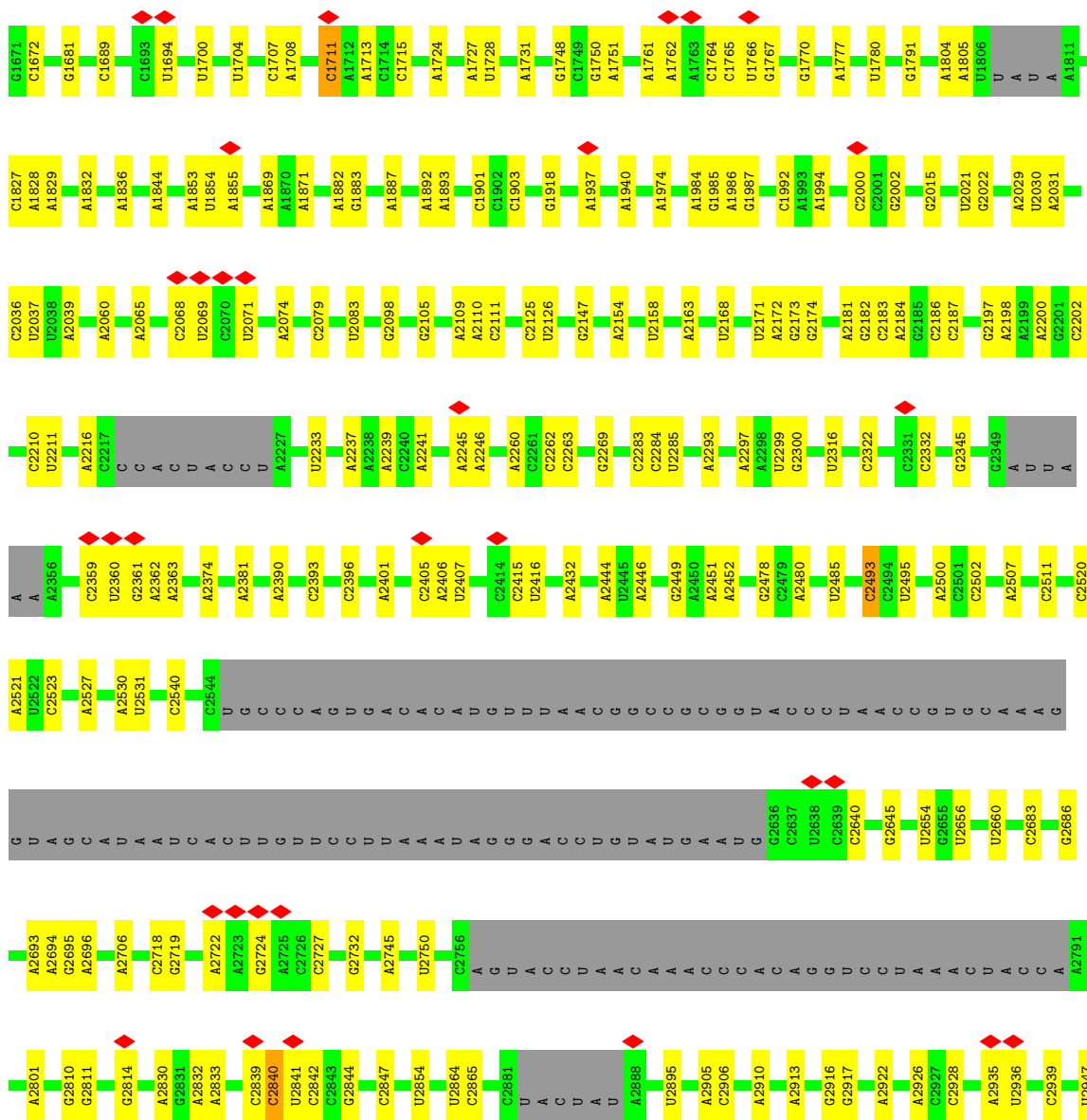
E128 M131 E132 R133 D134 T135 I136 R137 A138 M139 L140 E141 A142 Q143 Q144 E145 A146 L147 E148 E149 L150 Q151 L152 E153 S154 P155 K156 L157 H158 A159 K97 A161 I162 K163 R164 D165 P166 N167 L168 F169 P170 F171 E172 E173 P176 H177 Y178 T179 P180 P181 I182 P183 N184 Y185 Q186 P187 P188 E189

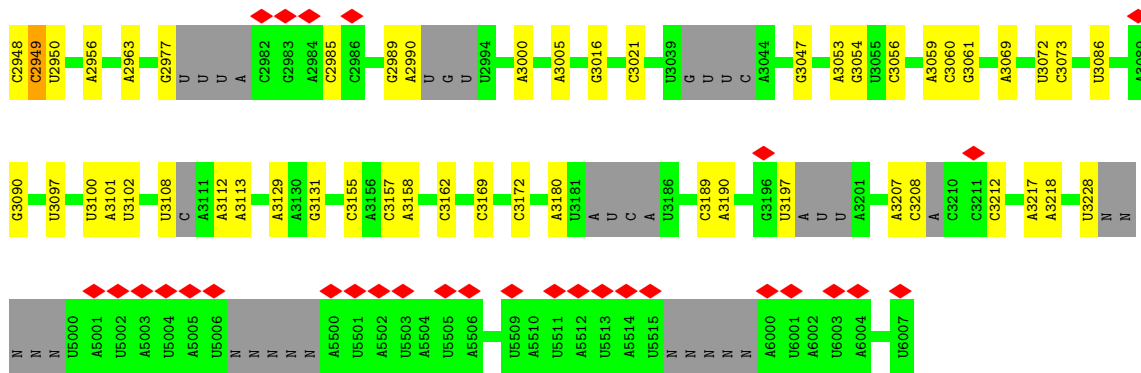


• Molecule 10: 39S ribosomal protein L41, mitochondrial

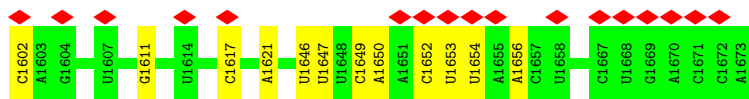
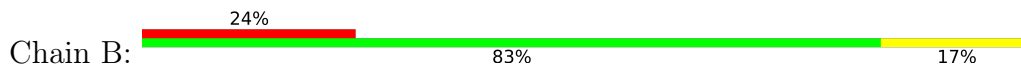


• Molecule 11: 16S rRNA

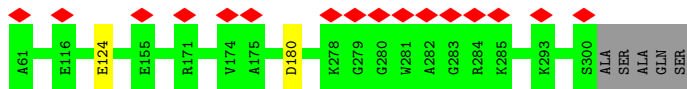
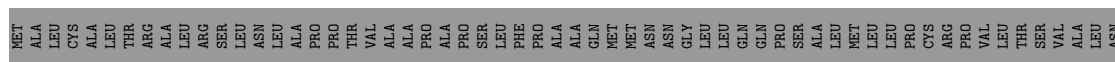
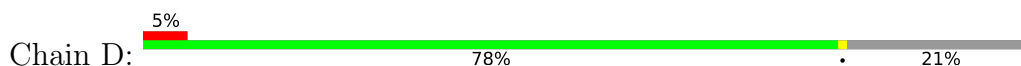




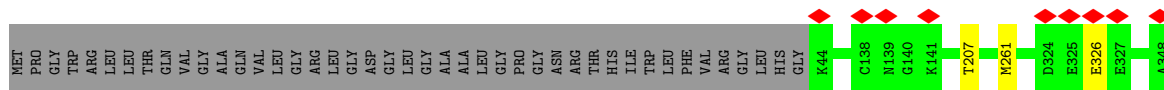
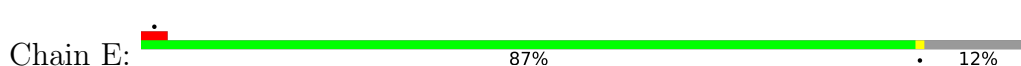
• Molecule 12: tRNA-Val



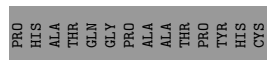
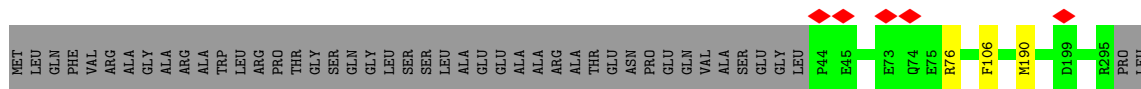
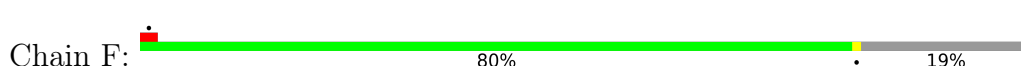
• Molecule 13: 39S ribosomal protein L2, mitochondrial



• Molecule 14: 39S ribosomal protein L3, mitochondrial

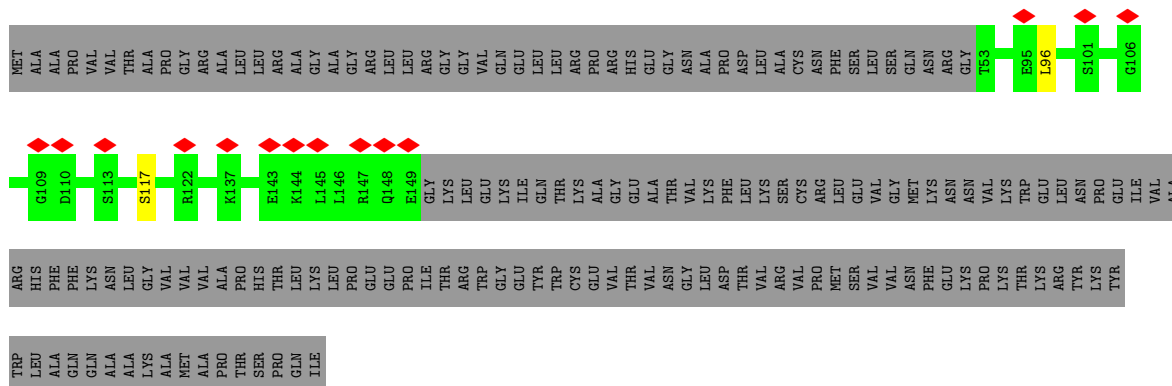


• Molecule 15: 39S ribosomal protein L4, mitochondrial

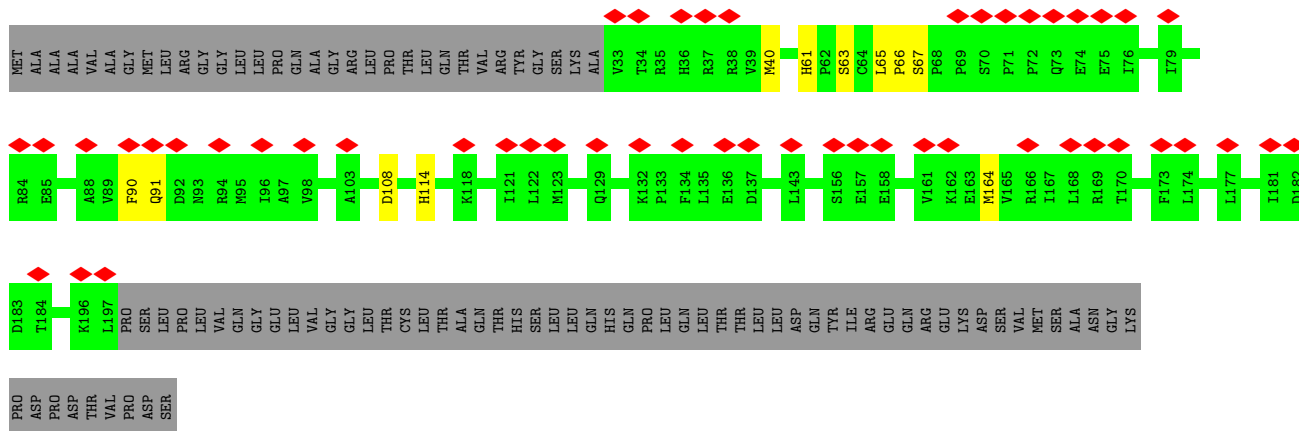


• Molecule 16: 39S ribosomal protein L9, mitochondrial

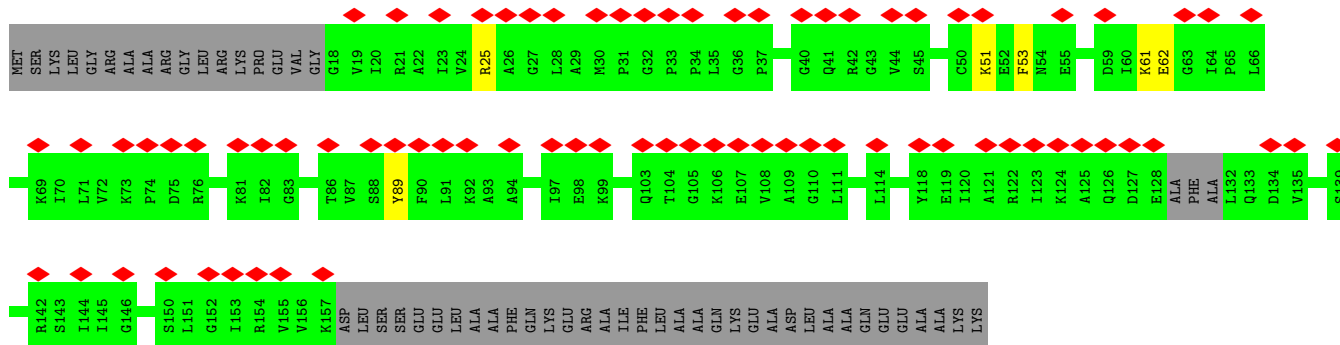
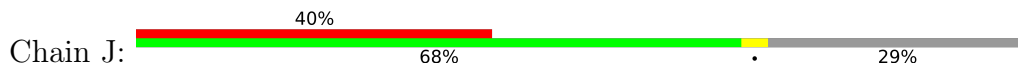




• Molecule 17: 39S ribosomal protein L10, mitochondrial

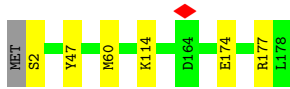


• Molecule 18: 39S ribosomal protein L11, mitochondrial

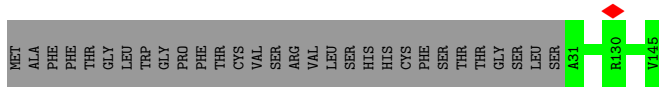
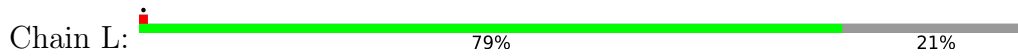


• Molecule 19: 39S ribosomal protein L13, mitochondrial

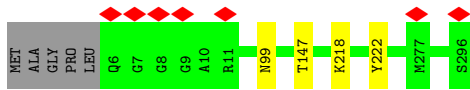




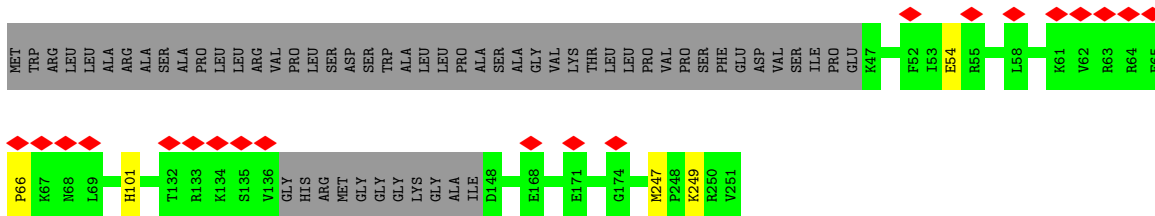
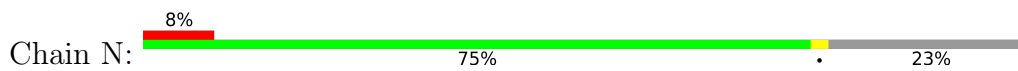
- Molecule 20: 39S ribosomal protein L14, mitochondrial



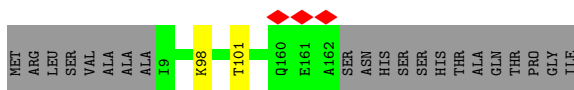
- Molecule 21: 39S ribosomal protein L15, mitochondrial



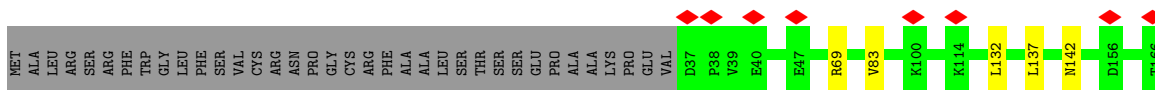
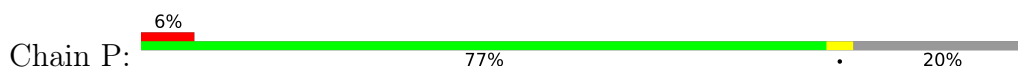
- Molecule 22: 39S ribosomal protein L16, mitochondrial



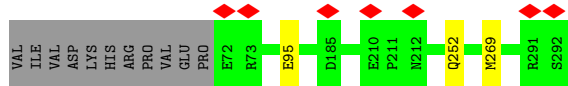
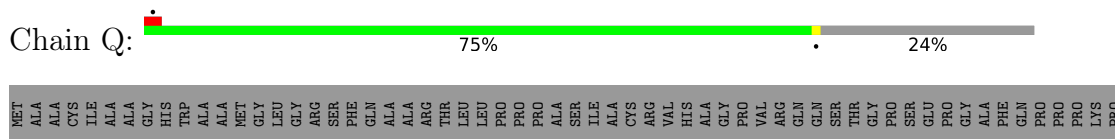
- Molecule 23: 39S ribosomal protein L17, mitochondrial



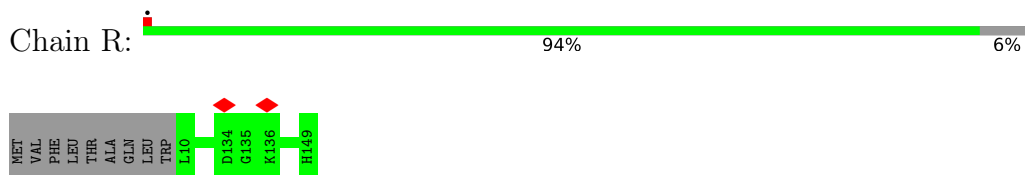
- Molecule 24: 39S ribosomal protein L18, mitochondrial



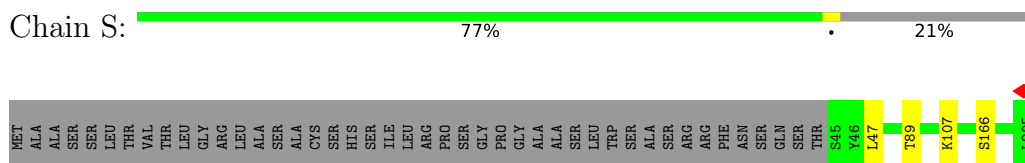
- Molecule 25: 39S ribosomal protein L19, mitochondrial



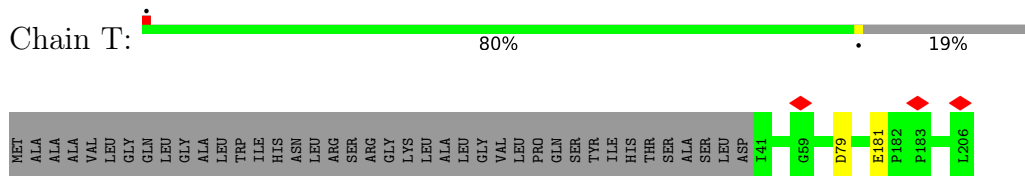
• Molecule 26: 39S ribosomal protein L20, mitochondrial



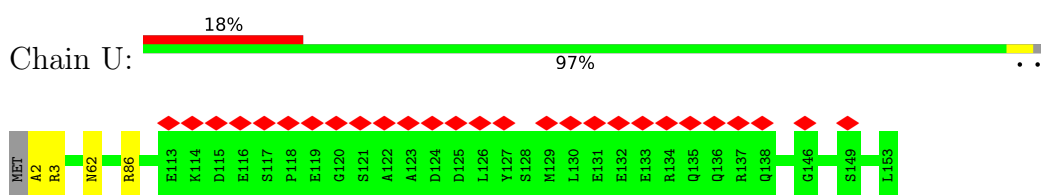
• Molecule 27: 39S ribosomal protein L21, mitochondrial



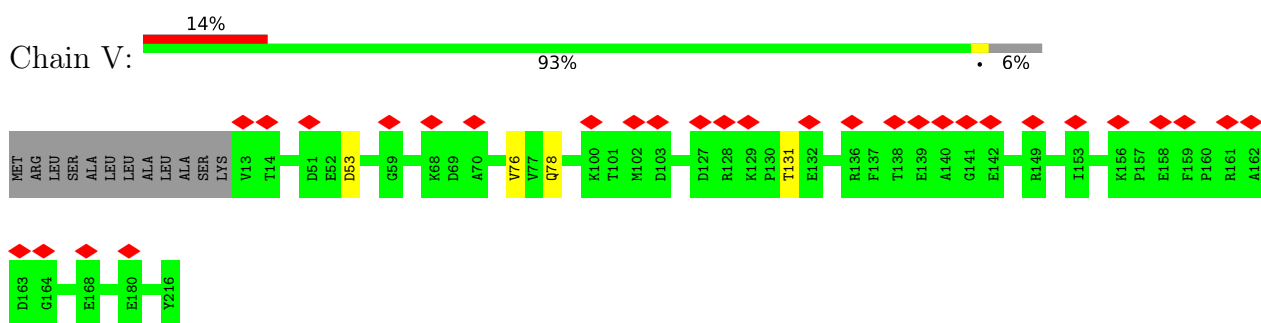
• Molecule 28: 39S ribosomal protein L22, mitochondrial



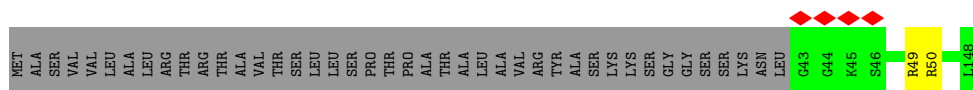
• Molecule 29: 39S ribosomal protein L23, mitochondrial



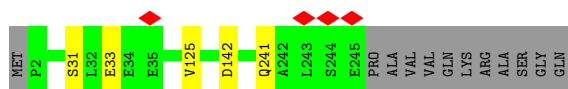
• Molecule 30: 39S ribosomal protein L24, mitochondrial



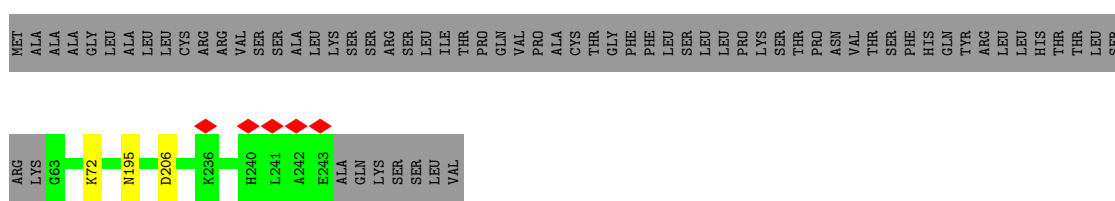
• Molecule 31: 39S ribosomal protein L27, mitochondrial



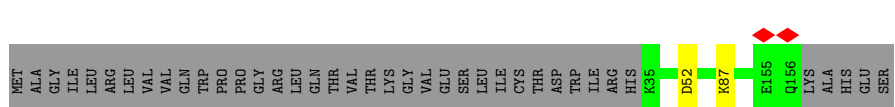
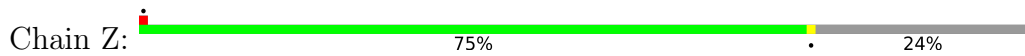
• Molecule 32: 39S ribosomal protein L28, mitochondrial



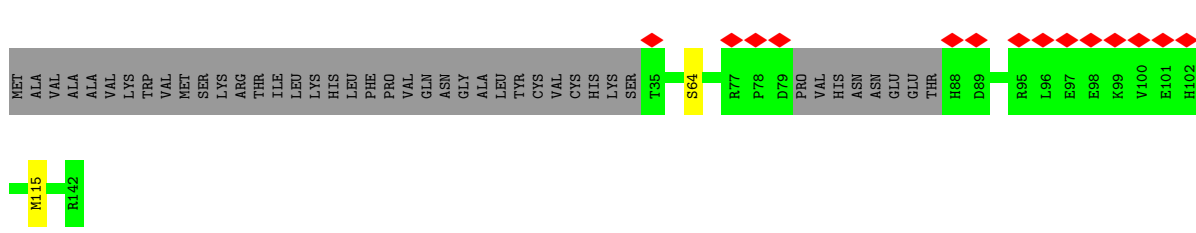
• Molecule 33: 39S ribosomal protein L47, mitochondrial



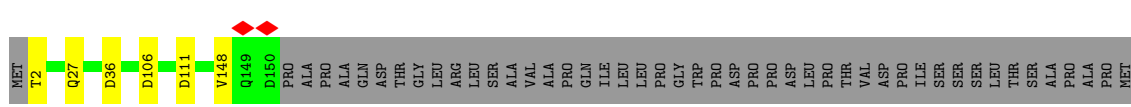
• Molecule 34: 39S ribosomal protein L30, mitochondrial



• Molecule 35: 39S ribosomal protein L42, mitochondrial

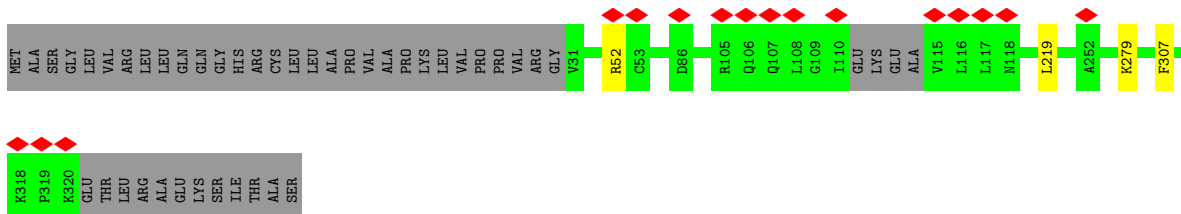
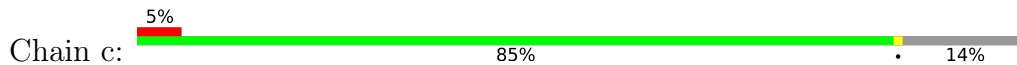


• Molecule 36: 39S ribosomal protein L43, mitochondrial

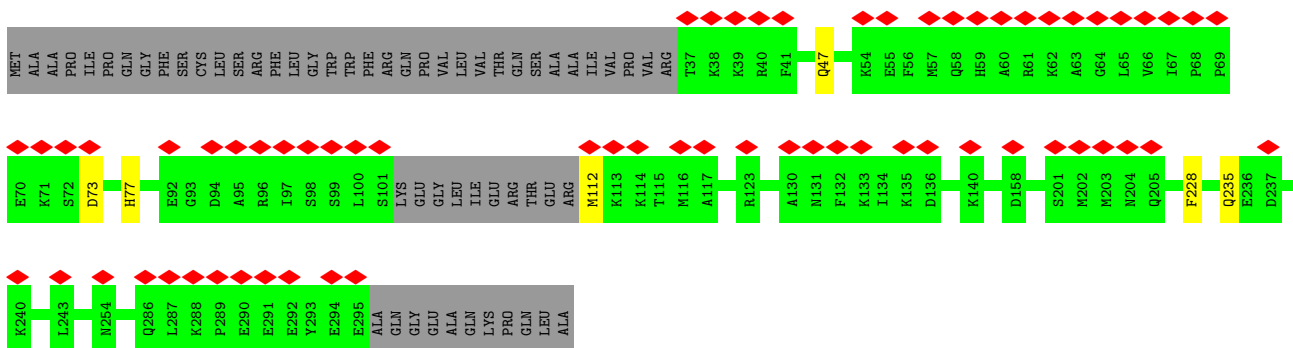
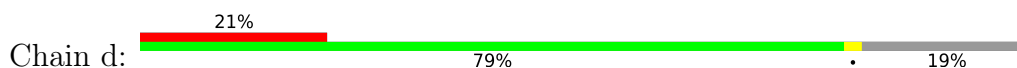


LEU
SER
ALA
VAL
SER
CYS
LEU
PRO
ILE
VAL
PRO
ALA
LEU
THR
THR
VAL
CYS
SER
ALA

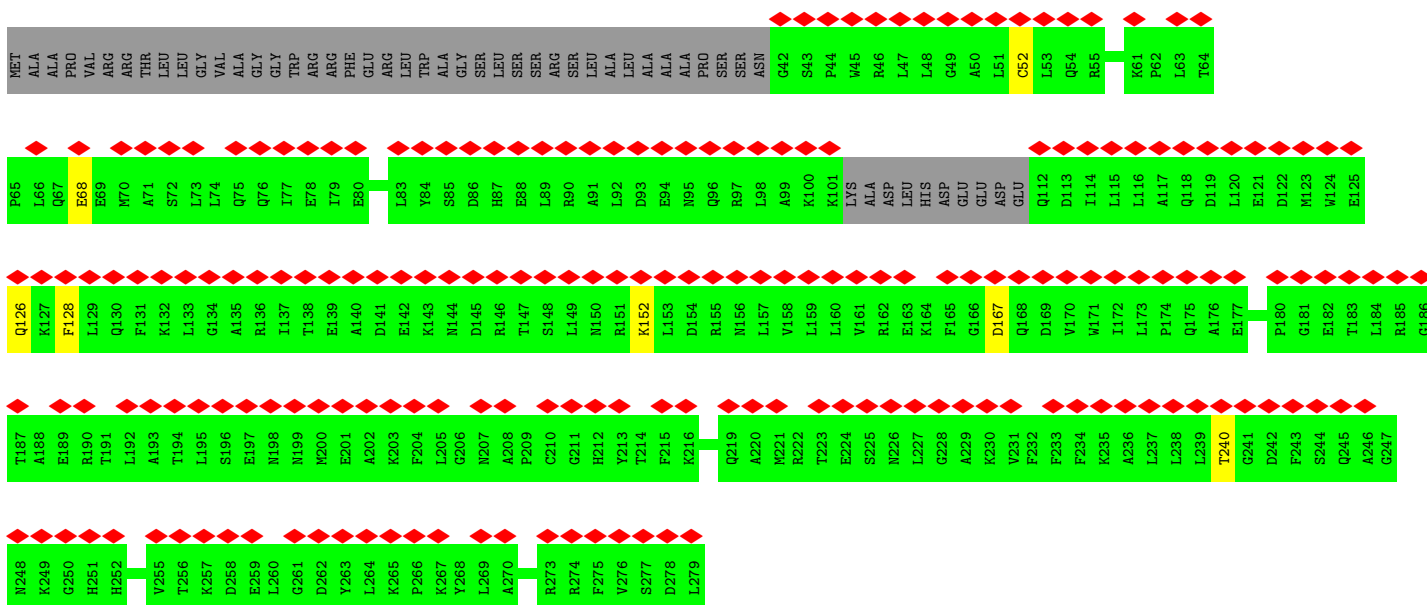
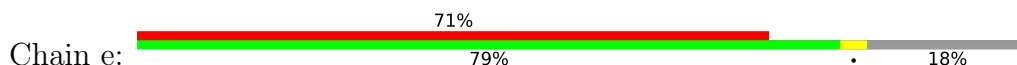
• Molecule 37: 39S ribosomal protein L44, mitochondrial

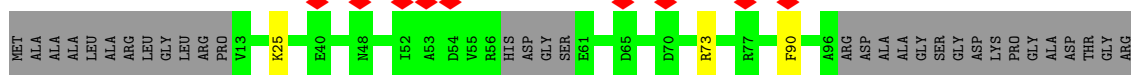


• Molecule 38: 39S ribosomal protein L45, mitochondrial

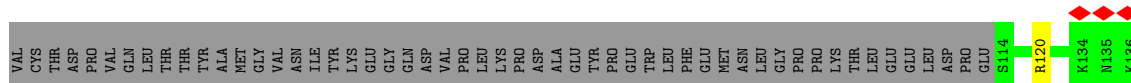
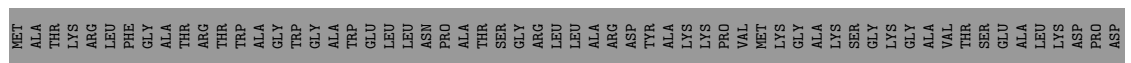


• Molecule 39: 39S ribosomal protein L46, mitochondrial

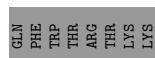
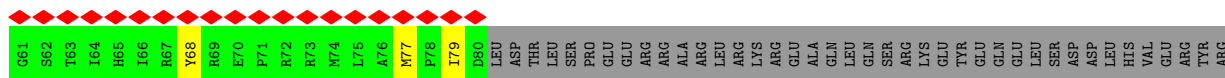
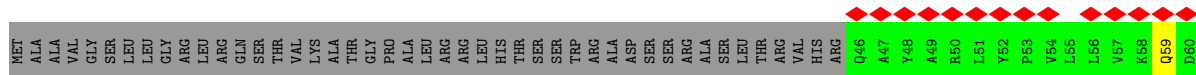




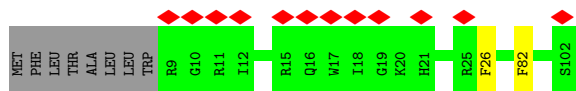
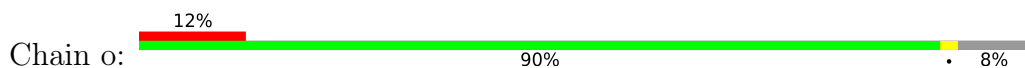
• Molecule 46: 39S ribosomal protein L54, mitochondrial



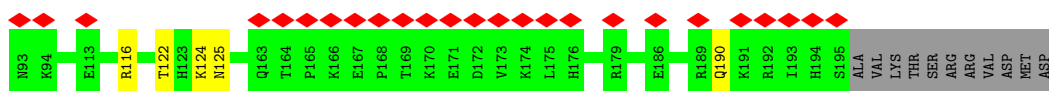
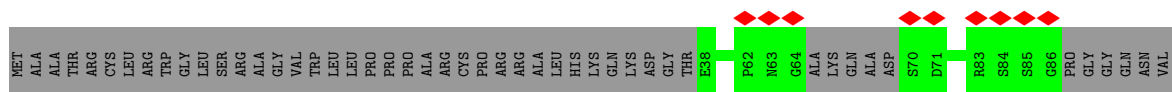
• Molecule 47: 39S ribosomal protein L55, mitochondrial

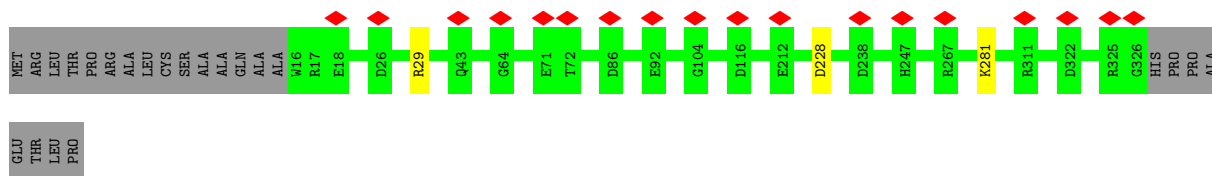


• Molecule 48: Ribosomal protein 63, mitochondrial



• Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68901	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	6.009	Depositor
Minimum map value	-2.665	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.204	Depositor
Recommended contour level	0.814	Depositor
Map size (Å)	518.4, 518.4, 518.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SAC, THC, SAM, PM8, ZN, MG, AYA, GNP, FES

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	0	0.24	0/913	0.50	0/1224
2	1	0.24	0/460	0.55	0/610
3	2	0.23	0/383	0.52	0/507
4	3	0.23	0/853	0.51	0/1136
5	4	0.24	0/341	0.57	0/451
6	5	0.24	0/3305	0.45	0/4502
7	6	0.24	0/3043	0.49	0/4140
8	7	0.24	0/2447	0.44	0/3310
9	8	0.25	0/880	0.52	0/1188
10	9	0.26	0/1025	0.48	0/1379
11	A	0.19	0/33679	0.76	16/52392 (0.0%)
12	B	0.30	1/1700 (0.1%)	0.73	0/2641
13	D	0.25	0/1910	0.55	0/2569
14	E	0.24	0/2475	0.44	0/3355
15	F	0.24	0/2090	0.48	0/2842
16	H	0.23	0/816	0.53	0/1097
17	I	0.26	0/1368	0.54	0/1849
18	J	0.24	0/1054	0.50	0/1419
19	K	0.24	0/1490	0.46	0/2021
20	L	0.24	0/905	0.53	0/1218
21	M	0.25	0/2381	0.50	0/3212
22	N	0.25	0/1624	0.52	0/2185
23	O	0.23	0/1283	0.51	0/1727
24	P	0.24	0/1199	0.53	0/1623
25	Q	0.24	0/1884	0.49	0/2535
26	R	0.24	0/1175	0.50	0/1572
27	S	0.24	0/1320	0.49	0/1789
28	T	0.25	0/1403	0.47	0/1886
29	U	0.25	0/1274	0.51	0/1723
30	V	0.24	0/1712	0.50	0/2322
31	W	0.24	0/857	0.48	0/1155
32	X	0.24	0/2099	0.44	0/2837

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.23	0/1593	0.49	0/2136
34	Z	0.23	0/1021	0.46	0/1378
35	a	0.24	0/866	0.49	0/1174
36	b	0.24	0/1203	0.53	0/1627
37	c	0.24	0/2347	0.45	0/3171
38	d	0.25	0/2095	0.47	0/2834
39	e	0.24	0/1885	0.47	0/2542
40	f	0.24	0/1216	0.45	0/1638
41	g	0.25	0/1151	0.50	0/1569
42	h	0.24	0/918	0.47	0/1249
43	i	0.24	0/850	0.50	0/1135
44	j	0.24	0/737	0.48	0/992
45	k	0.25	0/635	0.52	0/855
46	l	0.22	0/226	0.56	0/299
47	m	0.25	0/298	0.59	0/402
48	o	0.23	0/819	0.52	0/1097
49	p	0.23	0/1223	0.50	0/1641
50	q	0.24	0/1208	0.51	0/1633
51	r	0.25	0/1238	0.53	0/1676
52	s	0.24	0/3239	0.48	0/4400
53	u	0.24	0/1069	0.48	0/1447
54	v	0.24	0/597	0.59	0/796
55	w	0.25	0/647	0.44	0/871
56	x	0.24	0/2737	0.46	0/3714
57	y	0.24	0/2011	0.47	0/2702
58	z	0.24	0/2484	0.49	0/3349
All	All	0.23	1/113661 (0.0%)	0.60	16/160743 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
9	8	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	1602	C	OP3-P	-10.57	1.48	1.61

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	1711	C	C2-N1-C1'	8.13	127.74	118.80
11	A	1711	C	N1-C2-O2	8.06	123.74	118.90
11	A	2840	C	C2-N1-C1'	7.37	126.91	118.80
11	A	1728	U	N3-C4-O4	7.33	124.53	119.40
11	A	1711	C	N3-C2-O2	-6.50	117.35	121.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	8	169	PHE	Peptide

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	
1	0	108/188 (57%)	108 (100%)	0	0	100	100
2	1	53/65 (82%)	52 (98%)	1 (2%)	0	100	100
3	2	44/92 (48%)	44 (100%)	0	0	100	100
4	3	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
5	4	35/103 (34%)	35 (100%)	0	0	100	100
6	5	392/423 (93%)	383 (98%)	9 (2%)	0	100	100
7	6	352/380 (93%)	342 (97%)	10 (3%)	0	100	100
8	7	292/338 (86%)	283 (97%)	9 (3%)	0	100	100
9	8	100/206 (48%)	96 (96%)	4 (4%)	0	100	100
10	9	122/137 (89%)	119 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	D	238/305 (78%)	235 (99%)	3 (1%)	0	100	100
14	E	303/348 (87%)	298 (98%)	5 (2%)	0	100	100
15	F	250/311 (80%)	246 (98%)	4 (2%)	0	100	100
16	H	95/267 (36%)	95 (100%)	0	0	100	100
17	I	163/261 (62%)	151 (93%)	11 (7%)	1 (1%)	25	64
18	J	133/192 (69%)	120 (90%)	13 (10%)	0	100	100
19	K	175/178 (98%)	173 (99%)	2 (1%)	0	100	100
20	L	113/145 (78%)	111 (98%)	2 (2%)	0	100	100
21	M	289/296 (98%)	288 (100%)	1 (0%)	0	100	100
22	N	190/251 (76%)	181 (95%)	8 (4%)	1 (0%)	29	68
23	O	152/175 (87%)	150 (99%)	2 (1%)	0	100	100
24	P	142/180 (79%)	142 (100%)	0	0	100	100
25	Q	219/292 (75%)	216 (99%)	3 (1%)	0	100	100
26	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
27	S	159/205 (78%)	158 (99%)	1 (1%)	0	100	100
28	T	164/206 (80%)	162 (99%)	2 (1%)	0	100	100
29	U	150/153 (98%)	148 (99%)	2 (1%)	0	100	100
30	V	202/216 (94%)	200 (99%)	2 (1%)	0	100	100
31	W	104/148 (70%)	102 (98%)	2 (2%)	0	100	100
32	X	242/256 (94%)	239 (99%)	3 (1%)	0	100	100
33	Y	179/250 (72%)	178 (99%)	1 (1%)	0	100	100
34	Z	120/161 (74%)	118 (98%)	2 (2%)	0	100	100
35	a	96/142 (68%)	95 (99%)	1 (1%)	0	100	100
36	b	147/215 (68%)	144 (98%)	3 (2%)	0	100	100
37	c	282/332 (85%)	278 (99%)	4 (1%)	0	100	100
38	d	245/306 (80%)	239 (98%)	6 (2%)	0	100	100
39	e	224/279 (80%)	217 (97%)	7 (3%)	0	100	100
40	f	146/212 (69%)	139 (95%)	7 (5%)	0	100	100
41	g	132/166 (80%)	131 (99%)	1 (1%)	0	100	100
42	h	108/158 (68%)	106 (98%)	2 (2%)	0	100	100
43	i	95/128 (74%)	95 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	j	88/123 (72%)	87 (99%)	1 (1%)	0	100	100
45	k	76/112 (68%)	74 (97%)	2 (3%)	0	100	100
46	l	21/138 (15%)	21 (100%)	0	0	100	100
47	m	33/128 (26%)	32 (97%)	1 (3%)	0	100	100
48	o	92/102 (90%)	92 (100%)	0	0	100	100
49	p	141/206 (68%)	137 (97%)	4 (3%)	0	100	100
50	q	139/222 (63%)	139 (100%)	0	0	100	100
51	r	140/196 (71%)	132 (94%)	8 (6%)	0	100	100
52	s	382/439 (87%)	377 (99%)	5 (1%)	0	100	100
53	u	124/234 (53%)	121 (98%)	3 (2%)	0	100	100
54	v	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
55	w	77/156 (49%)	73 (95%)	4 (5%)	0	100	100
56	x	334/384 (87%)	323 (97%)	11 (3%)	0	100	100
57	y	242/381 (64%)	240 (99%)	2 (1%)	0	100	100
58	z	309/334 (92%)	301 (97%)	8 (3%)	0	100	100
All	All	9251/12228 (76%)	9060 (98%)	189 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	N	66	PRO
17	I	66	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	99/164 (60%)	96 (97%)	3 (3%)	41	75
2	1	52/60 (87%)	51 (98%)	1 (2%)	57	84
3	2	40/72 (56%)	40 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	88/166 (53%)	88 (100%)	0	100	100
5	4	36/89 (40%)	36 (100%)	0	100	100
6	5	353/368 (96%)	347 (98%)	6 (2%)	60	85
7	6	313/332 (94%)	308 (98%)	5 (2%)	62	86
8	7	270/303 (89%)	268 (99%)	2 (1%)	84	94
9	8	93/190 (49%)	88 (95%)	5 (5%)	22	57
10	9	104/112 (93%)	103 (99%)	1 (1%)	76	91
13	D	194/245 (79%)	192 (99%)	2 (1%)	76	91
14	E	260/290 (90%)	257 (99%)	3 (1%)	71	90
15	F	219/262 (84%)	216 (99%)	3 (1%)	67	88
16	H	88/228 (39%)	86 (98%)	2 (2%)	50	80
17	I	153/232 (66%)	143 (94%)	10 (6%)	17	50
18	J	112/150 (75%)	106 (95%)	6 (5%)	22	57
19	K	154/155 (99%)	149 (97%)	5 (3%)	39	74
20	L	98/124 (79%)	98 (100%)	0	100	100
21	M	246/249 (99%)	242 (98%)	4 (2%)	62	86
22	N	167/211 (79%)	163 (98%)	4 (2%)	49	79
23	O	134/150 (89%)	132 (98%)	2 (2%)	65	87
24	P	126/155 (81%)	121 (96%)	5 (4%)	31	68
25	Q	203/256 (79%)	200 (98%)	3 (2%)	65	87
26	R	118/126 (94%)	118 (100%)	0	100	100
27	S	146/180 (81%)	142 (97%)	4 (3%)	44	77
28	T	146/176 (83%)	144 (99%)	2 (1%)	67	88
29	U	134/135 (99%)	131 (98%)	3 (2%)	52	81
30	V	182/191 (95%)	178 (98%)	4 (2%)	52	81
31	W	86/119 (72%)	84 (98%)	2 (2%)	50	80
32	X	220/229 (96%)	215 (98%)	5 (2%)	50	80
33	Y	163/223 (73%)	160 (98%)	3 (2%)	59	85
34	Z	113/147 (77%)	111 (98%)	2 (2%)	59	85
35	a	96/133 (72%)	94 (98%)	2 (2%)	53	82
36	b	130/185 (70%)	125 (96%)	5 (4%)	33	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	c	251/288 (87%)	247 (98%)	4 (2%)	62	86
38	d	228/274 (83%)	222 (97%)	6 (3%)	46	78
39	e	198/236 (84%)	191 (96%)	7 (4%)	36	71
40	f	133/188 (71%)	127 (96%)	6 (4%)	27	64
41	g	124/148 (84%)	122 (98%)	2 (2%)	62	86
42	h	104/148 (70%)	103 (99%)	1 (1%)	76	91
43	i	86/110 (78%)	85 (99%)	1 (1%)	71	90
44	j	72/97 (74%)	70 (97%)	2 (3%)	43	77
45	k	71/90 (79%)	68 (96%)	3 (4%)	30	66
46	l	23/116 (20%)	22 (96%)	1 (4%)	29	66
47	m	31/113 (27%)	27 (87%)	4 (13%)	4	19
48	o	80/87 (92%)	78 (98%)	2 (2%)	47	79
49	p	135/181 (75%)	130 (96%)	5 (4%)	34	70
50	q	119/178 (67%)	116 (98%)	3 (2%)	47	79
51	r	133/169 (79%)	130 (98%)	3 (2%)	50	80
52	s	340/381 (89%)	331 (97%)	9 (3%)	46	78
53	u	118/200 (59%)	114 (97%)	4 (3%)	37	72
54	v	59/60 (98%)	57 (97%)	2 (3%)	37	72
55	w	73/136 (54%)	66 (90%)	7 (10%)	8	32
56	x	293/328 (89%)	283 (97%)	10 (3%)	37	72
57	y	226/350 (65%)	220 (97%)	6 (3%)	44	77
58	z	270/287 (94%)	267 (99%)	3 (1%)	73	90
All	All	8303/10572 (78%)	8108 (98%)	195 (2%)	53	80

5 of 195 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	e	68	GLU
49	p	116	ARG
39	e	167	ASP
43	i	42	LYS
50	q	141	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
22	N	98	HIS
56	x	193	GLN
38	d	211	GLN
57	y	110	ASN
54	v	42	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1401/1603 (87%)	260 (18%)	5 (0%)
12	B	71/72 (98%)	11 (15%)	0
All	All	1472/1675 (87%)	271 (18%)	5 (0%)

5 of 271 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	1672	C
11	A	1681	G
11	A	1689	C
11	A	1694	U
11	A	1700	U

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	2030	U
11	A	2186	C
11	A	2245	A
11	A	2530	A
11	A	2905	A

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

3 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
19	SAC	K	2	19	7,8,9	1.01	0	8,9,11	0.85	1 (12%)
29	AYA	U	2	29	6,7,8	1.27	1 (16%)	5,8,10	1.18	1 (20%)
36	THC	b	2	36	8,9,10	1.07	1 (12%)	9,11,13	0.78	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
19	SAC	K	2	19	-	3/7/8/10	-
29	AYA	U	2	29	-	0/4/6/8	-
36	THC	b	2	36	-	0/8/10/12	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	U	2	AYA	CA-N	-2.44	1.44	1.46
36	b	2	THC	CA-N1	-2.15	1.43	1.46

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	U	2	AYA	CB-CA-N	2.42	112.30	109.61
19	K	2	SAC	OG-CB-CA	-2.01	105.84	110.97

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	K	2	SAC	O-C-CA-CB
19	K	2	SAC	N-CA-CB-OG
19	K	2	SAC	C-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 44 ligands modelled in this entry, 40 are monoatomic - leaving 4 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
64	GNP	z	401	60	29,34,34	1.60	7 (24%)	33,54,54	2.13	6 (18%)
63	SAM	x	401	-	24,29,29	1.21	3 (12%)	23,42,42	1.58	4 (17%)
62	PM8	w	200	55	25,31,31	1.90	6 (24%)	30,38,38	1.75	6 (20%)
61	FES	r	201	51	0,4,4	-	-	-	-	-

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
64	GNP	z	401	60	-	4/14/38/38	0/3/3/3
63	SAM	x	401	-	-	4/12/33/33	0/3/3/3
62	PM8	w	200	55	-	13/36/38/38	-
61	FES	r	201	51	-	-	0/1/1/1

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	w	200	PM8	C34-N36	5.77	1.46	1.33
62	w	200	PM8	C39-N41	5.32	1.45	1.33
64	z	401	GNP	PB-O3A	4.29	1.64	1.59
63	x	401	SAM	C2-N3	4.01	1.38	1.32
64	z	401	GNP	C6-N1	3.09	1.38	1.33

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	z	401	GNP	C5-C6-N1	-8.42	111.92	123.43
62	w	200	PM8	C2-C1-S1	5.93	120.36	113.46
64	z	401	GNP	C2-N1-C6	5.84	125.21	115.93
63	x	401	SAM	N3-C2-N1	-5.31	120.38	128.68
62	w	200	PM8	O1-C1-C2	-3.40	119.97	123.99

There are no chirality outliers.

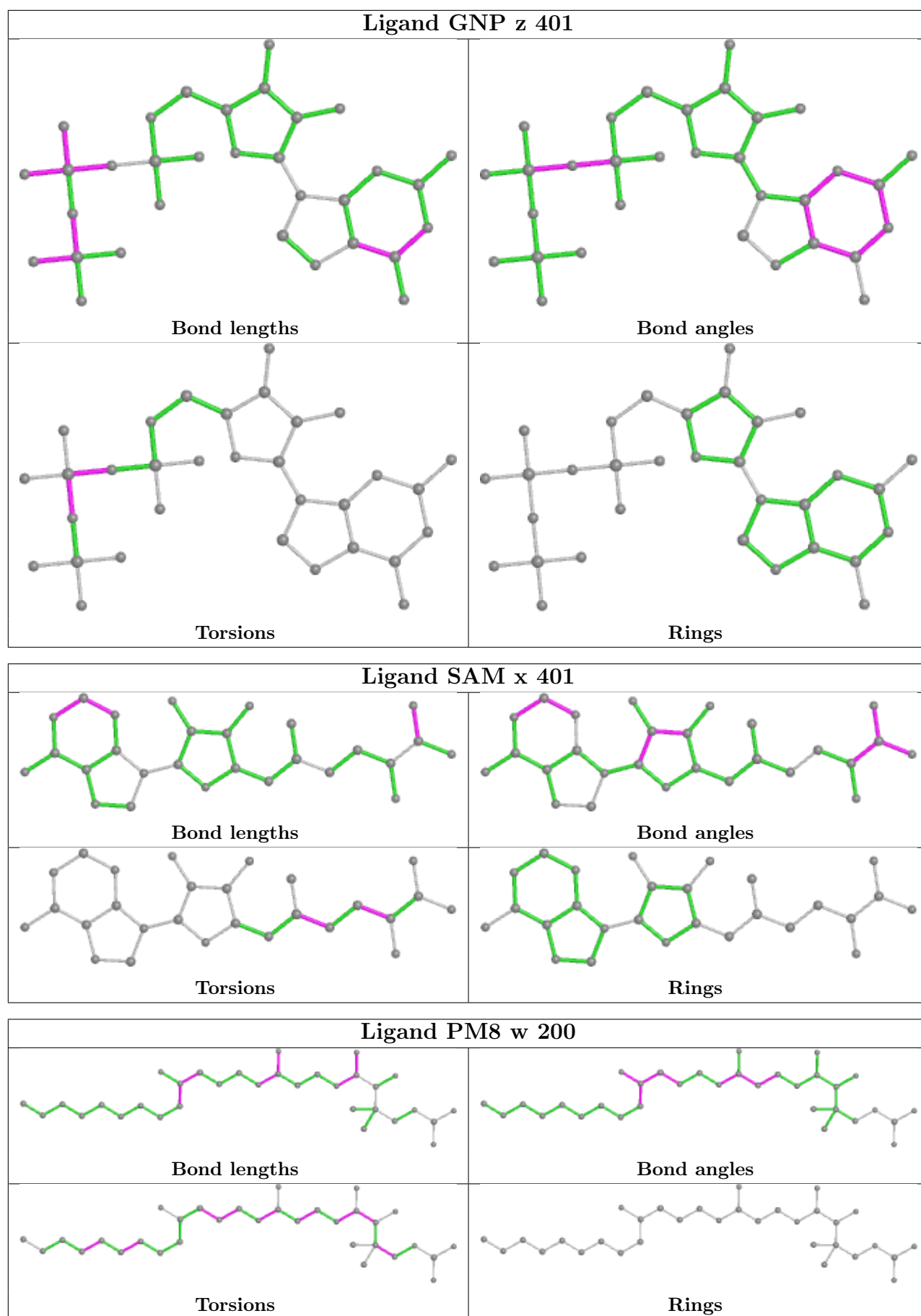
5 of 21 torsion outliers are listed below:

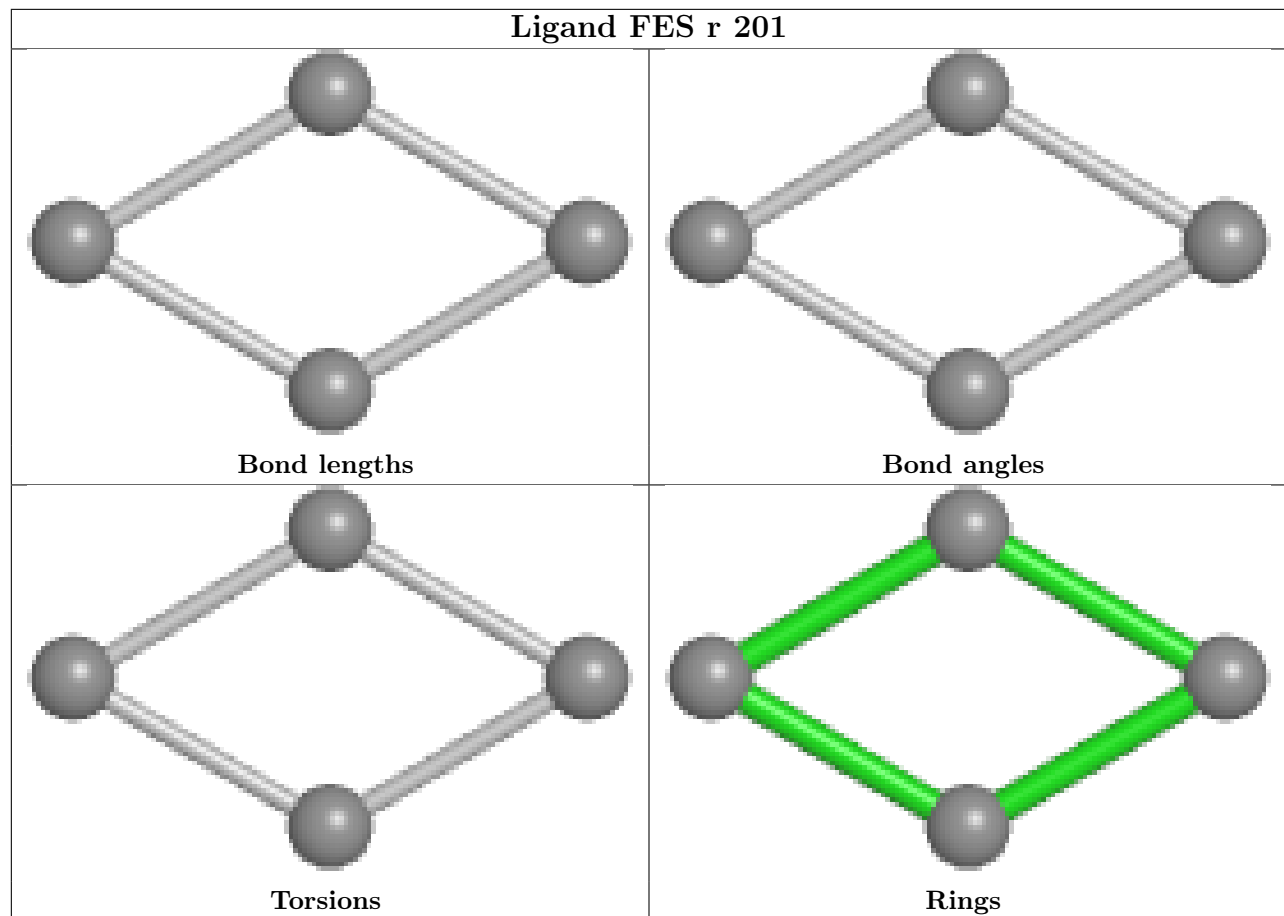
Mol	Chain	Res	Type	Atoms
62	w	200	PM8	O27-C28-C29-C32
62	w	200	PM8	C32-C34-N36-C37
62	w	200	PM8	N36-C37-C38-C39
62	w	200	PM8	N41-C42-C43-S1
62	w	200	PM8	C42-C43-S1-C1

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](#)

There are no chain breaks in this entry.

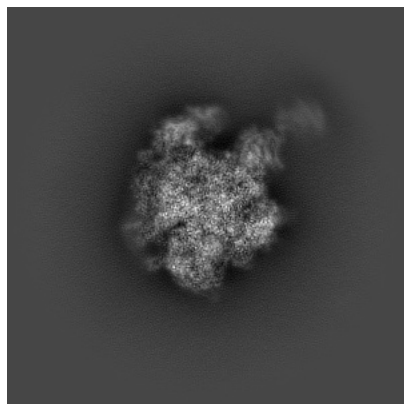
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17720. These allow visual inspection of the internal detail of the map and identification of artifacts.

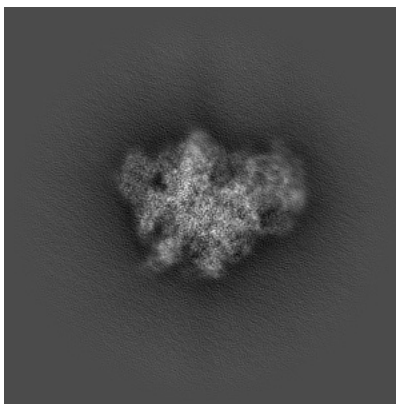
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

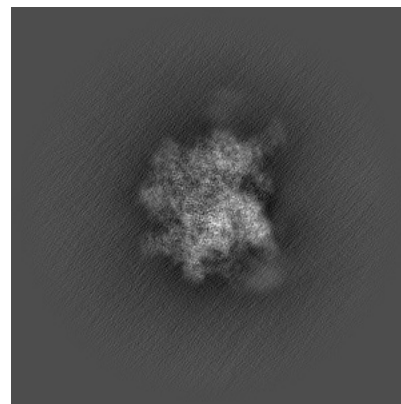
6.1.1 Primary map



X

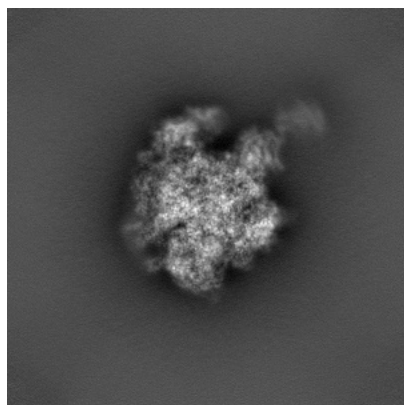


Y

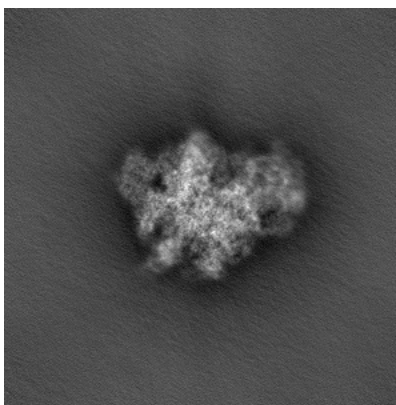


Z

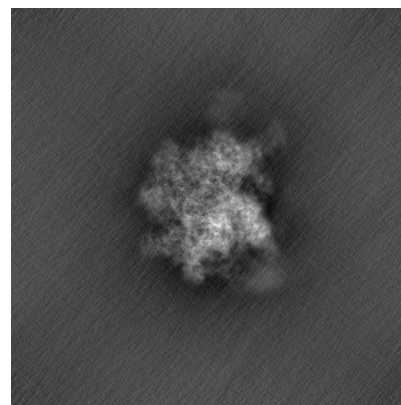
6.1.2 Raw map



X



Y

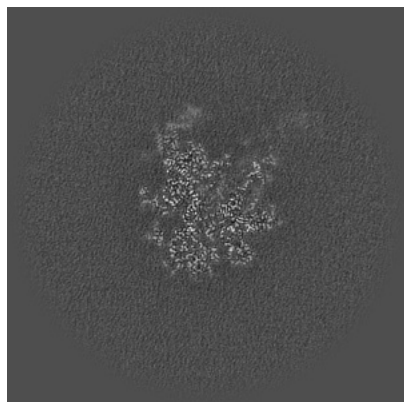


Z

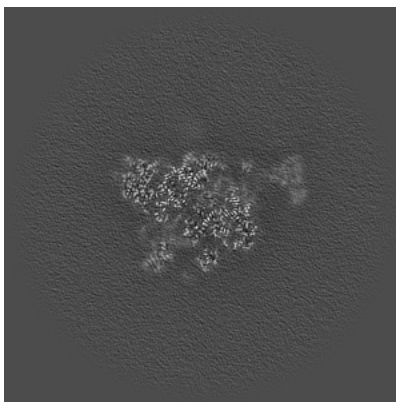
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

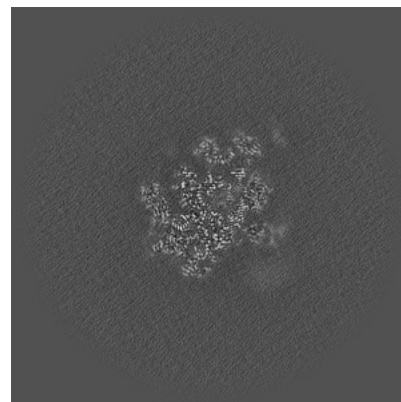
6.2.1 Primary map



X Index: 240

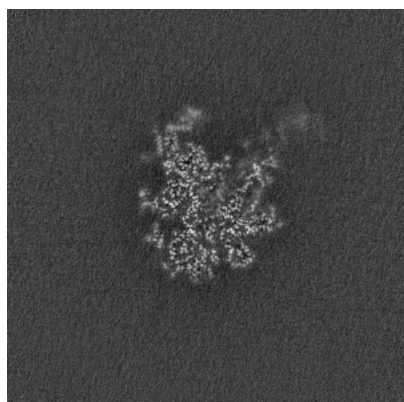


Y Index: 240

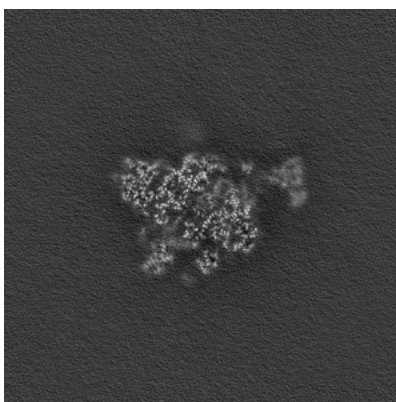


Z Index: 240

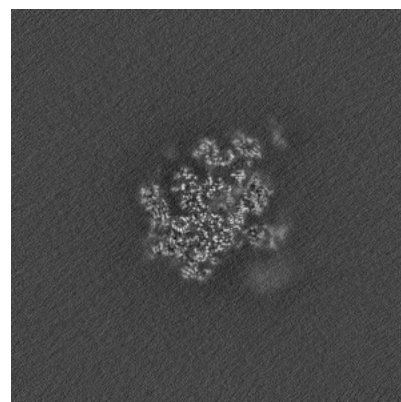
6.2.2 Raw map



X Index: 240



Y Index: 240

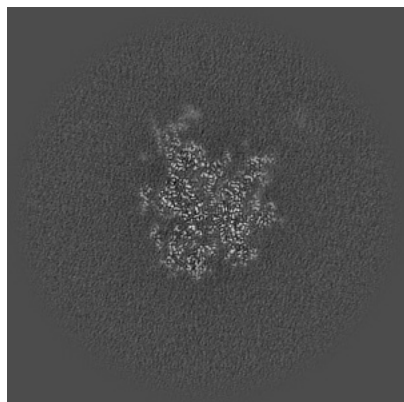


Z Index: 240

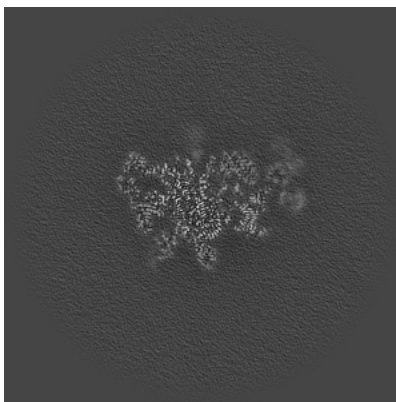
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

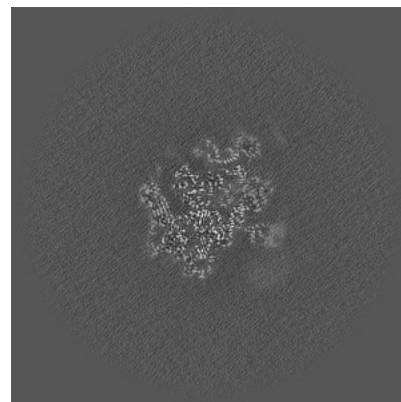
6.3.1 Primary map



X Index: 237

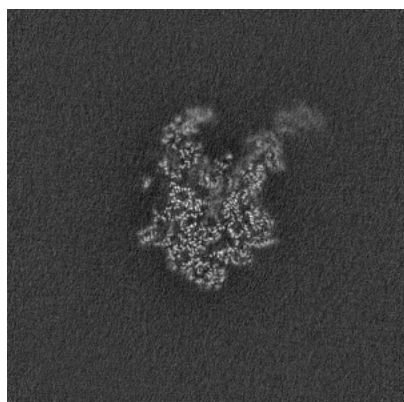


Y Index: 226

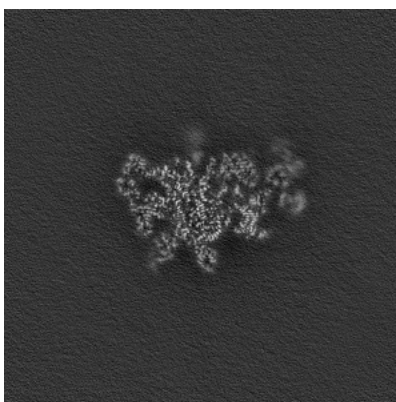


Z Index: 242

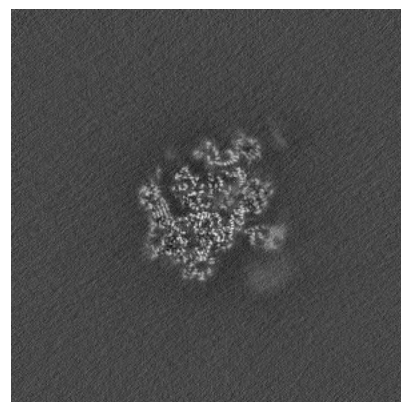
6.3.2 Raw map



X Index: 250



Y Index: 226

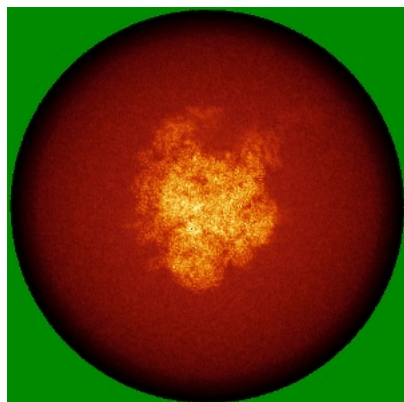


Z Index: 242

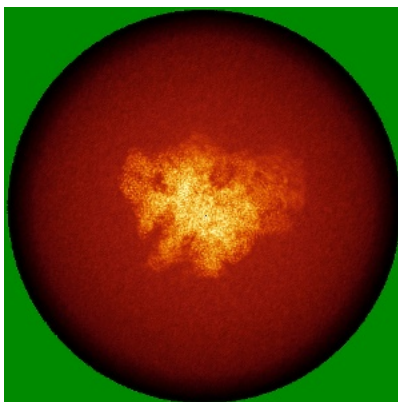
The images above show the largest variance slices of the map in three orthogonal directions.

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

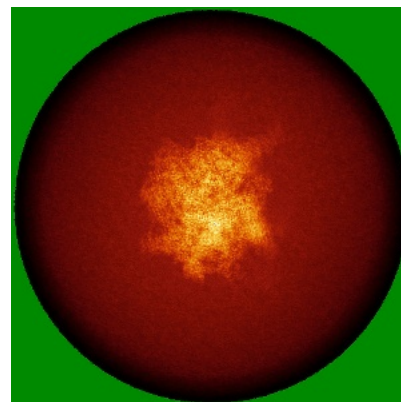
6.4.1 Primary map



X

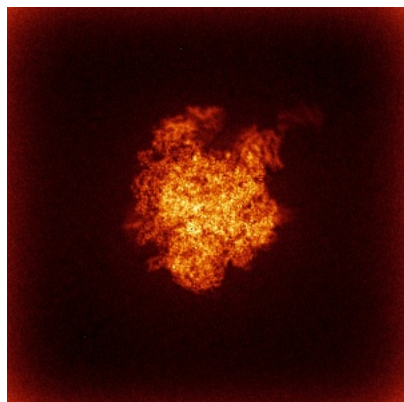


Y

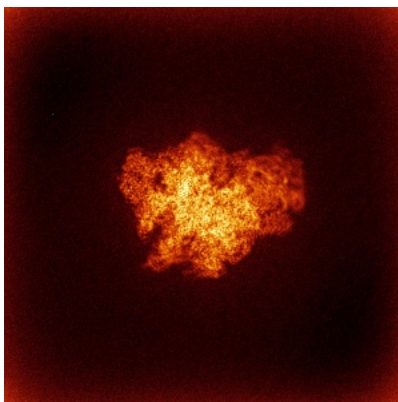


Z

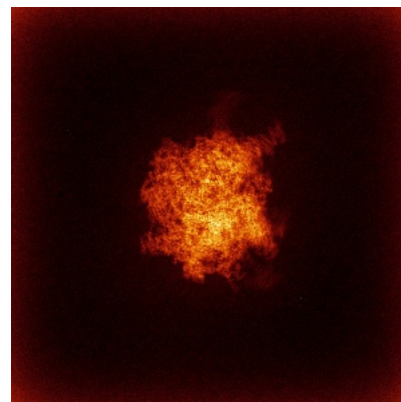
6.4.2 Raw map



X



Y

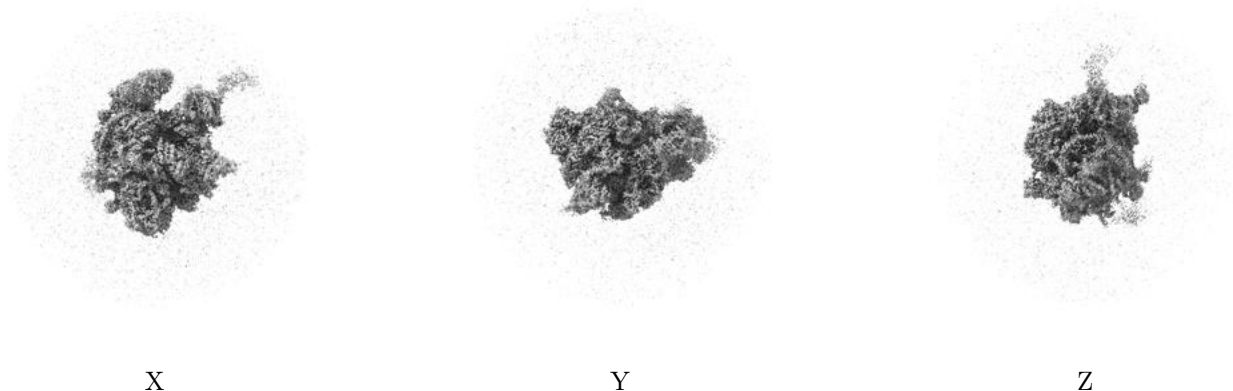


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

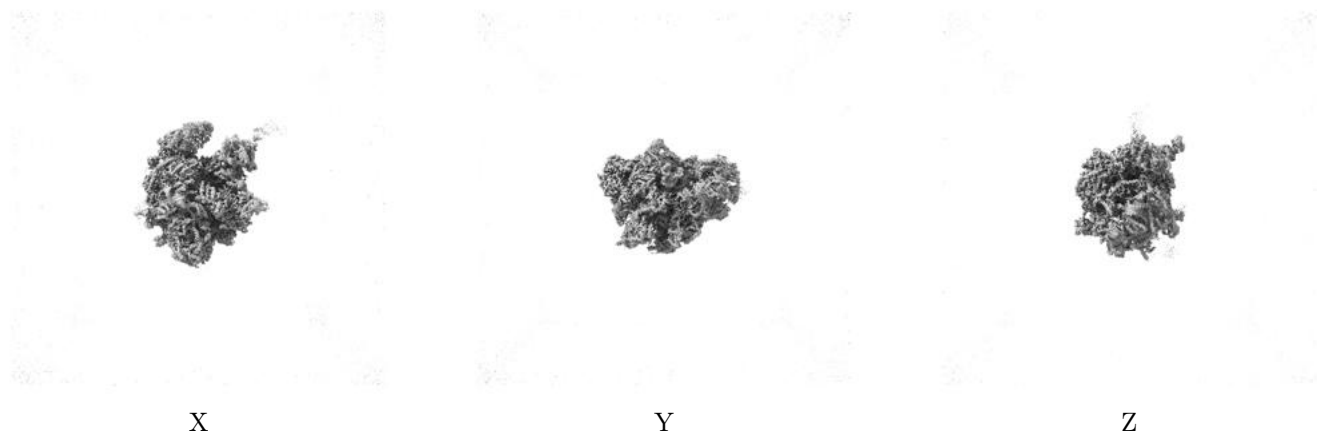
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.814. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 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.

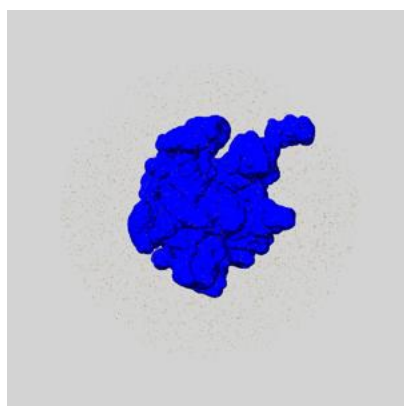
6.6 Mask visualisation [i](#)

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

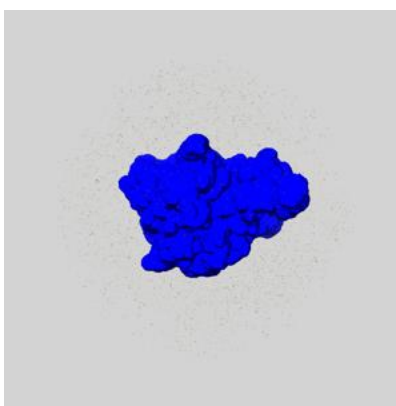
A mask typically either:

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

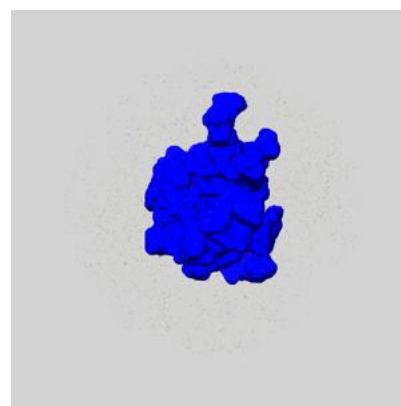
6.6.1 emd_17720_msk_1.map [i](#)



X



Y

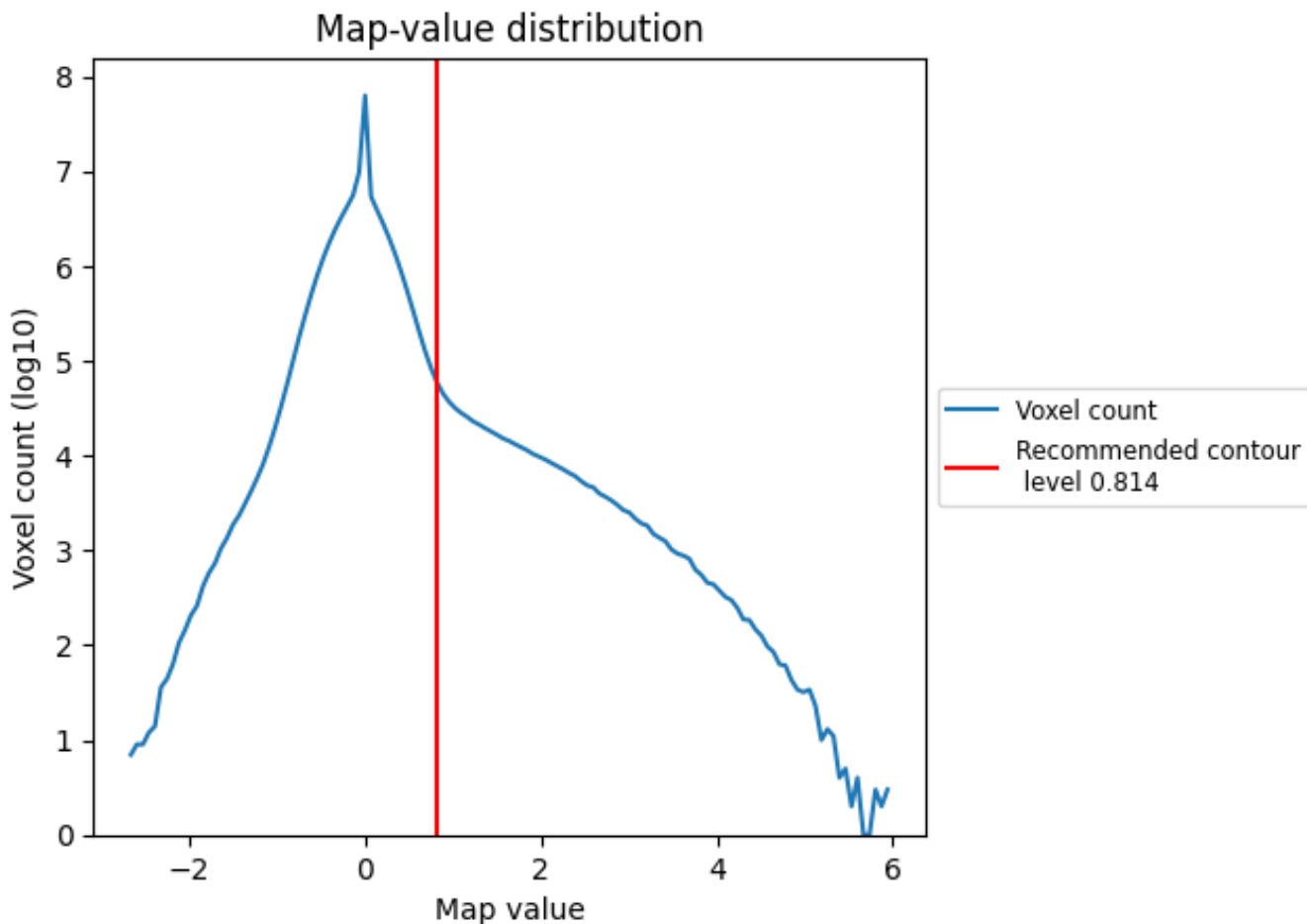


Z

7 Map analysis [i](#)

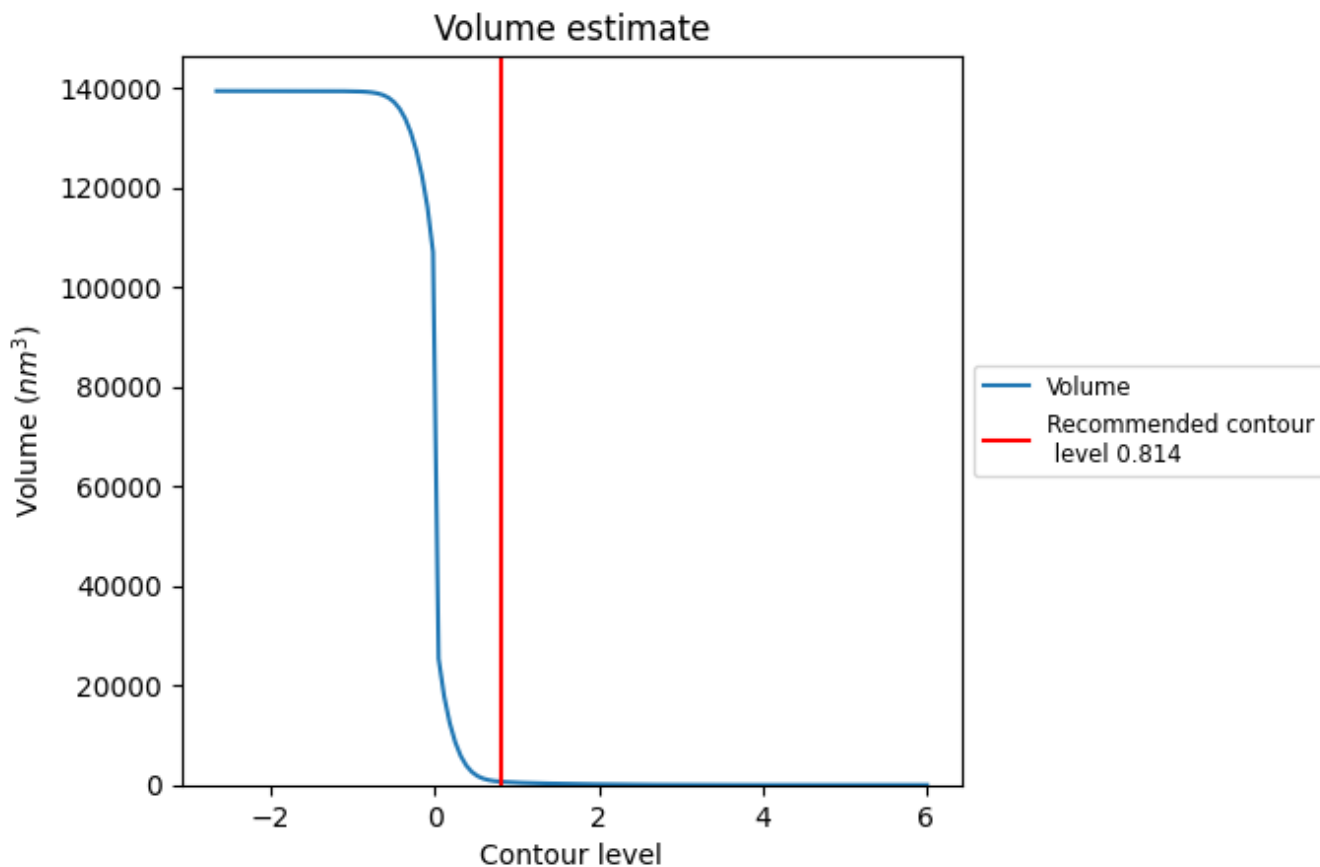
This section contains the results of statistical analysis of the map.

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.

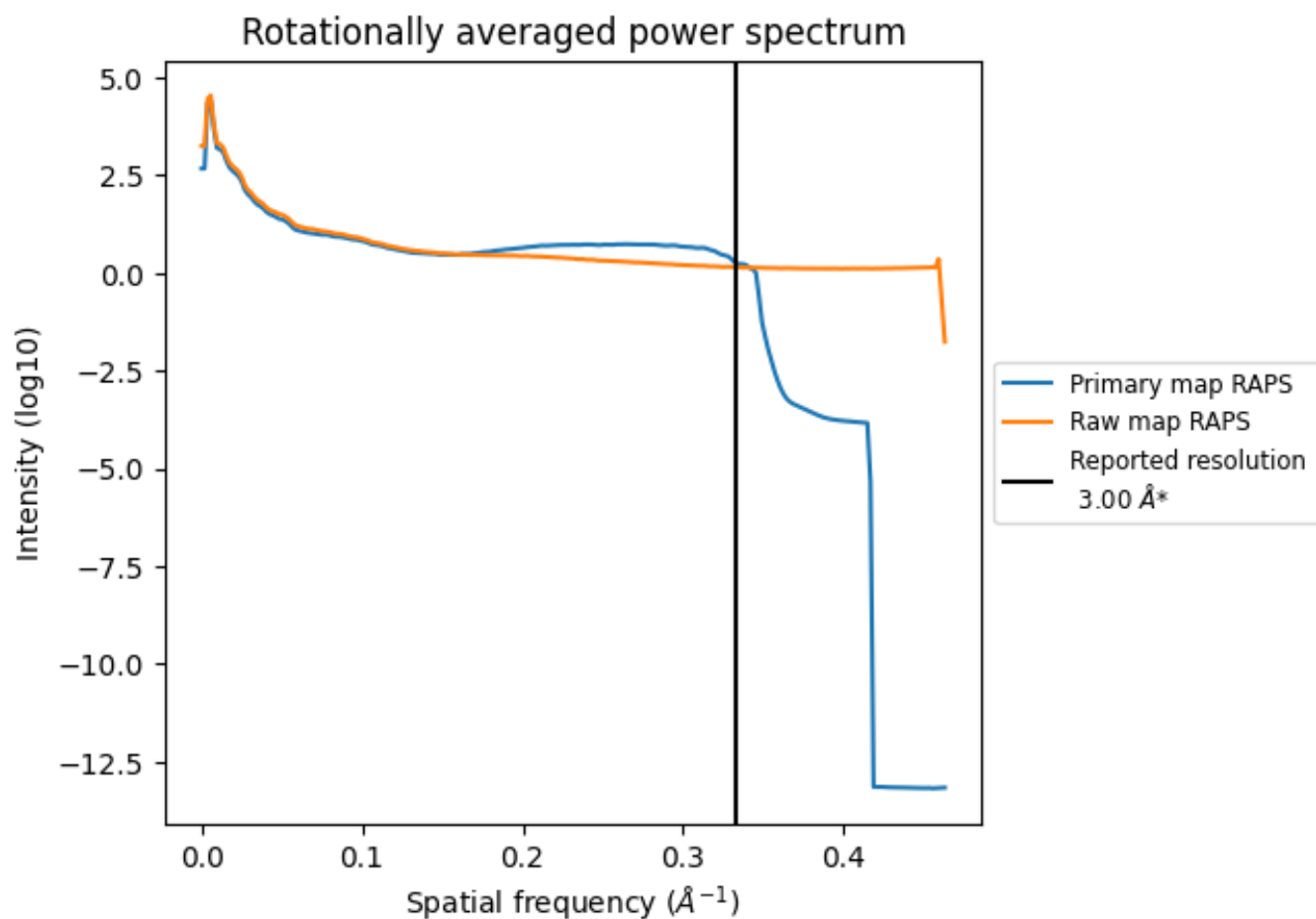
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 647 nm³; this corresponds to an approximate mass of 584 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](#)

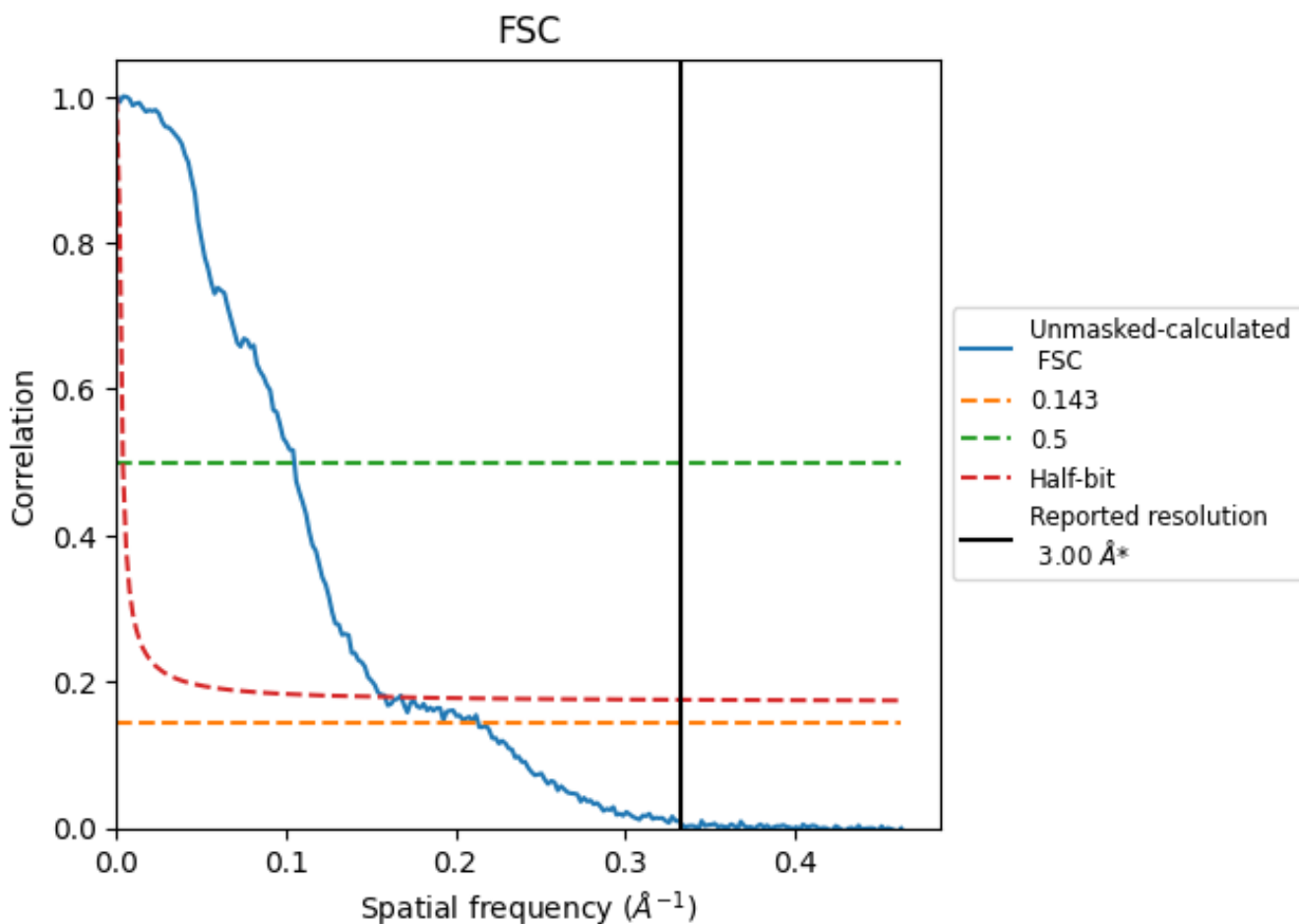


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 \AA^{-1}

8.2 Resolution estimates [i](#)

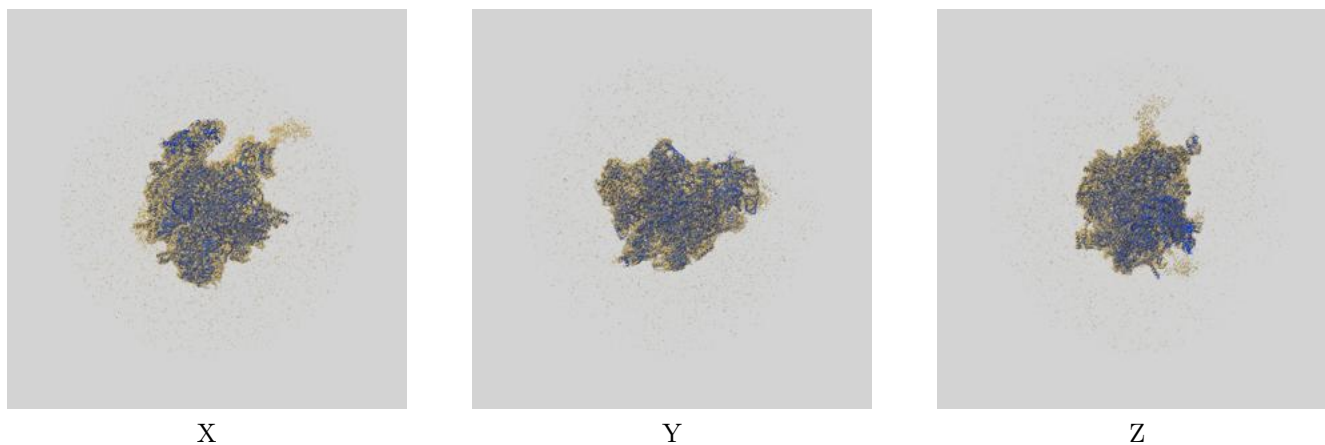
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.68	9.53	6.31

*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 4.68 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

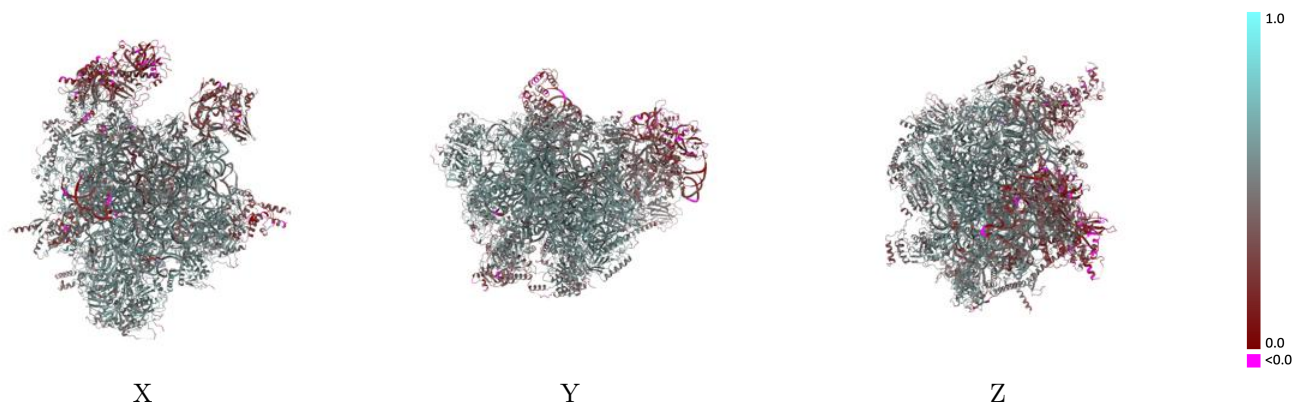
This section contains information regarding the fit between EMDB map EMD-17720 and PDB model 8QSJ. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



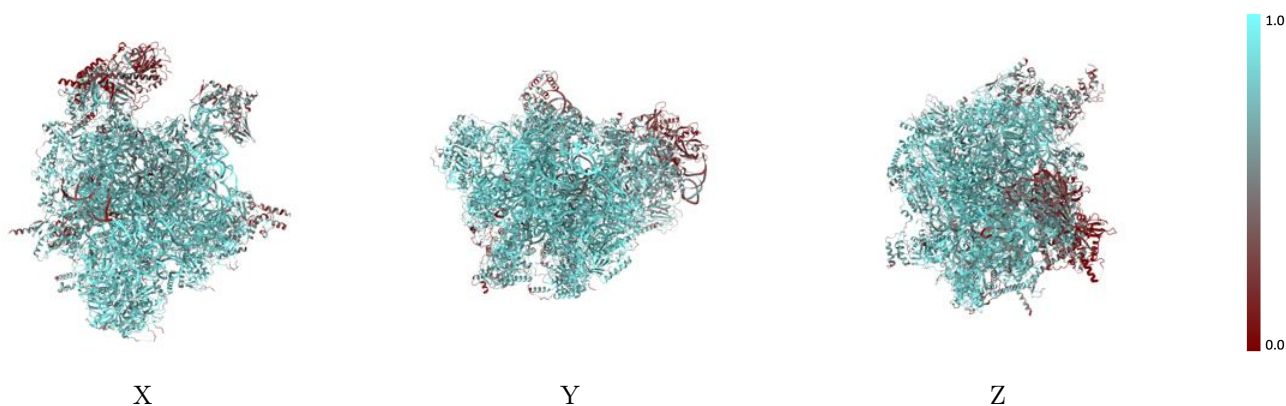
The images above show the 3D surface view of the map at the recommended contour level 0.814 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



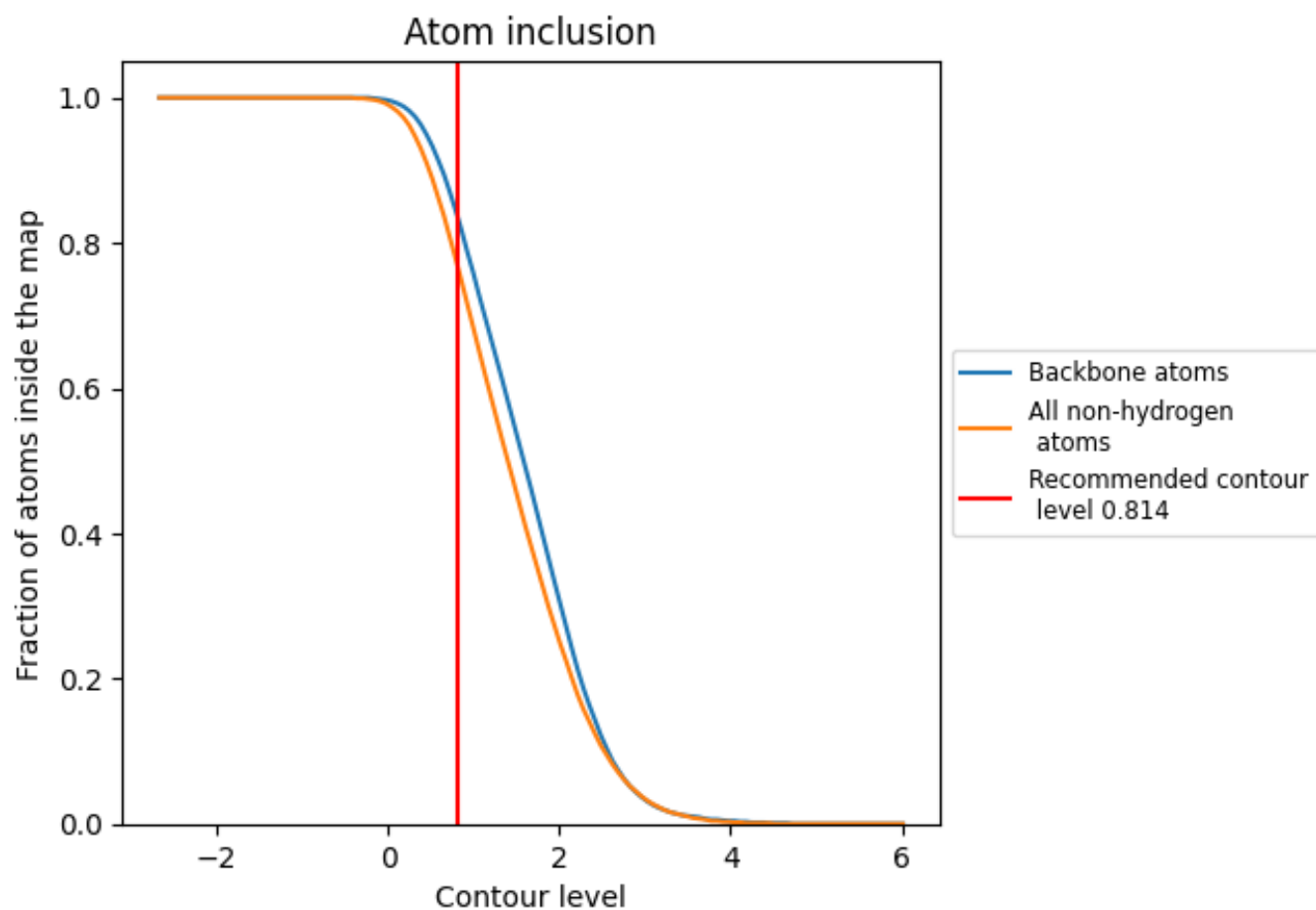
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.814).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

















































The table lists the average atom inclusion at the recommended contour level (0.814) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7680	 0.4930
0	 0.8060	 0.5410
1	 0.7600	 0.5180
2	 0.8970	 0.5980
3	 0.9240	 0.6070
4	 0.8650	 0.5570
5	 0.8100	 0.5290
6	 0.7070	 0.4530
7	 0.7230	 0.4500
8	 0.2770	 0.2360
9	 0.8000	 0.5130
A	 0.8780	 0.5350
B	 0.6300	 0.3020
D	 0.7990	 0.5340
E	 0.8500	 0.5550
F	 0.8420	 0.5390
H	 0.6910	 0.4750
I	 0.5260	 0.3510
J	 0.3570	 0.1980
K	 0.8710	 0.5760
L	 0.8170	 0.5460
M	 0.8470	 0.5590
N	 0.7100	 0.4730
O	 0.8620	 0.5680
P	 0.7210	 0.4550
Q	 0.8000	 0.5360
R	 0.8750	 0.5790
S	 0.8330	 0.5400
T	 0.8370	 0.5590
U	 0.7380	 0.5100
V	 0.6800	 0.4460
W	 0.8480	 0.5750
X	 0.7950	 0.5340
Y	 0.8210	 0.5340
Z	 0.8470	 0.5610



Continued on next page...

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Chain	Atom inclusion	Q-score
a	 0.7220	 0.4820
b	 0.8500	 0.5410
c	 0.7640	 0.4860
d	 0.5670	 0.3940
e	 0.1930	 0.1730
f	 0.3710	 0.2980
g	 0.8400	 0.5350
h	 0.6950	 0.4210
i	 0.8770	 0.5830
j	 0.7950	 0.5090
k	 0.6480	 0.3900
l	 0.6800	 0.3900
m	 0.1150	 0.1670
o	 0.7520	 0.5350
p	 0.6320	 0.4340
q	 0.6860	 0.4490
r	 0.8400	 0.5160
s	 0.8310	 0.5490
u	 0.6710	 0.4510
v	 0.5750	 0.3340
w	 0.3040	 0.2010
x	 0.6750	 0.4630
y	 0.6250	 0.4220
z	 0.7060	 0.4640