



wwPDB EM Validation Summary Report ⓘ

Jun 27, 2026 – 08:10 am BST

PDB ID : 9H55 / pdb_00009h55
EMDB ID : EMD-51877
Title : Assembly intermediate of human mitochondrial ribosome small subunit in complex with NOA1 and TFB1M (state N3)
Authors : Singh, V.; Shiriaev, D.; Khawaja, A.; Rorbach, J.
Deposited on : 2024-10-22
Resolution : 3.40 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:

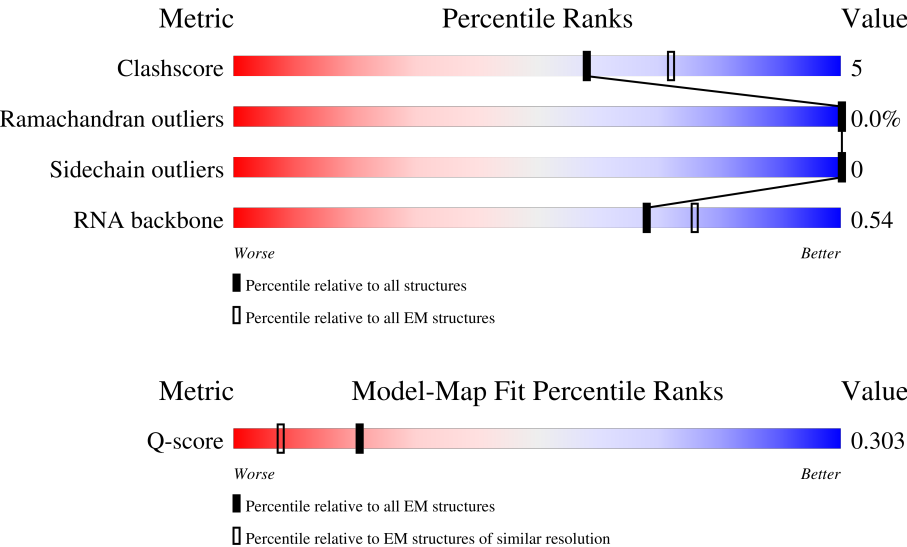
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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

Mol	Chain	Length	Quality of chain
1	A	955	20% 63% 23% 11%
2	B	296	68% 8% 24%
3	C	167	61% 65% 14% 21%

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Mol	Chain	Length	Quality of chain
4	D	430	
5	E	125	
6	F	242	
7	G	396	
8	H	201	
9	I	194	
10	J	138	
11	K	128	
12	L	257	
13	M	137	
14	N	130	
15	O	258	
16	P	142	
17	Q	87	
18	R	360	
19	S	190	
20	T	173	
21	U	205	
22	V	414	
23	W	187	
24	X	398	
25	Y	395	
26	Z	106	
27	0	215	
28	1	323	

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Mol	Chain	Length	Quality of chain
29	4	689	83% 74% 11% 15%
30	9	698	21% 46% 13% 41%
31	5	346	63% 73% 20% 8%
32	a	343	9% 8% 91%

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 129555 atoms, of which 60710 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	A	850	Total	C	H	N	O	P	0	0
			27223	8095	9165	3258	5855	850		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	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	C	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	D	332	Total	C	H	N	O	S	0	0
			5349	1660	2705	496	475	13		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	109	Total	C	H	N	O	S	0	0
			1747	544	882	158	159	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	201	Total	C	H	N	O	S	2	0
			3405	1071	1733	298	292	11		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	313	Total	C	H	N	O	S	0	0
			5147	1637	2570	456	470	14		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	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	I	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
I	184	5F0	ASN	variant	UNP P82912

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

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	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	K	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	L	164	Total	C	H	N	O	S	0	0
			2851	882	1467	256	239	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	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	N	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	O	193	Total	C	H	N	O	S	0	0
			3158	1014	1566	294	277	7		

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

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

- Molecule 17 is a protein called Small ribosomal subunit protein bS21m.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	87	Total	C	H	N	O	S	0	0
			1504	460	760	150	126	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	1	ACE	-	acetylation	UNP P82921
Q	50	ARG	CYS	conflict	UNP P82921

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

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	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	S	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	T	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	U	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	V	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	W	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	X	350	Total	C	H	N	O	S	0	0
			5678	1813	2842	497	515	11		

- Molecule 25 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Y	134	Total	C	H	N	O	S	0	0
			2236	736	1100	191	207	2		

- Molecule 26 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Z	96	Total	C	H	N	O	S	0	0
			1638	517	828	145	144	4		

- Molecule 27 is a protein called Small ribosomal subunit protein mS34.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	0	215	Total	C	H	N	O	S	0	0
			3589	1130	1802	339	313	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
28	1	277	Total	C	H	N	O	S	0	0
			4526	1424	2281	382	428	11		

- Molecule 29 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	4	586	Total	C	H	N	O	S	0	0
			9502	3035	4761	803	875	28		

- Molecule 30 is a protein called Nitric oxide-associated protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	9	415	Total	C	H	N	O	S	0	0
			6656	2108	3378	574	584	12		

- Molecule 31 is a protein called Dimethyladenosine transferase 1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	5	319	Total	C	H	N	O	S	0	0
			5229	1648	2661	458	451	11		

- Molecule 32 is a protein called Putative ribosome-binding factor A, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	a	32	Total	C	H	N	O		0	0
			520	162	271	42	45			

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	A	39	Total 39	Mg 39	0
33	B	1	Total 1	Mg 1	0
33	X	1	Total 1	Mg 1	0

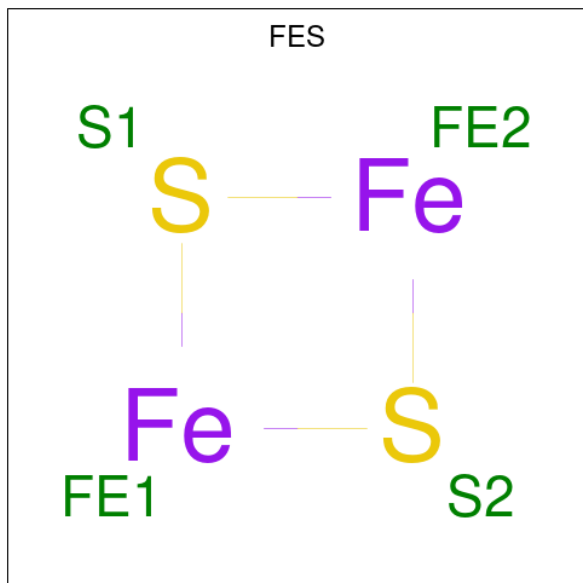
- Molecule 34 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
34	A	10	Total 10	K 10	0

- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

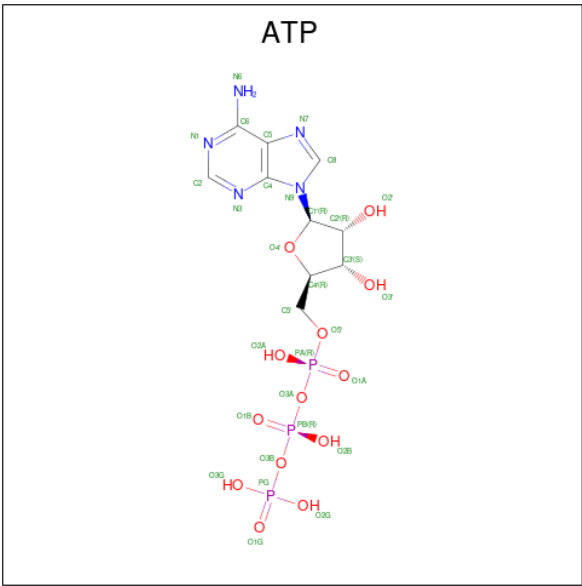
Mol	Chain	Residues	Atoms		AltConf
35	O	1	Total 1	Zn 1	0

- Molecule 36 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



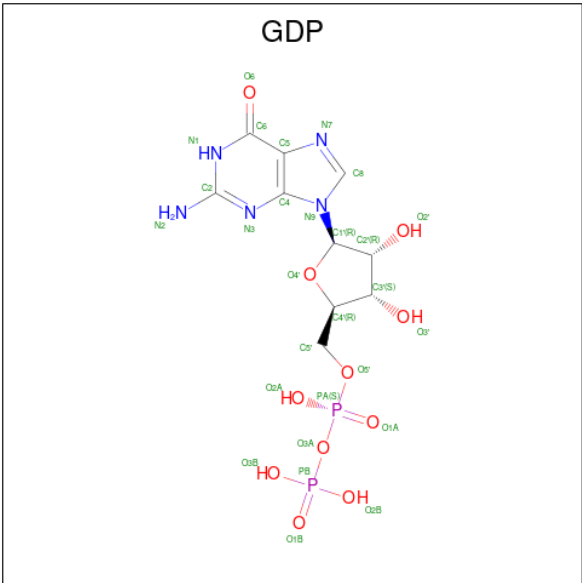
Mol	Chain	Residues	Atoms			AltConf
36	P	1	Total 4	Fe 2	S 2	0
36	T	1	Total 4	Fe 2	S 2	0

- Molecule 37 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

- Molecule 38 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

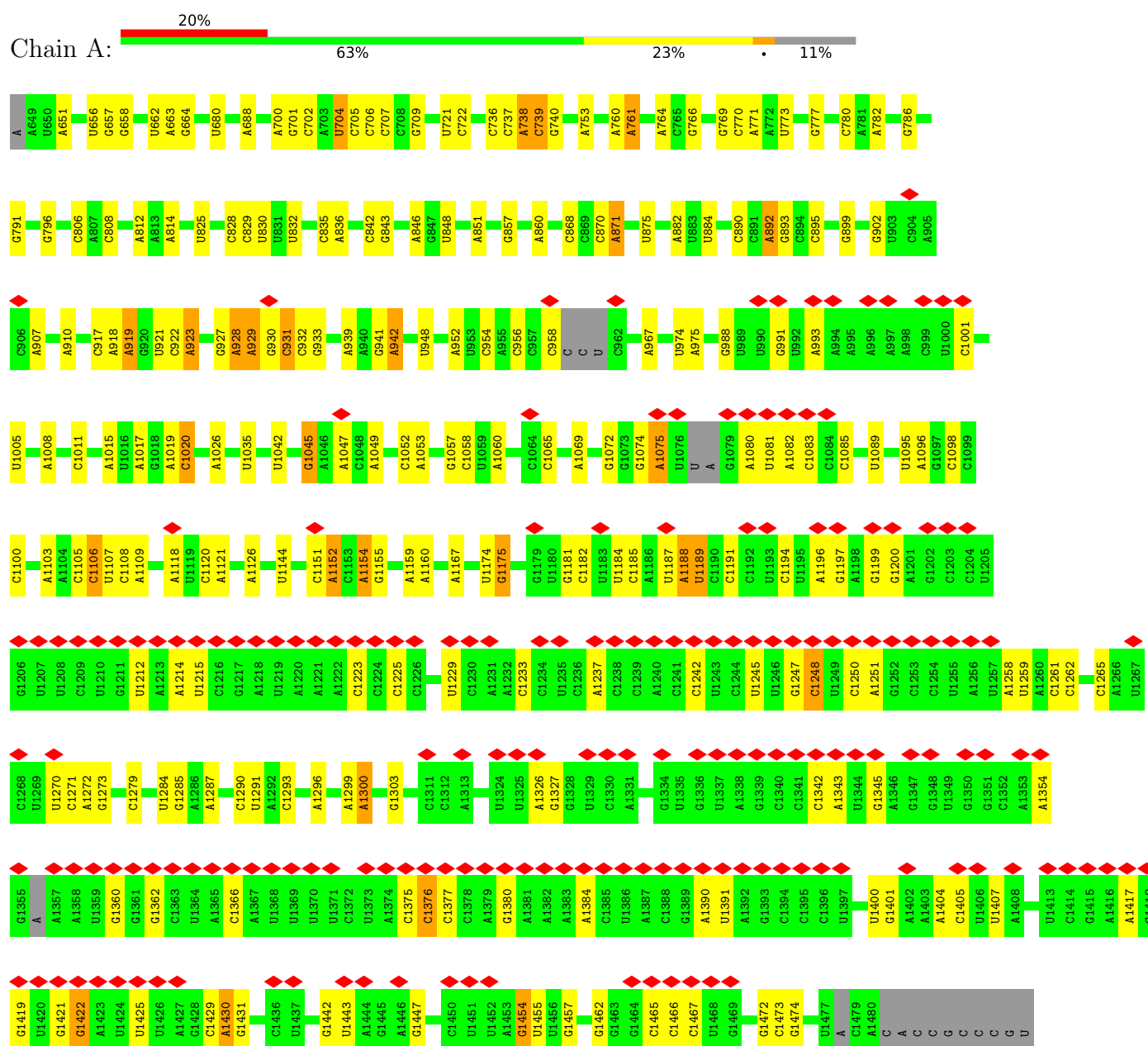


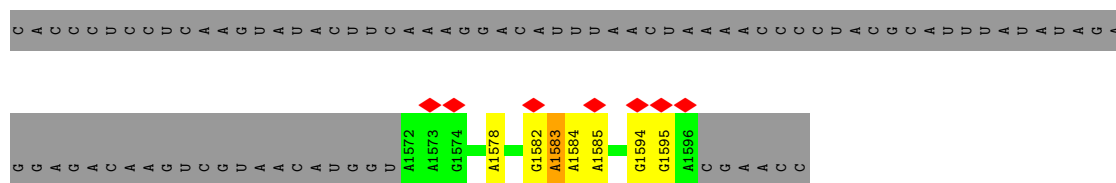
Mol	Chain	Residues	Atoms						AltConf
38	X	1	Total 38	C 10	H 10	N 5	O 11	P 2	0
38	9	1	Total 38	C 10	H 10	N 5	O 11	P 2	0

3 Residue-property plots

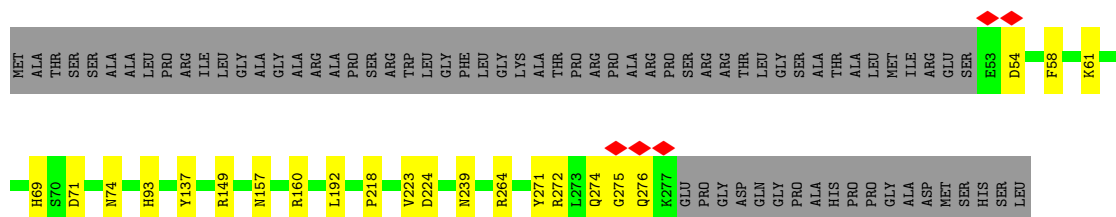
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 12S mitochondrial rRNA

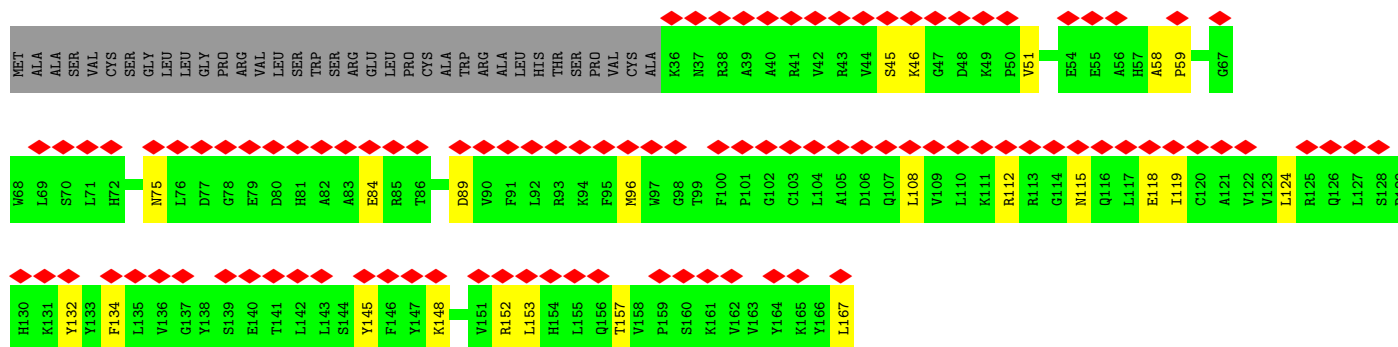




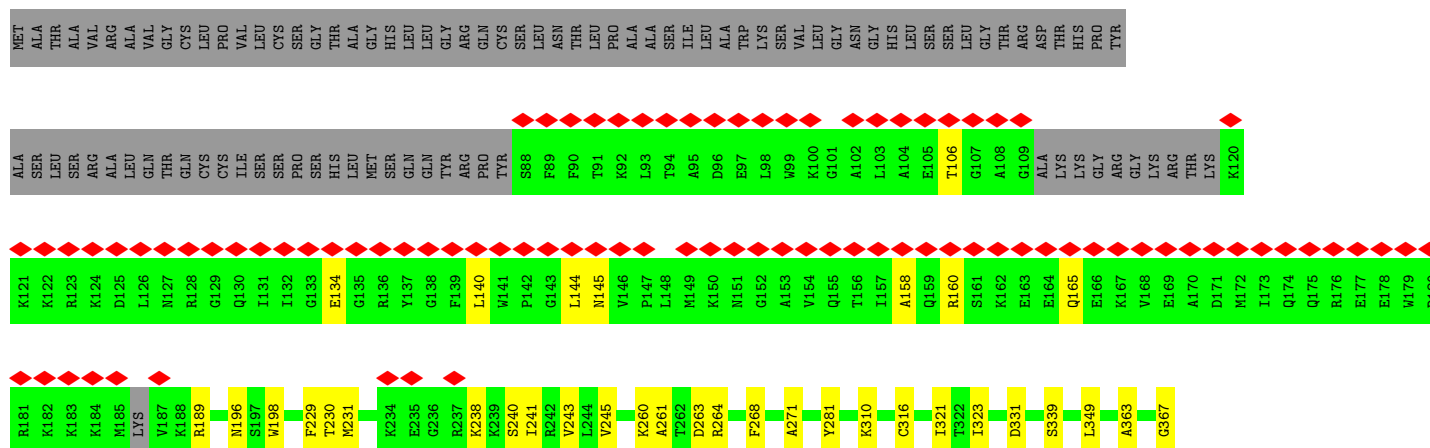
- Molecule 2: 28S ribosomal protein S2, mitochondrial

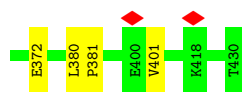


- Molecule 3: 28S ribosomal protein S24, mitochondrial

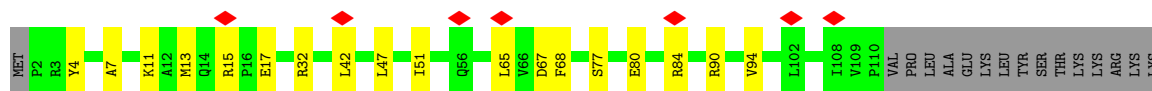
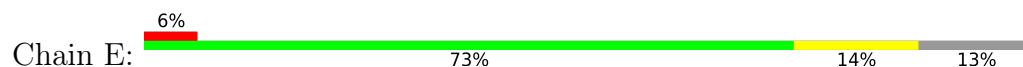


- Molecule 4: 28S ribosomal protein S5, mitochondrial

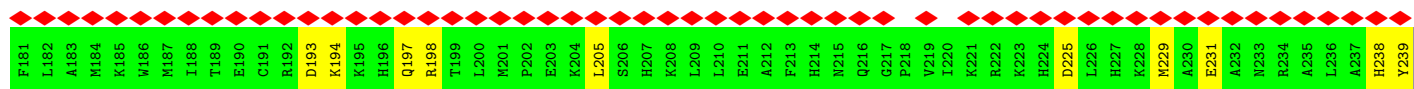
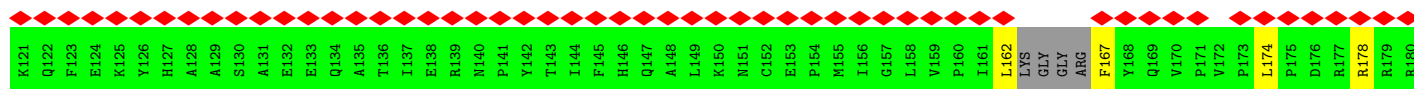
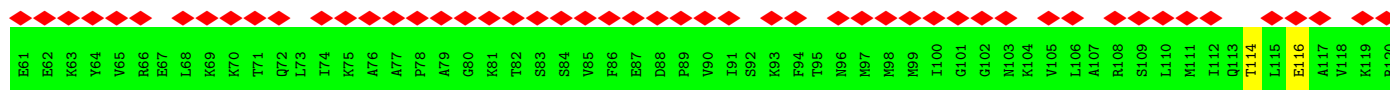
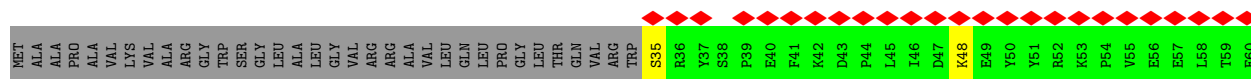
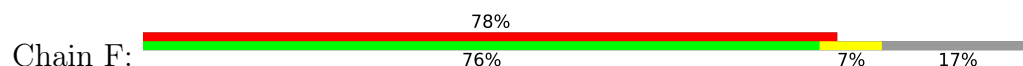




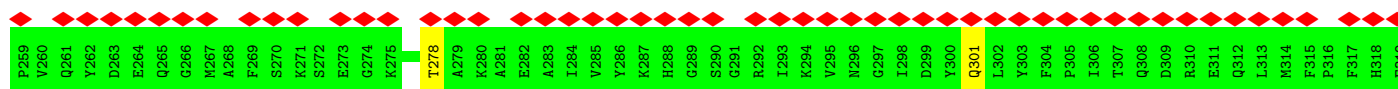
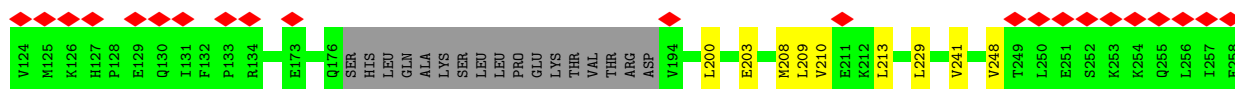
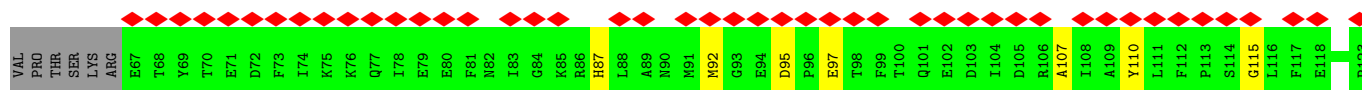
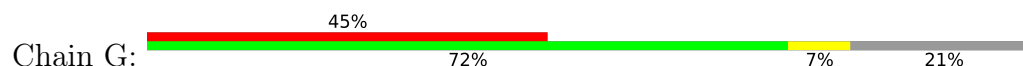
- Molecule 5: 28S ribosomal protein S6, mitochondrial

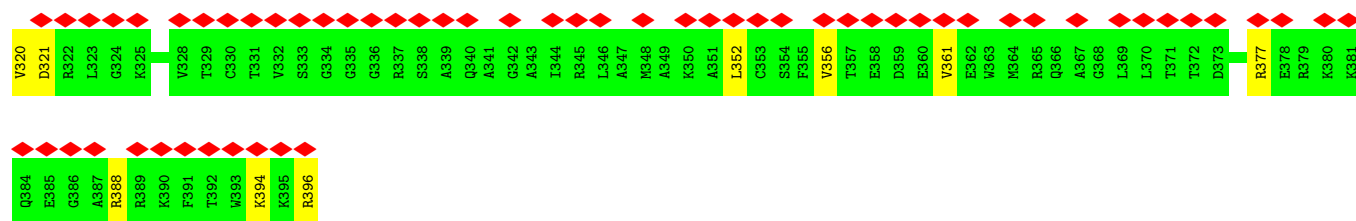


- Molecule 6: 28S ribosomal protein S7, mitochondrial

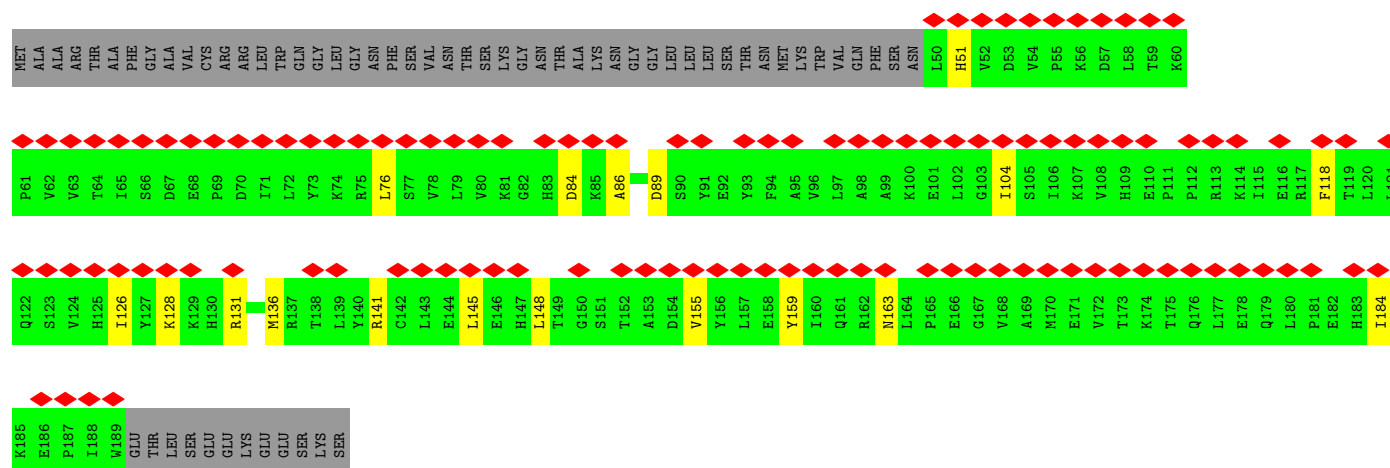


- Molecule 7: 28S ribosomal protein S9, mitochondrial

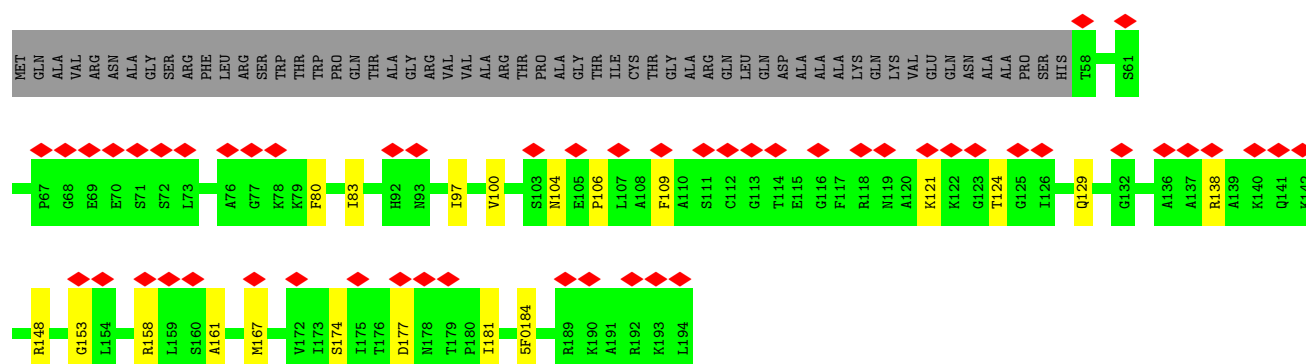




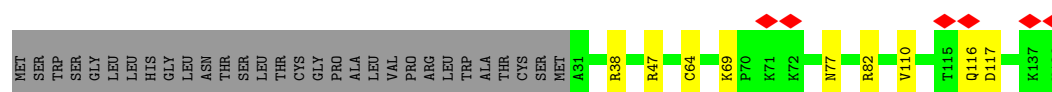
- Molecule 8: 28S ribosomal protein S10, mitochondrial



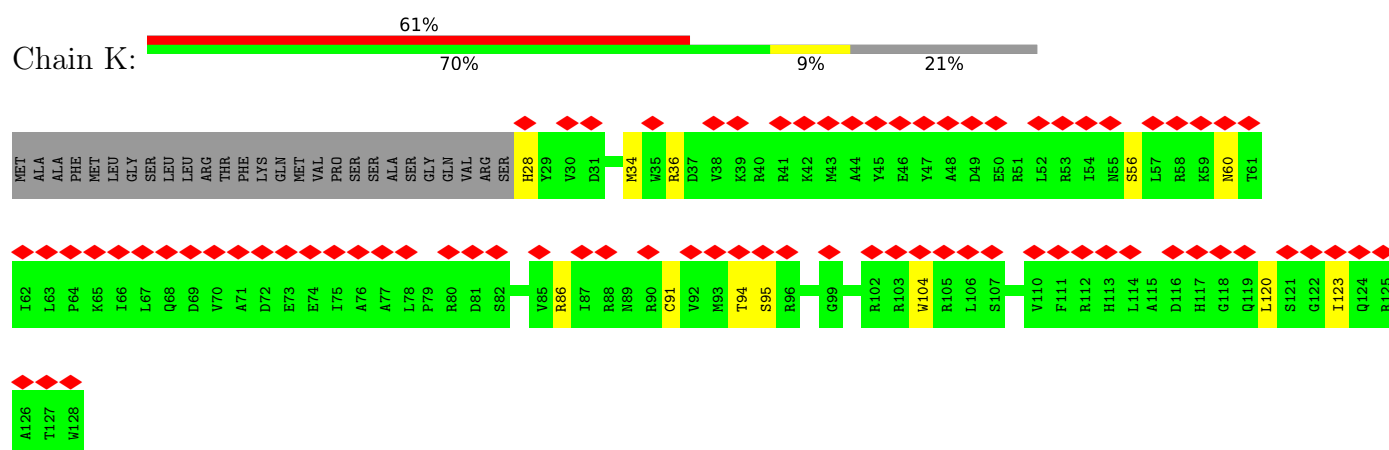
- Molecule 9: 28S ribosomal protein S11, mitochondrial



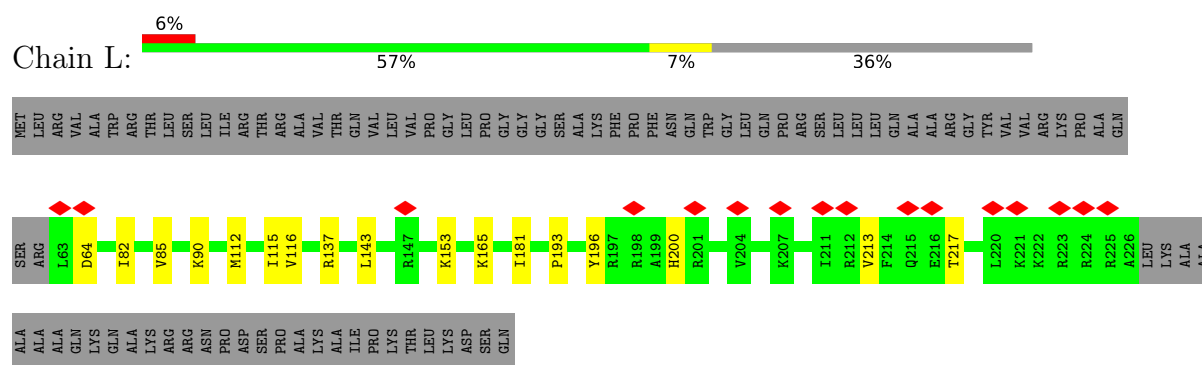
- Molecule 10: 28S ribosomal protein S12, mitochondrial



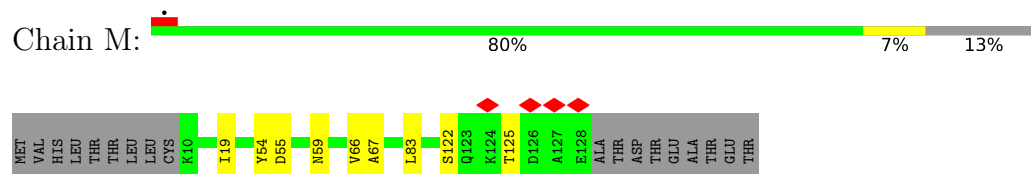
- Molecule 11: 28S ribosomal protein S14, mitochondrial



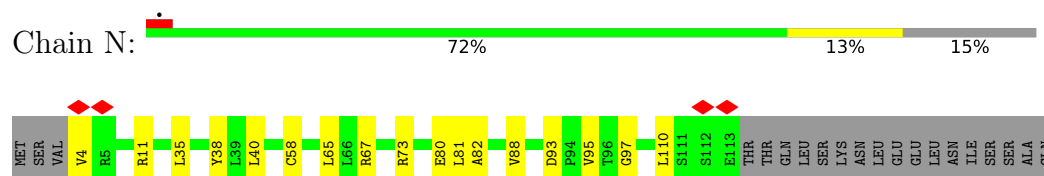
- Molecule 12: 28S ribosomal protein S15, mitochondrial



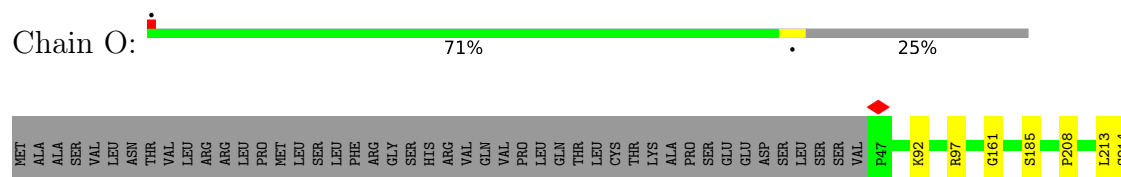
- Molecule 13: 28S ribosomal protein S16, mitochondrial

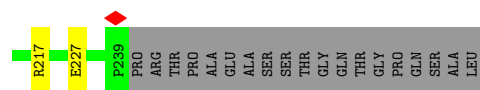


- Molecule 14: 28S ribosomal protein S17, mitochondrial

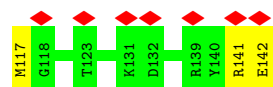
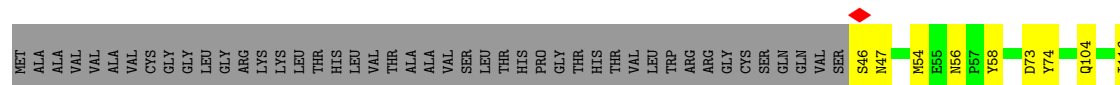


- Molecule 15: 28S ribosomal protein S18b, mitochondrial

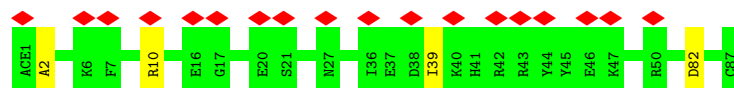




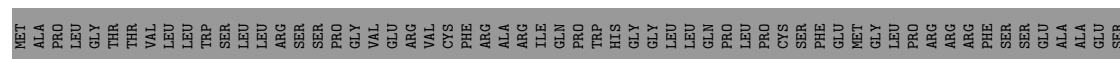
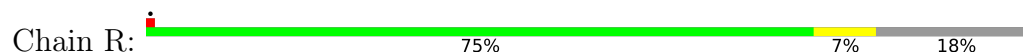
- Molecule 16: 28S ribosomal protein S18c, mitochondrial



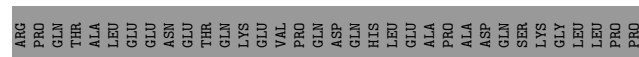
- Molecule 17: Small ribosomal subunit protein bS21m



- Molecule 18: 28S ribosomal protein S22, mitochondrial



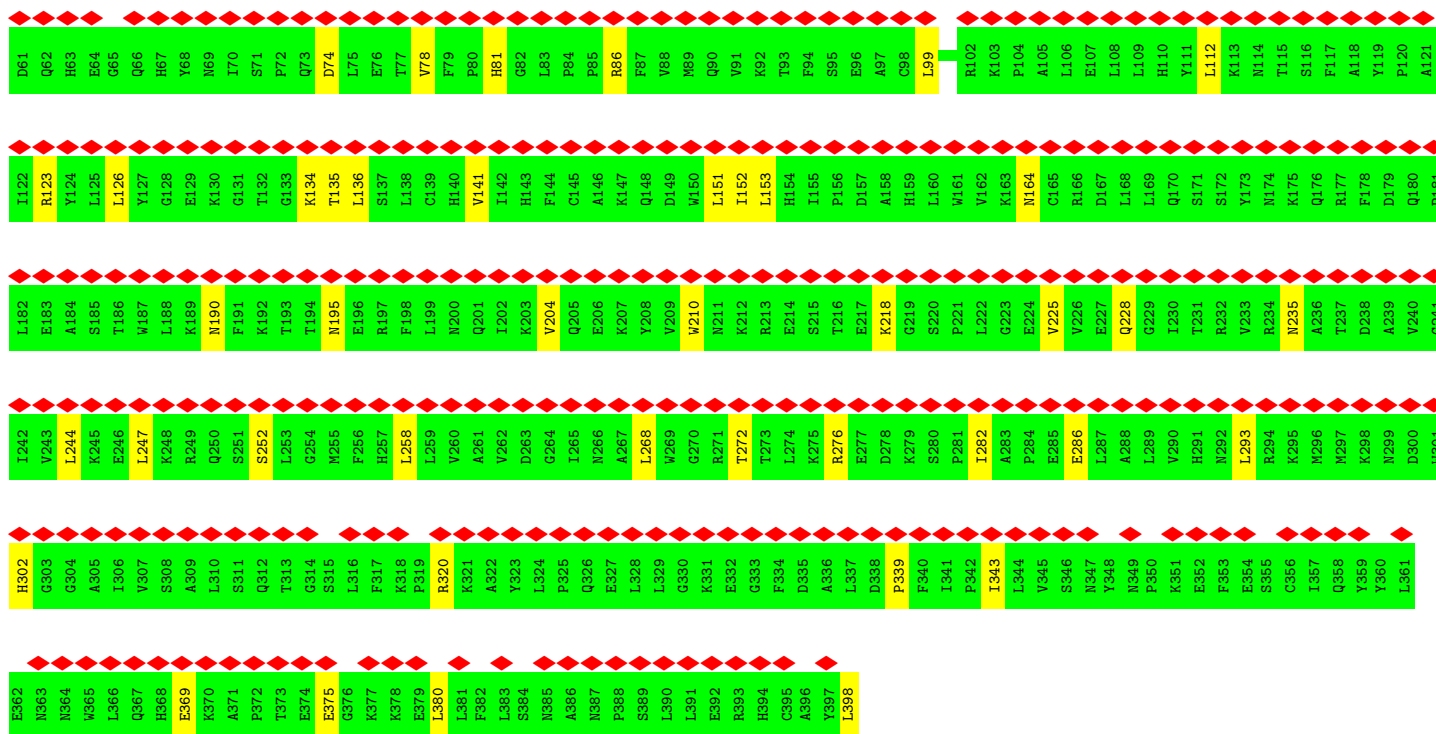
- Molecule 19: 28S ribosomal protein S23, mitochondrial



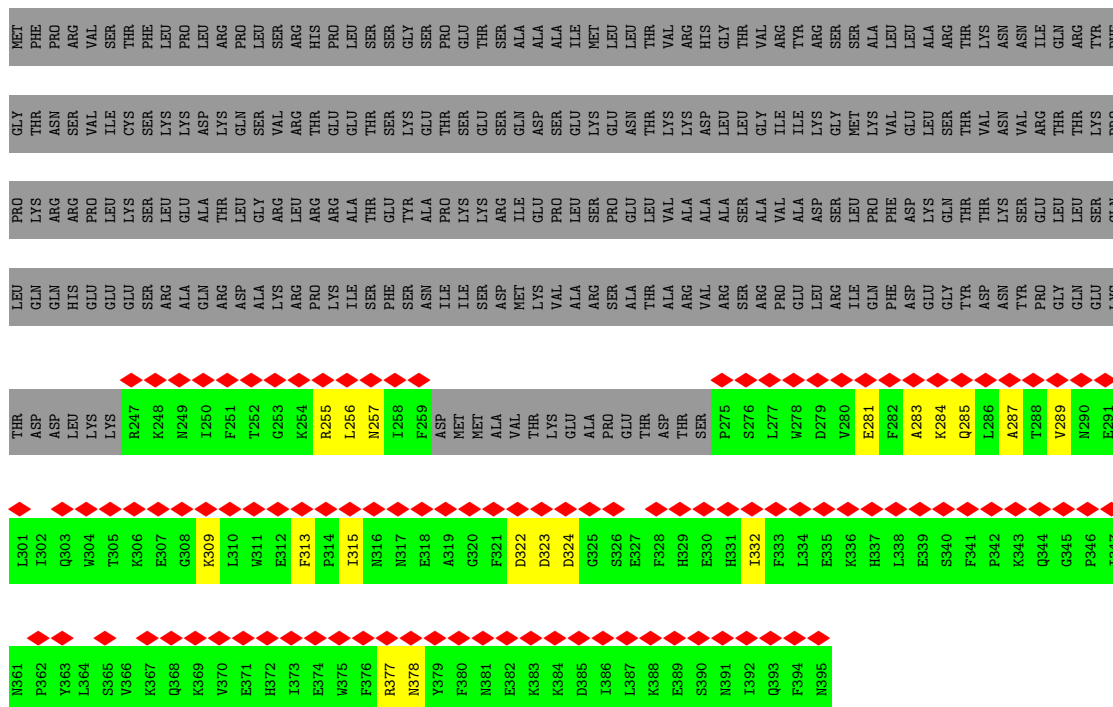
- Molecule 20: 28S ribosomal protein S25, mitochondrial



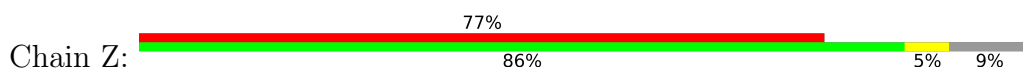
- | |
|-----|
| MET | MET | LEU | LYS | GLY | ILE | THR | ARG | LEU | ILE | SER | ARG | ILE | HIS | LYS | LEU | ASP | PRO | PRO | GLY | ARG | PHE | LEU | HIS | MET | GLY | THR | GLN | ALA | ALA | ARG | GLN | SER | ILE | ILE | ALA | ALA | HIS | LEU | ASP | ASN | GLN | VAL | PRO | VAL | GLU | SER | SER | ARG | ALA | ALA | ILE | S49 | R50 | T51 | N52 | E53 | N54 | D55 | P56 | A57 | K58 | H59 |
|-----|



- Molecule 25: 28S ribosomal protein S31, mitochondrial

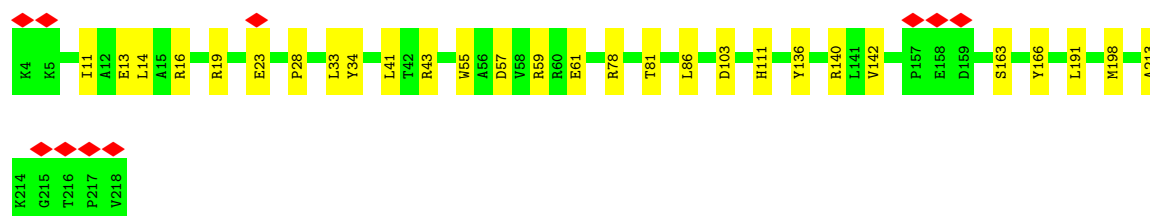
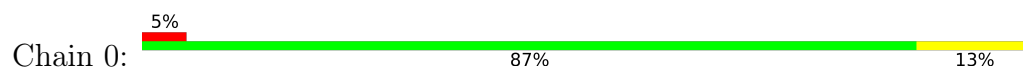


- Molecule 26: 28S ribosomal protein S33, mitochondrial

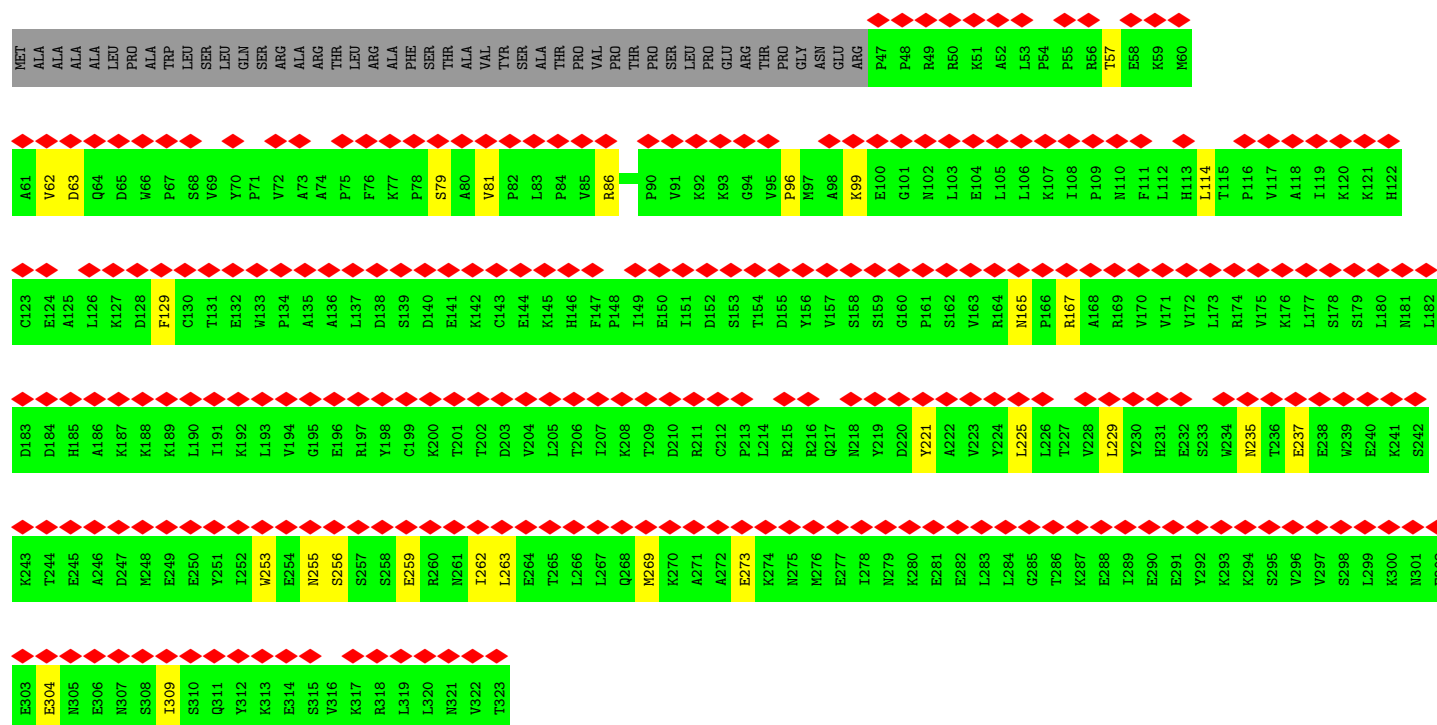
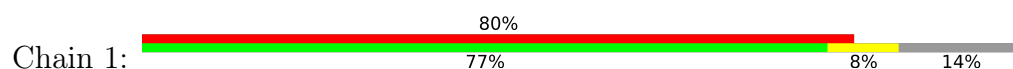




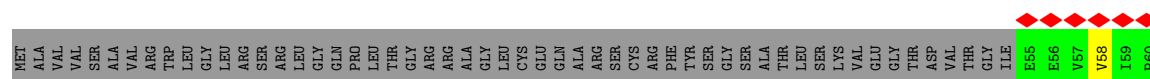
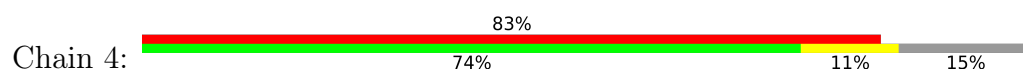
• Molecule 27: Small ribosomal subunit protein mS34



• Molecule 28: 28S ribosomal protein S35, mitochondrial



• Molecule 29: Pentatricopeptide repeat domain-containing protein 3, mitochondrial



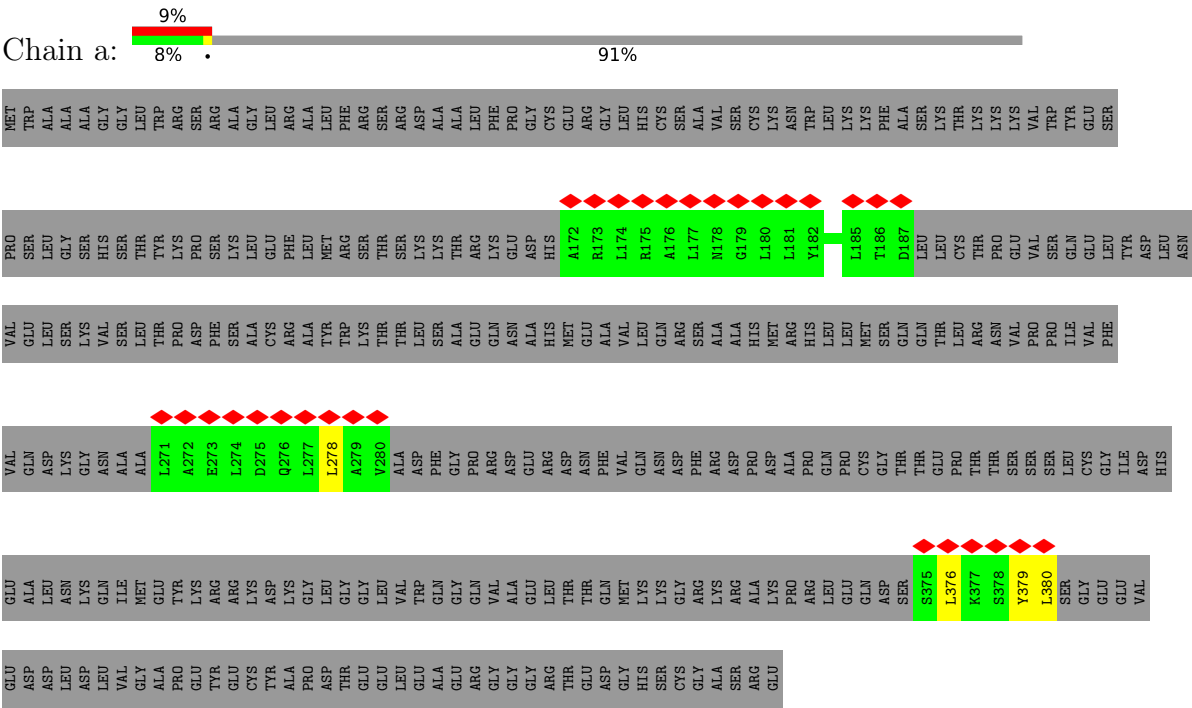
E661	K601	P541	L481	S421	K361	T301	K241	T181	I121	K61
A662	H602	P542	I482	I422	A362	V302	N242	T182	N122	K62
L663	N603	E543	C423	C423	P483	C303	K243	S183	S123	K63
S664	K604	L544	S484	S424	G364	A304	A244	S184	Y124	T64
N665	I605	Q545	A485	S425	I365	ILE	E245	L185	P125	W65
L666	P606	V546	Y486	L426	E366	ASN	R246	E186	K126	D66
T667	R607	A547	F487	R427	P367	LYS	I247	T187	Y127	V67
A668	S608	F548	P488	D428	S368	F309	F248	T188	F128	K68
E609	H489	L429	H489	L429	E310	E310	S249	N189	Q129	A69
L610	S490	E430	H489	L429	E311	E311	S249	S190	K130	V70
L611	S490	E430	H489	L429	E311	E311	S249	S190	D131	L71
A652	T492	L431	T492	L431	T371	K312	M251	L191	I132	Q72
A553	M493	A432	M493	A432	Y372	K313	P252	L192	A133	A73
D554	L494	Y433	L494	Y433	H373	S314	E253	D193	E133	A74
I555	H495	Q434	H495	Q434	H374	K315	K254	L194	E134	L75
K556	L496	V435	H495	V435	I375	I316	N255	L195	P135	S76
S557	L497	H436	L496	H436	I376	L317	E256	C196	H136	T77
A558	L497	G437	L497	G437	R377	E318	H257	Y197	I137	V78
A558	Q498	L438	Q498	L438	L378	L319	S258	Y198	C139	N79
Y559	A499	L439	A499	L439	F379	R320	Y259	G199	C139	R80
E560	L500	K440	L500	K440	D380	R321	C260	D200	L140	D81
S561	D501	T441	D501	T441	Q381	H322	T261	Q201	M141	T92
Q562	V502	G442	V502	G442	P382	K323	M262	E202	P142	T83
P563	A503	D443	A503	D443	G383	V324	I263	P203	E143	A84
I564	N504	N444	N504	N444	D384	A325	R264	S204	Y144	V85
R565	R505	W445	R505	W445	P385	Q326	G265	T205	F145	P86
Q566	L506	K446	L506	K446	L386	K327	M266	D206	E146	Y87
T567	E507	F447	E507	F447	K387	V328	V267	Y207	P147	V88
A627	A627	A627	A627	A627	R388	K329	K268	H208	Q148	F89
I628	V508	L448	V508	L448	S389	P330	H269	PHE	I149	Q90
Q569	I509	G449	I509	G449	S389	P330	H269	GLN	K150	D91
D570	P510	P450	P510	P450	S390	N331	R270	GLN	D151	D92
W571	K511	D451	K511	D451	F391	L332	A271	THR	I152	
P572	I512	Q452	I512	Q452	I392	Q333	Y272	GLY	S153	P93
A573	W513	H453	W513	H453	I393	T334	E273	GLN	E154	Y94
T574	K514	R454	K514	R454	Y394	F335	Q274	SER	A155	L96
S575	D515	M455	D515	M455	D395	N336	A275	ALA	A156	M96
L576	S516	F456	S516	F456	I396	T337	L276	LEU	L157	P97
N577	K517	Y457	K517	Y457	K397	I338	N277	GLU	K158	A98
C578	E518	Y458	E518	Y458	N398	L339	L278	GLU	E159	S99
F637	Y519	S459	Y519	S459	E399	K340	Y279	ASN	R160	S100
L639	G520	K460	G520	K460	L400	C341	T280	ASP	I161	L101
A580	H521	F461	H521	F461	M401	L342	E281	GLU	E162	E102
I581	T522	F462	T522	F462	G402	R343	L282	THR	S103	
L582	F523	D463	F523	D463	K403	R344	L283	SER	L163	S104
F583	R524	L464	R524	L464	R404	F345	N284	ARG	R164	R104
L584	S525	L464	S525	L464	F405	H346	N285	LYS	K165	S105
R585	D526	I465	D526	I465	S406	V347	R286	ALA	V166	F106
A586	L527	C466	A586	L527	P407	F348	L287	GLY	K167	L107
G587	R528	L467	G587	L467	K408	A349	H288	GLN	A168	L108
E588	E529	M468	E529	M468	R408	R349	A289	PHE	S169	A109
T589	E530	E469	T589	E469	D409	R350	C235		V170	K110
Q590	I531	Q470	Q590	I531	P410	S351	D290	V236	D171	S112
E591	L532	L471	E591	L532	D411	P352	V291	T237	M172	G113
A592	M533	D472	A592	M533	D412	A353	Y292	W238	F173	E114
W593	V473	V473	W593	V473	D413	L354	T293	R239	E114	N115
F653	L534	T474	F653	L534	K414	Q355	F294	A240	D174	V116
A654	M535	L475	A654	M535	F415	V356	N295		Q175	A117
M595	A536	T475	M595	A536	F416	L357	A296		L176	F119
L596	R537	K476	L596	R537	Q417	L357	I297		L177	
G597	D538	Y477	G597	D538	I417	R358	A296		Q178	
L598	K539	E478	L598	K539	S418	E359	I298		A179	
F599	F599	Y479	F599	F599	A419	R360	E299		G180	
Q659	R600	D480	Q659	R600	M420		A300			

● Molecule 30: Nitric oxide-associated protein 1



MET	LEU	PRO	ALA	ARG	LEU	LEU	PHE	ARG	GLY	ASP	THR	ASP	ALA	ALA	ALA	HIS	GLY	LEU	GLN	ARG	ALA	ALA	ALA	ARG	ARG	CYS	PHE	GLN	HIS	SER	SER	SER	ASN	LEU	GLY	ARG	GLU	GLU	LEU	PRO	TYR	ASP	PRO	VAL	VAL	ASP	THR	GLY
GLY	PHE	GLY	GLY	GLY	GLY	ASP	M68	Q69	E70	E76	Y77	I78	D80	P81	E82	P83	L91	L94	GLN	GLN	GLN	GLN	GLU	GLU	GLU	GLU	ARG	ARG	GLN	ARG	GLN	GLN	ASN	LEU	ARG	ALA	ARG	ARG	ARG	ARG	GLY	THR	GLY	GLY	GLY	GLY	GLY	

● Molecule 32: Putative ribosome-binding factor A, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16018	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.037	Depositor
Minimum map value	-0.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0054	Depositor
Map size (Å)	606.0, 606.0, 606.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.01, 1.01, 1.01	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: ACE, K, GDP, ATP, MG, FES, ZN, 5F0

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.18	0/20197	0.23	0/31437
2	B	0.19	0/1871	0.25	0/2531
3	C	0.16	0/1113	0.22	0/1505
4	D	0.18	0/2694	0.25	0/3608
5	E	0.13	0/880	0.27	0/1189
6	F	0.12	0/1709	0.23	0/2297
7	G	0.15	0/2632	0.23	0/3527
8	H	0.16	0/1178	0.25	0/1598
9	I	0.10	0/1030	0.23	0/1386
10	J	0.15	0/855	0.25	0/1148
11	K	0.14	0/880	0.24	0/1182
12	L	0.14	0/1408	0.25	0/1882
13	M	0.20	0/963	0.26	0/1295
14	N	0.19	0/886	0.25	0/1199
15	O	0.18	0/1648	0.24	0/2243
16	P	0.12	0/798	0.26	0/1070
17	Q	0.15	0/754	0.23	0/1003
18	R	0.18	0/2456	0.23	0/3317
19	S	0.16	0/1138	0.24	0/1533
20	T	0.18	0/1402	0.25	0/1883
21	U	0.14	0/1510	0.22	0/2025
22	V	0.10	0/3030	0.23	0/4093
23	W	0.15	0/801	0.26	0/1079
24	X	0.14	0/2908	0.25	0/3936
25	Y	0.14	0/1168	0.23	0/1570
26	Z	0.14	0/828	0.22	0/1104
27	0	0.14	0/1834	0.26	0/2484
28	1	0.13	0/2293	0.22	0/3102
29	4	0.10	0/4848	0.21	0/6560
30	9	0.12	0/3350	0.28	0/4549
31	5	0.13	0/2624	0.28	0/3552
32	a	0.14	0/248	0.32	0/331

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.15	0/71934	0.24	0/101218

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	18058	9165	9171	105	0
2	B	1828	1826	1815	14	0
3	C	1083	1096	1088	16	0
4	D	2644	2705	2693	29	0
5	E	865	882	878	13	0
6	F	1672	1733	1722	16	0
7	G	2577	2570	2560	21	0
8	H	1152	1191	1183	12	0
9	I	1020	1066	1053	11	0
10	J	839	892	887	8	0
11	K	862	889	885	8	0
12	L	1384	1467	1462	10	0
13	M	942	972	965	6	0
14	N	868	933	928	13	0
15	O	1592	1566	1557	8	0
16	P	781	809	806	8	0
17	Q	744	760	758	3	0
18	R	2409	2436	2428	16	0
19	S	1111	1117	1115	12	0
20	T	1371	1396	1393	10	0
21	U	1488	1505	1499	13	0
22	V	2969	2972	2961	39	0
23	W	789	806	802	12	0
24	X	2836	2842	2827	27	0
25	Y	1136	1100	1094	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	Z	810	828	824	5	0
27	0	1787	1802	1796	23	0
28	1	2245	2281	2276	17	0
29	4	4741	4761	4742	51	0
30	9	3278	3378	3371	70	0
31	5	2568	2661	2655	47	0
32	a	249	271	270	6	0
33	A	39	0	0	0	0
33	B	1	0	0	0	0
33	X	1	0	0	0	0
34	A	10	0	0	0	0
35	O	1	0	0	0	0
36	P	4	0	0	0	0
36	T	4	0	0	0	0
37	X	31	12	12	2	0
38	9	28	10	12	1	0
38	X	28	10	12	0	0
All	All	68845	60710	60500	572	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 572 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:9:623:ILE:HG22	30:9:653:LEU:HD11	1.46	0.94
1:A:1237:A:OP1	11:K:36:ARG:NH2	2.07	0.87
1:A:1429:C:OP1	7:G:388:ARG:NH1	2.12	0.83
30:9:624:LYS:O	30:9:653:LEU:HD12	1.89	0.72
22:V:167:VAL:HG13	22:V:172:ALA:HB3	1.72	0.71

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	223/296 (75%)	220 (99%)	3 (1%)	0	100	100
3	C	130/167 (78%)	127 (98%)	3 (2%)	0	100	100
4	D	326/430 (76%)	320 (98%)	6 (2%)	0	100	100
5	E	107/125 (86%)	104 (97%)	3 (3%)	0	100	100
6	F	199/242 (82%)	198 (100%)	1 (0%)	0	100	100
7	G	309/396 (78%)	303 (98%)	6 (2%)	0	100	100
8	H	138/201 (69%)	135 (98%)	2 (1%)	1 (1%)	18	47
9	I	134/194 (69%)	132 (98%)	2 (2%)	0	100	100
10	J	106/138 (77%)	102 (96%)	4 (4%)	0	100	100
11	K	99/128 (77%)	99 (100%)	0	0	100	100
12	L	162/257 (63%)	160 (99%)	2 (1%)	0	100	100
13	M	117/137 (85%)	117 (100%)	0	0	100	100
14	N	108/130 (83%)	108 (100%)	0	0	100	100
15	O	191/258 (74%)	188 (98%)	3 (2%)	0	100	100
16	P	95/142 (67%)	92 (97%)	3 (3%)	0	100	100
17	Q	85/87 (98%)	82 (96%)	2 (2%)	1 (1%)	10	35
18	R	293/360 (81%)	289 (99%)	4 (1%)	0	100	100
19	S	133/190 (70%)	128 (96%)	5 (4%)	0	100	100
20	T	166/173 (96%)	164 (99%)	2 (1%)	0	100	100
21	U	174/205 (85%)	173 (99%)	1 (1%)	0	100	100
22	V	358/414 (86%)	355 (99%)	3 (1%)	0	100	100
23	W	98/187 (52%)	96 (98%)	2 (2%)	0	100	100
24	X	348/398 (87%)	342 (98%)	6 (2%)	0	100	100
25	Y	130/395 (33%)	128 (98%)	2 (2%)	0	100	100
26	Z	94/106 (89%)	94 (100%)	0	0	100	100
27	0	213/215 (99%)	207 (97%)	6 (3%)	0	100	100
28	1	275/323 (85%)	273 (99%)	2 (1%)	0	100	100
29	4	580/689 (84%)	570 (98%)	10 (2%)	0	100	100
30	9	403/698 (58%)	385 (96%)	18 (4%)	0	100	100
31	5	317/346 (92%)	313 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	a	26/343 (8%)	26 (100%)	0	0	100	100
All	All	6137/8370 (73%)	6030 (98%)	105 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	126	ILE
17	Q	2	ALA

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	198/249 (80%)	198 (100%)	0	100	100
3	C	115/143 (80%)	115 (100%)	0	100	100
4	D	278/357 (78%)	278 (100%)	0	100	100
5	E	92/107 (86%)	92 (100%)	0	100	100
6	F	182/209 (87%)	182 (100%)	0	100	100
7	G	272/342 (80%)	272 (100%)	0	100	100
8	H	130/180 (72%)	130 (100%)	0	100	100
9	I	104/146 (71%)	104 (100%)	0	100	100
10	J	93/118 (79%)	93 (100%)	0	100	100
11	K	91/113 (80%)	91 (100%)	0	100	100
12	L	153/226 (68%)	153 (100%)	0	100	100
13	M	97/113 (86%)	97 (100%)	0	100	100
14	N	96/115 (84%)	96 (100%)	0	100	100
15	O	174/230 (76%)	174 (100%)	0	100	100
16	P	88/123 (72%)	88 (100%)	0	100	100
17	Q	78/78 (100%)	78 (100%)	0	100	100
18	R	264/318 (83%)	264 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	S	116/164 (71%)	116 (100%)	0	100	100
20	T	153/157 (98%)	153 (100%)	0	100	100
21	U	152/174 (87%)	152 (100%)	0	100	100
22	V	325/364 (89%)	325 (100%)	0	100	100
23	W	87/158 (55%)	87 (100%)	0	100	100
24	X	310/351 (88%)	310 (100%)	0	100	100
25	Y	124/357 (35%)	124 (100%)	0	100	100
26	Z	88/95 (93%)	88 (100%)	0	100	100
27	0	188/188 (100%)	188 (100%)	0	100	100
28	1	255/291 (88%)	255 (100%)	0	100	100
29	4	523/609 (86%)	523 (100%)	0	100	100
30	9	358/600 (60%)	358 (100%)	0	100	100
31	5	286/309 (93%)	286 (100%)	0	100	100
32	a	26/288 (9%)	26 (100%)	0	100	100
All	All	5496/7272 (76%)	5496 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
20	T	59	ASN
31	5	192	GLN
24	X	180	GLN
31	5	137	HIS
29	4	562	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	844/955 (88%)	132 (15%)	4 (0%)

5 of 132 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	651	A

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Mol	Chain	Res	Type
1	A	657	G
1	A	680	U
1	A	688	A
1	A	704	U

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	928	A
1	A	930	G
1	A	931	C
1	A	1154	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
9	5F0	I	184	9	8,8,9	0.58	0	7,9,11	1.09	1 (14%)

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
9	5F0	I	184	9	-	0/9/9/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	184	5F0	O-C-CB	-2.54	118.01	125.43

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 57 ligands modelled in this entry, 52 are monoatomic - leaving 5 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	$\# Z > 2$
36	FES	P	201	16,5	0,4,4	-	-	-		
37	ATP	X	501	33	29,33,33	0.49	0	44,52,52	0.58	0
38	GDP	X	502	-	28,30,30	0.43	0	44,47,47	0.41	0
38	GDP	9	801	-	28,30,30	0.44	0	44,47,47	0.49	0
36	FES	T	201	13,20	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
36	FES	P	201	16,5	-	-	0/1/1/1
37	ATP	X	501	33	-	0/22/38/38	0/3/3/3
38	GDP	X	502	-	-	3/16/32/32	0/3/3/3
38	GDP	9	801	-	-	0/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	FES	T	201	13,20	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

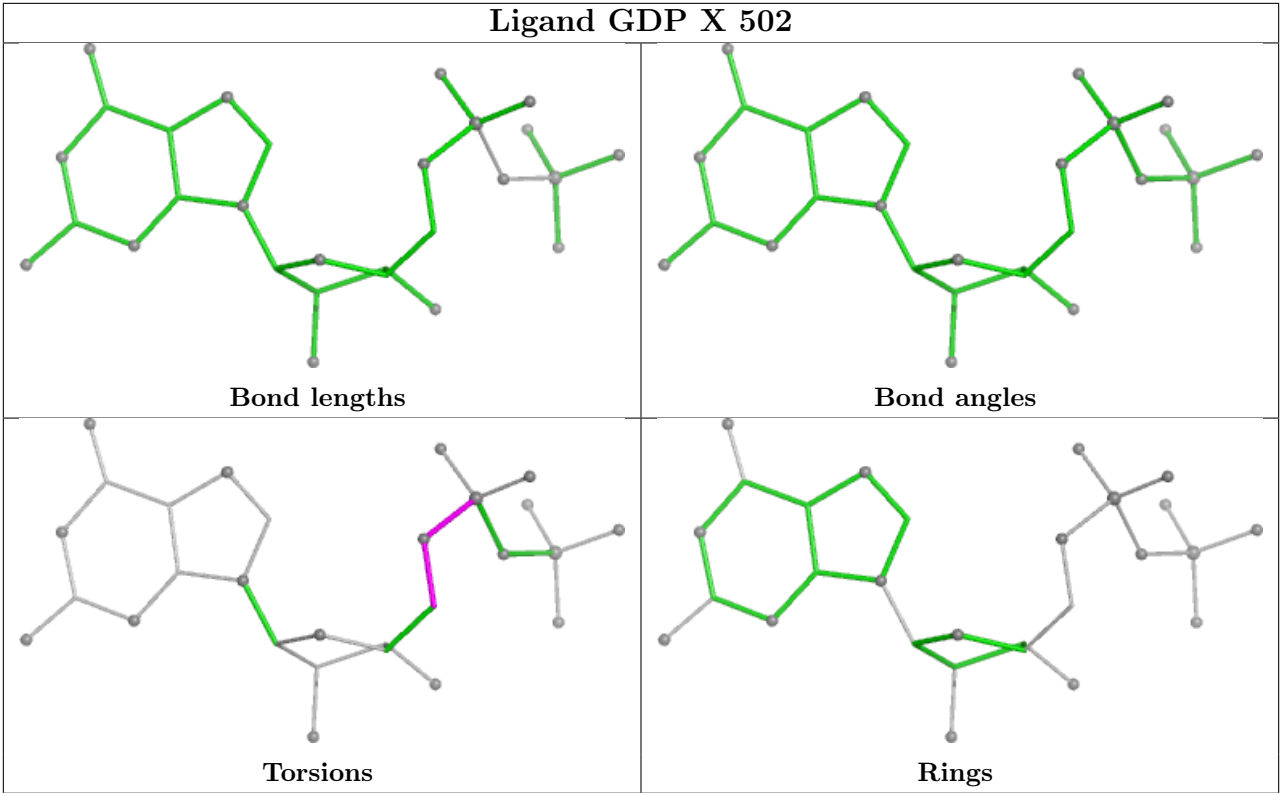
Mol	Chain	Res	Type	Atoms
38	X	502	GDP	C5'-O5'-PA-O1A
38	X	502	GDP	C5'-O5'-PA-O3A
38	X	502	GDP	C4'-C5'-O5'-PA

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
37	X	501	ATP	2	0
38	9	801	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
30	9	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	9	279:LEU	C	280:ALA	N	4.87

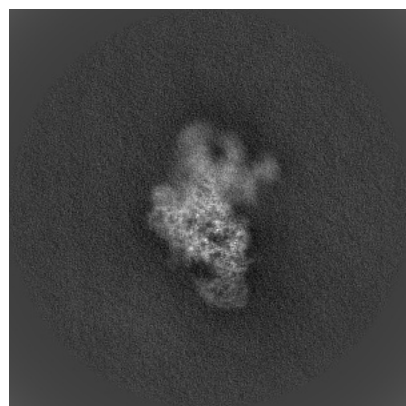
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51877. These allow visual inspection of the internal detail of the map and identification of artifacts.

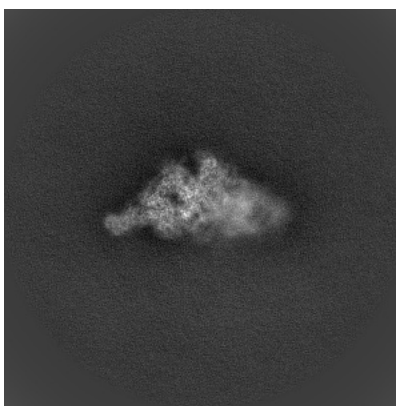
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

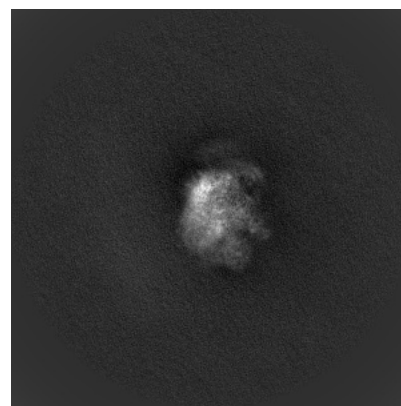
6.1.1 Primary map



X

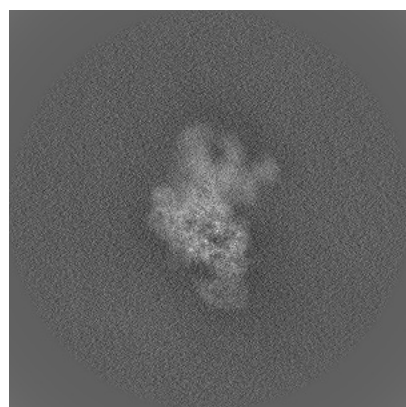


Y

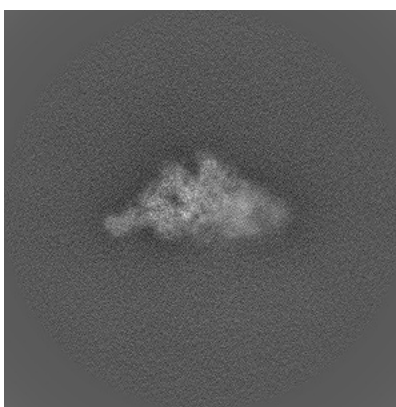


Z

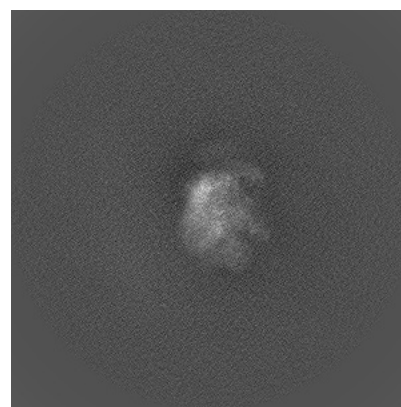
6.1.2 Raw map



X



Y

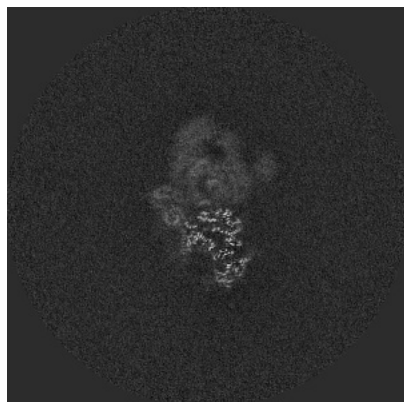


Z

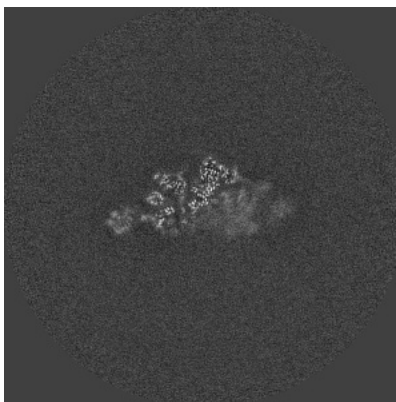
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

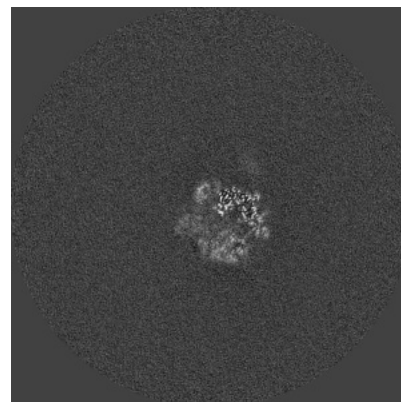
6.2.1 Primary map



X Index: 300

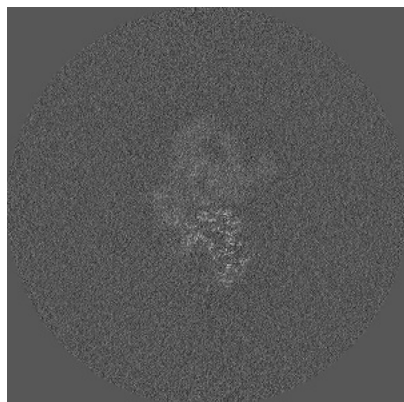


Y Index: 300

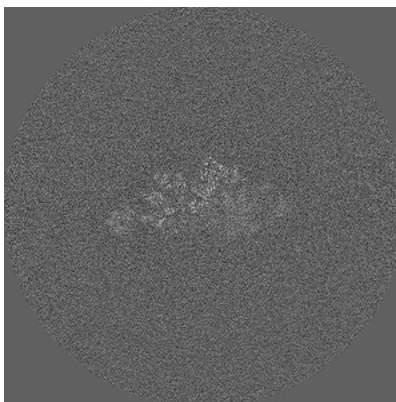


Z Index: 300

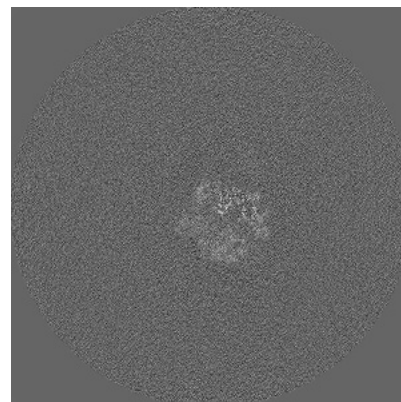
6.2.2 Raw map



X Index: 300



Y Index: 300

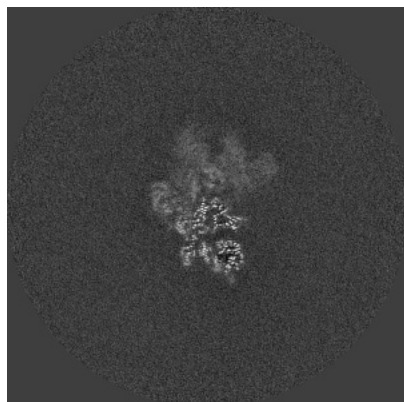


Z Index: 300

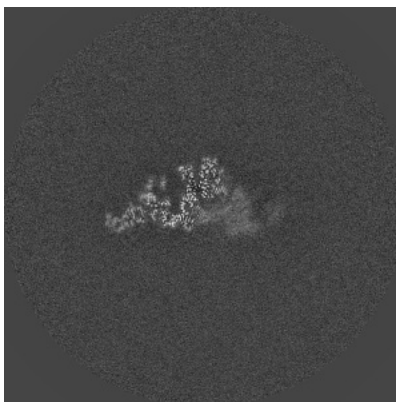
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

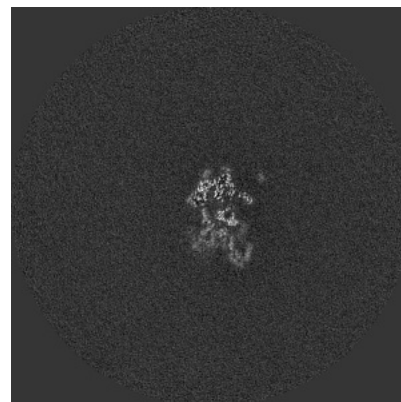
6.3.1 Primary map



X Index: 314

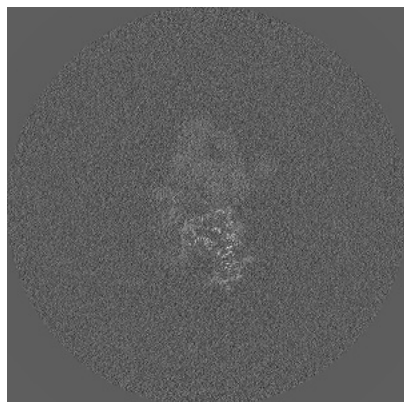


Y Index: 313

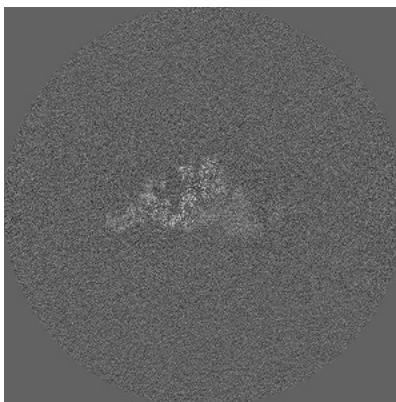


Z Index: 273

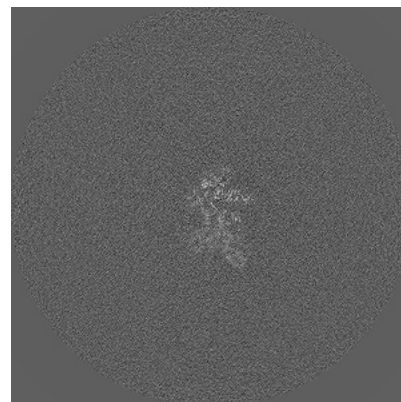
6.3.2 Raw map



X Index: 297



Y Index: 313

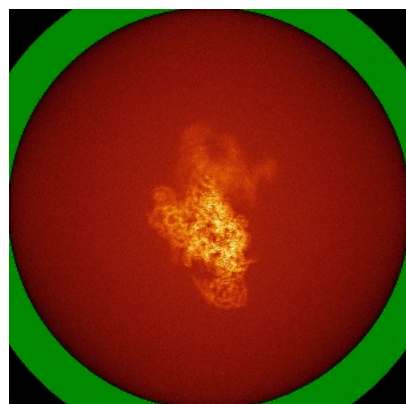


Z Index: 278

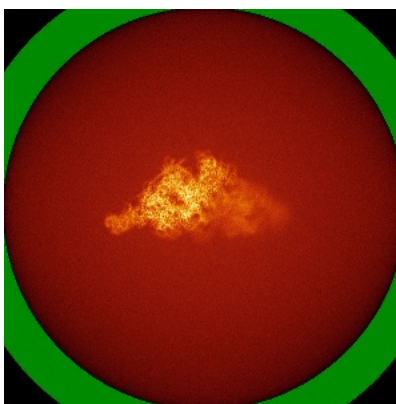
The images above show the largest variance slices of the map in three orthogonal directions.

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

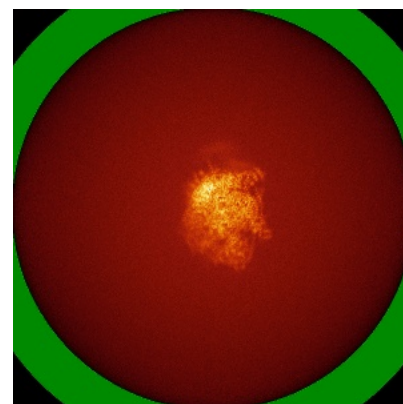
6.4.1 Primary map



X

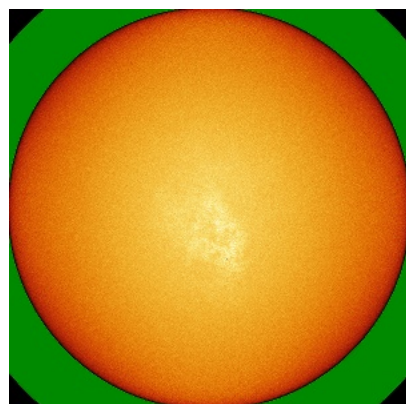


Y

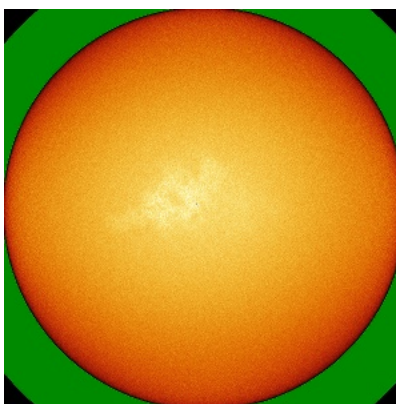


Z

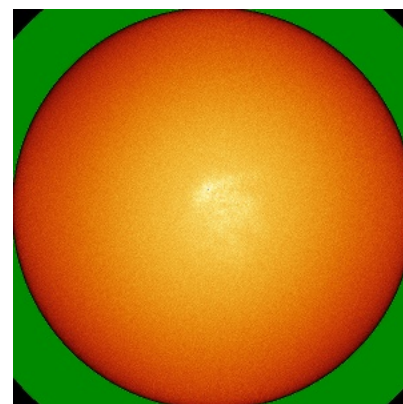
6.4.2 Raw map



X



Y

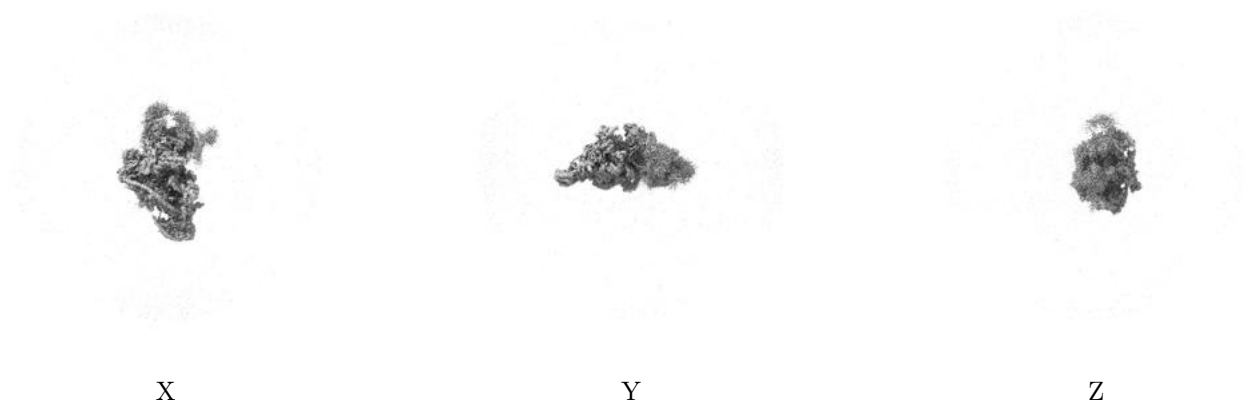


Z

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.

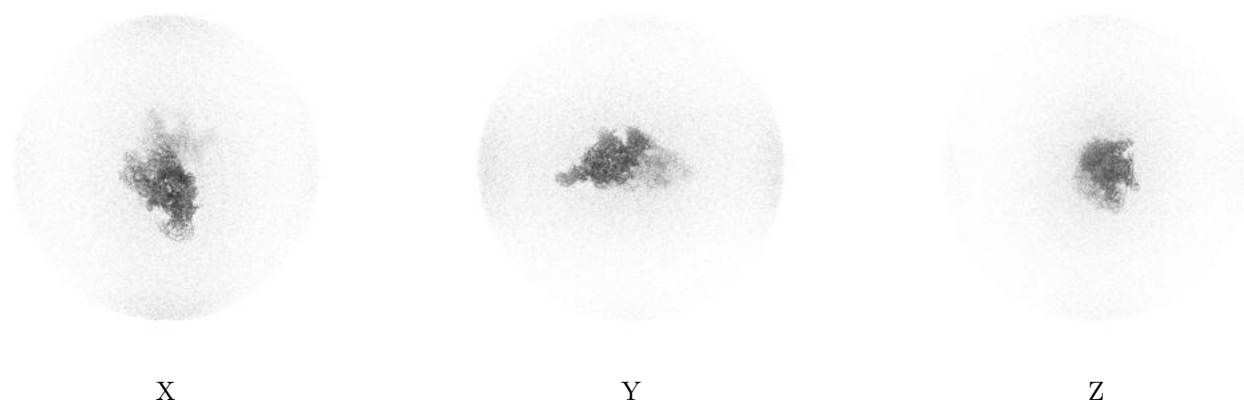
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0054. 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.

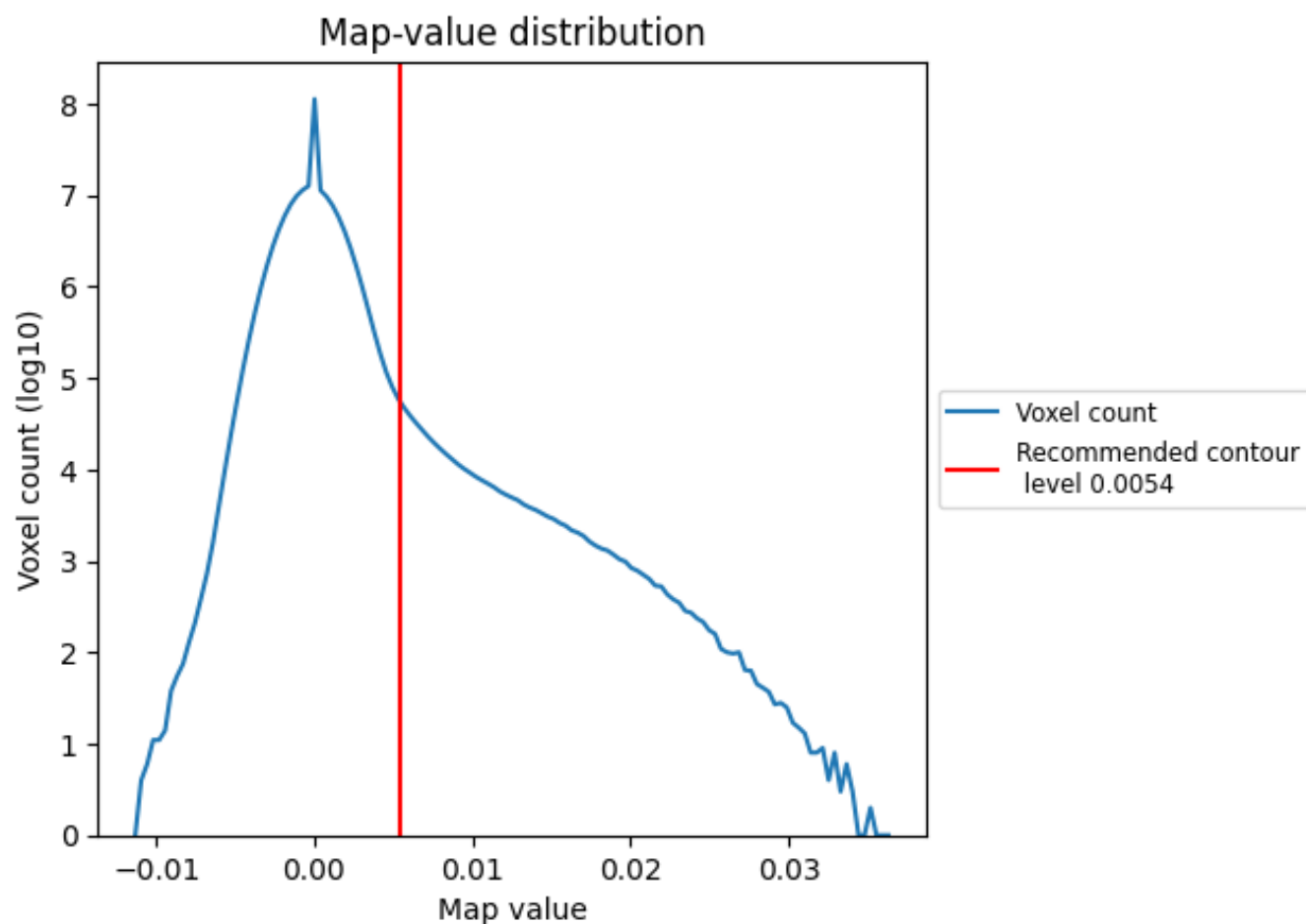
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

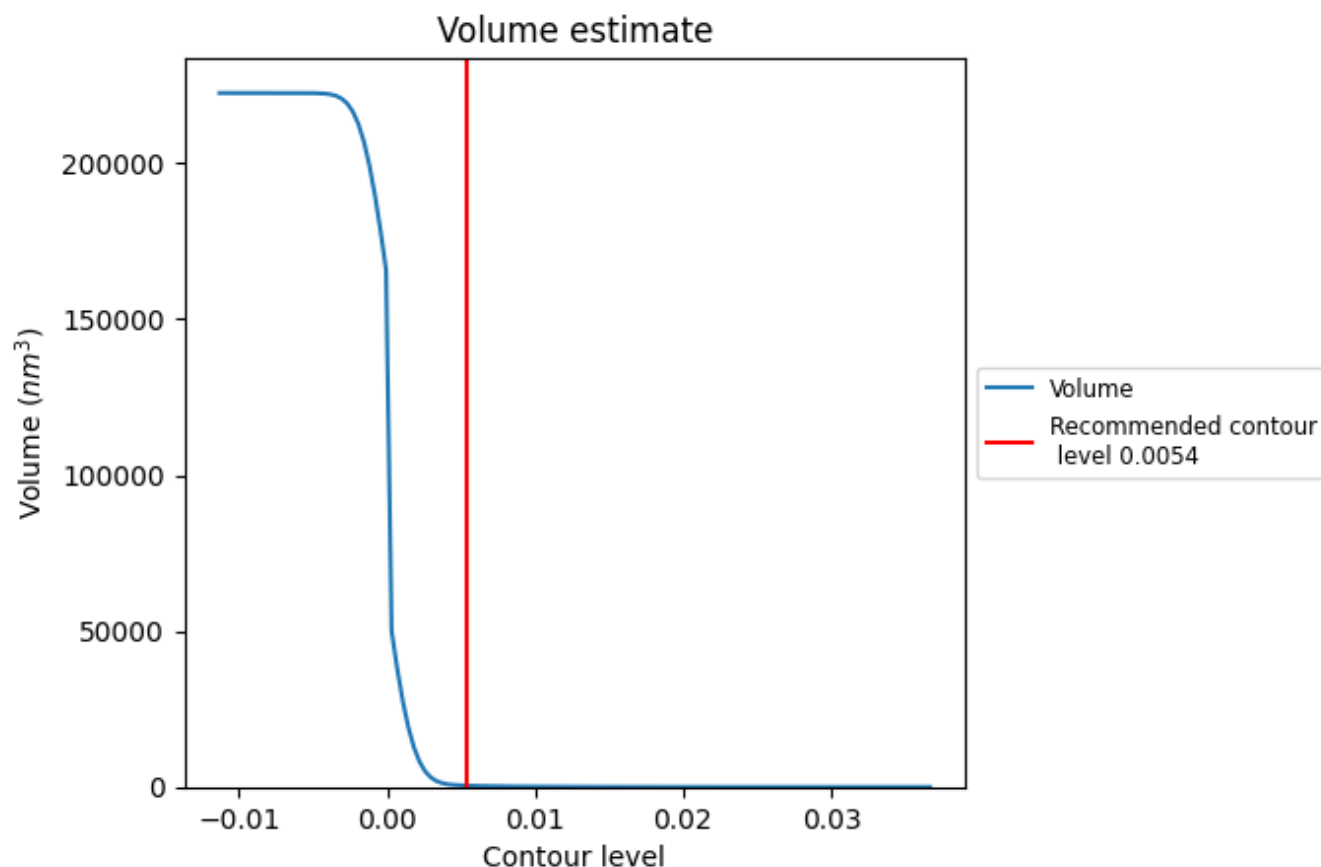
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

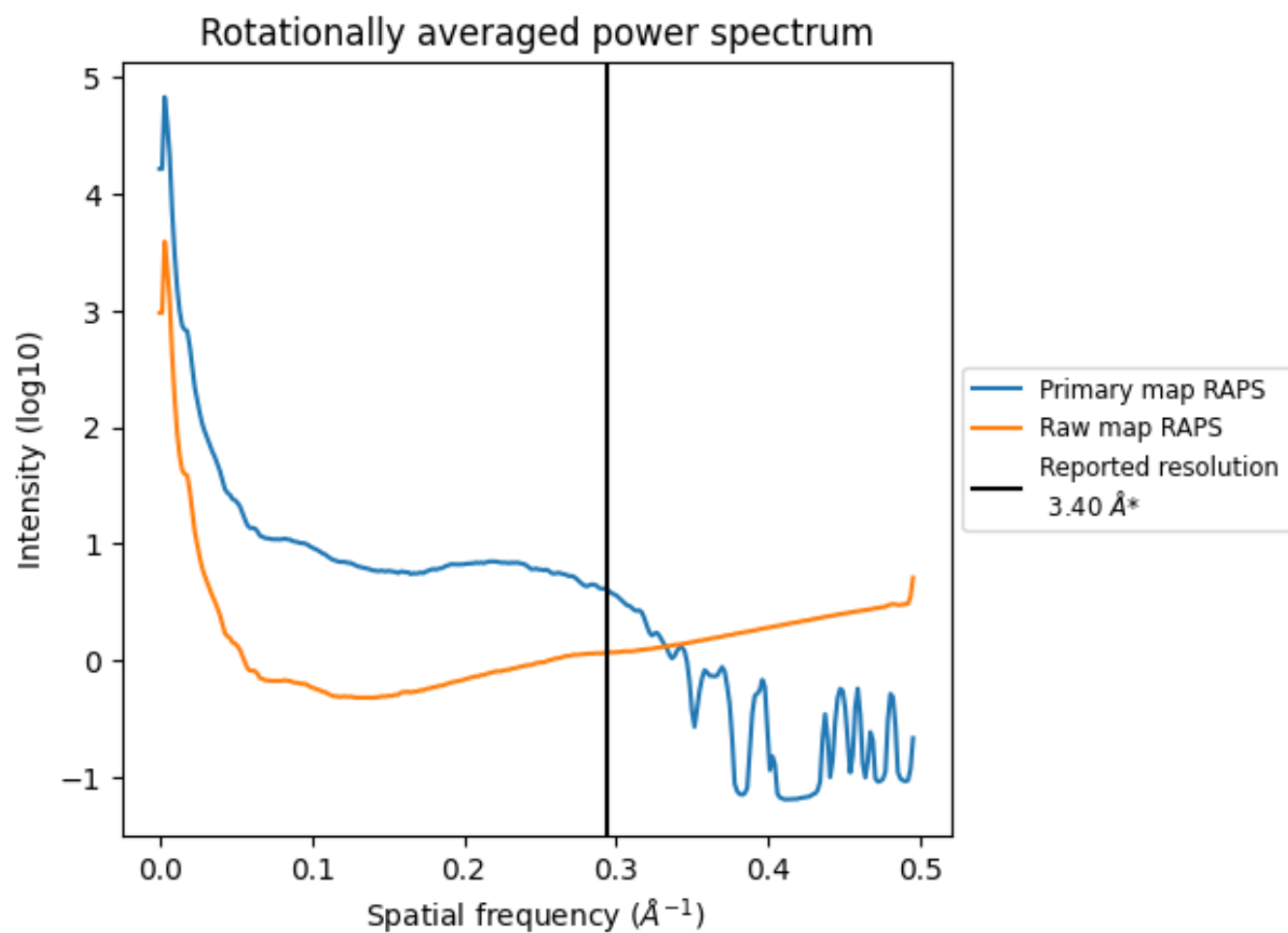
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 419 nm³; this corresponds to an approximate mass of 379 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

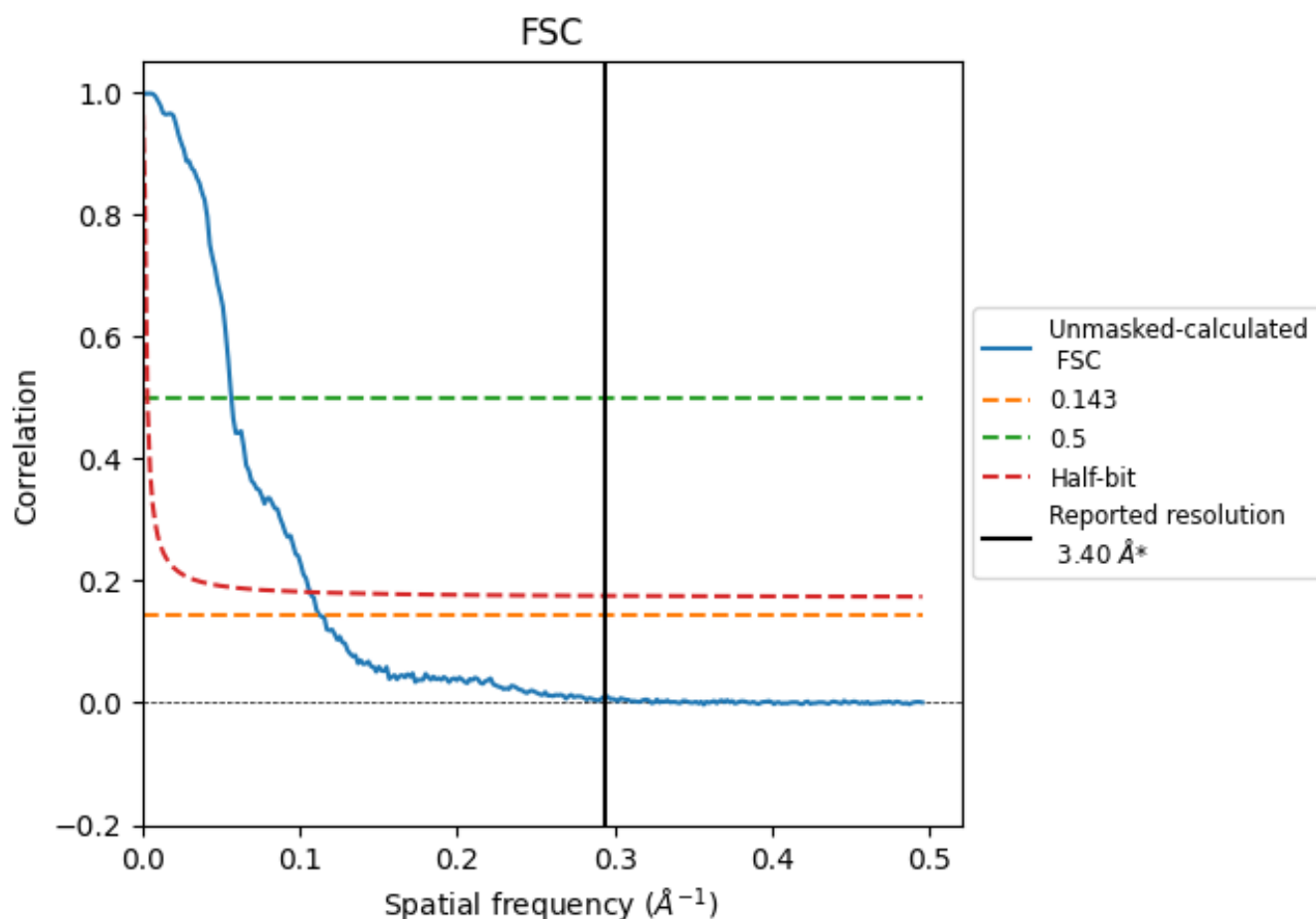


*Reported resolution corresponds to spatial frequency of $0.294 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

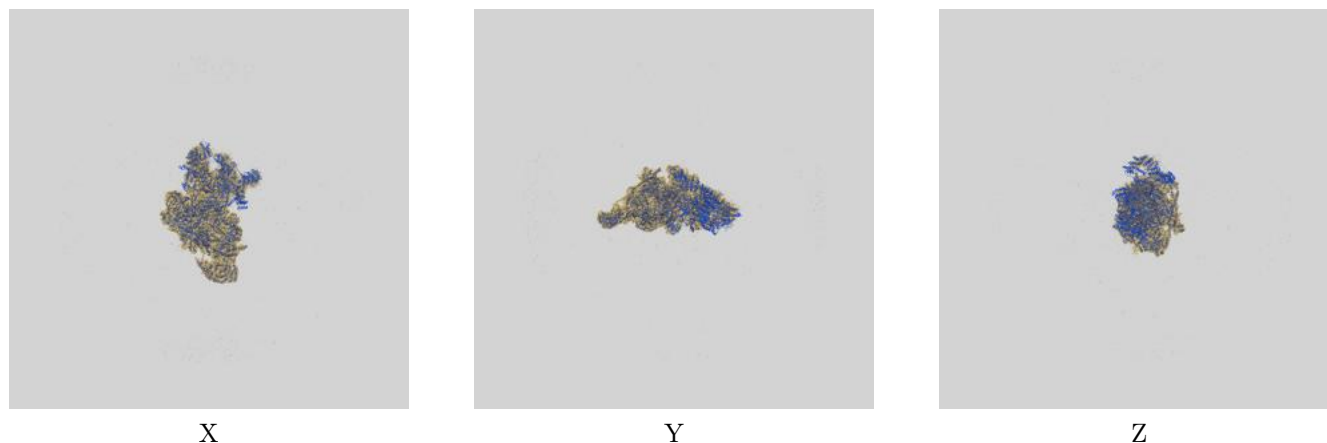
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	3.40	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.87	17.70	9.39

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.5 CUT-OFF 17.70 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

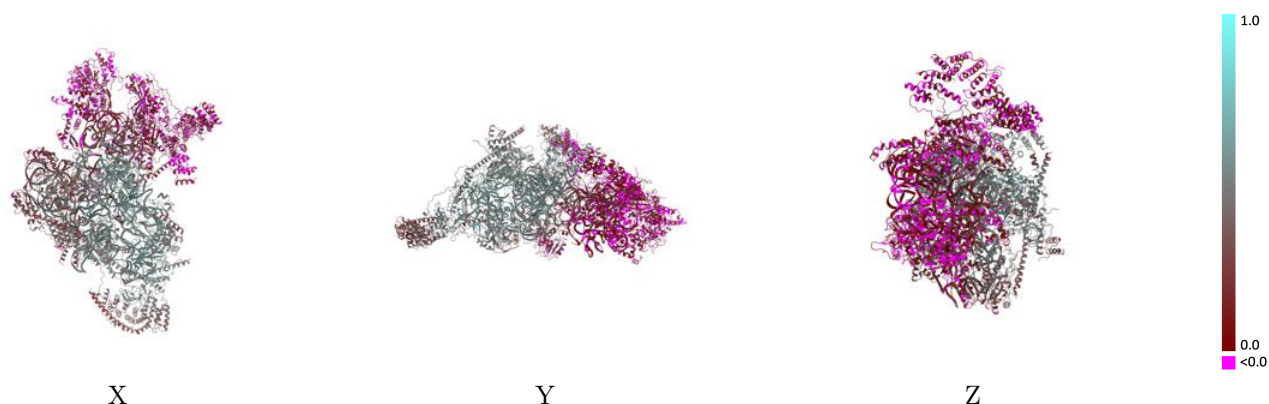
This section contains information regarding the fit between EMDB map EMD-51877 and PDB model 9H55. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



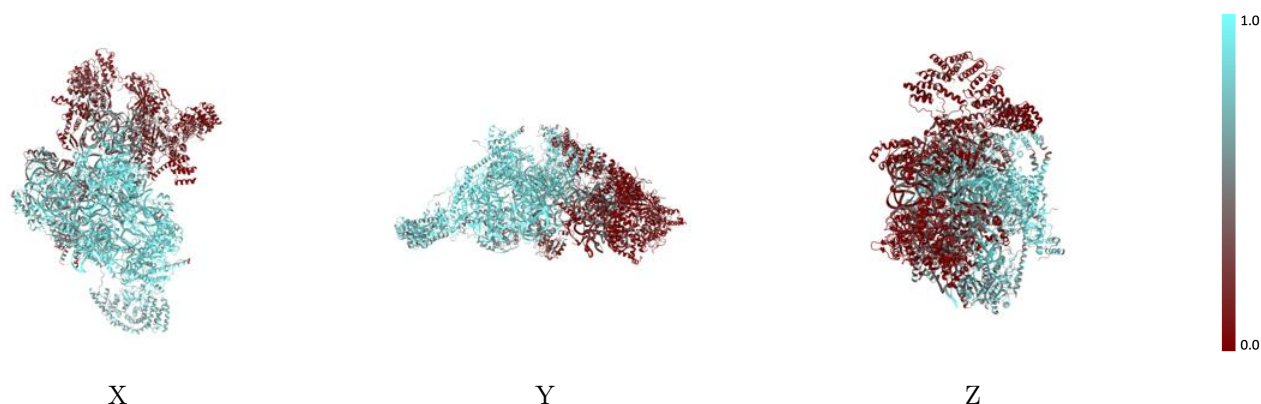
The images above show the 3D surface view of the map at the recommended contour level 0.0054 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



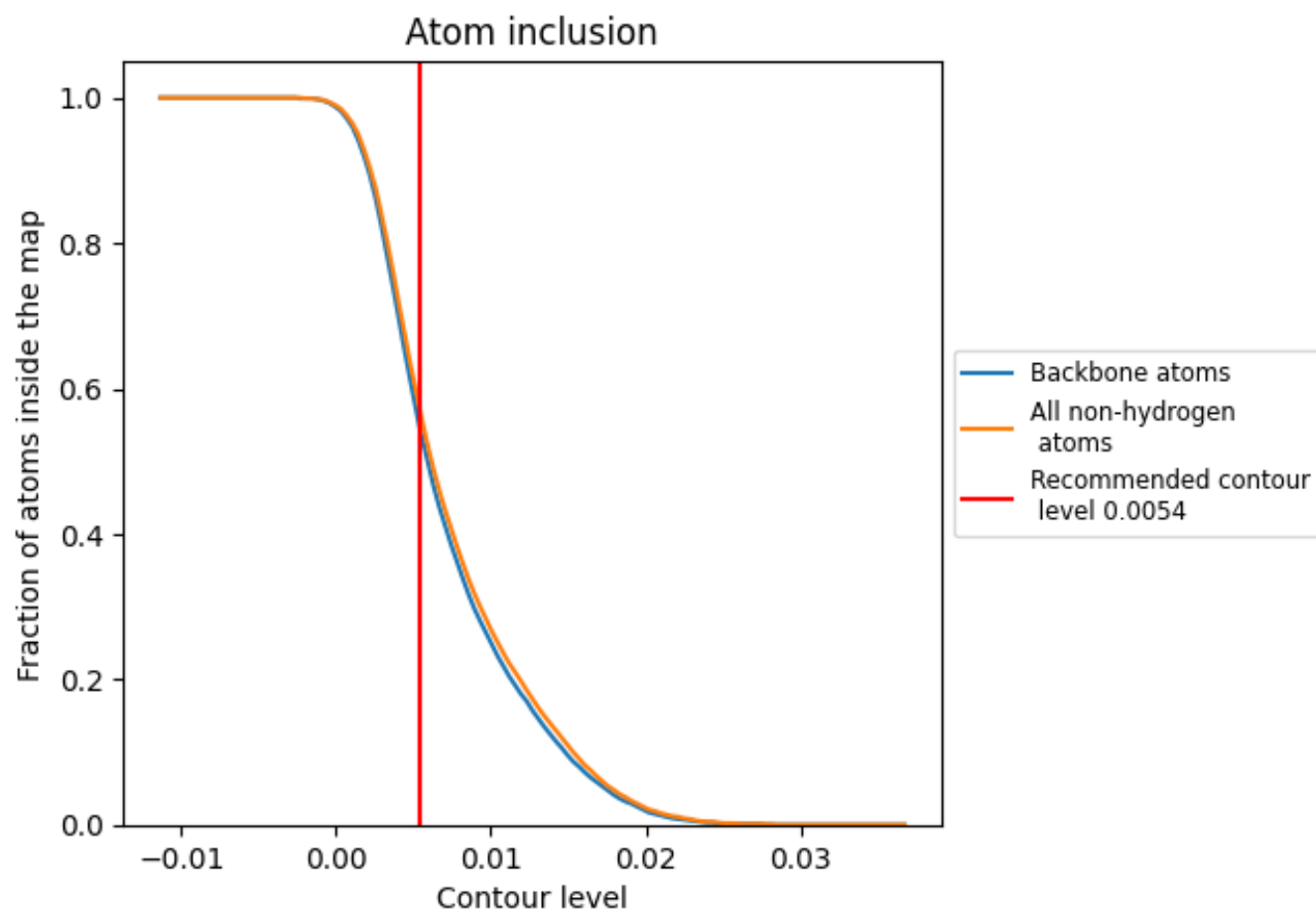
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0054).

9.4 Atom inclusion [i](#)



At the recommended contour level, 55% of all backbone atoms, 57% 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 (0.0054) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5710	 0.3030
0	 0.8260	 0.4810
1	 0.1190	 0.0360
4	 0.0860	 0.0430
5	 0.2970	 0.1760
9	 0.4940	 0.2860
A	 0.7210	 0.3670
B	 0.8910	 0.5310
C	 0.2420	 0.1160
D	 0.6660	 0.4240
E	 0.7240	 0.3530
F	 0.1110	 0.0300
G	 0.4150	 0.2050
H	 0.2110	 0.0980
I	 0.4950	 0.2520
J	 0.7880	 0.4850
K	 0.2530	 0.0780
L	 0.7280	 0.4230
M	 0.9070	 0.5610
N	 0.8720	 0.5330
O	 0.9030	 0.5410
P	 0.7320	 0.3830
Q	 0.6240	 0.3680
R	 0.8700	 0.5130
S	 0.8200	 0.4500
T	 0.8650	 0.5210
U	 0.7710	 0.4110
V	 0.7030	 0.3220
W	 0.8050	 0.4860
X	 0.0910	 0.0340
Y	 0.0920	 0.0630
Z	 0.1700	 0.0910
a	 0.0950	 0.1280

