



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 12:27 AM UTC

PDB ID : 6HIY / pdb_00006hiy
EMDB ID : EMD-0232
Title : Cryo-EM structure of the Trypanosoma brucei mitochondrial ribosome - This entry contains the body of the small mitoribosomal subunit in complex with mt-IF-3
Authors : Ramrath, D.J.F.; Niemann, M.; Leibundgut, M.; Bieri, P.; Prange, C.; Horn, E.K.; Leitner, A.; Boehringer, D.; Schneider, A.; Ban, N.
Deposited on : 2018-08-31
Resolution : 3.27 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

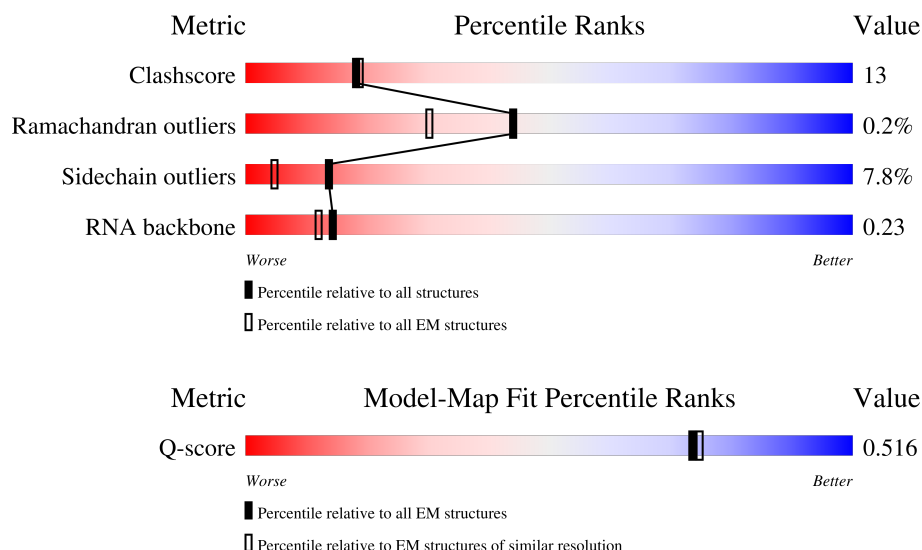
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.27 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.



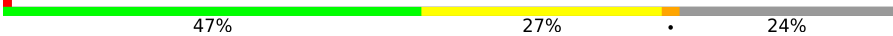
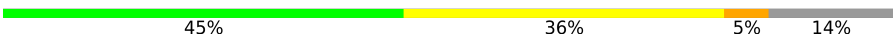
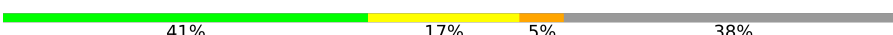
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14508 (2.77 - 3.77)

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	DA	1788	
2	DD	812	
3	DI	407	

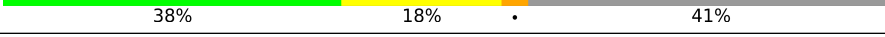
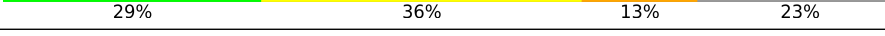
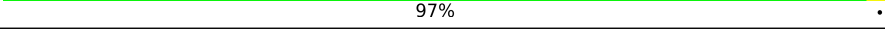
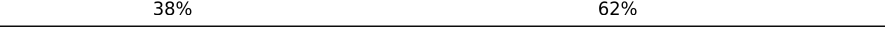
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Mol	Chain	Length	Quality of chain
4	DL	307	
5	DM	294	
6	DN	293	
7	DO	282	
8	DP	274	
9	DQ	268	
10	DR	270	
11	DS	261	
12	DU	228	
13	DZ	94	
14	Da	64	
15	CE	435	
16	CF	160	
17	CH	282	
18	CI	443	
19	CK	326	
20	CL	87	
21	CO	429	
22	CP	188	
23	CQ	307	
24	CR	320	
25	CU	193	
26	CZ	360	
27	Ca	602	
28	Cb	324	

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Mol	Chain	Length	Quality of chain
29	Cd	440	
30	Cj	257	
31	Cm	215	
32	Cn	250	
33	Cp	187	
34	Cq	263	
35	Cr	439	
36	Cv	1211	
37	CA	621	
38	UQ	32	
39	UR	8	
40	US	54	
41	UT	44	

2 Entry composition [i](#)

There are 45 unique types of molecules in this entry. The entry contains 100780 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 mS48.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	DA	1426	Total	C	N	O	S	0	0
			11489	7252	2052	2151	34		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DA	894	HIS	ASN	conflict	UNP Q57UJ2
DA	1181	THR	ILE	conflict	UNP Q57UJ2
DA	1333	ALA	VAL	conflict	UNP Q57UJ2
DA	1700	ARG	HIS	conflict	UNP Q57UJ2
DA	1761	LYS	ARG	conflict	UNP Q57UJ2

- Molecule 2 is a protein called mS51.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	DD	791	Total	C	N	O	S	0	0
			6523	4127	1184	1171	41		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DD	371	PRO	SER	conflict	UNP Q385L8
DD	599	ALA	VAL	conflict	UNP Q385L8

- Molecule 3 is a protein called mS56.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	DI	390	Total	C	N	O	S	0	0
			3182	2020	554	594	14		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DI	92	GLU	GLY	conflict	UNP Q587C2
DI	116	ASP	GLU	conflict	UNP Q587C2

- Molecule 4 is a protein called mS59.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	DL	140	Total	C	N	O	S	0	0
			1134	718	208	199	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DL	274	THR	ALA	conflict	UNP Q38BS2

- Molecule 5 is a protein called mS60.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	DM	294	Total	C	N	O	S	0	0
			2430	1533	459	426	12		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DM	69	PHE	TYR	conflict	UNP Q57XL2
DM	97	ASN	SER	conflict	UNP Q57XL2
DM	138	SER	PRO	conflict	UNP Q57XL2
DM	173	ALA	THR	conflict	UNP Q57XL2
DM	206	ALA	THR	conflict	UNP Q57XL2

- Molecule 6 is a protein called mS61.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	DN	257	Total	C	N	O	S	0	0
			2091	1331	379	371	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DN	51	GLY	SER	conflict	UNP Q38D60

- Molecule 7 is a protein called mS62.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	DO	222	Total	C	N	O	S	0	0
			1804	1127	327	340	10		

- Molecule 8 is a protein called mS63.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	DP	207	Total	C	N	O	S	0	0
			1760	1132	312	307	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DP	3	HIS	ARG	conflict	UNP Q38F25

- Molecule 9 is a protein called mS64.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	DQ	256	Total	C	N	O	S	0	0
			2061	1293	389	370	9		

- Molecule 10 is a protein called mS65.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	DR	251	Total	C	N	O	S	0	0
			2025	1304	369	342	10		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DR	65	GLY	SER	conflict	UNP Q57UA2
DR	94	GLY	GLU	conflict	UNP Q57UA2
DR	128	PRO	SER	conflict	UNP Q57UA2
DR	229	ARG	GLN	conflict	UNP Q57UA2

- Molecule 11 is a protein called mS66.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	DS	238	Total	C	N	O	S	0	0
			1904	1185	356	348	15		

- Molecule 12 is a protein called mS68.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	DU	213	Total	C	N	O	S	0	0
			1754	1103	310	335	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DU	119	ILE	LEU	conflict	UNP Q582T9
DU	152	ILE	VAL	conflict	UNP Q582T9

- Molecule 13 is a protein called mS73.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	DZ	82	Total	C	N	O	S	0	0
			697	457	113	123	4		

- Molecule 14 is a protein called mS74.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Da	55	Total	C	N	O	S	0	0
			501	315	109	74	3		

- Molecule 15 is a protein called mS55m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CE	417	Total	C	N	O	S	0	0
			3399	2151	632	600	16		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CE	341	ARG	LYS	conflict	UNP Q38AX6

- Molecule 16 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CF	159	Total	C	N	O	S	0	0
			1292	821	228	237	6		

- Molecule 17 is a protein called uS8m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CH	273	Total	C	N	O	S	0	0
			2228	1387	432	398	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CH	74	ASN	SER	conflict	UNP Q388R7

- Molecule 18 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CI	202	Total	C	N	O	S	0	0
			1632	1035	281	309	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CI	370	ALA	VAL	conflict	UNP Q57W62

- Molecule 19 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CK	241	Total	C	N	O	S	0	0
			1980	1234	368	363	15		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CK	3	ARG	GLN	conflict	UNP Q389T7
CK	138	UNK	ILE	conflict	UNP Q389T7

- Molecule 20 is a protein called uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CL	87	Total	C	N	O	S	0	0
			733	503	113	107	10		

- Molecule 21 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CO	361	Total	C	N	O	S	0	0
			3003	1907	560	520	16		

- Molecule 22 is a protein called bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CP	180	Total	C	N	O	S	0	0
			1489	956	274	250	9		

- Molecule 23 is a protein called uS17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	CQ	190	Total	C	N	O	S	0	0
			1584	1015	302	259	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CQ	138	ALA	VAL	conflict	UNP Q38DP8

- Molecule 24 is a protein called bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	CR	314	Total	C	N	O	S	0	0
			2567	1623	471	465	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CR	8	ILE	VAL	conflict	UNP Q38AS2

- Molecule 25 is a protein called uS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	CU	184	Total	C	N	O	S	0	0
			1538	965	307	254	12		

- Molecule 26 is a protein called mt-IF-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	CZ	151	Total	C	N	O	S	0	0
			1212	759	231	215	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CZ	6	SER	GLY	conflict	UNP Q57WU2
CZ	30	THR	ILE	conflict	UNP Q57WU2
CZ	172	THR	ALA	conflict	UNP Q57WU2

- Molecule 27 is a protein called mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ca	592	Total	C	N	O	S	0	0
			5004	3201	898	882	23		

- Molecule 28 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Cb	252	Total	C	N	O	S	0	0
			2056	1300	368	380	8		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cb	244	SER	ASN	conflict	UNP Q57VB2
Cb	?	-	GLU	deletion	UNP Q57VB2
Cb	312	CYS	-	expression tag	UNP Q57VB2
Cb	313	SER	-	expression tag	UNP Q57VB2
Cb	314	ARG	-	expression tag	UNP Q57VB2
Cb	315	ASP	-	expression tag	UNP Q57VB2
Cb	316	GLY	-	expression tag	UNP Q57VB2
Cb	317	PHE	-	expression tag	UNP Q57VB2
Cb	318	ALA	-	expression tag	UNP Q57VB2
Cb	319	LEU	-	expression tag	UNP Q57VB2
Cb	320	MET	-	expression tag	UNP Q57VB2
Cb	321	LYS	-	expression tag	UNP Q57VB2
Cb	322	ALA	-	expression tag	UNP Q57VB2
Cb	323	ASN	-	expression tag	UNP Q57VB2
Cb	324	LYS	-	expression tag	UNP Q57VB2

- Molecule 29 is a protein called mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Cd	291	Total	C	N	O	S	0	0
			2389	1491	442	446	10		

- Molecule 30 is a protein called mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Cj	226	Total	C	N	O	S	0	0
			1792	1138	310	340	4		

- Molecule 31 is a protein called mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Cm	196	Total	C	N	O	S	0	0
			1577	975	304	289	9		

- Molecule 32 is a protein called mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Cn	110	Total	C	N	O	S	0	0
			912	585	181	143	3		

- Molecule 33 is a protein called mS41.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Cp	175	Total	C	N	O	S	0	0
			1483	937	268	273	5		

- Molecule 34 is a protein called mS42.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Cq	252	Total	C	N	O	S	0	0
			2005	1285	342	369	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cq	48	THR	ALA	conflict	UNP Q586A1
Cq	167	MET	VAL	conflict	UNP Q586A1

- Molecule 35 is a protein called mS43.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Cr	257	Total	C	N	O	S	0	0
			1999	1261	368	356	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cr	351	LYS	GLU	conflict	UNP Q585I1

- Molecule 36 is a protein called mS47.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Cv	1059	Total	C	N	O	S	0	0
			8557	5387	1535	1596	39		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cv	16	CYS	PRO	conflict	UNP Q383R4
Cv	718	THR	ALA	conflict	UNP Q383R4
Cv	1179	GLU	GLY	conflict	UNP Q383R4

- Molecule 37 is a RNA chain called 9S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	CA	478	Total	C	N	O	P	0	0
			10092	4542	1705	3367	478		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CA	298	U	C	conflict	GB 343546
CA	614	U	-	insertion	GB 343546
CA	615	U	-	insertion	GB 343546
CA	616	U	-	insertion	GB 343546
CA	617	U	-	insertion	GB 343546
CA	618	U	-	insertion	GB 343546
CA	619	U	-	insertion	GB 343546
CA	620	U	-	insertion	GB 343546
CA	621	U	-	insertion	GB 343546

- Molecule 38 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	UQ	32	Total	C	N	O	0	0
			192	128	32	32		

- Molecule 39 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	UR	8	Total	C	N	O	0	0
			48	32	8	8		

- Molecule 40 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	US	54	Total	C	N	O	0	0
			324	216	54	54		

- Molecule 41 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	UT	44	Total	C	N	O	0	0
			264	176	44	44		

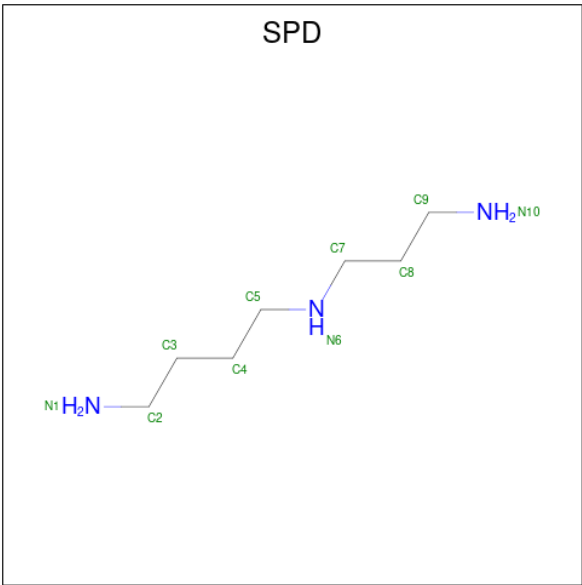
- Molecule 42 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
42	DA	1	Total	Zn	0
			1	1	
42	DS	2	Total	Zn	0
			2	2	
42	Cr	1	Total	Zn	0
			1	1	

- Molecule 43 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

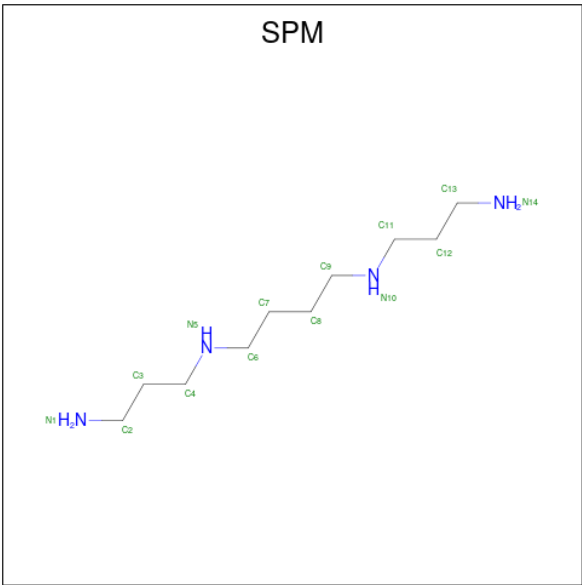
Mol	Chain	Residues	Atoms		AltConf
43	CO	1	Total	Mg	0
			1	1	
43	CQ	1	Total	Mg	0
			1	1	
43	Ca	1	Total	Mg	0
			1	1	
43	Cv	1	Total	Mg	0
			1	1	
43	CA	32	Total	Mg	0
			32	32	

- Molecule 44 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



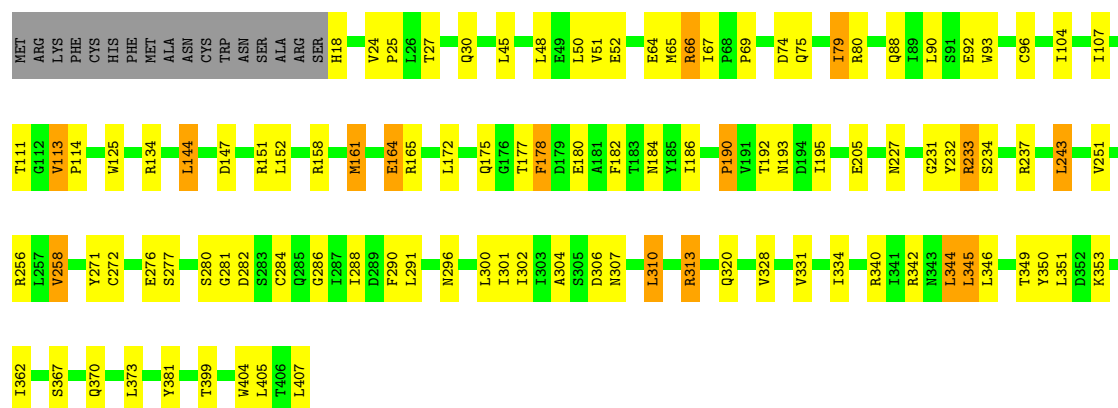
Mol	Chain	Residues	Atoms			AltConf
44	CA	1	Total	C	N	0
			10	7	3	
44	CA	1	Total	C	N	0
			10	7	3	

- Molecule 45 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



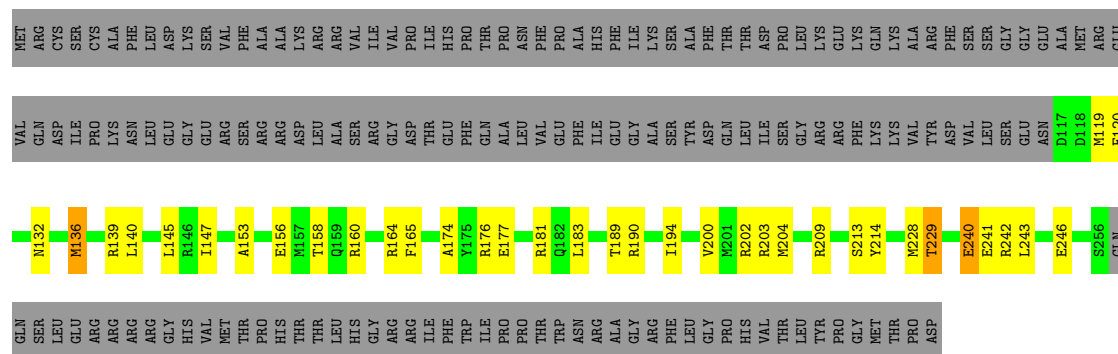
Mol	Chain	Residues	Atoms			AltConf
45	CA	1	Total	C	N	0
			14	10	4	

Chain DI: 



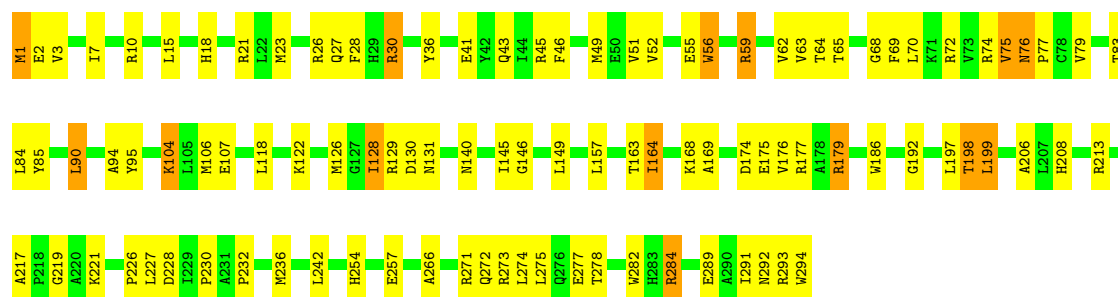
• Molecule 4: mS59

Chain DL: 



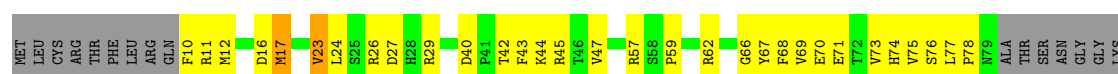
• Molecule 5: mS60

Chain DM: 

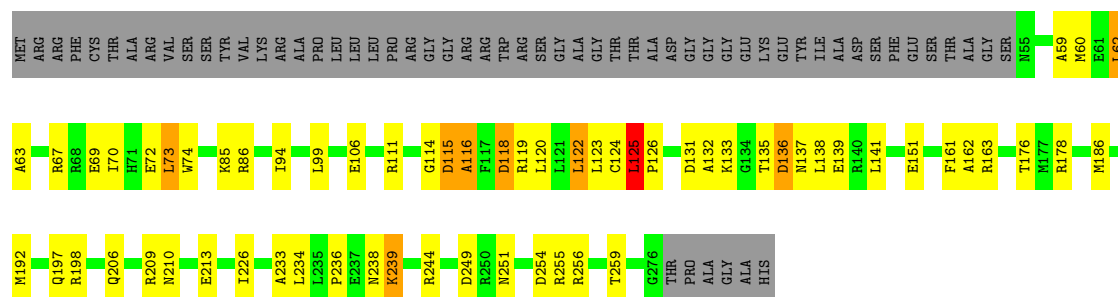


• Molecule 6: mS61

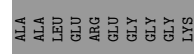
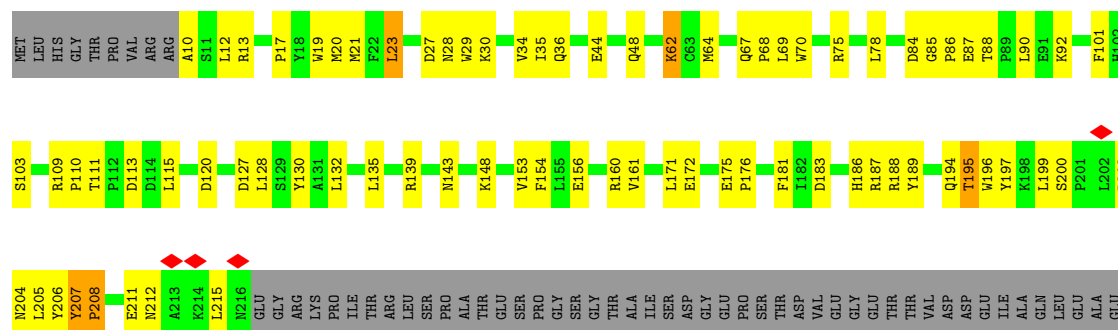
Chain DN: 



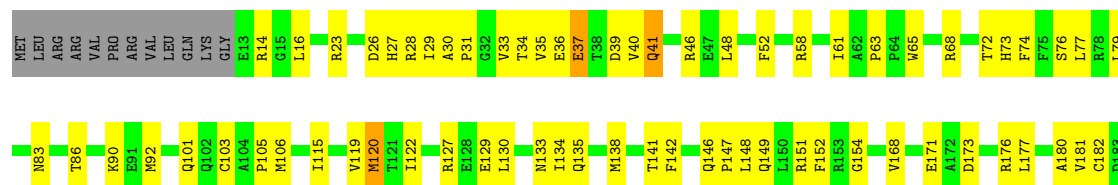
- Molecule 7: mS62

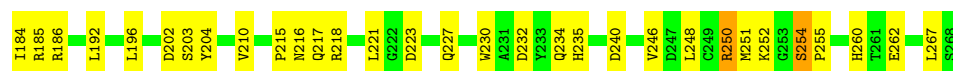


- Molecule 8: mS63



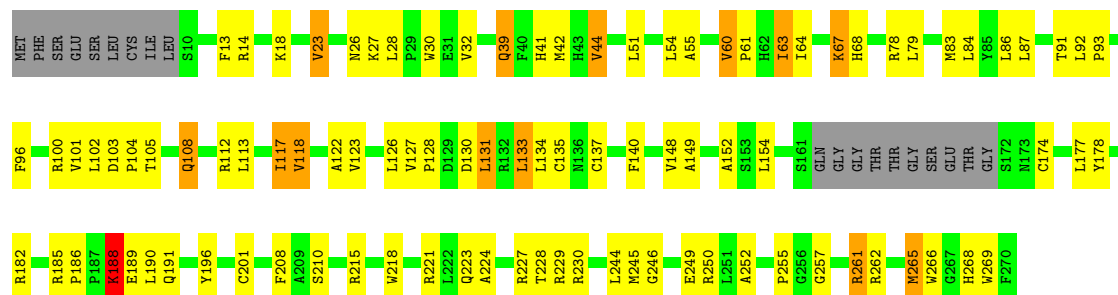
- Molecule 9: mS64





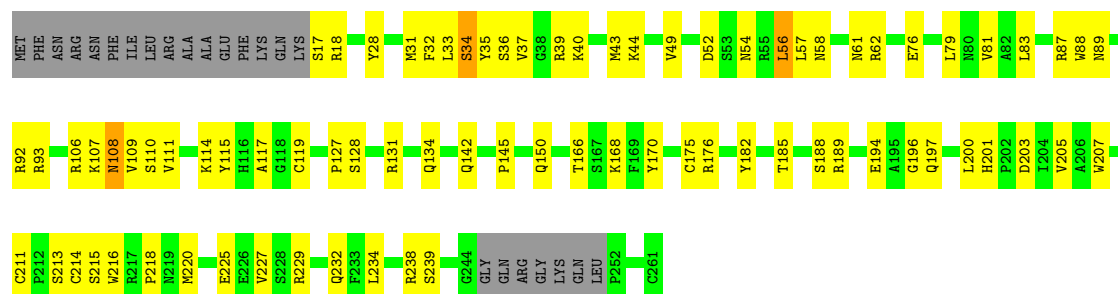
• Molecule 10: mS65

Chain DR: 57% 30% 5% 7%



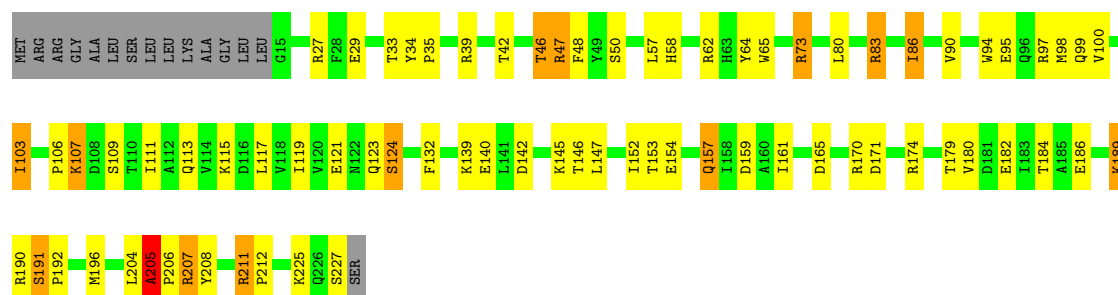
• Molecule 11: mS66

Chain DS: 61% 29% 9%



• Molecule 12: mS68

Chain DU: 61% 27% 6% 7%

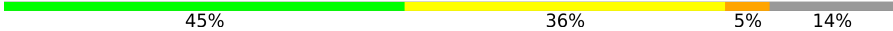


• Molecule 13: mS73

Chain DZ: 64% 20% 13%



• Molecule 14: mS74

Chain Da:  45% 36% 5% 14%

MET PHE SER LEU THR GLN THR TRP LEU
 T10 A11 H12 H13 Y14 C15 G16
 H21 R22 R25 R28 H30 P31 S32 L33 Q34 A35 S36 H37 D38 R40 R41 R42
 K45 R46 T51 R52 R53 W54 R61 P64

• Molecule 15: mS55m

Chain CE:  59% 34% • •

MET PHE ARG SER LEU THR ALA ALA GLN
 K10 N11 L12 M13 S14 W15 Y16 T17 K18
 M21 R22 G23 G24 R27 I28 Y29 Y30 Y31 W32 M33 R34 P35 R40 R41 R42
 R47 N48 S48 L59 Y60 F61 R62 T64 R65 D66 S67 A68 E69 A70 I71 A72
 I80 K81 G82
 M83 D84 N85 A86 I87 D88 L89 R94 I95 E102 Q105 K109 L110 N111 T112 E113 Y114 N115 Q116 W117 R118
 T121 W122 Y123 A124 G134 R135 F136 L137 I144 M149 V152 K153 P156 Q161 W162 I163 Y164 C165
 S171 G172 K173 G174 E188 A189 K190 K191
 E192 R195 I201 D205 L206 E209 G210 Y213 V217 D220 G221 V222 R223 Y227 R231 I232 V233 D240 C243 A244 F245 R253 I254 N255 L256 K257 N260 H267 L279 R280 I285 A286 A287 S288 V292 P293 H294 P302 E306 I307 R308
 R309 R310 G312 G313 M314 A315 R316 R317 P318 R319 G320 L325 M326 P327 D328 D332 P336 L339 R340 R341 G342 Y343 D345 Y348 S356 D357 E358 E362 P363 R364 N365 G366 L367 D370 R373 L376 Q380
 THR SER PRO ALA PRO THR THR ALA LYS D390
 T391 R394 T395 L396 E397 L400 K401 R402 G403 K405 T406 R407 R408 D409 L410 I415 V416 N417 V420 D421 V422 P425 H435

• Molecule 16: bS6m

Chain CF:  74% 22% • •

MET V2 K11 P12 R15 R16 L22 G34 L35 I36 I37 R37 S38 I39 E42 G43 I44 P47 R50 F51 T60 Y61 A62 R63 R64 I65 I66 L67 Q68 L69 D70 M71 M76 M81 L90 L93 S106
 E110 L111 Q112 R123 L124 E127 T128 N129
 Q133 A136 D137 I138 Q141 E143 V146 F149 T152 N160

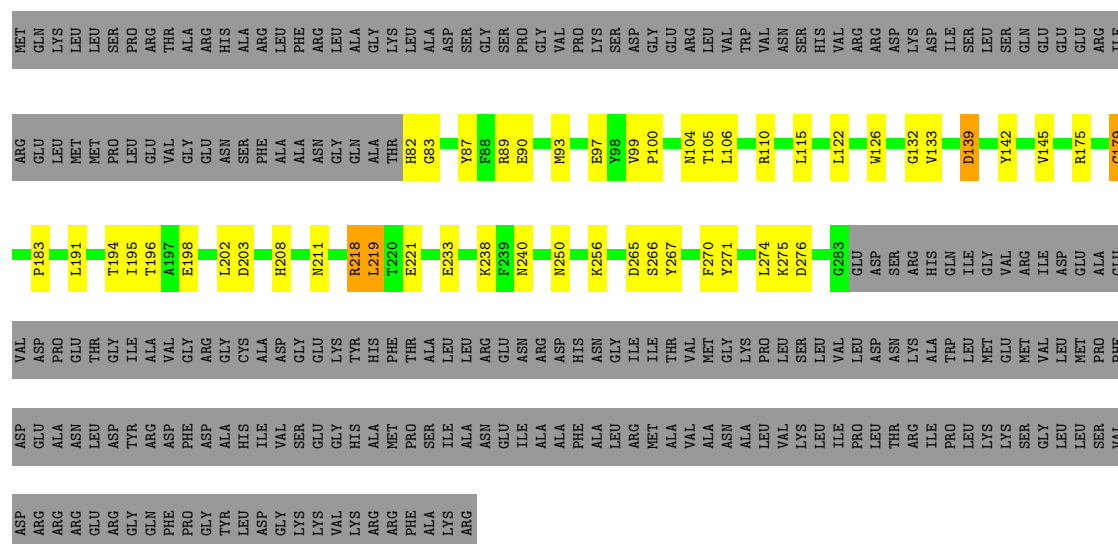
• Molecule 17: uS8m

Chain CH:  68% 25% • •

MET LEU ARG GLN SER LEU LEU SER LEU
 A10 V16 P17 P18 L19 G24 H25 R26 H29 R53 L59 L60 Q68 V77 V78 P84 L88 V89 P92 R97 T105 T106 R107 L108 K113 H116 A117 Y118 Y120 K125 V128 D131 D132 R133
 V134 K138 R142 R143 R144 E146 Y149 T150 P151 T152 T153 D154 R158 T163 K167 V170 V171 V172 P173 I176 E177 T178 R179 H186 R195 D196 R201 A202 F203 Q211 T215 I216 N217 V218 D225 G226 T227 T228 E229 S233 M236 R239
 N248 R249 L250 V251 V252 Y253 D259 R260 R261 L262 L263 D264 H265 L266 E271 R276 M279 M280 V281 H282

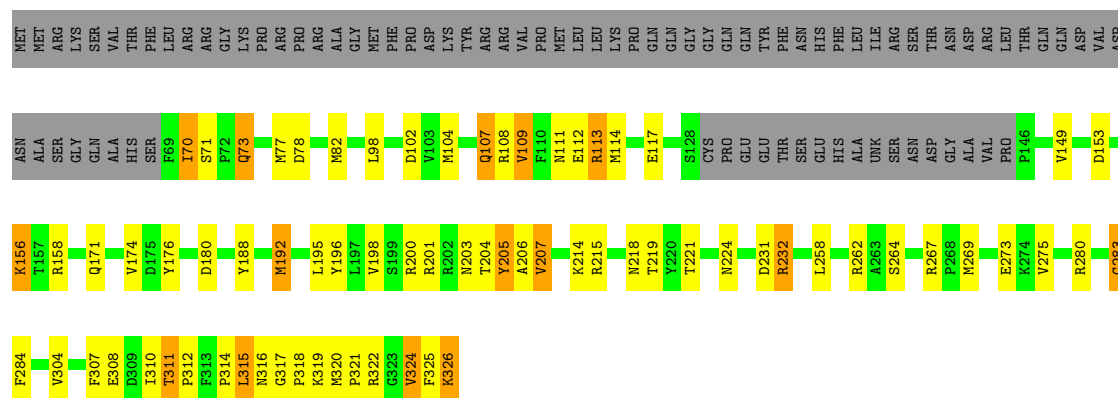
• Molecule 18: uS9m

Chain CI:  35% 10% 54%



• Molecule 19: uS11m

Chain CK:  52% 18% 5% 26%



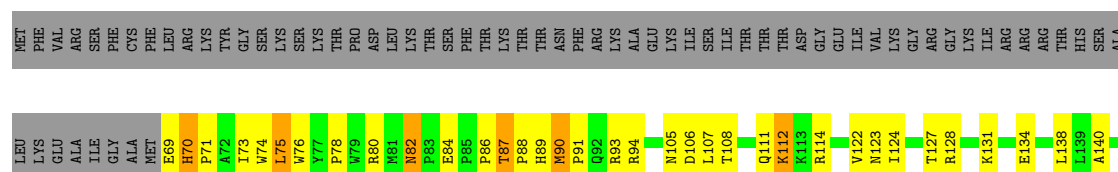
• Molecule 20: uS12m

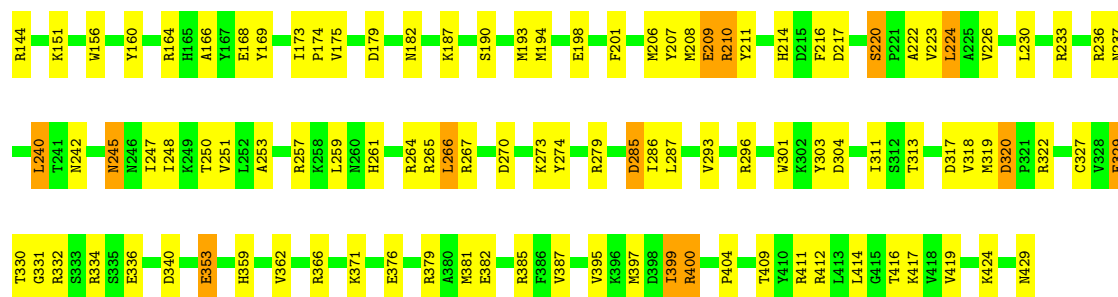
Chain CL:  59% 37% 5%



• Molecule 21: uS15m

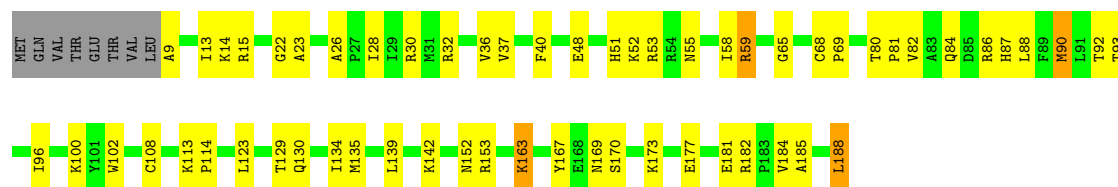
Chain CO:  52% 28% 16%





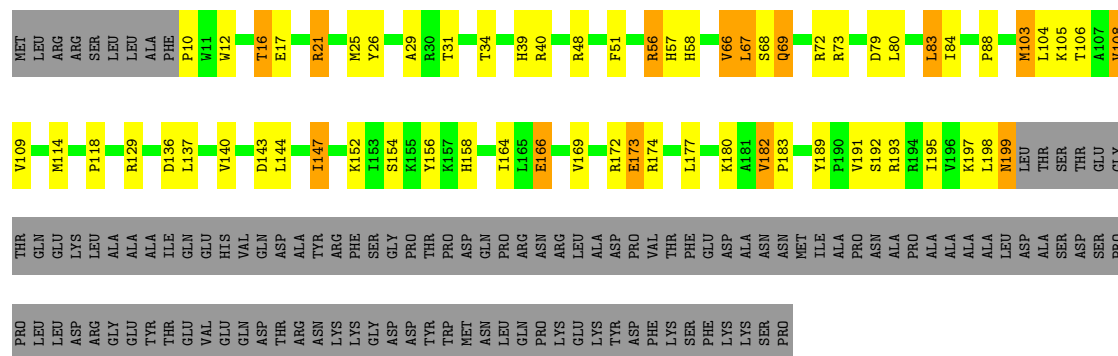
• Molecule 22: bS16m

Chain CP: 64% 29%



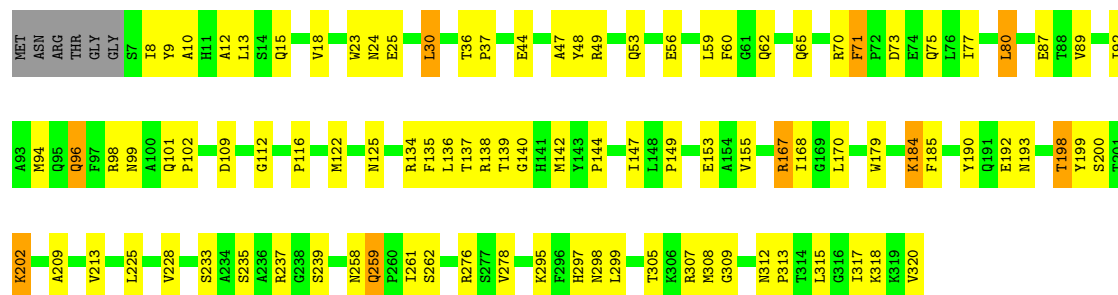
• Molecule 23: uS17m

Chain CQ: 41% 17% 5% 38%



• Molecule 24: bS18m

Chain CR: 68% 28%



• Molecule 25: uS21m

MET	LEU	HIS	THR	THR	ARG	LEU	TRP	LEU	G10	M13	M14	M15	M16	M17	M18	M19	M20	K27	H32	I35	F38	R41	P42	P43	M44	V48	E52	V57	D58	R59	R60	I61	M62	V65	R69	L70	R71	H72	F73	Q74	R77	S78	Y79	Q80	E81	X82	S83	M84	S85	T86	L90	E94	L104	Q105	K106	S107	F108	K115	Q123	P142	M143	M148	K154	Q161	V168	M169	V170	V171	Q180	I181	H182	R185	F186	M187	Y188	R189	M193
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I273	H276	F277	T278	S279	V281	A282	F281	A282	P286	H305	I306	K307	Y308	P309	W314	T315	L318	R319	R320	M321	G332	K341	M359	D360	L370	M371	T372	A373	S374	V375	A376	P377	H378	T379	A380	S381	V382	A383	P384	H385	T386	A387	S388	V389	A390	P391	H392	T393	A394	S395	V396	A397	P398	H399	T400	A401	S402	V403	A404	P405	H406	T407	A408	S409	V410	A411	P412	H413	T414	A415	S416	V417	A418	P419	H420	T421	A422	S423	V424	A425	P426	H427	T428	A429	S430	V431	A432	P433	H434	T435	A436	S437	V438	A439	P440	H441	T442	A443	S444	V445	A446	P447	H448	T449	A450	S451	V452	A453	P454	H455	T456	A457	S458	V459	A460	P461	H462	T463	A464	S465	V466	A467	P468	H469	T470	A471	S472	V473	A474	P475	H476	T477	A478	S479	V480	A481	P482	H483	T484	A485	S486	V487	A488	P489	H490	T491	A492	S493	V494	A495	P496	H497	T498	A499	S500	V501	A502	P503	H504	T505	A506	S507	V508	A509	P510	H511	T512	A513	S514	V515	A516	P517	H518	T519	A520	S521	V522	A523	P524	H525	T526	A527	S528	V529	A530	P531	H532	T533	A534	S535	V536	A537	P538	H539	T540	A541	S542	V543	A544	P545	H546	T547	A548	S
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S556	R470	R369	R254	L134	LEU
S557	F471	E370	Y255	R149	ARG
A558	R473	V376	E266	K153	ALA
G559	R474	D380	L267	E154	TTR
F560	Q475				ILE
R564	G478	Y383	F272	K157	ARG
R568	T479	R384	S276	T158	GLN
R569	L480			E160	R10
T570	R481	Q387	R286		Y11
	K484	Q390	M230	R164	N14
W576	M488	D391		Y168	K15
F578		Y392	L293	F172	E31
V579	Y491	E393	D294	G173	P32
	Y492	Q397	F295	D174	P33
Q585	E496	D398	L296		K34
F586		N399	L297		P35
Q587	F500	Y400	V298	Q177	
K588	F501	Y402	R299	F178	W38
	F502	Y403	X300	L179	R39
K597		R404	L301	R180	
A598	Q506	R405	V303	E181	V43
F599	M507	N406	A309	E189	R46
E601	E508	F407		G190	L61
LEU	W509	P408	C314	M191	W62
		E409		Q192	
	N513	M410	D318	R193	P66
	T514		L194	L195	R67
	P515	T414			S68
			K323	R201	
	E518	V418	W330		W71
	Q519		I331	L205	
	Y520	Q423	R332	L206	L75
	Q521		D333	A207	Q76
	E522	W427	V334	V208	
	H523		R335		M79
	W524	R432		L217	
	P525	Q433	K338	T221	P82
			H339		
	D529	S438	G340	P225	R88
	R536	M443	L341	R227	R89
	E537	F444		H226	Y90
	I538		R347	K228	D91
	Q539	T447	F348	E229	P98
	S540		A349		
	R541	V451	E350	Q232	W102
	P542		F355	R233	
		K457			A121
	F546	K458	R359	S240	
	Y547	L459		T243	I124
	E548	E460	L365	P244	Y130
	S549	L461	V366	E245	M131
			R367		
	T552	K467	P368		
	R552				

Device Type	Percentage
Smartphones	56%
Tablets	20%
Feature phones	2%
Other devices	22%



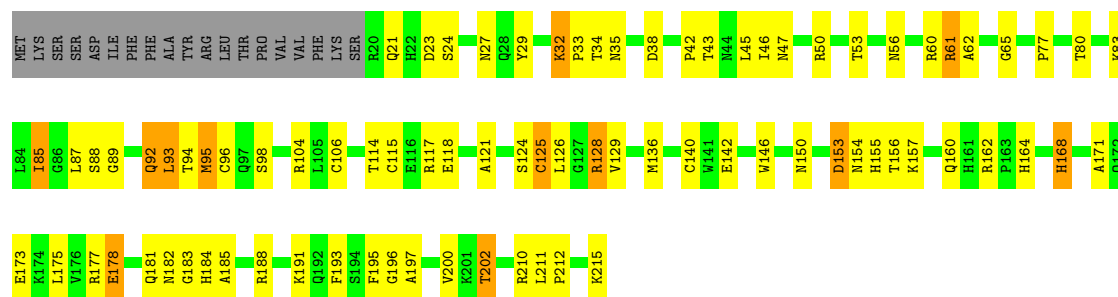
Response	Percentage
Good country	48%
Not a good country	15%
Don't know	34%



Frequency	Percentage
Daily	65%
Weekly	19%
Monthly	5%
Never	12%

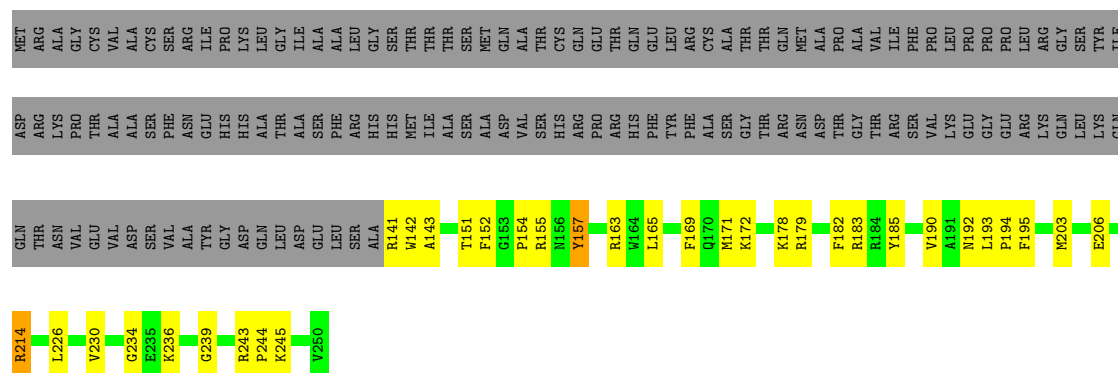


Age Group	Percentage
18-24	53%
25-34	33%
35-44	6%
45-54	9%



• Molecule 32: mS38

Chain Cn: 30% 13% 56%



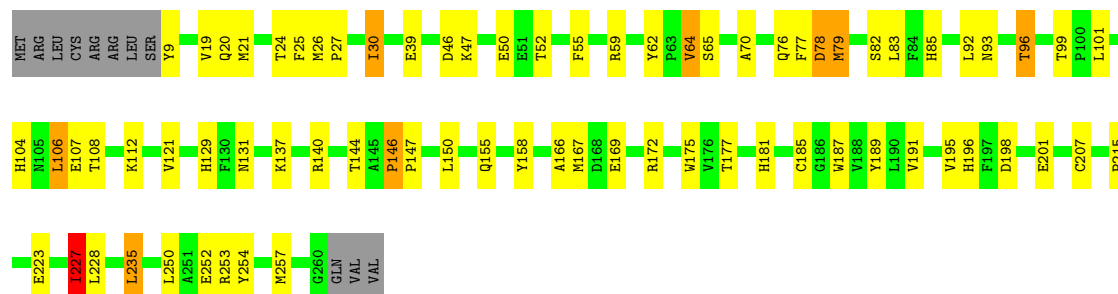
• Molecule 33: mS41

Chain Cp: 53% 39% 6%



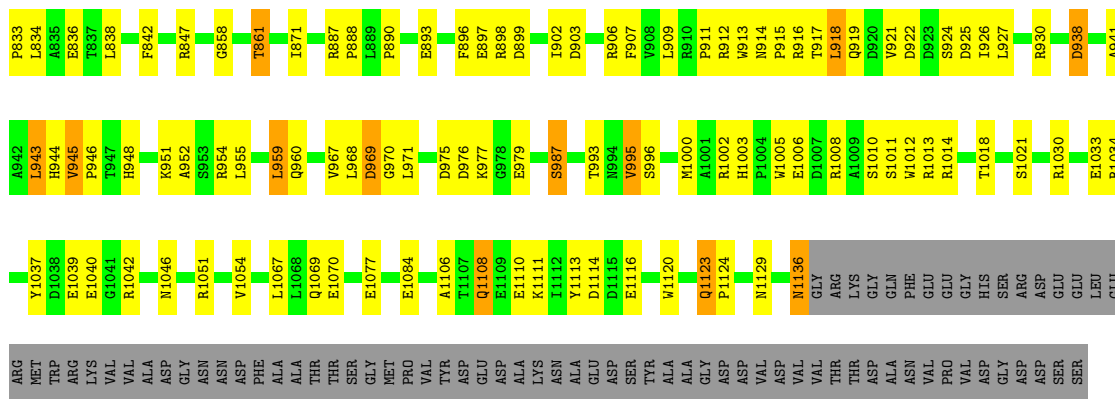
• Molecule 34: mS42

Chain Cq: 68% 25% 7%

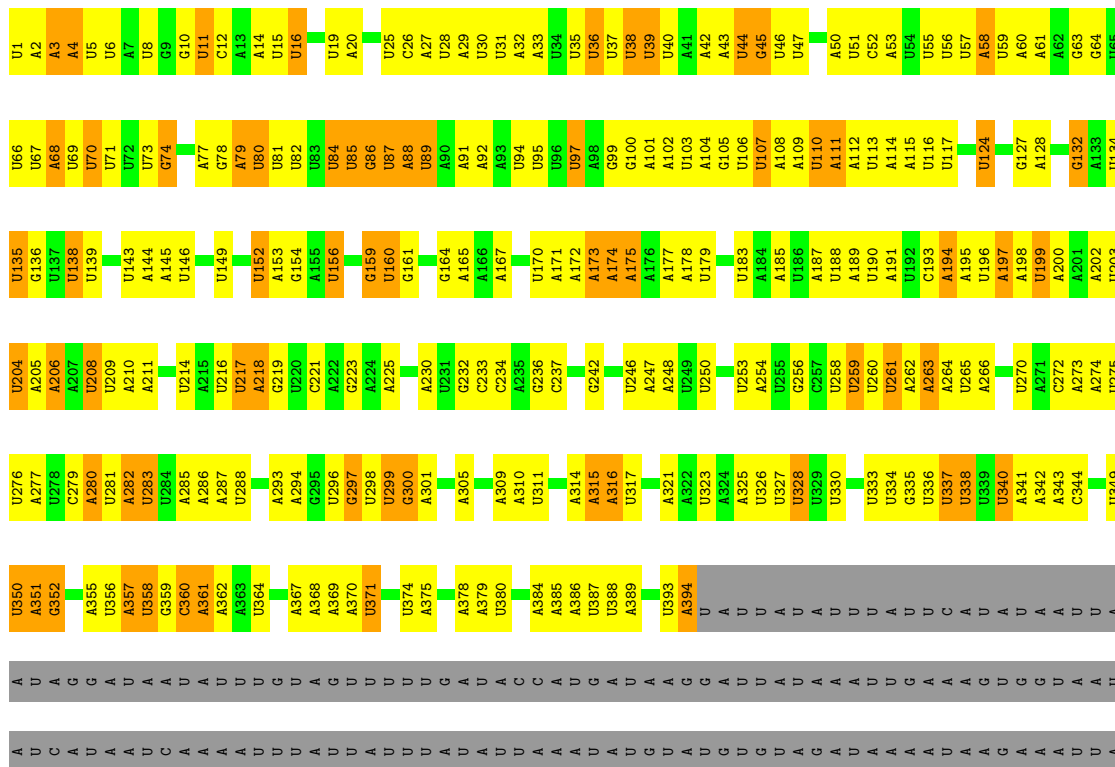


Chain Cr: 38% 18% . 41%

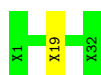




• Molecule 37: 9S rRNA



• Molecule 38: Unknown protein



• Molecule 39: Unknown protein

Chain UR:  38% 62%



- Molecule 40: Unknown protein

Chain US:  87% 13%



- Molecule 41: Unknown protein

Chain UT:  66% 34%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31911	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.514	Depositor
Minimum map value	-0.265	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.0115	Depositor
Map size (Å)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	DA	0.48	4/11769 (0.0%)	0.88	29/15925 (0.2%)
2	DD	0.48	0/6710	0.91	11/9087 (0.1%)
3	DI	0.46	0/3248	0.88	3/4401 (0.1%)
4	DL	0.50	0/1160	0.90	6/1560 (0.4%)
5	DM	0.49	0/2488	0.88	7/3362 (0.2%)
6	DN	0.53	0/2148	0.99	8/2916 (0.3%)
7	DO	0.46	0/1840	0.89	5/2482 (0.2%)
8	DP	0.57	0/1813	0.89	2/2457 (0.1%)
9	DQ	0.47	0/2111	0.92	0/2863
10	DR	0.48	0/2090	0.92	4/2849 (0.1%)
11	DS	0.43	0/1950	0.82	0/2633
12	DU	0.46	0/1799	0.86	4/2438 (0.2%)
13	DZ	0.45	0/725	0.87	2/984 (0.2%)
14	Da	0.45	0/520	0.83	0/694
15	CE	0.53	0/3484	0.90	4/4708 (0.1%)
16	CF	0.46	0/1319	0.81	0/1783
17	CH	0.52	0/2276	0.95	6/3071 (0.2%)
18	CI	0.44	0/1670	0.77	0/2260
19	CK	0.43	0/2024	0.88	1/2715 (0.0%)
20	CL	0.46	0/759	0.87	2/1026 (0.2%)
21	CO	0.48	0/3085	0.89	2/4165 (0.0%)
22	CP	0.55	0/1533	0.93	5/2074 (0.2%)
23	CQ	0.56	0/1631	0.98	4/2203 (0.2%)
24	CR	0.49	0/2640	0.88	3/3572 (0.1%)
25	CU	0.45	0/1576	0.80	0/2115
26	CZ	0.51	0/1237	0.88	1/1659 (0.1%)
27	Ca	0.49	0/5159	0.90	13/6980 (0.2%)
28	Cb	0.49	0/2105	0.88	0/2842
29	Cd	0.50	0/2446	0.81	0/3299
30	Cj	0.44	0/1842	0.87	2/2511 (0.1%)
31	Cm	0.53	0/1616	0.97	5/2175 (0.2%)
32	Cn	0.49	0/934	0.91	3/1248 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Cp	0.44	0/1528	0.85	3/2072 (0.1%)
34	Cq	0.48	0/2066	0.85	3/2815 (0.1%)
35	Cr	0.45	0/2038	0.90	7/2759 (0.3%)
36	Cv	0.46	0/8780	0.90	15/11901 (0.1%)
37	CA	0.28	0/11286	0.45	0/17548
All	All	0.47	4/103405 (0.0%)	0.85	160/142152 (0.1%)

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
1	DA	0	1
2	DD	0	2
6	DN	0	2
7	DO	0	2
10	DR	0	1
17	CH	0	1
27	Ca	0	1
30	Cj	0	1
36	Cv	0	2
All	All	0	13

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	DA	323	HIS	CG-CD2	10.30	1.47	1.35
1	DA	529	ILE	C-O	5.88	1.30	1.24
1	DA	323	HIS	CD2-NE2	-5.66	1.31	1.37
1	DA	323	HIS	CB-CG	-5.29	1.42	1.50

The worst 5 of 160 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	CK	283	GLY	N-CA-C	14.42	132.53	114.37
2	DD	255	VAL	CA-C-N	12.41	135.36	119.84
2	DD	255	VAL	C-N-CA	12.41	135.36	119.84
27	Ca	32	PRO	N-CA-CB	8.14	110.98	103.08
7	DO	125	LEU	CA-C-N	-7.86	110.57	120.23

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	DA	166	TYR	Peptide
2	DD	248	ASP	Peptide
2	DD	255	VAL	Peptide
6	DN	142	ARG	Peptide
6	DN	292	TYR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DA	11489	0	11135	280	0
2	DD	6523	0	6307	215	0
3	DI	3182	0	3153	71	0
4	DL	1134	0	1128	31	0
5	DM	2430	0	2427	86	0
6	DN	2091	0	2076	120	0
7	DO	1804	0	1752	51	0
8	DP	1760	0	1723	77	0
9	DQ	2061	0	2041	85	0
10	DR	2025	0	2029	107	0
11	DS	1904	0	1855	61	0
12	DU	1754	0	1687	82	0
13	DZ	697	0	644	26	0
14	Da	501	0	473	26	0
15	CE	3399	0	3376	145	0
16	CF	1292	0	1261	30	0
17	CH	2228	0	2204	65	0
18	CI	1632	0	1568	54	0
19	CK	1980	0	1922	85	0
20	CL	733	0	738	35	0
21	CO	3003	0	2995	111	0
22	CP	1489	0	1510	58	0
23	CQ	1584	0	1601	52	0
24	CR	2567	0	2508	87	0
25	CU	1538	0	1539	54	0
26	CZ	1212	0	1178	27	0
27	Ca	5004	0	4776	184	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	Cb	2056	0	2031	79	0
29	Cd	2389	0	2232	67	0
30	Cj	1792	0	1744	55	0
31	Cm	1577	0	1505	66	0
32	Cn	912	0	969	33	0
33	Cp	1483	0	1438	58	0
34	Cq	2005	0	1916	52	0
35	Cr	1999	0	2007	62	0
36	Cv	8557	0	8252	265	0
37	CA	10092	0	5051	221	0
38	UQ	192	0	194	2	0
39	UR	48	0	50	6	0
40	US	324	0	326	8	0
41	UT	264	0	267	10	0
42	Cr	1	0	0	0	0
42	DA	1	0	0	0	0
42	DS	2	0	0	0	0
43	CA	32	0	0	0	0
43	CO	1	0	0	0	0
43	CQ	1	0	0	0	0
43	Ca	1	0	0	0	0
43	Cv	1	0	0	0	0
44	CA	20	0	38	1	0
45	CA	14	0	26	1	0
All	All	100780	0	93652	2556	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 13.

The worst 5 of 2556 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)
10:DR:128:PRO:CD	10:DR:133:LEU:O	1.77	1.31
10:DR:261:ARG:HH21	37:CA:81:U:P	1.53	1.29
22:CP:23:ALA:HB2	22:CP:51:HIS:CG	1.68	1.28
2:DD:339:ARG:NH2	37:CA:85:U:O2	1.65	1.25
10:DR:128:PRO:HD2	10:DR:133:LEU:O	1.34	1.22

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	DA	1420/1788 (79%)	1370 (96%)	48 (3%)	2 (0%)	48	76
2	DD	787/812 (97%)	747 (95%)	38 (5%)	2 (0%)	36	66
3	DI	388/407 (95%)	366 (94%)	21 (5%)	1 (0%)	36	66
4	DL	138/307 (45%)	130 (94%)	8 (6%)	0	100	100
5	DM	292/294 (99%)	283 (97%)	9 (3%)	0	100	100
6	DN	253/293 (86%)	242 (96%)	11 (4%)	0	100	100
7	DO	220/282 (78%)	213 (97%)	6 (3%)	1 (0%)	24	55
8	DP	205/274 (75%)	195 (95%)	9 (4%)	1 (0%)	24	55
9	DQ	254/268 (95%)	246 (97%)	6 (2%)	2 (1%)	16	44
10	DR	247/270 (92%)	239 (97%)	8 (3%)	0	100	100
11	DS	234/261 (90%)	227 (97%)	7 (3%)	0	100	100
12	DU	211/228 (92%)	202 (96%)	7 (3%)	2 (1%)	14	43
13	DZ	80/94 (85%)	75 (94%)	5 (6%)	0	100	100
14	Da	53/64 (83%)	52 (98%)	1 (2%)	0	100	100
15	CE	413/435 (95%)	395 (96%)	18 (4%)	0	100	100
16	CF	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
17	CH	271/282 (96%)	265 (98%)	5 (2%)	1 (0%)	30	60
18	CI	200/443 (45%)	196 (98%)	4 (2%)	0	100	100
19	CK	237/326 (73%)	225 (95%)	12 (5%)	0	100	100
20	CL	85/87 (98%)	80 (94%)	5 (6%)	0	100	100
21	CO	359/429 (84%)	343 (96%)	14 (4%)	2 (1%)	21	51
22	CP	178/188 (95%)	171 (96%)	7 (4%)	0	100	100
23	CQ	188/307 (61%)	182 (97%)	6 (3%)	0	100	100
24	CR	312/320 (98%)	297 (95%)	14 (4%)	1 (0%)	36	66
25	CU	182/193 (94%)	177 (97%)	4 (2%)	1 (0%)	24	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	CZ	149/360 (41%)	142 (95%)	6 (4%)	1 (1%)	18	48
27	Ca	590/602 (98%)	556 (94%)	29 (5%)	5 (1%)	16	44
28	Cb	248/324 (76%)	242 (98%)	6 (2%)	0	100	100
29	Cd	289/440 (66%)	281 (97%)	6 (2%)	2 (1%)	18	48
30	Cj	224/257 (87%)	216 (96%)	7 (3%)	1 (0%)	30	60
31	Cm	194/215 (90%)	184 (95%)	10 (5%)	0	100	100
32	Cn	108/250 (43%)	103 (95%)	5 (5%)	0	100	100
33	Cp	173/187 (92%)	169 (98%)	4 (2%)	0	100	100
34	Cq	250/263 (95%)	243 (97%)	7 (3%)	0	100	100
35	Cr	253/439 (58%)	243 (96%)	9 (4%)	1 (0%)	30	60
36	Cv	1051/1211 (87%)	1011 (96%)	40 (4%)	0	100	100
All	All	10893/13360 (82%)	10460 (96%)	407 (4%)	26 (0%)	44	71

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	CZ	296	PRO
27	Ca	32	PRO
27	Ca	33	PRO
27	Ca	35	PRO
24	CR	10	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DA	1211/1514 (80%)	1130 (93%)	81 (7%)	15	42
2	DD	694/711 (98%)	651 (94%)	43 (6%)	16	44
3	DI	350/365 (96%)	323 (92%)	27 (8%)	12	37
4	DL	118/263 (45%)	109 (92%)	9 (8%)	12	38
5	DM	252/252 (100%)	232 (92%)	20 (8%)	11	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	DN	229/256 (90%)	209 (91%)	20 (9%)	9	32
7	DO	186/229 (81%)	176 (95%)	10 (5%)	20	48
8	DP	187/239 (78%)	179 (96%)	8 (4%)	26	54
9	DQ	228/239 (95%)	218 (96%)	10 (4%)	25	54
10	DR	220/235 (94%)	196 (89%)	24 (11%)	6	23
11	DS	209/228 (92%)	196 (94%)	13 (6%)	16	44
12	DU	190/201 (94%)	171 (90%)	19 (10%)	7	27
13	DZ	72/84 (86%)	68 (94%)	4 (6%)	19	47
14	Da	50/59 (85%)	46 (92%)	4 (8%)	11	36
15	CE	358/372 (96%)	321 (90%)	37 (10%)	7	26
16	CF	136/144 (94%)	126 (93%)	10 (7%)	13	39
17	CH	237/246 (96%)	217 (92%)	20 (8%)	10	34
18	CI	171/371 (46%)	167 (98%)	4 (2%)	44	66
19	CK	210/283 (74%)	191 (91%)	19 (9%)	9	31
20	CL	79/79 (100%)	73 (92%)	6 (8%)	12	38
21	CO	318/377 (84%)	290 (91%)	28 (9%)	9	32
22	CP	160/168 (95%)	143 (89%)	17 (11%)	6	24
23	CQ	171/270 (63%)	151 (88%)	20 (12%)	5	21
24	CR	275/279 (99%)	256 (93%)	19 (7%)	14	42
25	CU	160/169 (95%)	149 (93%)	11 (7%)	14	42
26	CZ	121/313 (39%)	110 (91%)	11 (9%)	9	31
27	Ca	516/543 (95%)	477 (92%)	39 (8%)	12	38
28	Cb	219/277 (79%)	207 (94%)	12 (6%)	19	47
29	Cd	240/381 (63%)	218 (91%)	22 (9%)	8	30
30	Cj	193/219 (88%)	180 (93%)	13 (7%)	15	42
31	Cm	165/184 (90%)	141 (86%)	24 (14%)	3	15
32	Cn	95/210 (45%)	90 (95%)	5 (5%)	20	49
33	Cp	163/175 (93%)	152 (93%)	11 (7%)	15	42
34	Cq	210/221 (95%)	193 (92%)	17 (8%)	11	36
35	Cr	211/369 (57%)	189 (90%)	22 (10%)	7	25
36	Cv	912/1034 (88%)	830 (91%)	82 (9%)	9	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	9516/11559 (82%)	8775 (92%)	741 (8%)	14	37

5 of 741 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	CR	202	LYS
30	Cj	138	ASP
25	CU	74	GLN
24	CR	198	THR
27	Ca	433	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 245 such sidechains are listed below:

Mol	Chain	Res	Type
12	DU	96	GLN
35	Cr	142	ASN
19	CK	107	GLN
35	Cr	80	HIS
36	Cv	739	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
37	CA	476/621 (76%)	213 (44%)	2 (0%)

5 of 213 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
37	CA	2	A
37	CA	3	A
37	CA	4	A
37	CA	5	U
37	CA	6	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
37	CA	38	U
37	CA	39	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 43 ligands modelled in this entry, 40 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
45	SPM	CA	735	-	13,13,13	0.33	0	12,12,12	0.84	0
44	SPD	CA	734	-	9,9,9	0.34	0	8,8,8	0.67	0
44	SPD	CA	733	-	9,9,9	0.48	0	8,8,8	0.48	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
45	SPM	CA	735	-	-	8/11/11/11	-
44	SPD	CA	734	-	-	3/7/7/7	-
44	SPD	CA	733	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
45	CA	735	SPM	C2-C3-C4-N5
45	CA	735	SPM	N10-C11-C12-C13
44	CA	733	SPD	C3-C4-C5-N6
45	CA	735	SPM	C6-C7-C8-C9
45	CA	735	SPM	C7-C8-C9-N10

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	CA	735	SPM	1	0
44	CA	733	SPD	1	0

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.

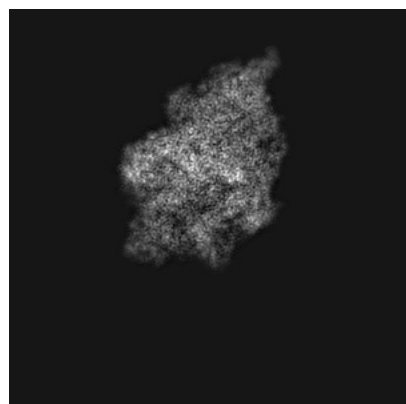
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0232. These allow visual inspection of the internal detail of the map and identification of artifacts.

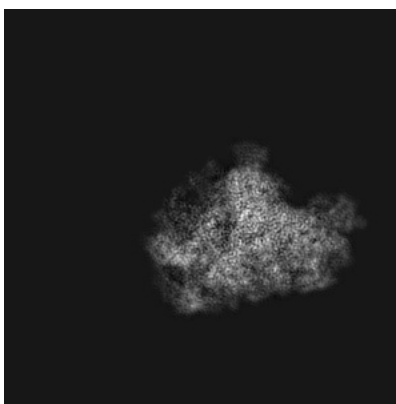
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

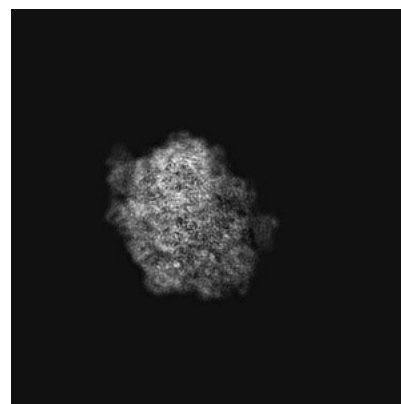
6.1.1 Primary map



X

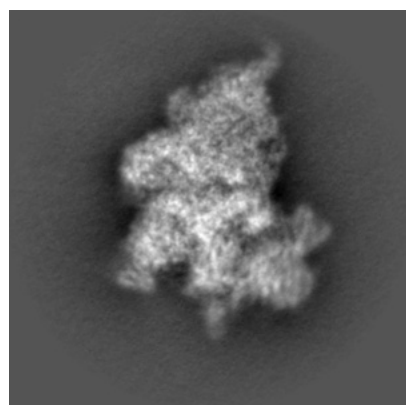


Y

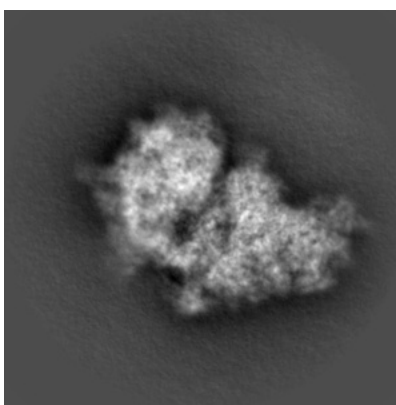


Z

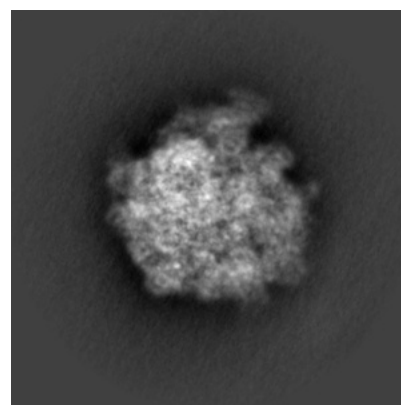
6.1.2 Raw map



X



Y

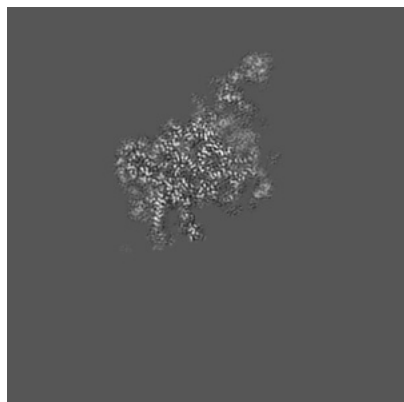


Z

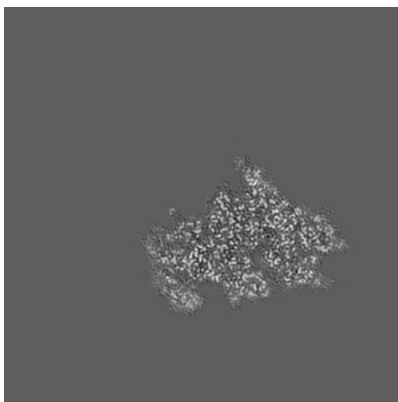
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

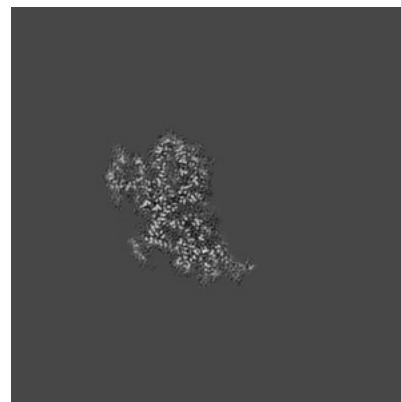
6.2.1 Primary map



X Index: 160

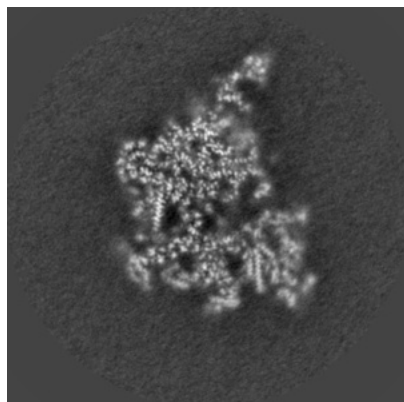


Y Index: 160

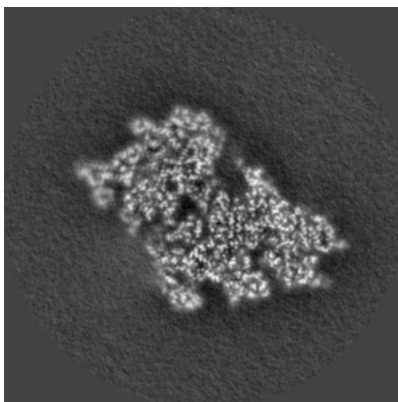


Z Index: 160

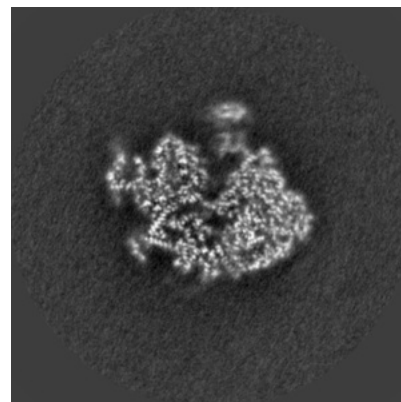
6.2.2 Raw map



X Index: 160



Y Index: 160

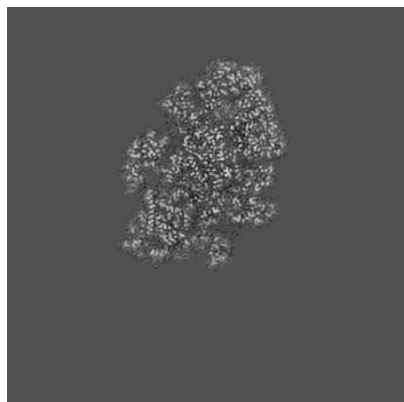


Z Index: 160

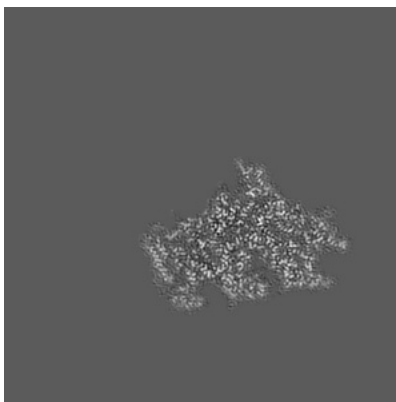
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

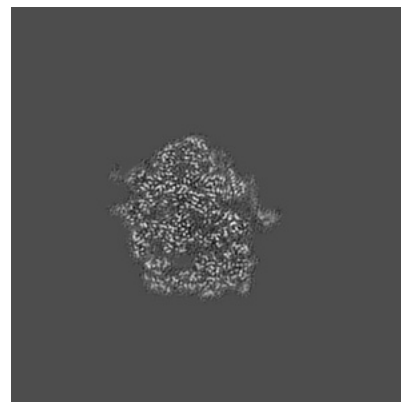
6.3.1 Primary map



X Index: 133

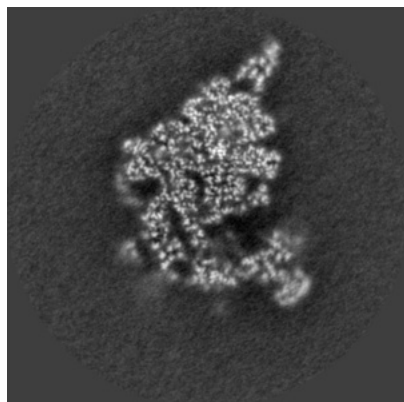


Y Index: 162

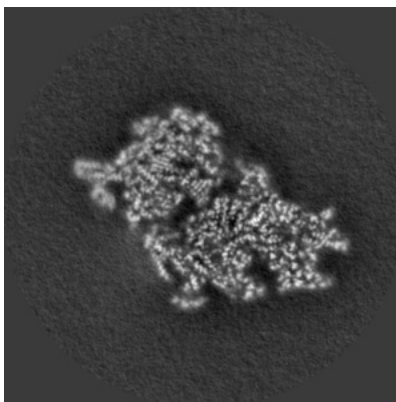


Z Index: 187

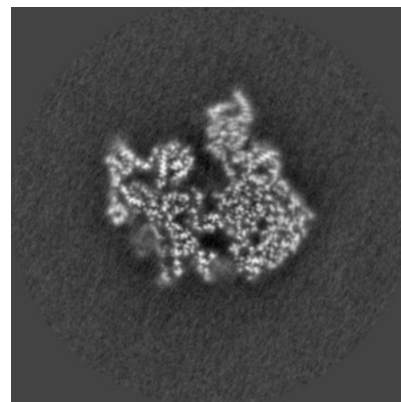
6.3.2 Raw map



X Index: 151



Y Index: 164

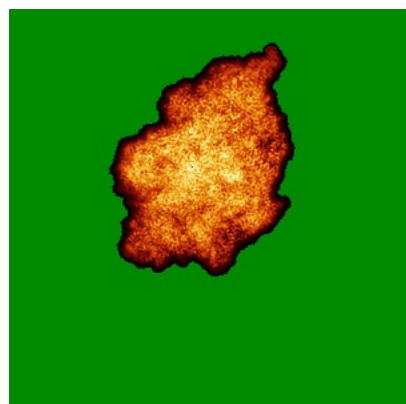


Z Index: 152

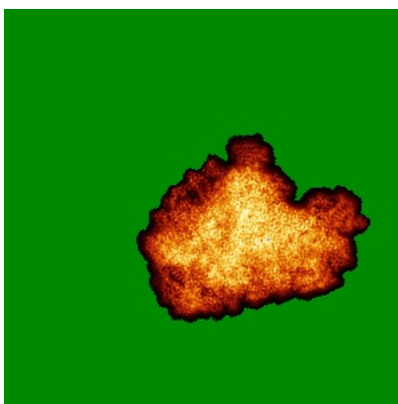
The images above show the largest variance slices of the map in three orthogonal directions.

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

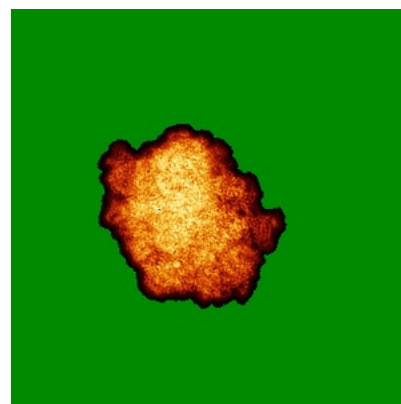
6.4.1 Primary map



X

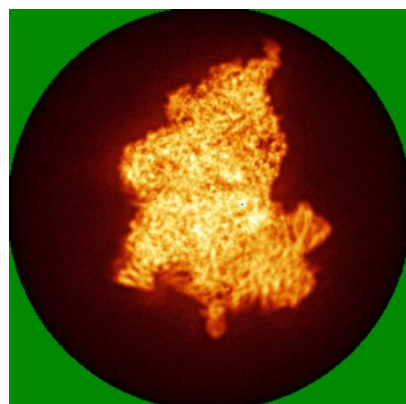


Y

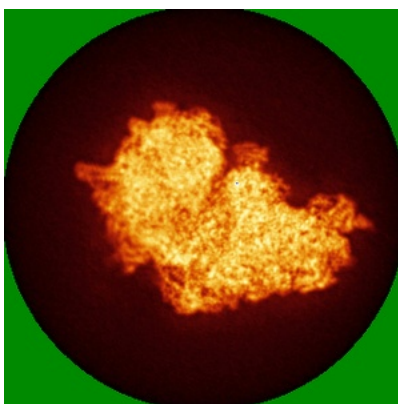


Z

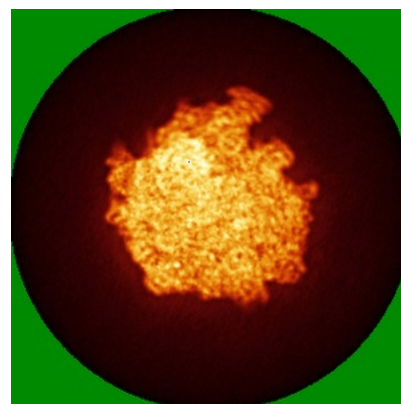
6.4.2 Raw map



X



Y

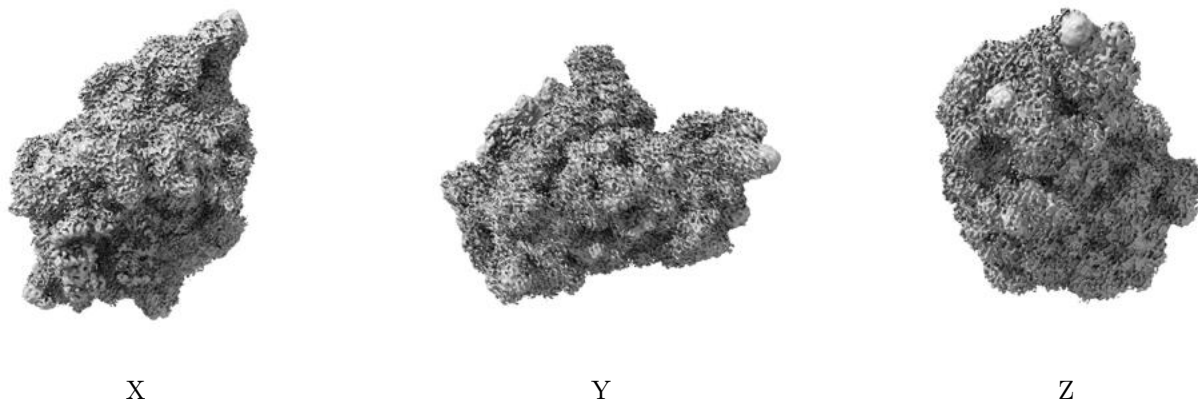


Z

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.

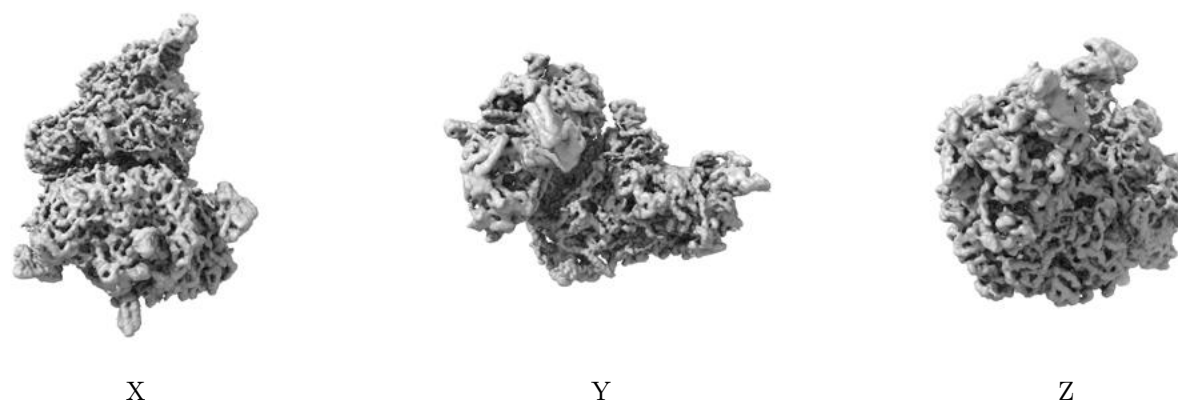
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0115. 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.

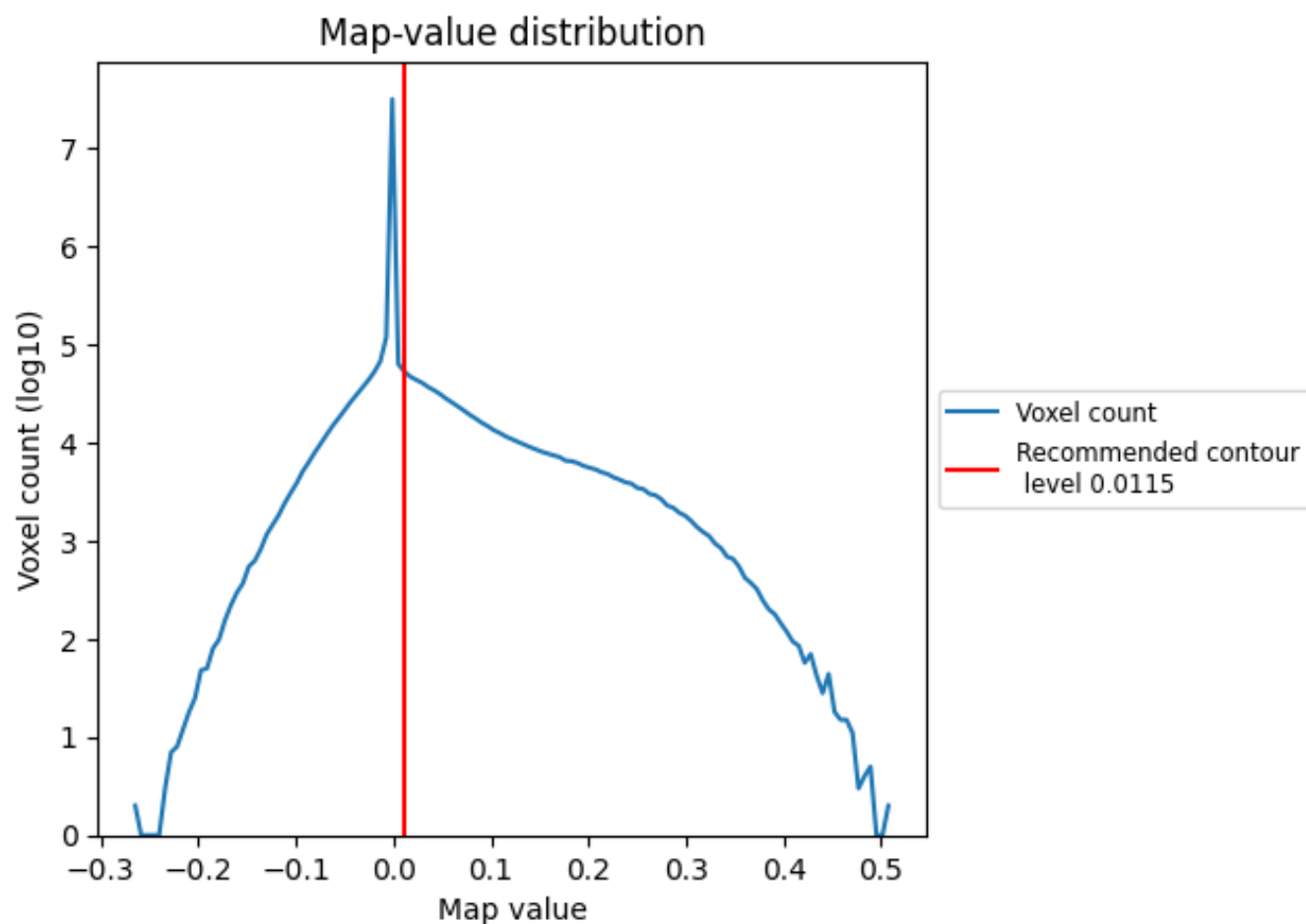
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

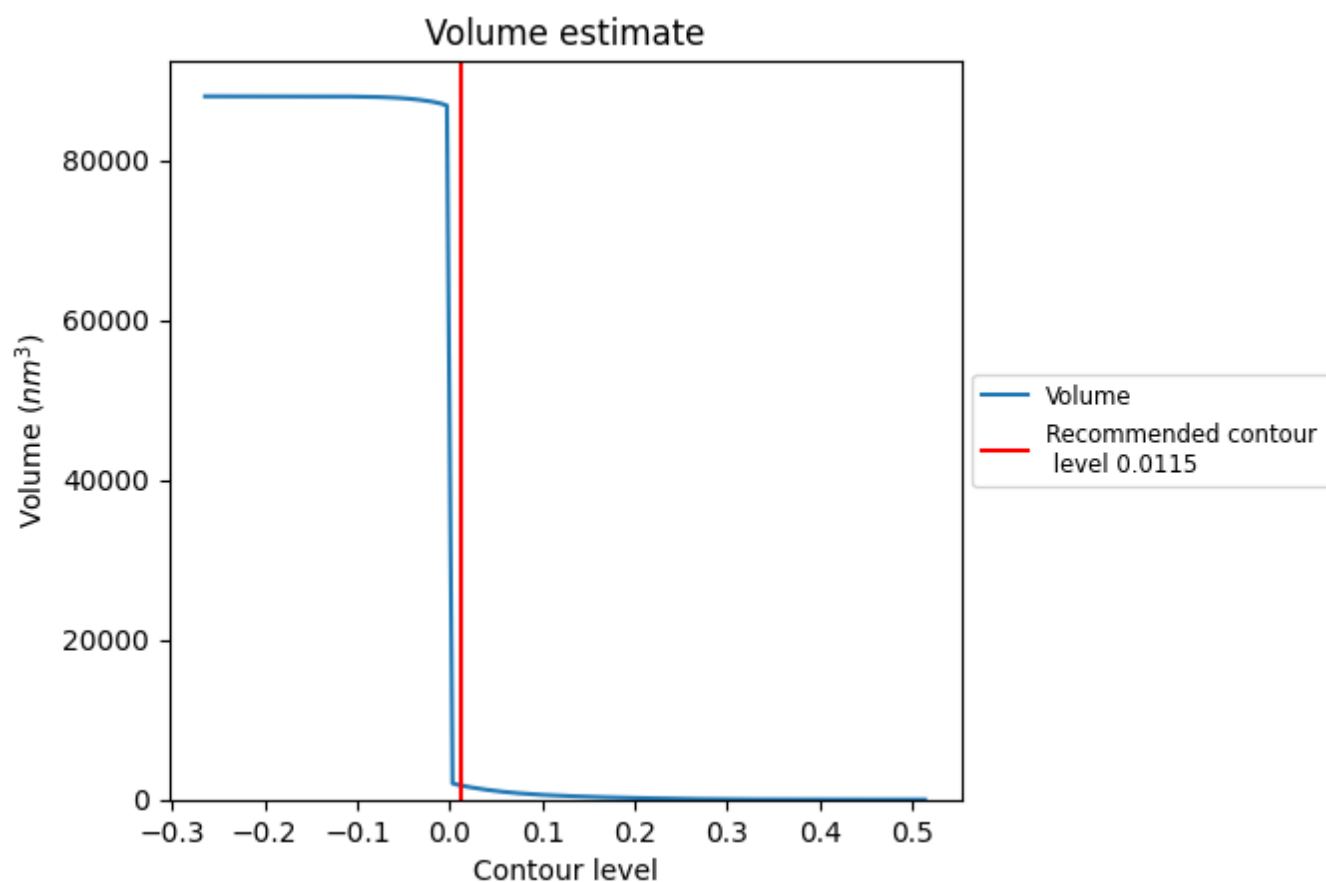
This section contains the results of statistical analysis of the map.

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.

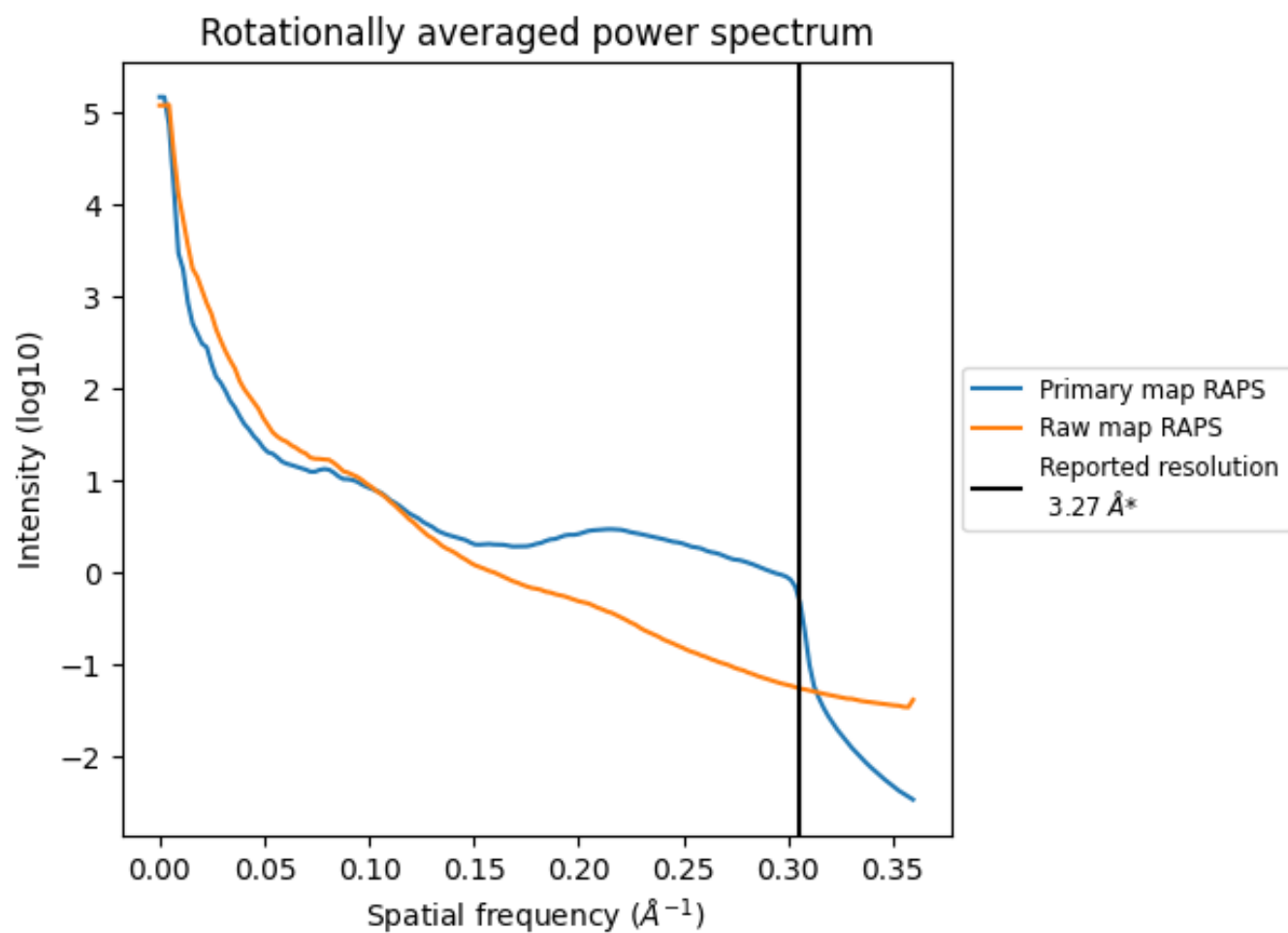
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1779 nm³; this corresponds to an approximate mass of 1607 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 ⓘ

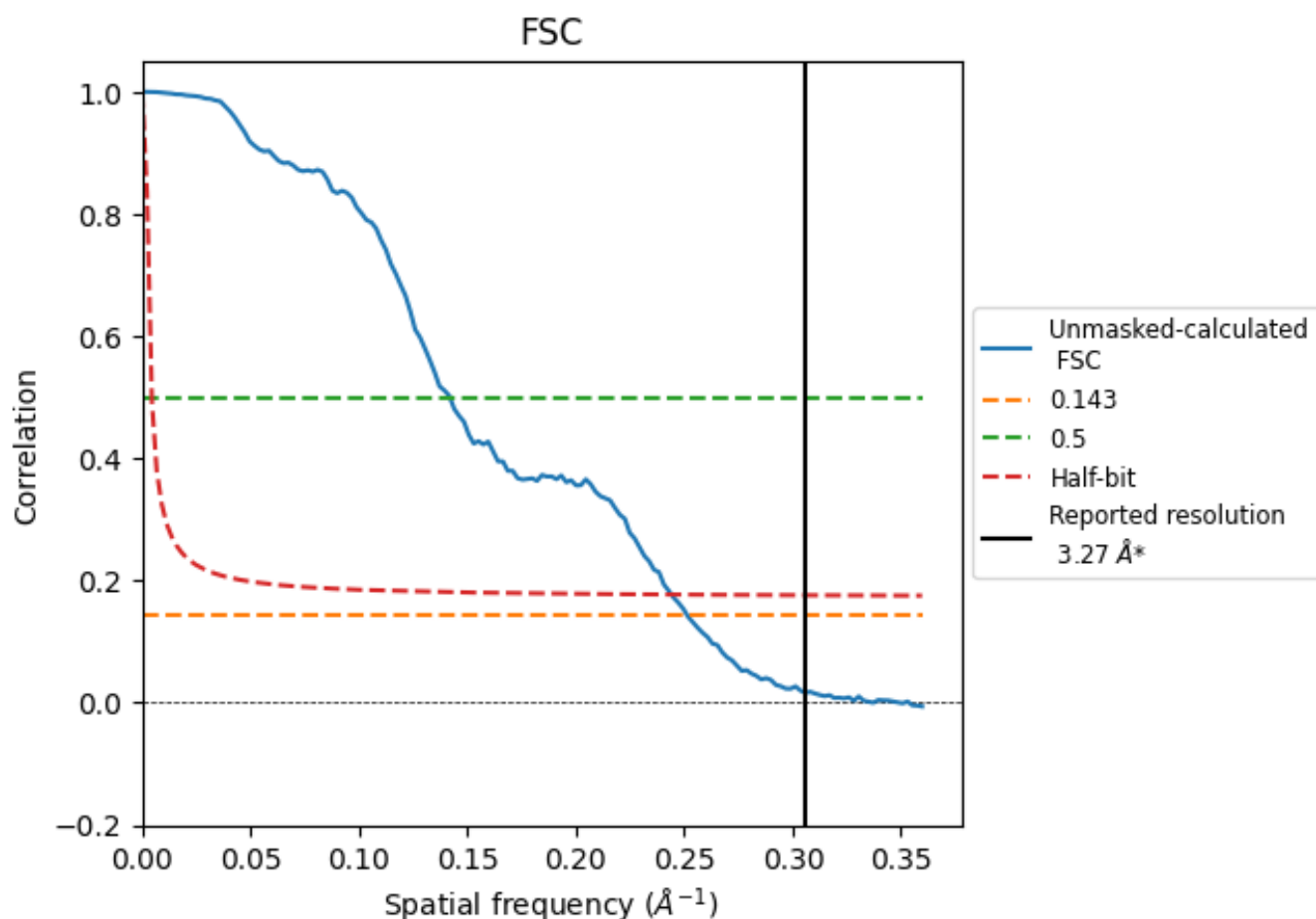


*Reported resolution corresponds to spatial frequency of $0.306 \text{ \AA}^{-1}$

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 0.306 Å⁻¹

8.2 Resolution estimates [i](#)

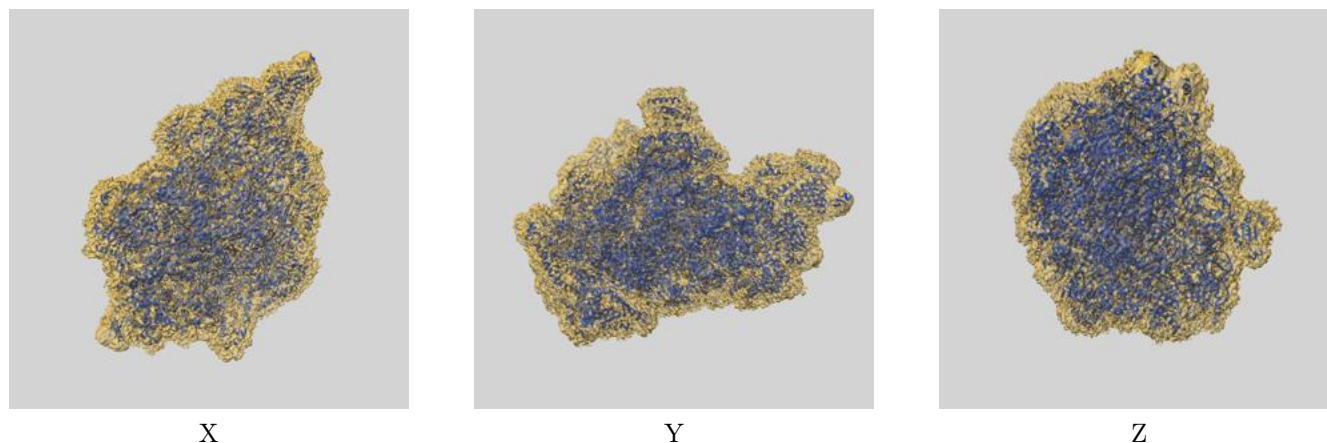
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.27	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.98	7.05	4.10

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.98 differs from the reported value 3.27 by more than 10 %

9 Map-model fit [i](#)

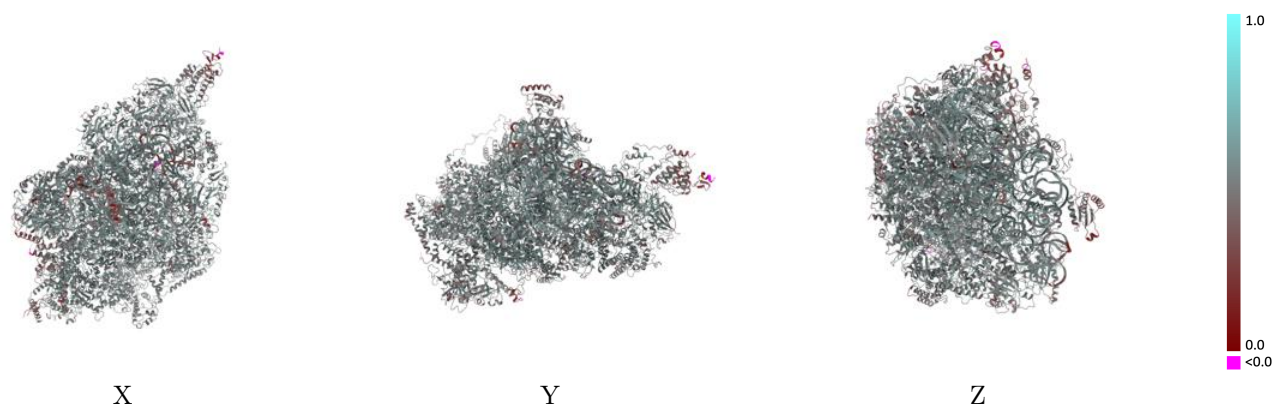
This section contains information regarding the fit between EMDB map EMD-0232 and PDB model 6HIY. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



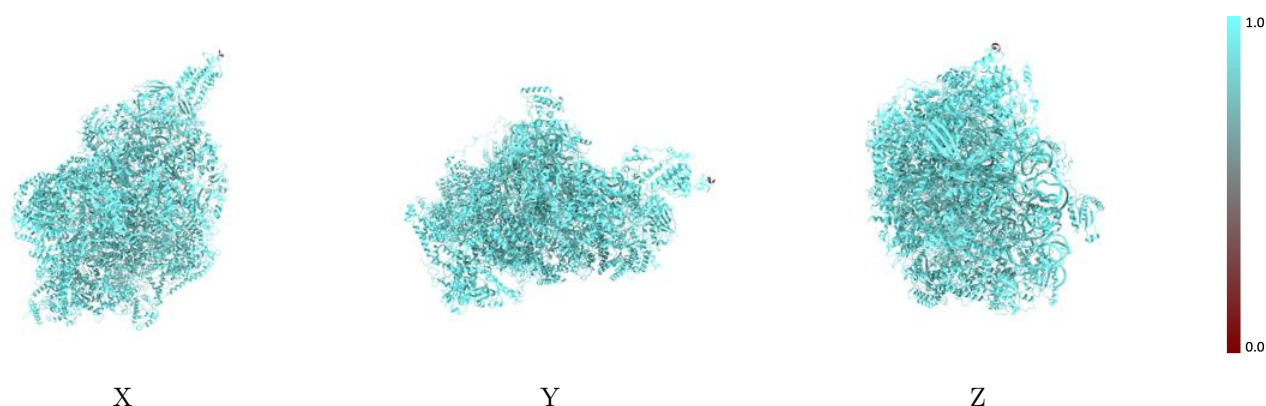
The images above show the 3D surface view of the map at the recommended contour level 0.0115 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



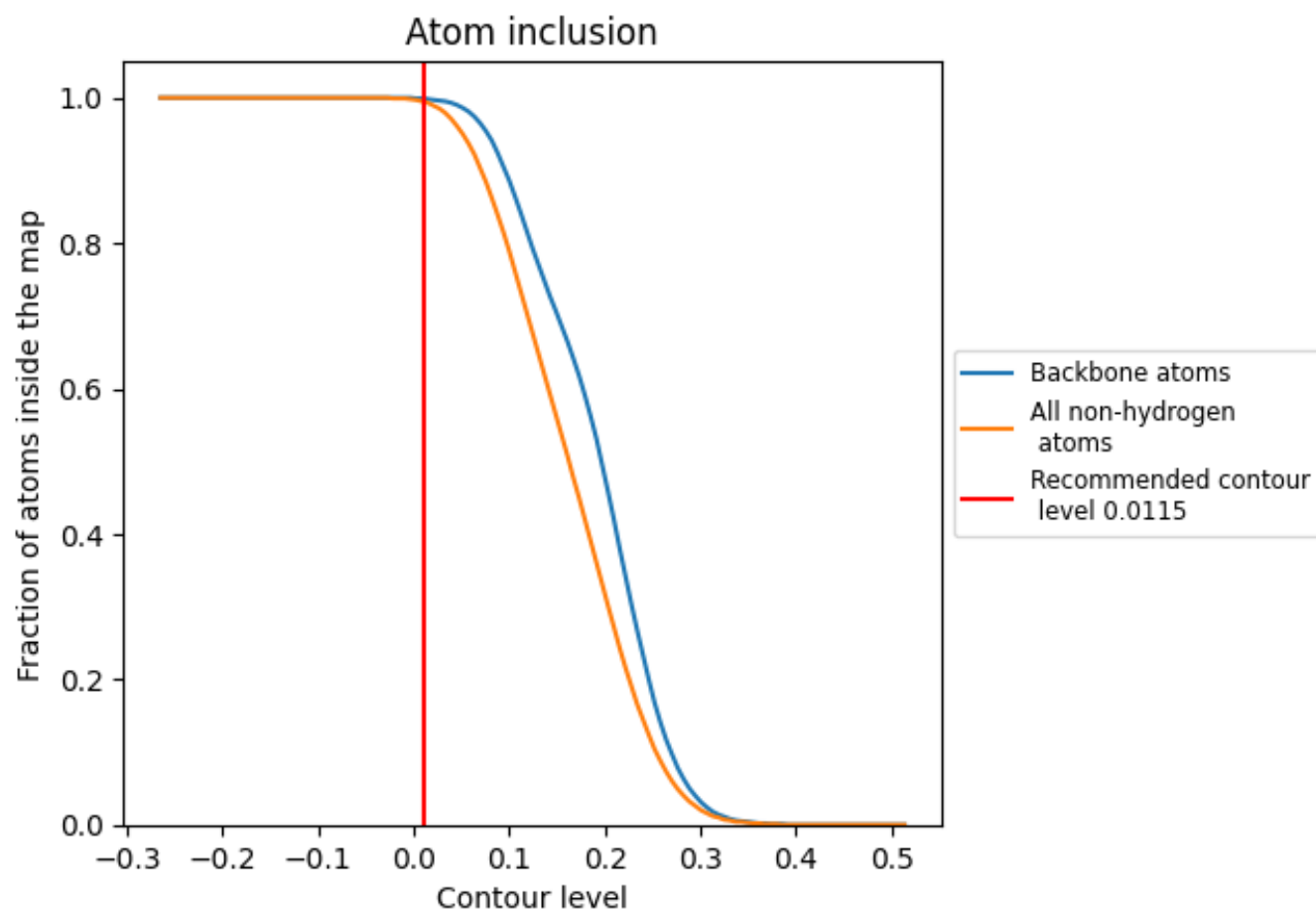
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0115).

9.4 Atom inclusion ⓘ



At the recommended contour level, 100% of all backbone atoms, 99% 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 (0.0115) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9940	 0.5160
CA	 0.9960	 0.5150
CE	 0.9910	 0.5410
CF	 0.9820	 0.5040
CH	 0.9910	 0.5270
CI	 0.9910	 0.5300
CK	 0.9950	 0.5020
CL	 0.9970	 0.5380
CO	 0.9990	 0.5330
CP	 0.9980	 0.5360
CQ	 0.9980	 0.5640
CR	 0.9880	 0.5220
CU	 0.9970	 0.5270
CZ	 0.9800	 0.4120
Ca	 0.9930	 0.5320
Cb	 0.9930	 0.5060
Cd	 0.9930	 0.5030
Cj	 0.9990	 0.5140
Cm	 0.9840	 0.5160
Cn	 0.9980	 0.5310
Cp	 0.9990	 0.4980
Cq	 0.9910	 0.5240
Cr	 0.9970	 0.4760
Cv	 0.9950	 0.5290
DA	 0.9950	 0.5030
DD	 0.9930	 0.5250
DI	 0.9970	 0.5100
DL	 0.9880	 0.5430
DM	 0.9960	 0.5400
DN	 0.9910	 0.5360
DO	 0.9970	 0.4930
DP	 0.9840	 0.4450
DQ	 0.9970	 0.5010
DR	 1.0000	 0.5020
DS	 0.9970	 0.5160



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Chain	Atom inclusion	Q-score
DU	 0.9960	 0.5150
DZ	 0.9930	 0.5400
Da	 0.9980	 0.5600
UQ	 1.0000	 0.4100
UR	 1.0000	 0.4000
US	 0.9880	 0.4230
UT	 0.9660	 0.3910