



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 07:02 pm GMT

PDB ID : 5O9Z
EMDB ID : EMD-3766
Title : Cryo-EM structure of a pre-catalytic human spliceosome primed for activation (B complex)
Authors : Bertram, K.; Kastner, B.
Deposited on : 2017-06-20
Resolution : 4.50 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:

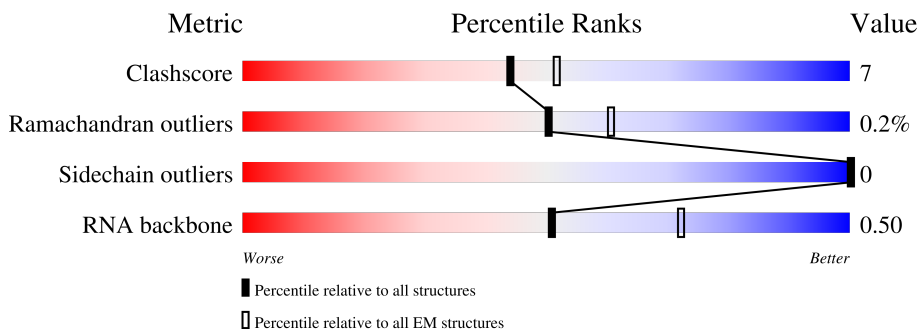
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 4.50 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.



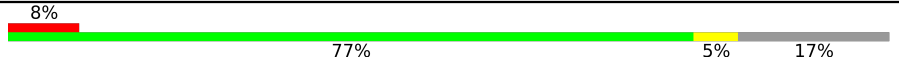
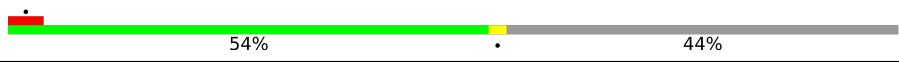
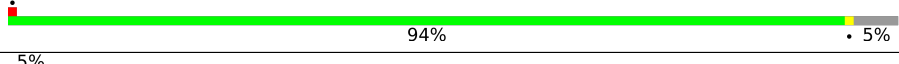

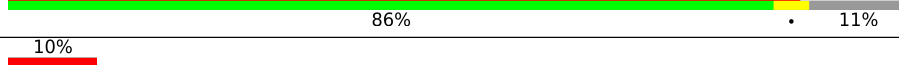
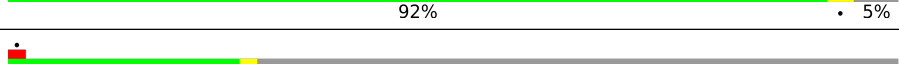
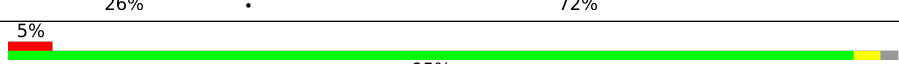
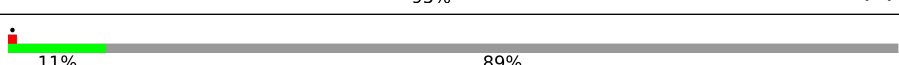

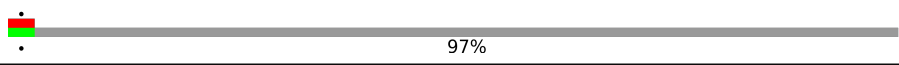
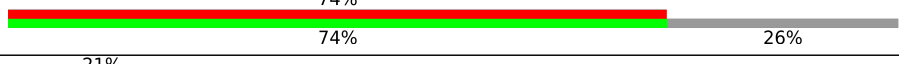
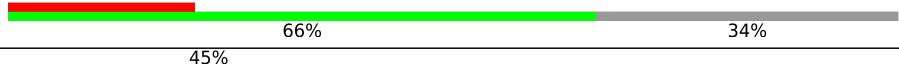






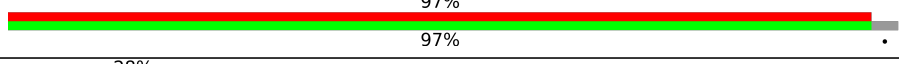
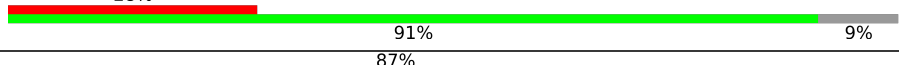
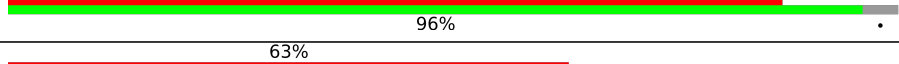




Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	2335	 7% 89% 5% 6%
2	B	972	 81% 6% 13%
3	C	2136	 43% 75% 21%
4	D	357	 78% 85% 15%
5	E	683	 28% 68%
6	F	521	 72% 9% 19%
7	G	941	 7% 79% 6% 15%

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Mol	Chain	Length	Quality of chain
8	H	499	
9	I	312	
10	J	142	
11	K	439	
12	L	513	
13	M	177	
14	N	199	
15	O	128	
16	P	800	
17	Q	376	
18	R	557	
19	S	118	
19	a	118	
19	h	118	
20	T	86	
20	b	86	
20	i	86	
21	U	92	
21	c	92	
21	j	92	
22	V	76	
22	d	76	
22	k	76	
23	W	126	
23	e	126	

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Mol	Chain	Length	Quality of chain
23	l	126	47% 56% 44%
24	X	240	30% 30% 70%
24	f	240	8% 27% 73%
24	m	240	22% 27% 73%
25	Z	119	69% 69% 31%
25	g	119	36% 78% 22%
25	n	119	53% 69% 31%
26	o	95	95% 95% 5%
27	p	102	72% 72% 28%
28	q	139	58% 58% 42%
29	r	91	84% 84% 16%
30	s	80	86% 86% 14%
31	t	103	77% 77% 23%
32	u	96	65% 65% 35%
33	v	1304	62% 62% 38%
34	w	1217	94% 94% 6%
35	x	86	63% 63% 37%
36	y	110	81% 81% 19%
37	z	256	63% 63% 37%
38	1	225	42% 42% 58%
39	Y	324	6% 6% 5% 86%
40	2	188	53% 16% 15% 20% 47%
41	4	145	37% 47% 40% 8% 6%
42	5	116	15% 41% 43% 14%
43	6	106	37% 48% 30% 7% 15%

2 Entry composition

There are 43 unique types of molecules in this entry. The entry contains 59243 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 Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	2190	11100	6725	2190	2185	0	0

- Molecule 2 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	844	4264	2577	844	843	0	0

- Molecule 3 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	C	1693	8538	5154	1693	1691	0	0

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
4	D	302	302	302	0	302

- Molecule 5 is a protein called U4/U6 small nuclear ribonucleoprotein Prp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	E	219	1101	663	219	219	0	0

- Molecule 6 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	F	420	2100	1260	420	420	0	0

- Molecule 7 is a protein called Pre-mRNA-processing factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	G	804	4057	2449	804	804	0	0

- Molecule 8 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	H	413	2068	1243	413	412	0	0

- Molecule 9 is a protein called Pre-mRNA-splicing factor 38A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	I	176	883	531	176	176	0	0

- Molecule 10 is a protein called Thioredoxin-like protein 4A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	J	135	677	408	135	134	0	0

- Molecule 11 is a protein called Microfibrillar-associated protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	K	45	225	135	45	45	0	0

- Molecule 12 is a protein called WD40 repeat-containing protein SMU1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	L	459	2288	1370	459	459	0	0

- Molecule 13 is a protein called Peptidyl-prolyl cis-trans isomerase H.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	M	169	844	506	169	169	0	0

- Molecule 14 is a protein called Zinc finger matrin-type protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	N	56	277	165	56	56	0	0

- Molecule 15 is a protein called NHP2-like protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	O	126	636	385	126	125	0	0

- Molecule 16 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	P	91	458	276	91	91	0	0

- Molecule 17 is a protein called WW domain-binding protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	Q	75	378	228	75	75	0	0

- Molecule 18 is a protein called Protein Red.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	R	16	79	47	16	16	0	0

- Molecule 19 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	a	78	393	237	78	78	0	0
19	h	74	371	223	74	74	0	0
19	S	87	Total	C			0	87
			87	87				

- Molecule 20 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	b	73	364	218	73	73	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
20	i	71	Total	C	N	O	0	0
			354	212	71	71		
20	T	74	Total	C			0	74
			74	74				

- Molecule 21 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	c	78	Total	C	N	O	0	0
			388	232	78	78		
21	j	78	Total	C	N	O	0	0
			388	232	78	78		
21	U	79	Total	C			0	79
			79	79				

- Molecule 22 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	d	69	Total	C	N	O	0	0
			344	206	69	69		
22	k	73	Total	C	N	O	0	0
			364	218	73	73		
22	V	74	Total	C			0	74
			74	74				

- Molecule 23 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	e	78	Total	C	N	O	0	0
			390	234	78	78		
23	l	71	Total	C	N	O	0	0
			353	211	71	71		
23	W	80	Total	C			0	80
			80	80				

- Molecule 24 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	f	64	Total	C	N	O	0	0
			319	191	64	64		

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Mol	Chain	Residues	Atoms				AltConf	Trace
24	m	64	Total	C	N	O	0	0
			316	188	64	64		
24	X	71	Total	C			0	71
			71	71				

- Molecule 25 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	g	93	Total	C	N	O	0	0
			469	283	93	93		
25	n	82	Total	C	N	O	0	0
			412	248	82	82		
25	Z	82	Total	C			0	82
			82	82				

- Molecule 26 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms		AltConf	Trace
26	o	90	Total	C	0	90
			90	90		

- Molecule 27 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms		AltConf	Trace
27	p	73	Total	C	0	73
			73	73		

- Molecule 28 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms		AltConf	Trace
28	q	80	Total	C	0	80
			80	80		

- Molecule 29 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms		AltConf	Trace
29	r	76	Total	C	0	76
			76	76		

- Molecule 30 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms	AltConf	Trace
30	s	69	Total C 69 69	0	69

- Molecule 31 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms	AltConf	Trace
31	t	79	Total C 79 79	0	79

- Molecule 32 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms	AltConf	Trace
32	u	62	Total C 62 62	0	62

- Molecule 33 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms	AltConf	Trace
33	v	806	Total C 806 806	0	806

- Molecule 34 is a protein called Splicing factor 3B subunit 3 (SF3B3).

Mol	Chain	Residues	Atoms	AltConf	Trace
34	w	1140	Total C 1140 1140	0	1140

- Molecule 35 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms	AltConf	Trace
35	x	54	Total C 54 54	0	54

- Molecule 36 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms	AltConf	Trace
36	y	89	Total C 89 89	0	89

- Molecule 37 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms	AltConf	Trace
37	z	162	Total C 162 162	0	162

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	89	ASP	CYS	conflict	UNP P09661
z	119	CYS	SER	conflict	UNP P09661
z	151A	PHE	-	insertion	UNP P09661

- Molecule 38 is a protein called U2 small nuclear ribonucleoprotein B”.

Mol	Chain	Residues	Atoms	AltConf	Trace
38	1	94	Total C 94 94	0	94

- Molecule 39 is a RNA chain called MINX pre-mRNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
39	Y	46	Total C N O P 972 435 167 324 46	0	0

- Molecule 40 is a RNA chain called Human gene for small nuclear RNA U2 (snRNA U2).

Mol	Chain	Residues	Atoms	AltConf	Trace
40	2	100	Total C N O P 2123 947 367 709 100	0	0

- Molecule 41 is a RNA chain called Homo sapiens U4A snRNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
41	4	137	Total C N O P 2904 1298 501 968 137	0	0

- Molecule 42 is a RNA chain called Homo sapiens U5 A small nuclear RNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
42	5	114	Total C N O P 2397 1074 399 810 114	0	0

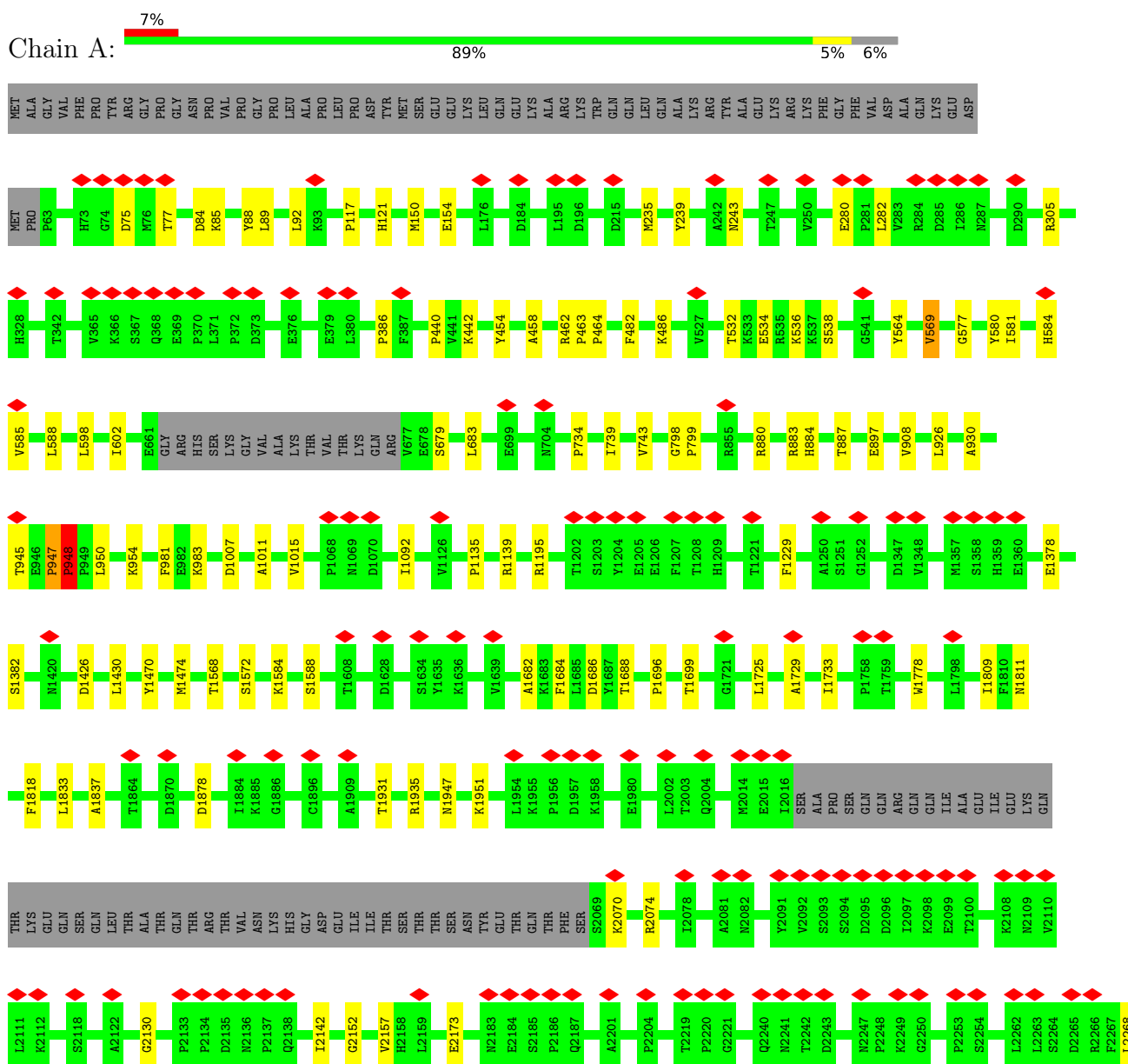
- Molecule 43 is a RNA chain called Homo sapiens RNA, U6 small nuclear 1 (RNU6-1), small nuclear RNA.

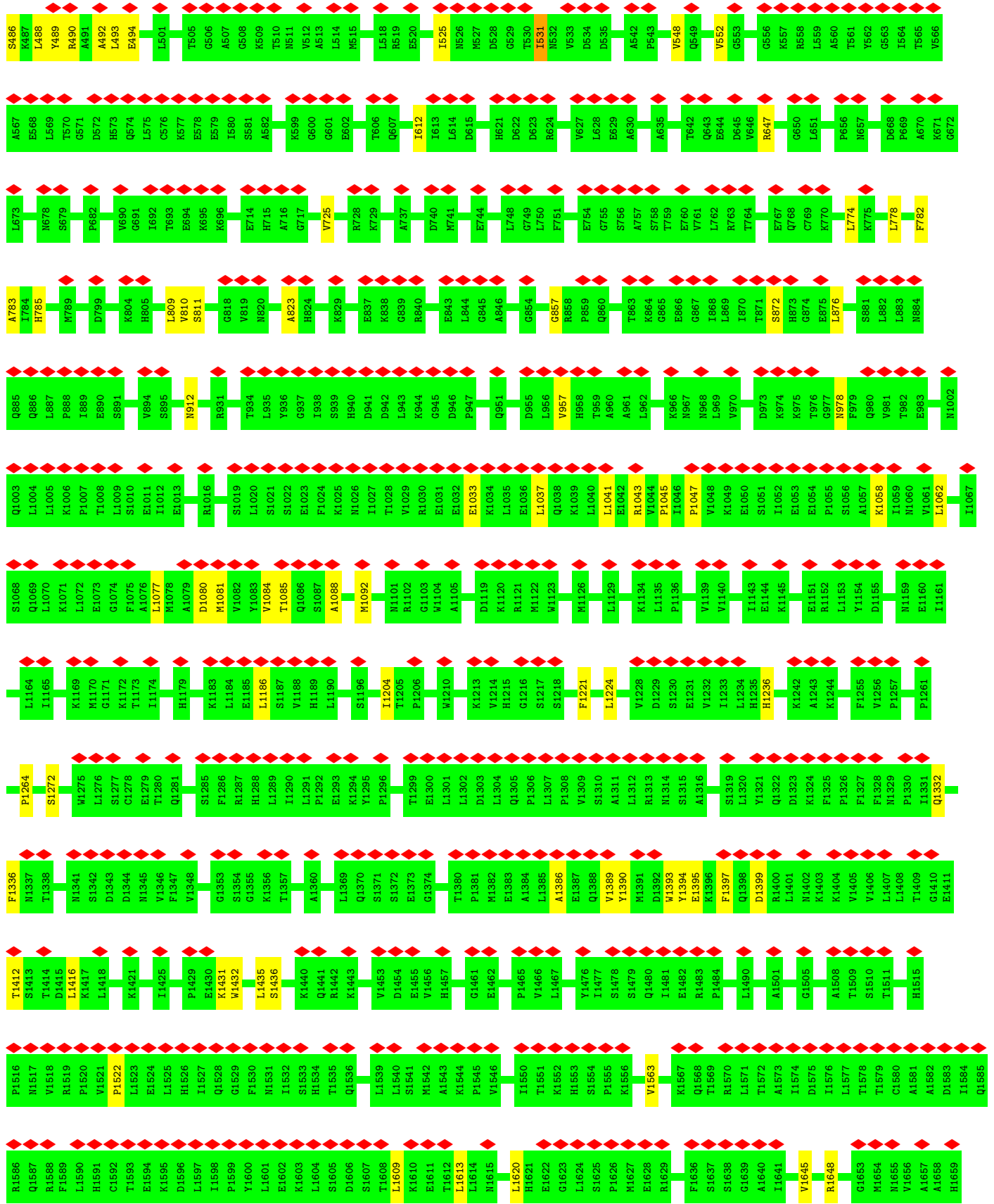
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
43	6	90	1926	861	353	622	90	0	0

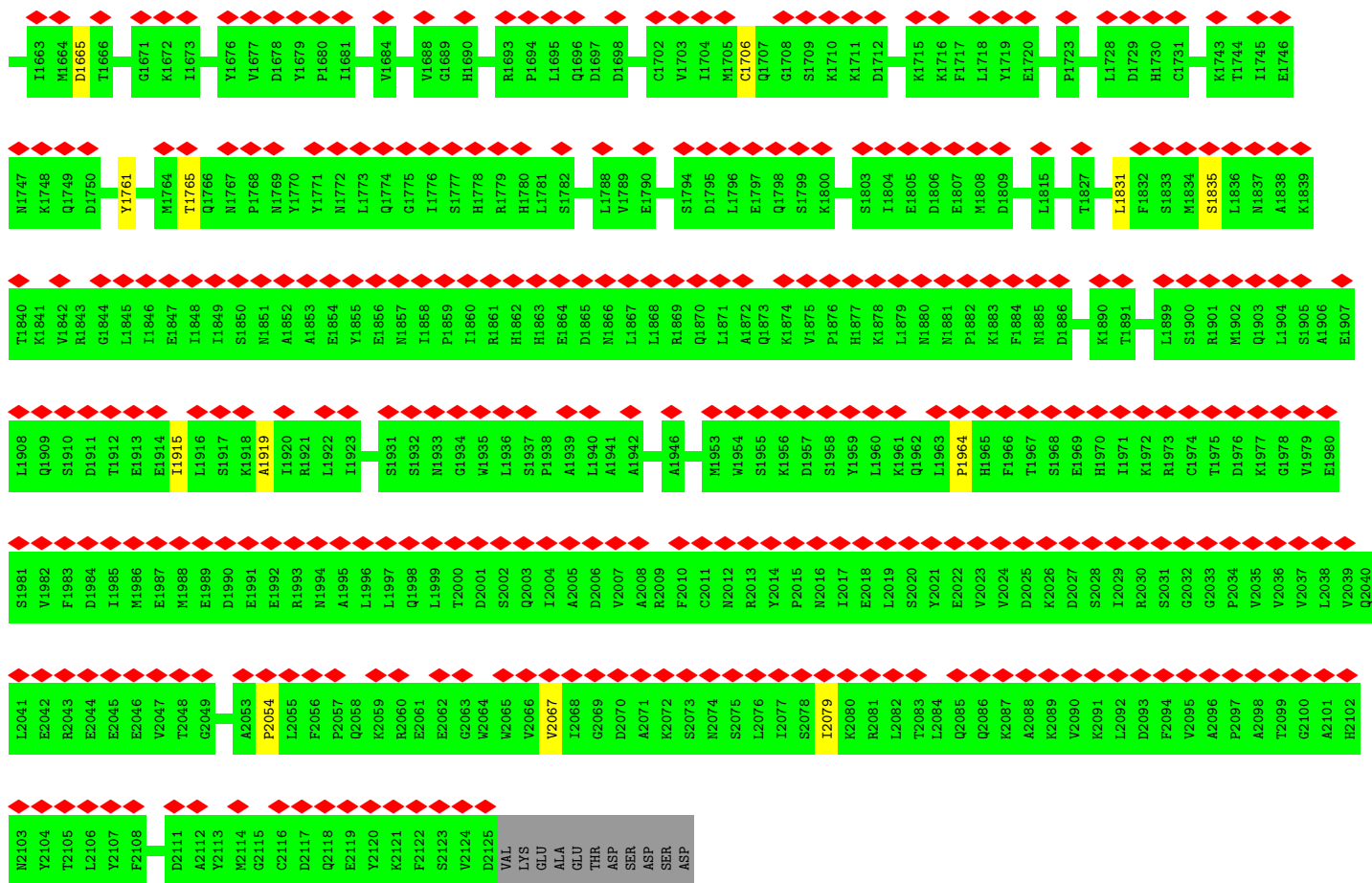
3 Residue-property plots

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.

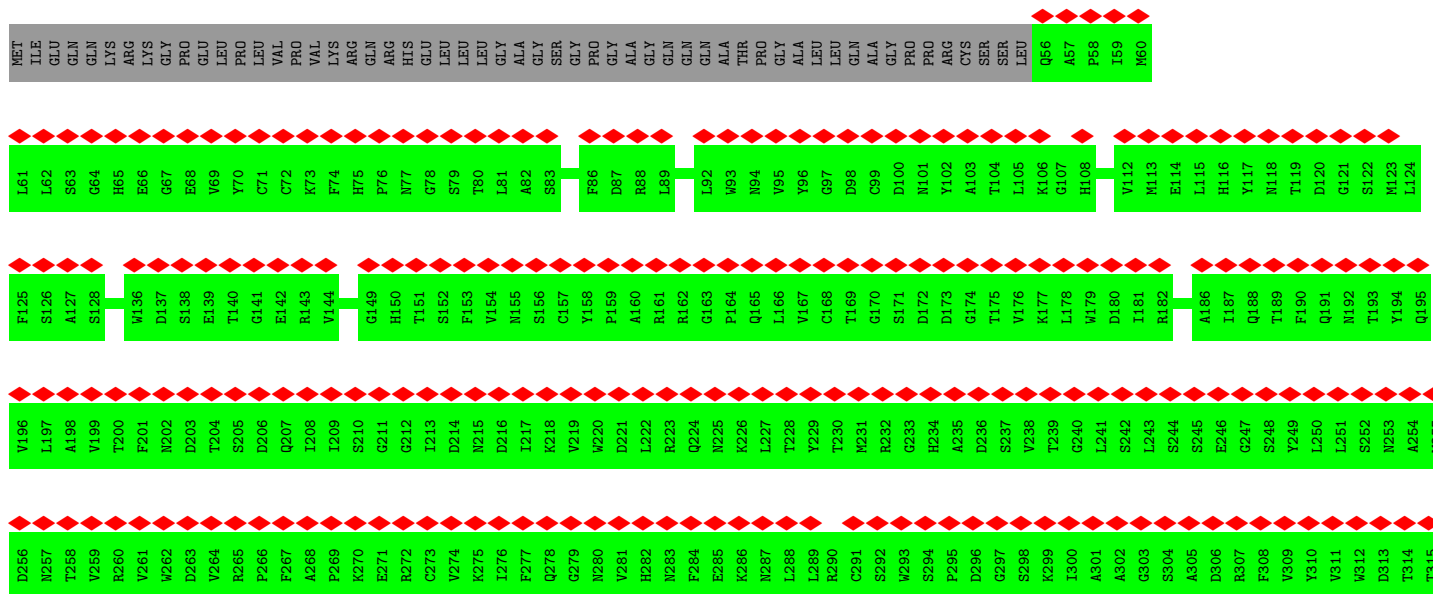
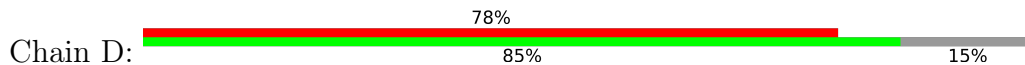
- Molecule 1: Pre-mRNA-processing-splicing factor 8

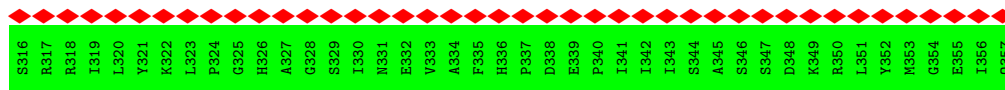




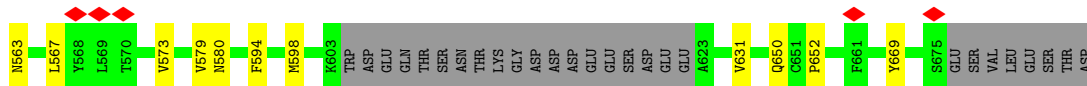
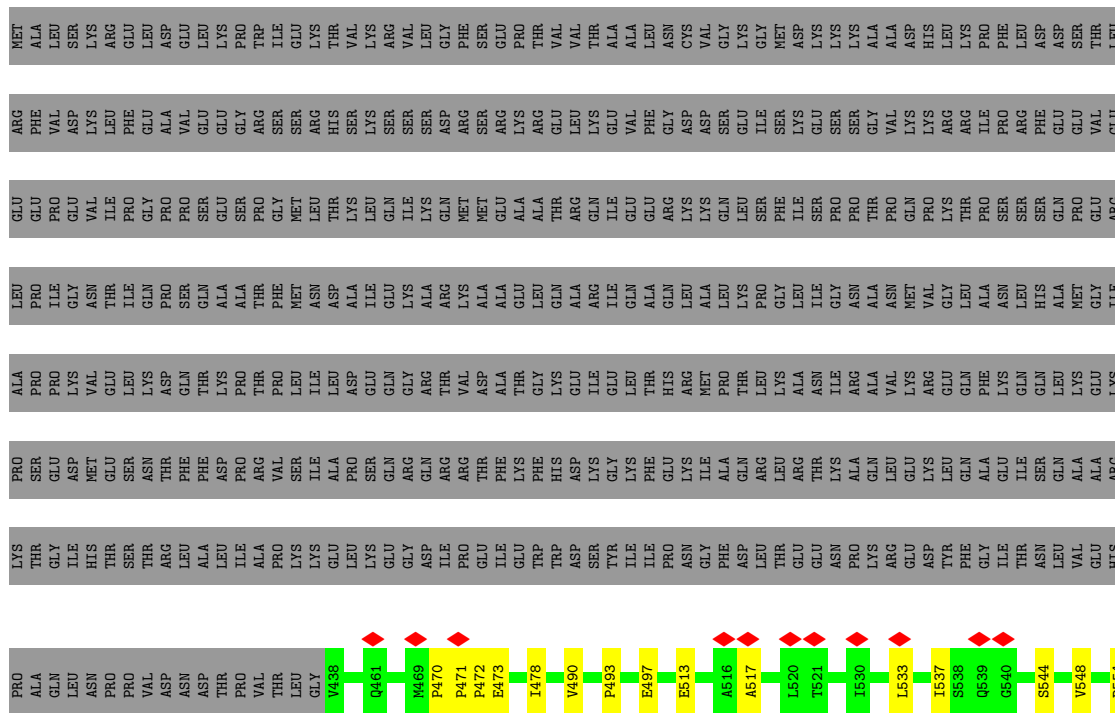


• Molecule 4: U5 small nuclear ribonucleoprotein 40 kDa protein

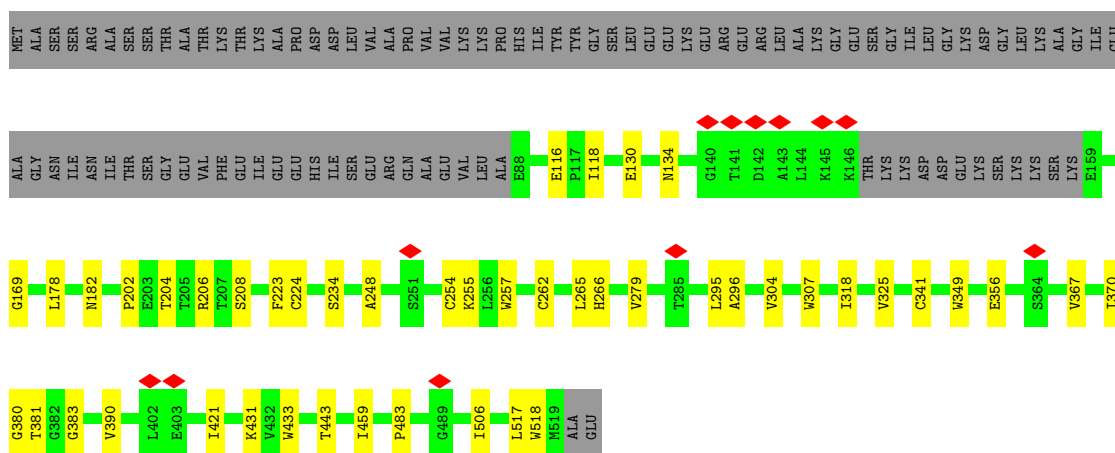




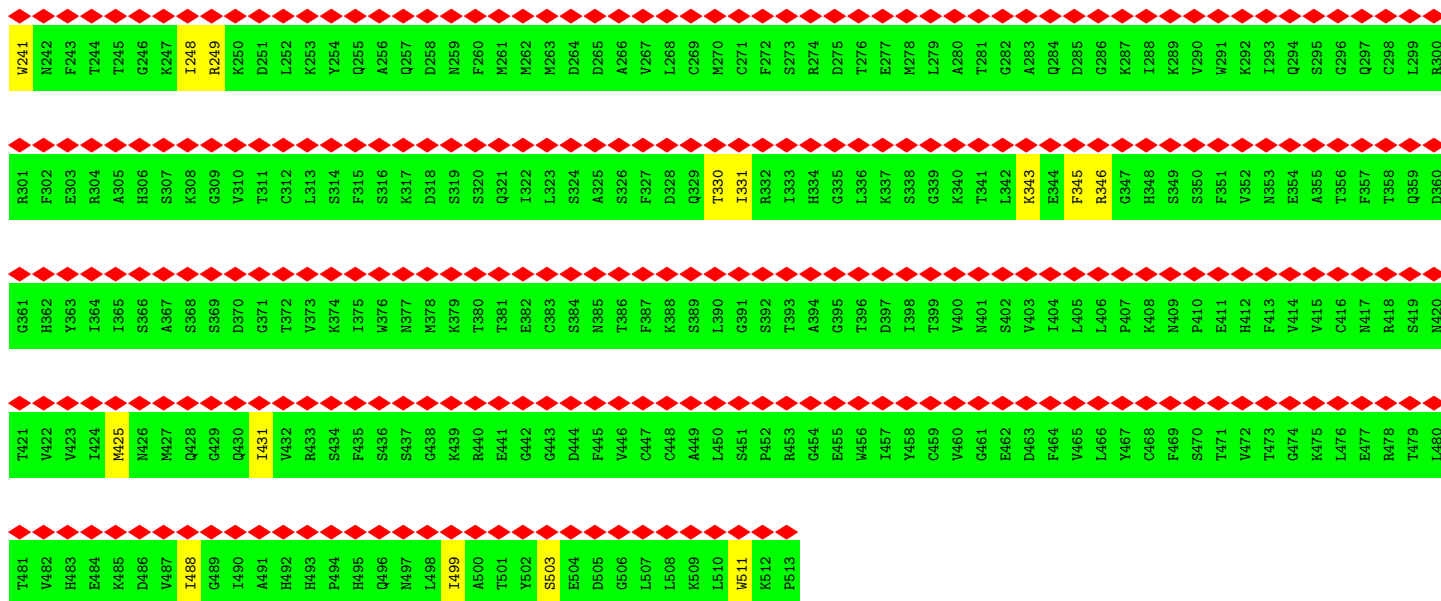
• Molecule 5: U4/U6 small nuclear ribonucleoprotein Prp3



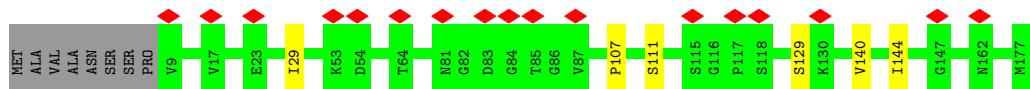
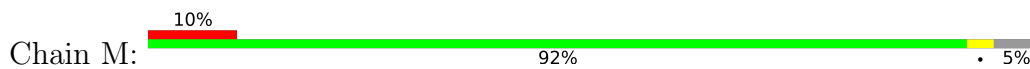
• Molecule 6: U4/U6 small nuclear ribonucleoprotein Prp4



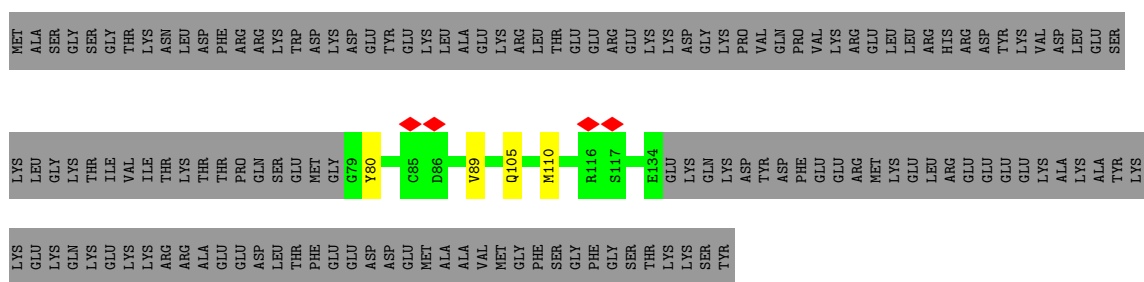
• Molecule 7: Pre-mRNA-processing factor 6



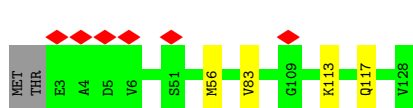
• Molecule 13: Peptidyl-prolyl cis-trans isomerase H



• Molecule 14: Zinc finger matrin-type protein 2

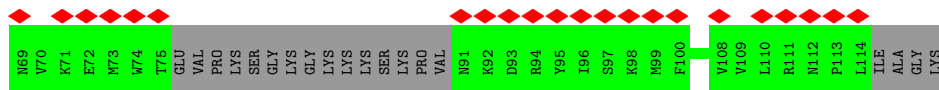


• Molecule 15: NHP2-like protein 1

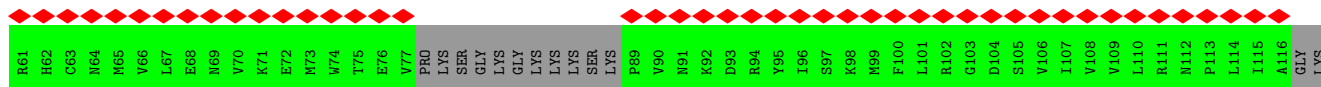
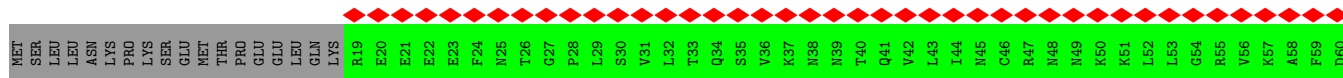
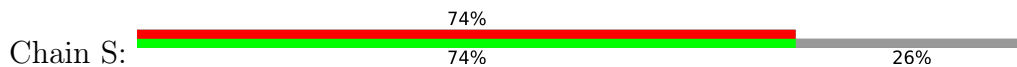


• Molecule 16: U4/U6.U5 tri-snRNP-associated protein 1

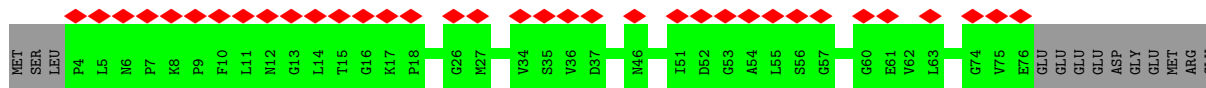
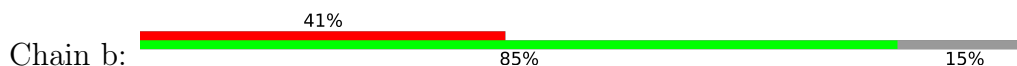




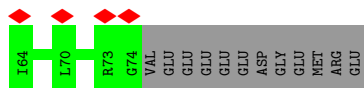
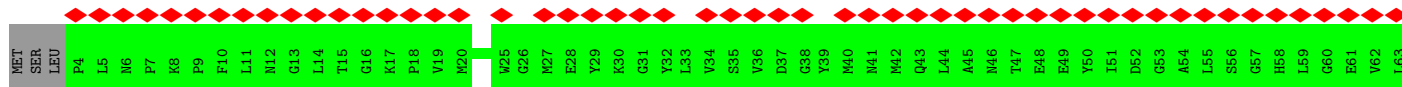
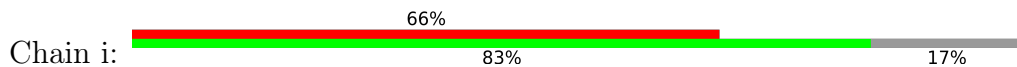
• Molecule 19: Small nuclear ribonucleoprotein Sm D2



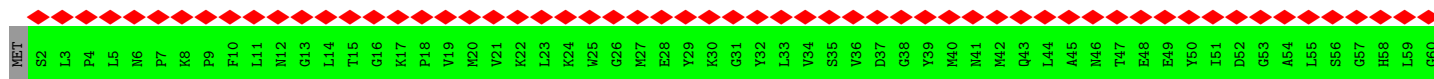
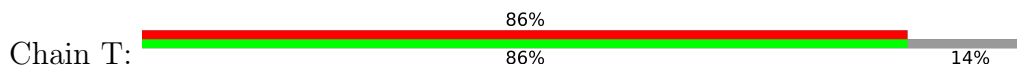
• Molecule 20: Small nuclear ribonucleoprotein F



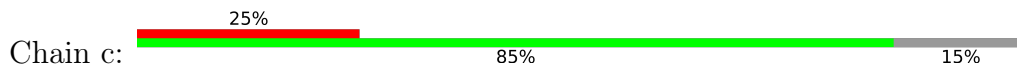
• Molecule 20: Small nuclear ribonucleoprotein F

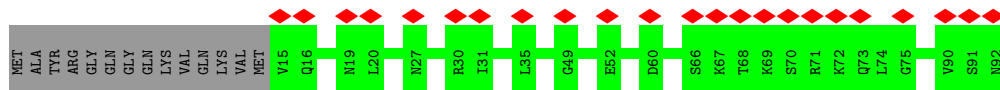


• Molecule 20: Small nuclear ribonucleoprotein F

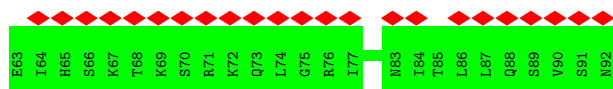
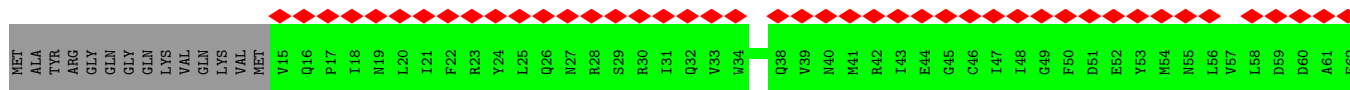
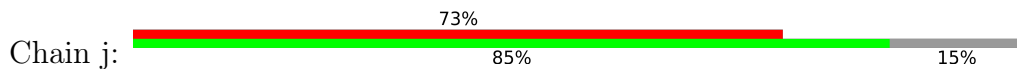


• Molecule 21: Small nuclear ribonucleoprotein E

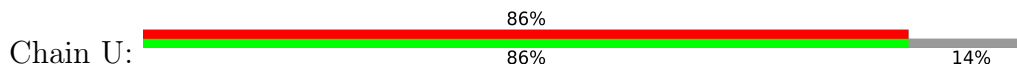




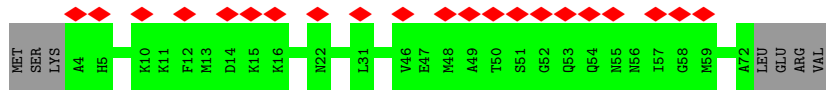
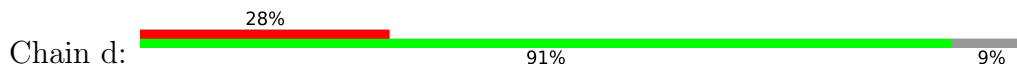
• Molecule 21: Small nuclear ribonucleoprotein E



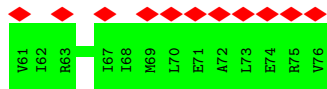
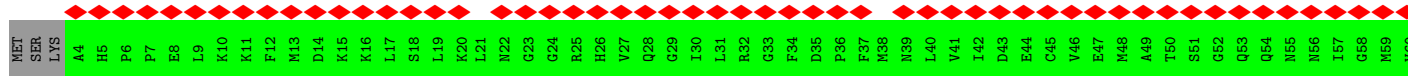
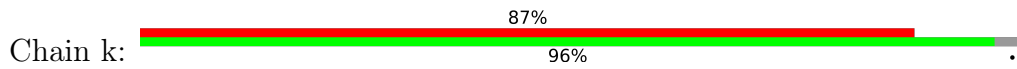
• Molecule 21: Small nuclear ribonucleoprotein E



• Molecule 22: Small nuclear ribonucleoprotein G

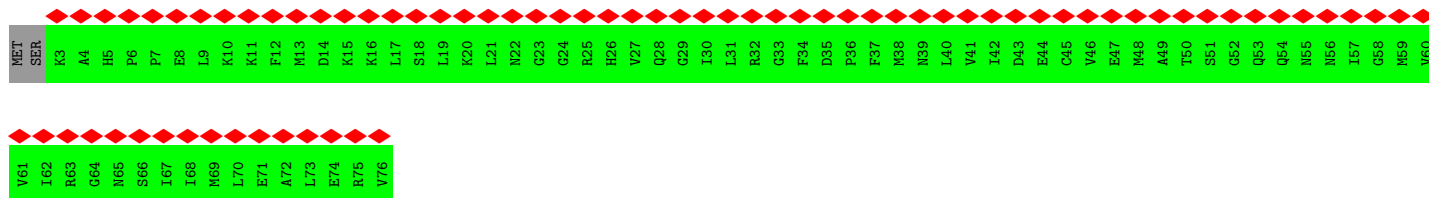


• Molecule 22: Small nuclear ribonucleoprotein G

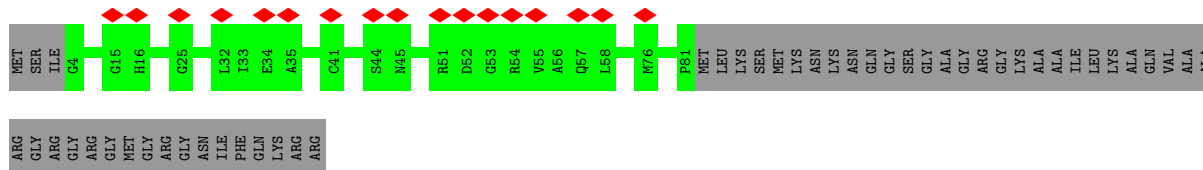


• Molecule 22: Small nuclear ribonucleoprotein G

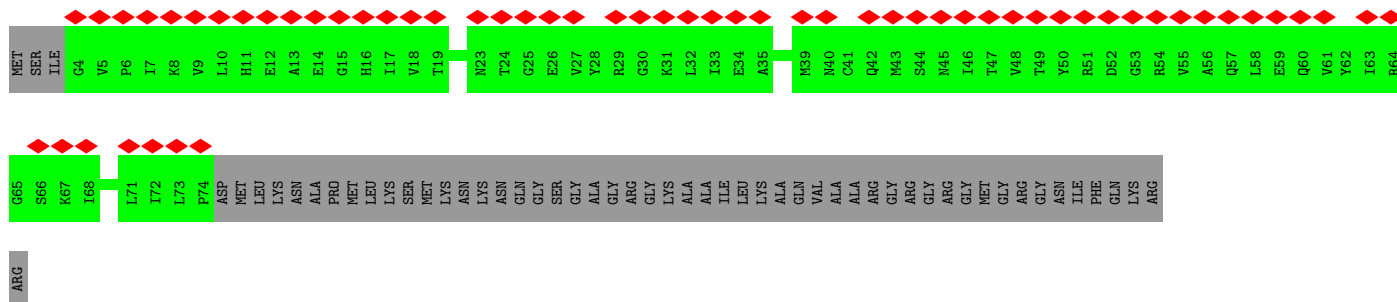




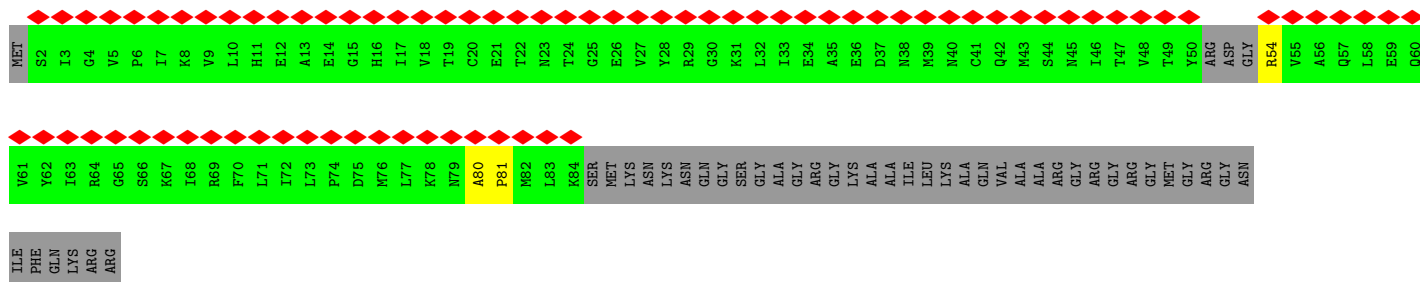
• Molecule 23: Small nuclear ribonucleoprotein Sm D3



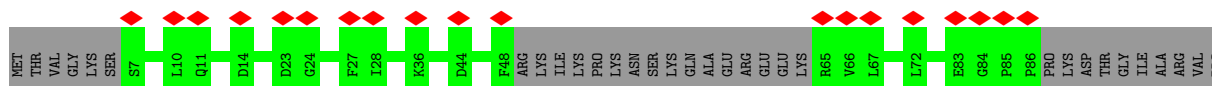
• Molecule 23: Small nuclear ribonucleoprotein Sm D3

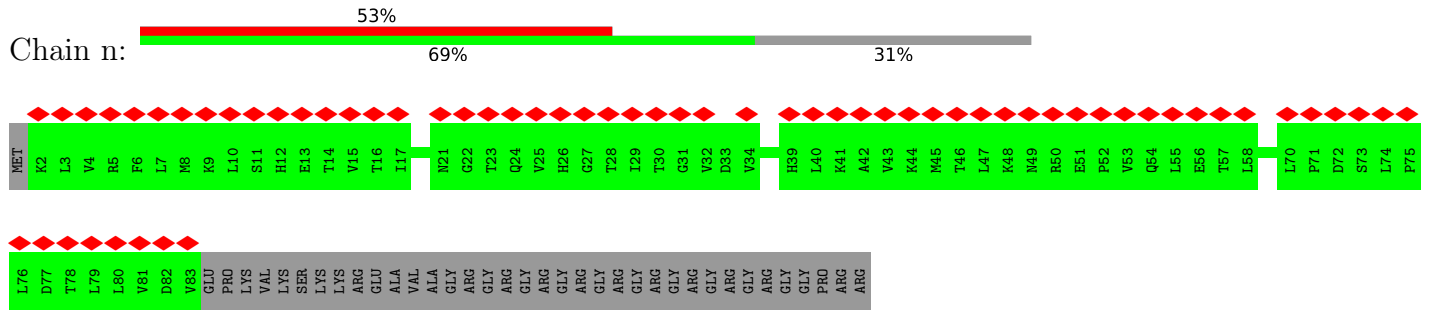


• Molecule 23: Small nuclear ribonucleoprotein Sm D3

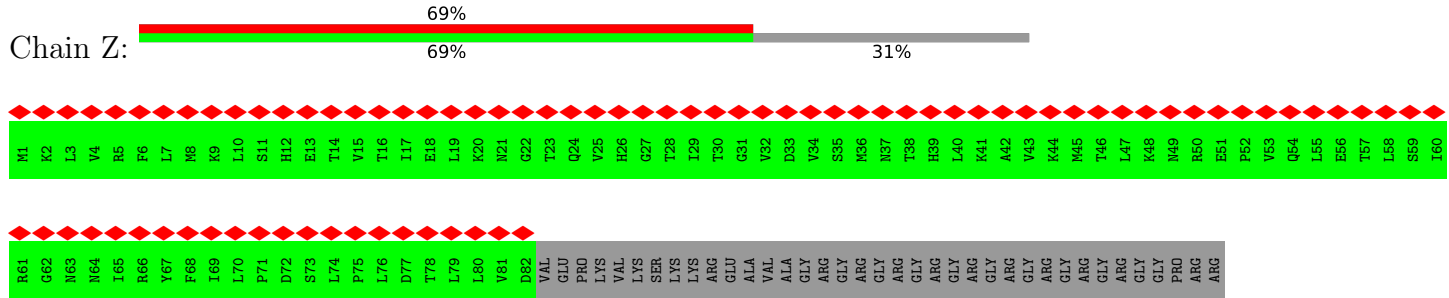


• Molecule 24: Small nuclear ribonucleoprotein-associated proteins B and B'

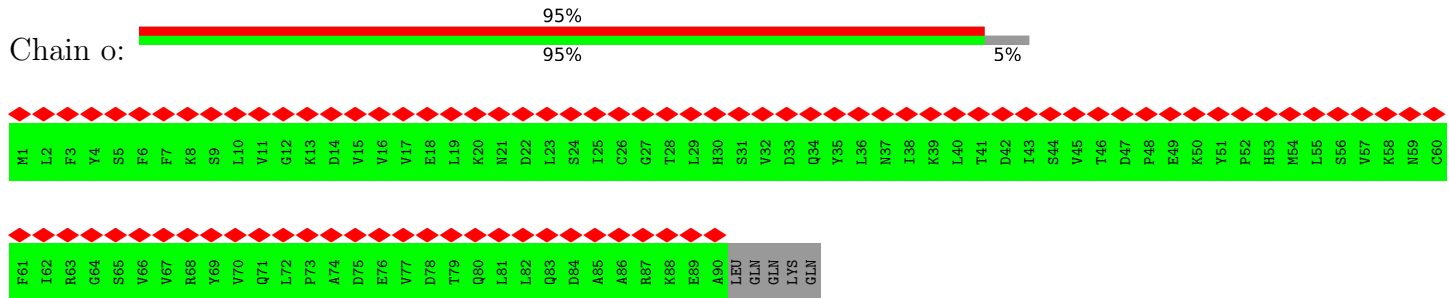




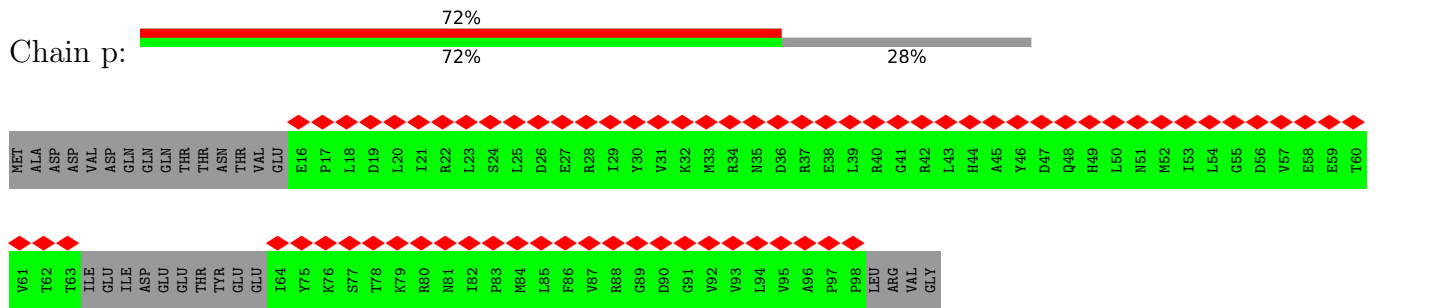
• Molecule 25: Small nuclear ribonucleoprotein Sm D1



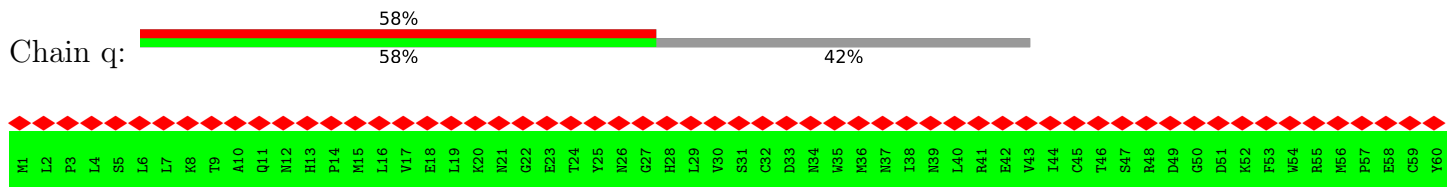
• Molecule 26: U6 snRNA-associated Sm-like protein LSm2

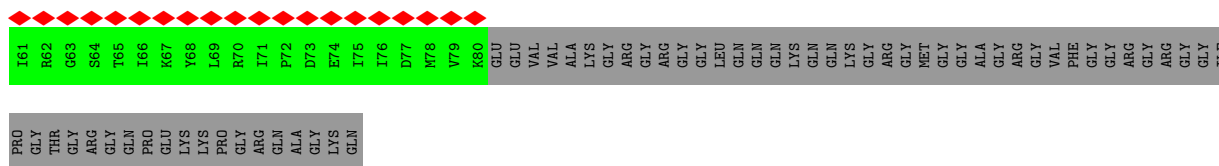


• Molecule 27: U6 snRNA-associated Sm-like protein LSm3

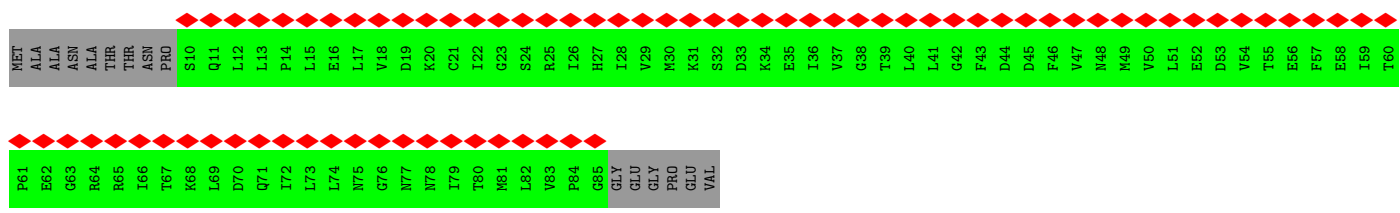
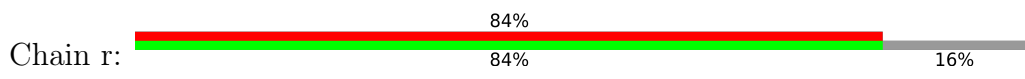


• Molecule 28: U6 snRNA-associated Sm-like protein LSm4

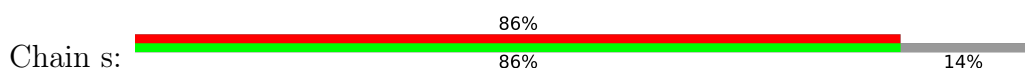




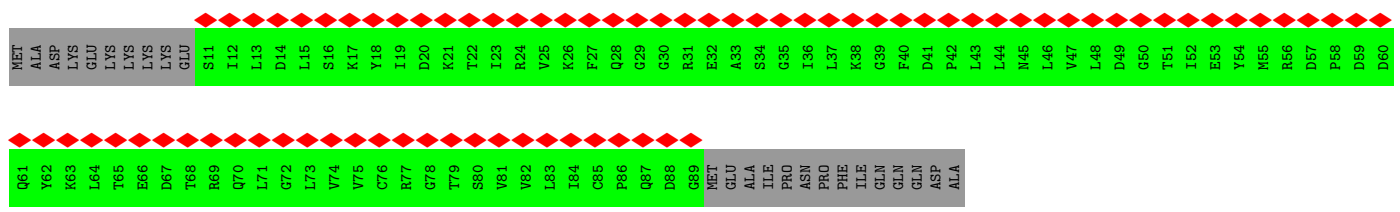
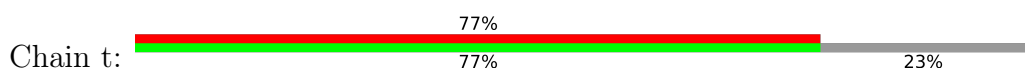
• Molecule 29: U6 snRNA-associated Sm-like protein LSM5



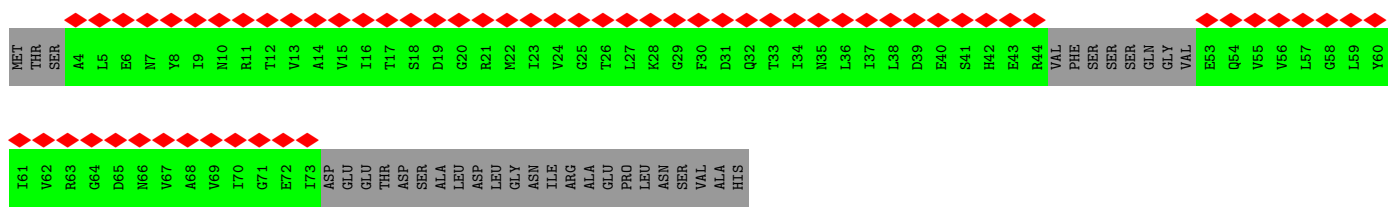
• Molecule 30: U6 snRNA-associated Sm-like protein LSM6



• Molecule 31: U6 snRNA-associated Sm-like protein LSM7



• Molecule 32: U6 snRNA-associated Sm-like protein LSM8



• Molecule 33: Splicing factor 3B subunit 1

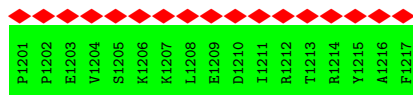
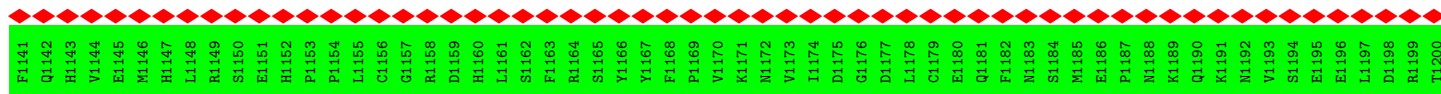
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R963	I1023	Y1083	V1143	G1203	L1263
T964	L1024	I1084	Q1144	C1204	V1264
C965	K1025	A1085	M1145	E1205	Y1265
Q966	N1026	K1086	G1146	D1206	W1266
E967	I1027	A1087	V1147	S1207	L1267
E968	H1028	I1088	L1148	L1208	I1268
R969	E1029	G1089	K1149	M1209	R1269
L970	K1030	P1090	S1150	H1210	M1270
H971	V1031	H1091	L1151	L1211	S1271
G972	Q1032	D1092	S1152	L1212	I1272
H973	N1033	V1093	F1153	M1213	Y1273
L974	N1034	L1094	L1154	Y1214	I1274
G975	C1035	A1095	F1155	V1215	G1275
V976	I1036	T1096	E1156	W1216	S1276
Y977	D1037	L1097	Y1157	Q1217	Q1277
L978	L1038	L1098	I1158	M1218	I1278
Y979	V1039	M1099	G1159	V1219	A1279
E980	G1040	ASN	E1160	F1220	L1280
Y981	R1041	LEU	M1161	I1221	I1281
L982	I1042	LYS	G1162	T1222	A1282
G983	A1043	VAL	K1163	S1223	H1283
E984	D1044	GLN	D1164	P1224	Y1284
E985	R1045	ARG	Y1165	H1225	P1285
Y986	G1046	GLN	I1166	V1226	I1286
P987	A1047	M1108	Y1167	I1227	I1287
E988	E1048	R1109	A1168	Q1228	Y1288
Y989	Y1049	V1110	V1169	A1229	M1289
L990	V1050	C1111	T1170	V1230	D1290
G991	S1051	T1112	P1171	M1231	D1291
S992	A1052	T1113	L1172	G1232	K1292
Y993	R1053	V1114	L1173	A1233	M1293
L994	E1054	A1115	E1174	L1234	T1294
G995	W1055	I1116	D1175	E1235	Y1295
A996	M1056	A1117	A1176	G1236	I1296
L997	R1057	I1118	L1177	L1237	R1297
K998	I1058	V1119	M1178	R1238	Y1298
A999	C1059	E1120	D1179	V1239	E1299
I1000	F1060	A1121	R1180	A1240	L1300
V1001	E1061	T1122	D1181	I1241	L1301
N1002	L1062	C1123	L1182	G1242	Y1302
V1003	L1063	S1124	V1183	P1243	I1303
I1004	E1064	F1125	H1184	C1244	L1304
G1005	L1065	T1127	R1185	R1245	
M1006	L1066	V1128	Q1186	M1246	
H1007	K1067	L1129	T1187	L1247	
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P1012	A1072	M1134	V1192	Q1252	
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K1014	R1074	Y1136	H1194	L1254	
D1015	R1075	R1137	M1195	F1255	
L1016	A1076	V1138	S1196	H1256	
L1017	T1077	P1139	L1197	P1257	
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• Molecule 34: Splicing factor 3B subunit 3 (SF3B3)

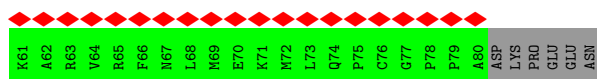
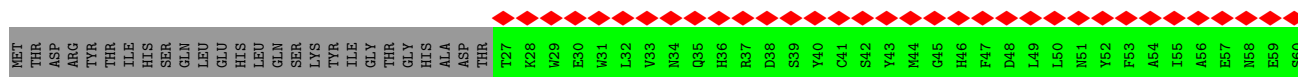


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Y4	S64	D124	C184	G244	Q304
N5	L65	P125	L185	P245	T305
L6	M66	K126	E186	S246	E306
T7	A67	G127	M187	G247	Q307
L8	F68	R128	D188	V248	G308
Q9	R69	A129	Y189	L249	D309
R10	L70	V130	E190	I250	I310
A11	T71	M131	E191	C251	F311
T12	G72	I132	A192	S252	K312
G13	G73	S133	D193	E253	I313
I14	T74	A134	M194	N254	T314
S15	K75	I135	D195	Y255	L315
F16	D76	E136	P196	I256	E316
A17	Y77	K137	T197	T257	T317
I18	I78	Q138	G198	Y258	D318
H19	V79	K139	E199	K259	E319
G20	V80	L140	A200	N260	D320
N21	G81	V141	A201	F261	M321
F22	S82	Y142	A202	G262	V322
S23	D83	I143	N203	D263	T323
G24	S84	L144	T204	Q264	E324
T25	G85	M145	Q205	P265	I325
K26	R86	R146	Q206	D266	R326
Q27	I87	D147	T207	L267	L327
Q28	V88	A148	L208	R268	K328
E29	I89	A149	T209	C269	Y329
I30	L90	A150	F210	P270	F330
V31	E91	R151	Y211	L271	D331
V32	Y92	L152	E212	P272	T332
S33	Q93	T153	L213	R273	V333
R34	P94	I154	D214	R274	P334
G35	S95	S155	L215	R275	V335
K36	K96	S156	G216	N276	A336
I37	M97	P157	L217	D277	A337
L38	M98	L158	N218	L278	A338
E39	F99	E159	H219	D279	M339
L40	E100	A160	V220	D280	C340
L41	K101	H161	V221	P281	V341
R42	I102	K162	R222	E282	L342
P43	H103	A163	K223	R283	K343
D44	Q104	M164	Y224	G284	T344
P45	E105	T165	S225	M285	G345
M46	T106	L166	E226	I286	F346
T47	F107	V167	P227	F287	L347
G48	G108	Y168	L228	V288	F348
K49	K109	H169	E229	C289	V349
V50	S110	V170	E230	S290	A350
H51	G111	V171	H231	A291	S351
T52	C112	G172	G232	T292	E352
L53	R113	V173	N233	H293	F353
L54	L114	D174	F234	K294	G354
T55	I115	V175	L235	T295	N355
V56	V116	G176	I236	K296	H356
E57	F117	F177	T237	S297	Y357
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G60	F120	P180	G240	F300	Q360

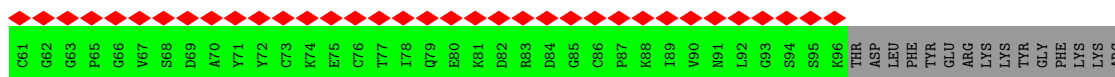
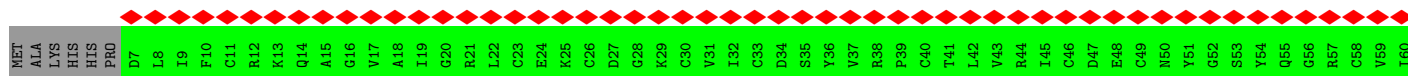
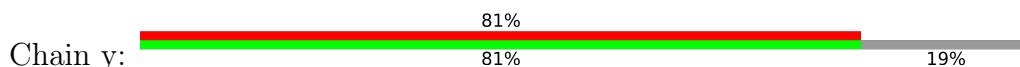
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L721	S722	Y723	S724	Y725	Q726	S727	R728	F729	H730	L731	T732	P733	L734	S735	Y736	E737	T738	L739	E740	F741	A742	S743	G744	F745	S747	E748	Q749	C750	P751	E752	G753	L754	V755	A756	I757	S758	T759	N760	I761	L762	R763	I764	L765	L766	L767	LYS	LEU	G771	A772	V773	F774	N775	Q776	V777	A778	F779	P780										
Q782	Y783	T784	P785	R786	K787	F788	V789	I790	H791	P792	E793	S794	N795	N796	L797	I798	I799	L800	E801	T802	D803	H804	N805	A806	THR	GLU	ALA	THR	LYS	ALA	GLN	ARG	LYS	GLN	GLN	MET	ALA	GLU	GLU	MET	VAL	GLU	GLU	ALA	ALA	GLY	GLU	ASP	GLU	ARG	GLU	LEU	ALA	ALA	ALA	MET	ALA	ALA	A772	V773	F774	N775	Q776	V777	A778	F779	P780
ALA	PHE	LEU	ASN	GLU	ASN	LEU	P848	E849	S850	L851	F852	G853	P855	K856	A857	C858	N859	C860	Q861	W862	A863	S864	V865	L866	R867	V868	N869	N870	P871	L872	Q873	C874	N875	T876	L877	D878	L879	Q881	L882	E883	Q884	N885	E886	A887	A888	F889	V891	A892	V893	C894	R895	F896	S897	N898	T899	G900											
E901	D902	W903	Y904	Y905	L906	Y907	G908	V909	A910	K911	D912	L913	I914	L915	N916	P917	R918	S919	W920	A921	G922	G923	F924	V925	Y926	T927	Y928	K929	L930	Y931	N932	N933	G934	E935	K936	L937	E938	F939	L940	H941	K942	T943	P944	V945	E946	E947	V948	F949	A950	A951	N952	A953	P954	F955	N956	G957	R958	V959	L960								
I961	G962	V963	G964	K965	L966	L967	R968	V969	Y970	Y971	L972	G973	K974	K975	K976	L977	L978	R979	K980	C981	E982	N983	K984	H985	I986	A987	N988	Y989	I990	S991	G992	I993	Q994	T995	I996	G997	H998	R999	V1000	I1001	V1002	S1003	D1004	V1005	Q1006	E1007	S1008	F1009	P1010	W1011	ASN	L1012	ALA	LEU	H1013	H1014	K1015	R1016	N1017	E1018	N1019	Q1020					
L1021	I1022	I1023	F1024	A1025	D1026	D1027	T1028	A1029	E1030	R1031	W1032	V1033	K1034	T1035	A1036	S1037	L1038	L1039	D1040	Y1041	D1042	T1043	V1044	A1045	G1046	A1047	D1048	K1049	F1050	G1051	N1052	I1053	C1054	V1055	V1056	R1057	L1058	P1059	P1060	M1061	T1062	M1063	D1064	E1065	V1066	D1067	ASP	PRO	THR	GLY	ASN	LYS	ALA	LEU	TRP	ASP	ARG	GLY	H1138	D1139	F1140						
LEU	N1083	G1084	A1085	S1086	Q1087	K1088	A1089	E1089	V1091	I1092	M1093	N1094	Y1095	H1096	V1097	G1098	E1099	T1100	V1101	L1102	S1103	L1104	Q1105	K1106	T1107	T1108	L1109	I1110	P1111	G1112	G1113	S1114	E1115	S1116	L1117	V1118	Y1119	T1120	T1121	L1122	S1123	G1124	G1125	I1126	G1127	I1128	L1129	V1130	P1131	F1132	T1133	S1134	H1135	E1136	D1137	H1138	D1139	F1140									



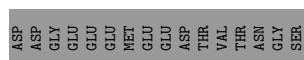
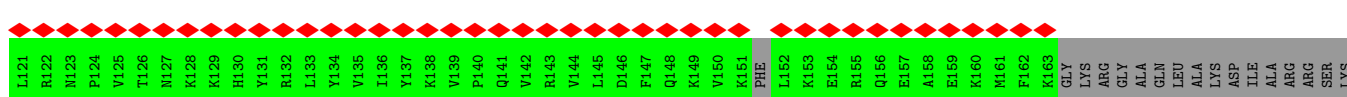
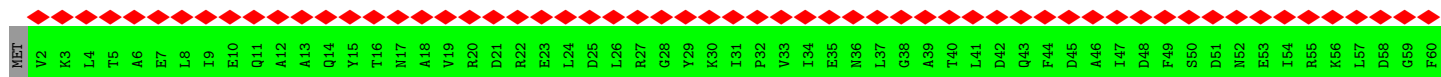
• Molecule 35: Splicing factor 3B subunit 5



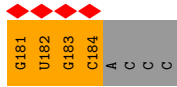
• Molecule 36: PHD finger-like domain-containing protein 5A



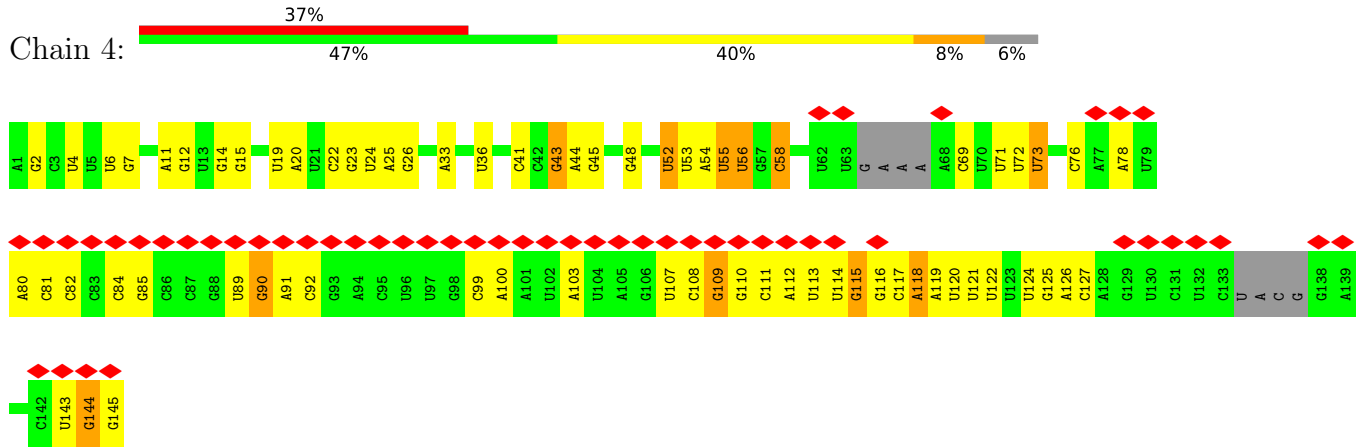
• Molecule 37: U2 small nuclear ribonucleoprotein A'



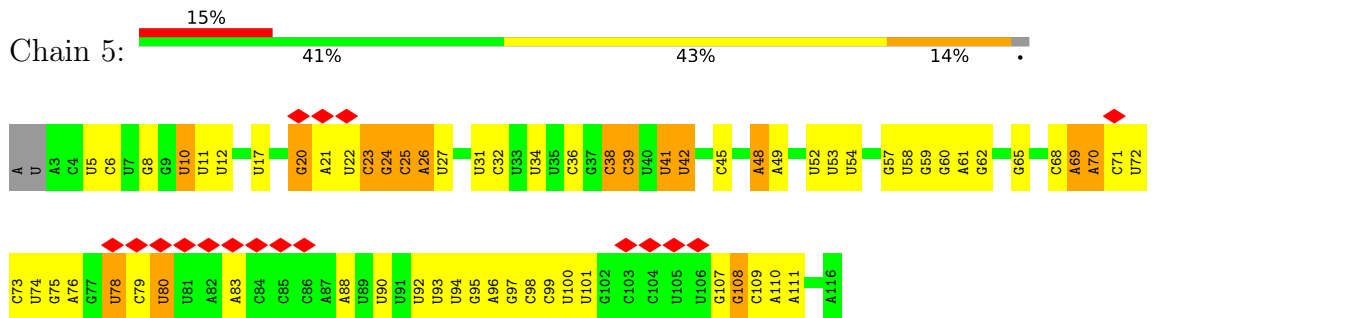
• Molecule 38: U2 small nuclear ribonucleoprotein B''



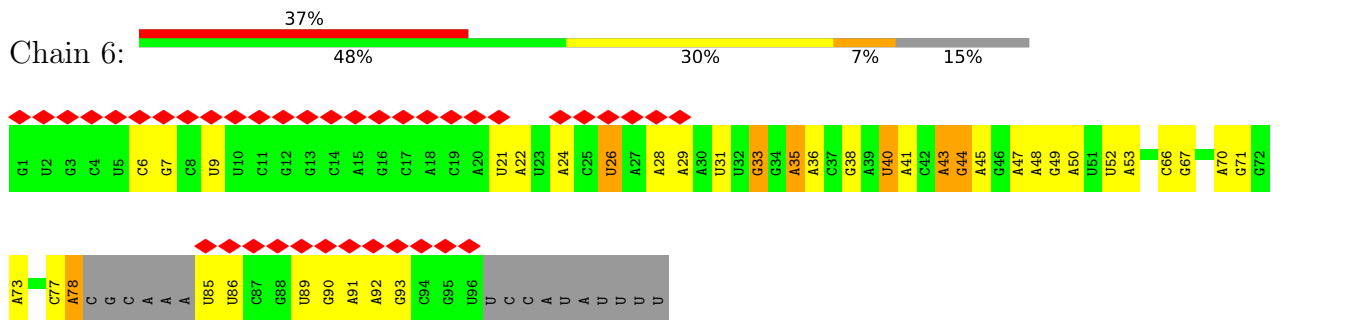
• Molecule 41: Homo sapiens U4A snRNA



• Molecule 42: Homo sapiens U5 A small nuclear RNA



• Molecule 43: Homo sapiens RNA, U6 small nuclear 1 (RNU6-1), small nuclear RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44629	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 ($e^-/\text{\AA}^2$)	1.5	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	0.144	Depositor
Minimum map value	-0.041	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	501.12, 501.12, 501.12	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality i

5.1 Standard geometry i

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	0.23	0/11222	0.41	0/15747
2	B	0.24	0/4312	0.43	0/6043
3	C	0.23	0/8613	0.41	0/12069
5	E	0.23	0/1107	0.42	0/1547
6	F	0.24	0/2115	0.45	0/2951
7	G	0.26	1/4089 (0.0%)	0.40	0/5728
8	H	0.49	1/2082 (0.0%)	0.40	0/2910
9	I	0.23	0/888	0.40	0/1241
10	J	0.23	0/681	0.38	0/952
11	K	0.22	0/224	0.29	0/312
12	L	0.24	0/2295	0.44	0/3198
13	M	0.24	0/853	0.47	0/1188
14	N	0.22	0/276	0.43	0/383
15	O	0.22	0/641	0.39	0/898
16	P	0.22	0/459	0.36	0/640
17	Q	0.24	0/379	0.35	0/530
18	R	0.21	0/78	0.35	0/107
19	a	0.22	0/394	0.44	0/548
19	h	0.22	0/371	0.44	0/516
20	b	0.24	0/367	0.45	0/509
20	i	0.24	0/357	0.46	0/495
21	c	0.22	0/388	0.46	0/540
21	j	0.22	0/388	0.45	0/540
22	d	0.23	0/346	0.48	0/481
22	k	0.23	0/366	0.47	0/509
23	e	0.23	0/392	0.47	0/546
23	l	0.23	0/354	0.45	0/492
24	f	0.23	0/319	0.43	0/442
24	m	0.22	0/314	0.44	0/434
25	g	0.23	0/471	0.42	0/657
25	n	0.22	0/414	0.45	0/578
39	Y	0.44	4/1083 (0.4%)	0.75	0/1681
40	2	0.88	16/2366 (0.7%)	1.55	70/3677 (1.9%)
41	4	0.16	0/3240	0.71	0/5039

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
42	5	0.16	0/2672	0.76	0/4154
43	6	0.14	0/2155	0.70	0/3355
All	All	0.30	22/57071 (0.0%)	0.58	70/81637 (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	A	0	2
7	G	0	3
All	All	0	5

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	268	LEU	C-N	19.79	1.71	1.34
40	2	150	U	C1'-N1	6.93	1.59	1.48
40	2	111	G	C1'-N9	-6.89	1.37	1.46
40	2	182	U	C1'-N1	6.86	1.59	1.48
40	2	142	U	C1'-N1	6.77	1.58	1.48

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	2	167	U	C5-C4-O4	11.77	132.96	125.90
40	2	164	C	N1-C2-O2	-10.19	112.78	118.90
40	2	162	U	N3-C2-O2	-9.05	115.87	122.20
40	2	164	C	C5'-C4'-O4'	-8.38	99.04	109.10
40	2	169	C	P-O3'-C3'	8.20	129.53	119.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	462	ARG	Peptide
1	A	948	PRO	Peptide
7	G	308	HIS	Peptide
7	G	840	ASP	Peptide
7	G	841	PRO	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	A	11100	0	5431	72	0
2	B	4264	0	2120	32	0
3	C	8538	0	4146	60	0
4	D	302	0	0	0	0
5	E	1101	0	543	15	0
6	F	2100	0	1038	24	0
7	G	4057	0	2089	37	0
8	H	2068	0	1019	20	0
9	I	883	0	414	4	0
10	J	677	0	316	1	0
11	K	225	0	98	2	0
12	L	2288	0	1076	10	0
13	M	844	0	426	3	0
14	N	277	0	114	2	0
15	O	636	0	322	2	0
16	P	458	0	225	1	0
17	Q	378	0	190	1	0
18	R	79	0	32	0	0
19	S	87	0	0	0	0
19	a	393	0	176	0	0
19	h	371	0	162	0	0
20	T	74	0	0	0	0
20	b	364	0	181	0	0
20	i	354	0	177	0	0
21	U	79	0	0	0	0
21	c	388	0	167	0	0
21	j	388	0	167	0	0
22	V	74	0	0	0	0
22	d	344	0	168	0	0
22	k	364	0	176	0	0
23	W	80	0	0	2	0
23	e	390	0	188	0	0
23	l	353	0	166	0	0
24	X	71	0	0	0	0
24	f	319	0	144	0	0
24	m	316	0	133	0	0
25	Z	82	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	g	469	0	214	0	0
25	n	412	0	185	0	0
26	o	90	0	0	0	0
27	p	73	0	0	0	0
28	q	80	0	0	0	0
29	r	76	0	0	0	0
30	s	69	0	0	0	0
31	t	79	0	0	0	0
32	u	62	0	0	0	0
33	v	806	0	0	0	0
34	w	1140	0	0	0	0
35	x	54	0	0	0	0
36	y	89	0	0	0	0
37	z	162	0	0	0	0
38	1	94	0	0	0	0
39	Y	972	0	495	31	0
40	2	2123	0	1076	178	0
41	4	2904	0	1470	44	0
42	5	2397	0	1216	40	0
43	6	1926	0	973	33	0
All	All	59243	0	27233	553	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 7.

The worst 5 of 553 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)
40:2:153:A:H2	40:2:178:A:N1	1.00	1.46
1:A:2313:HIS:CB	3:C:1045:PRO:HB3	1.47	1.44
40:2:153:A:C2'	40:2:154:C:H5'	1.46	1.42
8:H:268:LEU:C	8:H:269:PRO:N	1.71	1.39
40:2:153:A:N1	40:2:178:A:N6	1.73	1.37

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	A	2184/2335 (94%)	1969 (90%)	208 (10%)	7 (0%)	41	76
2	B	842/972 (87%)	772 (92%)	70 (8%)	0	100	100
3	C	1689/2136 (79%)	1624 (96%)	63 (4%)	2 (0%)	51	85
5	E	215/683 (32%)	174 (81%)	37 (17%)	4 (2%)	8	41
6	F	416/521 (80%)	376 (90%)	39 (9%)	1 (0%)	47	81
7	G	798/941 (85%)	700 (88%)	94 (12%)	4 (0%)	29	68
8	H	411/499 (82%)	359 (87%)	49 (12%)	3 (1%)	22	62
9	I	174/312 (56%)	158 (91%)	15 (9%)	1 (1%)	25	65
10	J	133/142 (94%)	126 (95%)	7 (5%)	0	100	100
11	K	43/439 (10%)	42 (98%)	1 (2%)	0	100	100
12	L	451/513 (88%)	437 (97%)	14 (3%)	0	100	100
13	M	167/177 (94%)	158 (95%)	9 (5%)	0	100	100
14	N	54/199 (27%)	47 (87%)	7 (13%)	0	100	100
15	O	124/128 (97%)	119 (96%)	5 (4%)	0	100	100
16	P	87/800 (11%)	79 (91%)	8 (9%)	0	100	100
17	Q	73/376 (19%)	70 (96%)	3 (4%)	0	100	100
18	R	14/557 (2%)	13 (93%)	1 (7%)	0	100	100
19	a	74/118 (63%)	71 (96%)	3 (4%)	0	100	100
19	h	70/118 (59%)	68 (97%)	2 (3%)	0	100	100
20	b	71/86 (83%)	70 (99%)	1 (1%)	0	100	100
20	i	69/86 (80%)	67 (97%)	2 (3%)	0	100	100
21	c	76/92 (83%)	70 (92%)	6 (8%)	0	100	100
21	j	76/92 (83%)	70 (92%)	6 (8%)	0	100	100
22	d	67/76 (88%)	63 (94%)	4 (6%)	0	100	100
22	k	71/76 (93%)	67 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	e	76/126 (60%)	73 (96%)	3 (4%)	0	100	100
23	l	69/126 (55%)	69 (100%)	0	0	100	100
24	f	60/240 (25%)	57 (95%)	3 (5%)	0	100	100
24	m	60/240 (25%)	57 (95%)	3 (5%)	0	100	100
25	g	89/119 (75%)	84 (94%)	5 (6%)	0	100	100
25	n	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
All	All	8883/13444 (66%)	8186 (92%)	675 (8%)	22 (0%)	50	81

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	957	VAL
7	G	842	HIS
7	G	373	VAL
8	H	434	VAL
1	A	1015	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	125/2108 (6%)	125 (100%)	0	100	100
2	B	49/866 (6%)	49 (100%)	0	100	100
3	C	77/1908 (4%)	77 (100%)	0	100	100
5	E	8/599 (1%)	8 (100%)	0	100	100
6	F	17/441 (4%)	17 (100%)	0	100	100
7	G	35/792 (4%)	35 (100%)	0	100	100
8	H	15/424 (4%)	15 (100%)	0	100	100
9	I	6/293 (2%)	6 (100%)	0	100	100
10	J	5/130 (4%)	5 (100%)	0	100	100
12	L	11/450 (2%)	11 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	M	10/148 (7%)	10 (100%)	0	100	100
15	O	6/111 (5%)	6 (100%)	0	100	100
16	P	3/681 (0%)	3 (100%)	0	100	100
17	Q	2/333 (1%)	2 (100%)	0	100	100
19	a	3/110 (3%)	3 (100%)	0	100	100
19	h	2/110 (2%)	2 (100%)	0	100	100
20	b	4/74 (5%)	4 (100%)	0	100	100
20	i	4/74 (5%)	4 (100%)	0	100	100
21	c	1/84 (1%)	1 (100%)	0	100	100
21	j	1/84 (1%)	1 (100%)	0	100	100
22	d	3/66 (4%)	3 (100%)	0	100	100
22	k	3/66 (4%)	3 (100%)	0	100	100
23	e	3/101 (3%)	3 (100%)	0	100	100
23	l	2/101 (2%)	2 (100%)	0	100	100
24	f	2/177 (1%)	2 (100%)	0	100	100
25	g	4/101 (4%)	4 (100%)	0	100	100
25	n	3/101 (3%)	3 (100%)	0	100	100
All	All	404/10533 (4%)	404 (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. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
39	Y	44/324 (13%)	14 (31%)	0
40	2	96/188 (51%)	18 (18%)	3 (3%)
41	4	134/145 (92%)	41 (30%)	4 (2%)
42	5	113/116 (97%)	36 (31%)	2 (1%)
43	6	88/106 (83%)	22 (25%)	3 (3%)
All	All	475/879 (54%)	131 (27%)	12 (2%)

5 of 131 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
39	Y	50	C
39	Y	51	U
39	Y	52	C
39	Y	53	C
39	Y	54	G

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
42	5	78	U
42	5	94	U
43	6	77	C
43	6	28	A
41	4	43	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
12	L	1
3	C	1
8	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L	39:ASN	C	40:THR	N	8.39
1	C	1296:PRO	C	1297:PRO	N	3.45
1	H	268:LEU	C	269:PRO	N	1.71

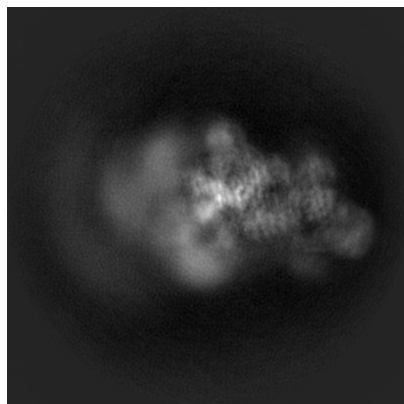
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3766. These allow visual inspection of the internal detail of the map and identification of artifacts.

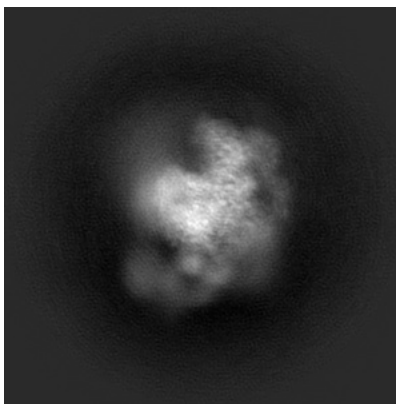
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

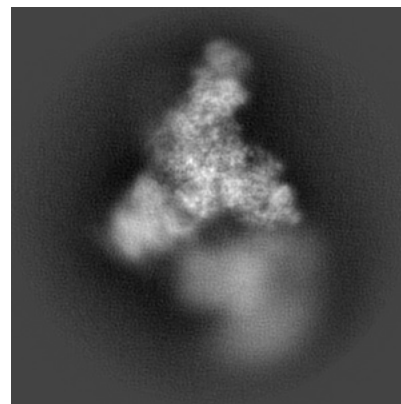
6.1.1 Primary map



X

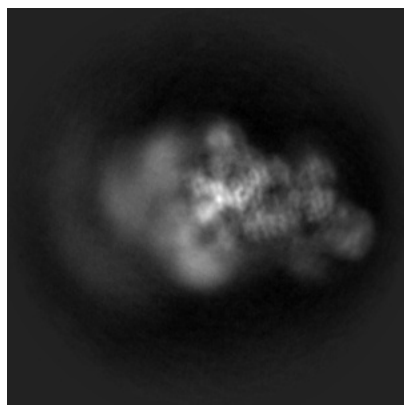


Y

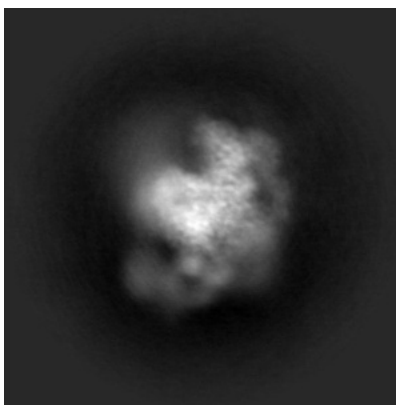


Z

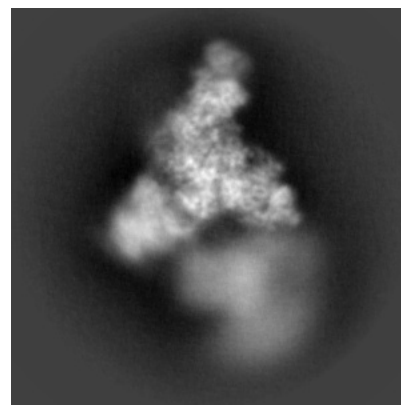
6.1.2 Raw map



X



Y

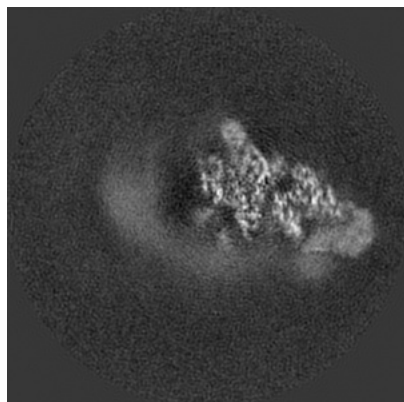


Z

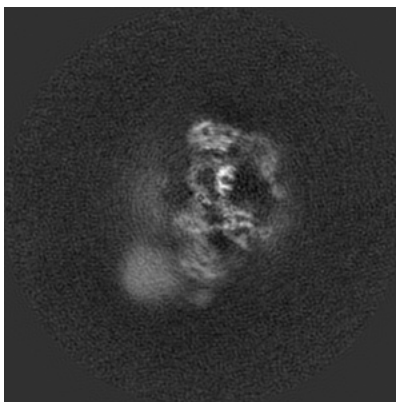
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

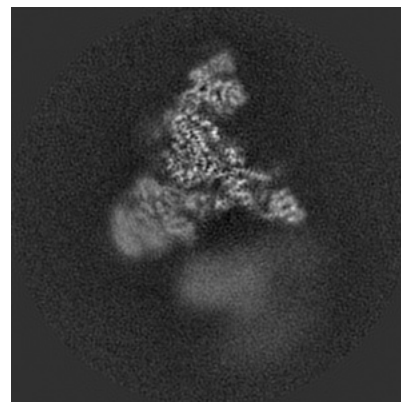
6.2.1 Primary map



X Index: 216

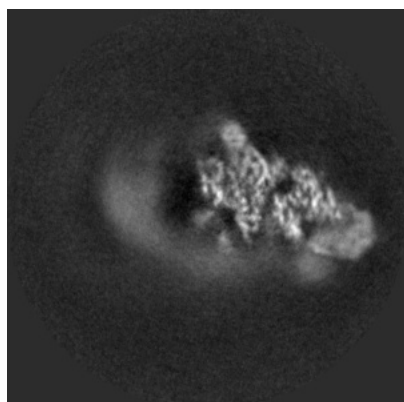


Y Index: 216

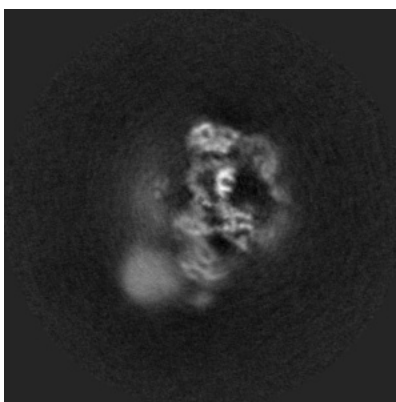


Z Index: 216

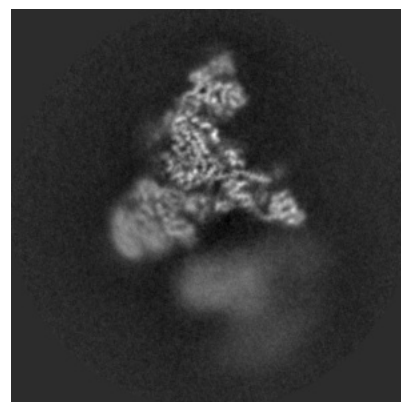
6.2.2 Raw map



X Index: 216



Y Index: 216

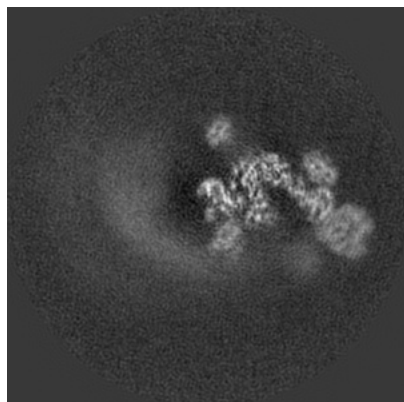


Z Index: 216

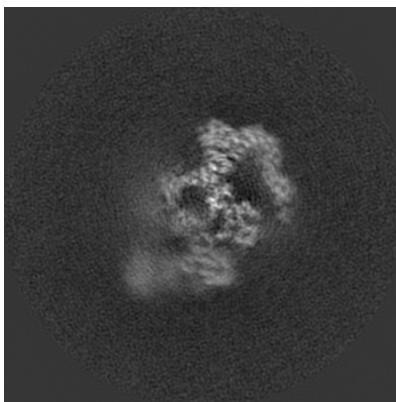
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

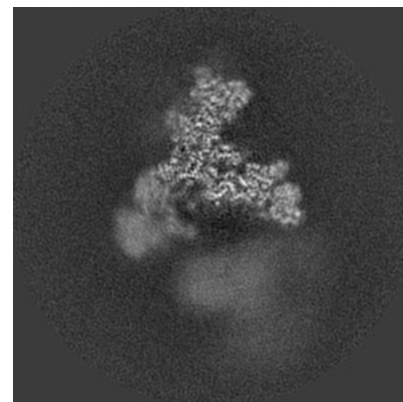
6.3.1 Primary map



X Index: 237

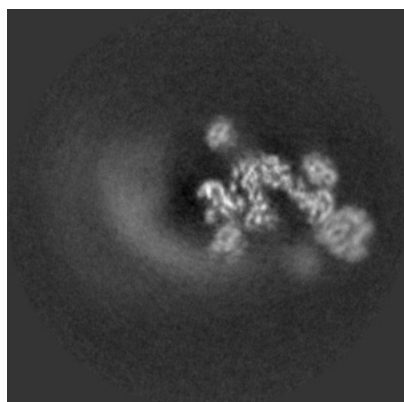


Y Index: 229

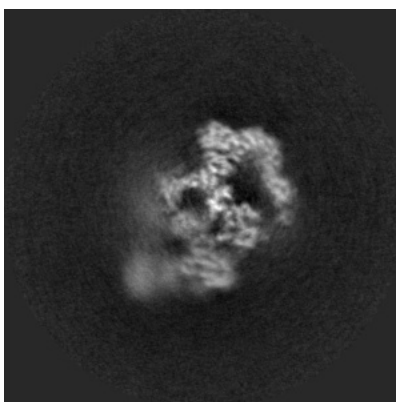


Z Index: 225

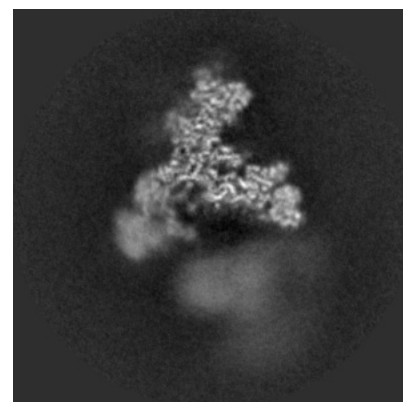
6.3.2 Raw map



X Index: 237



Y Index: 229

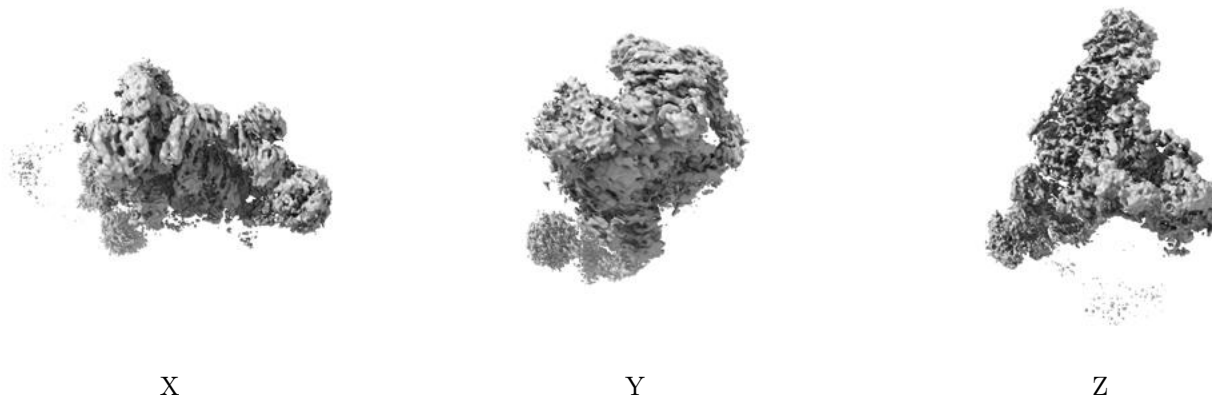


Z Index: 225

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

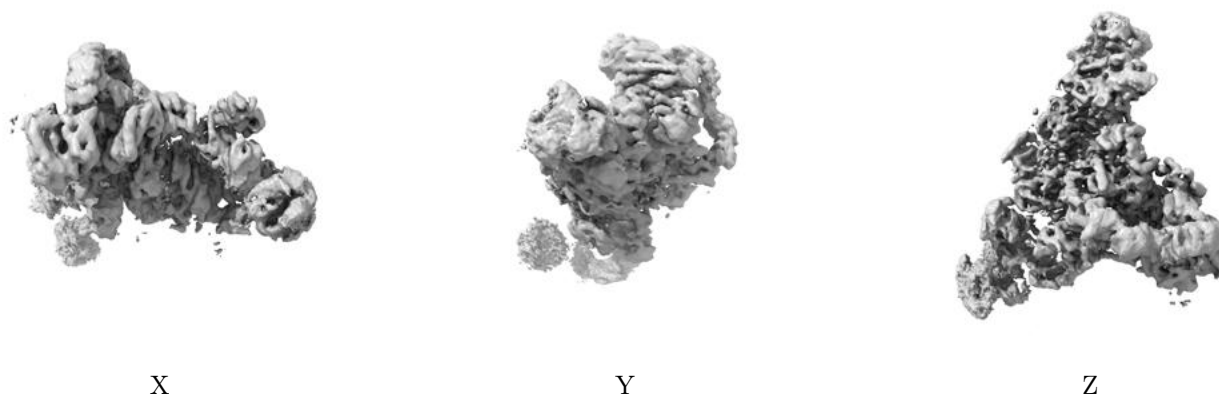
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



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

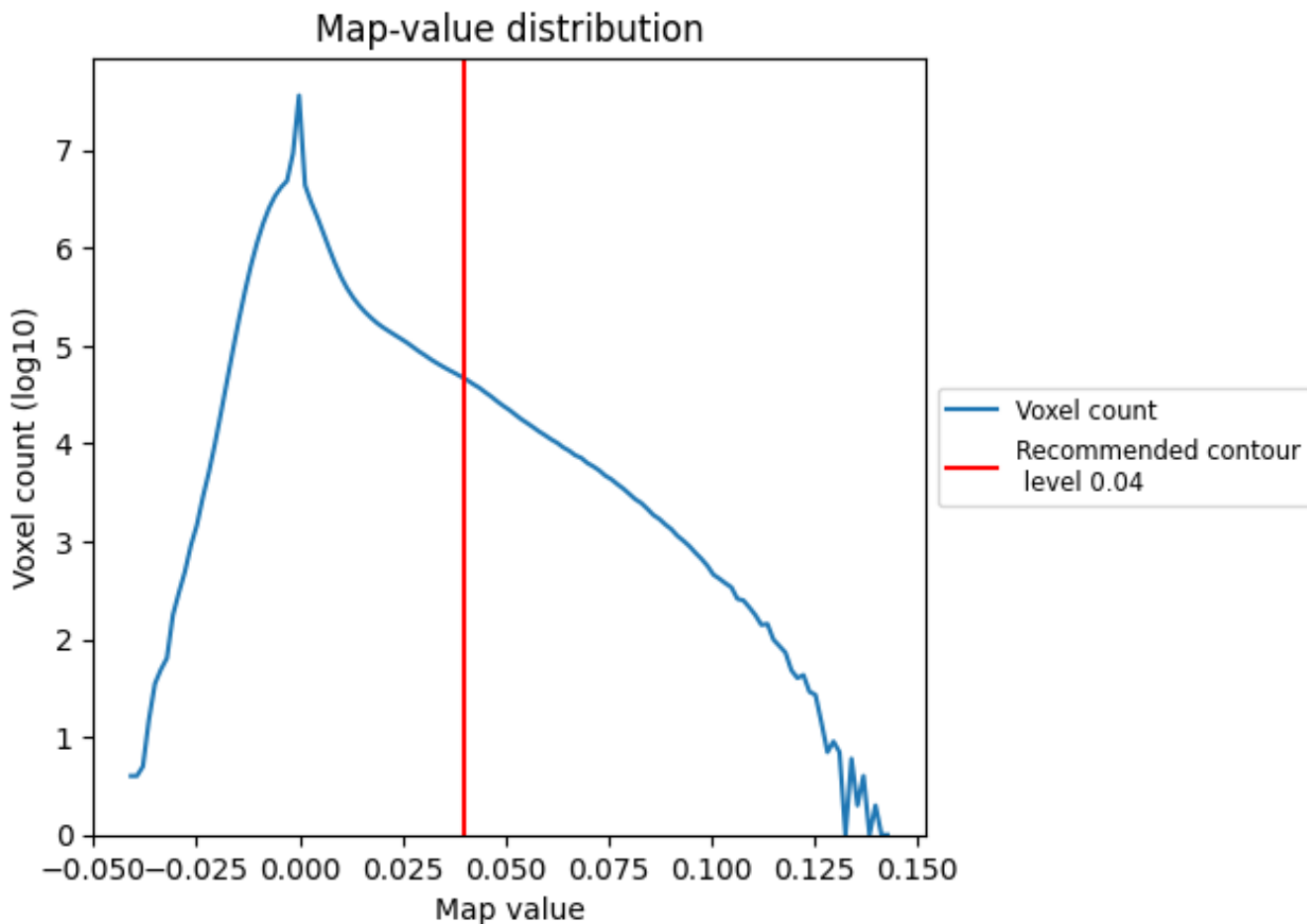
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

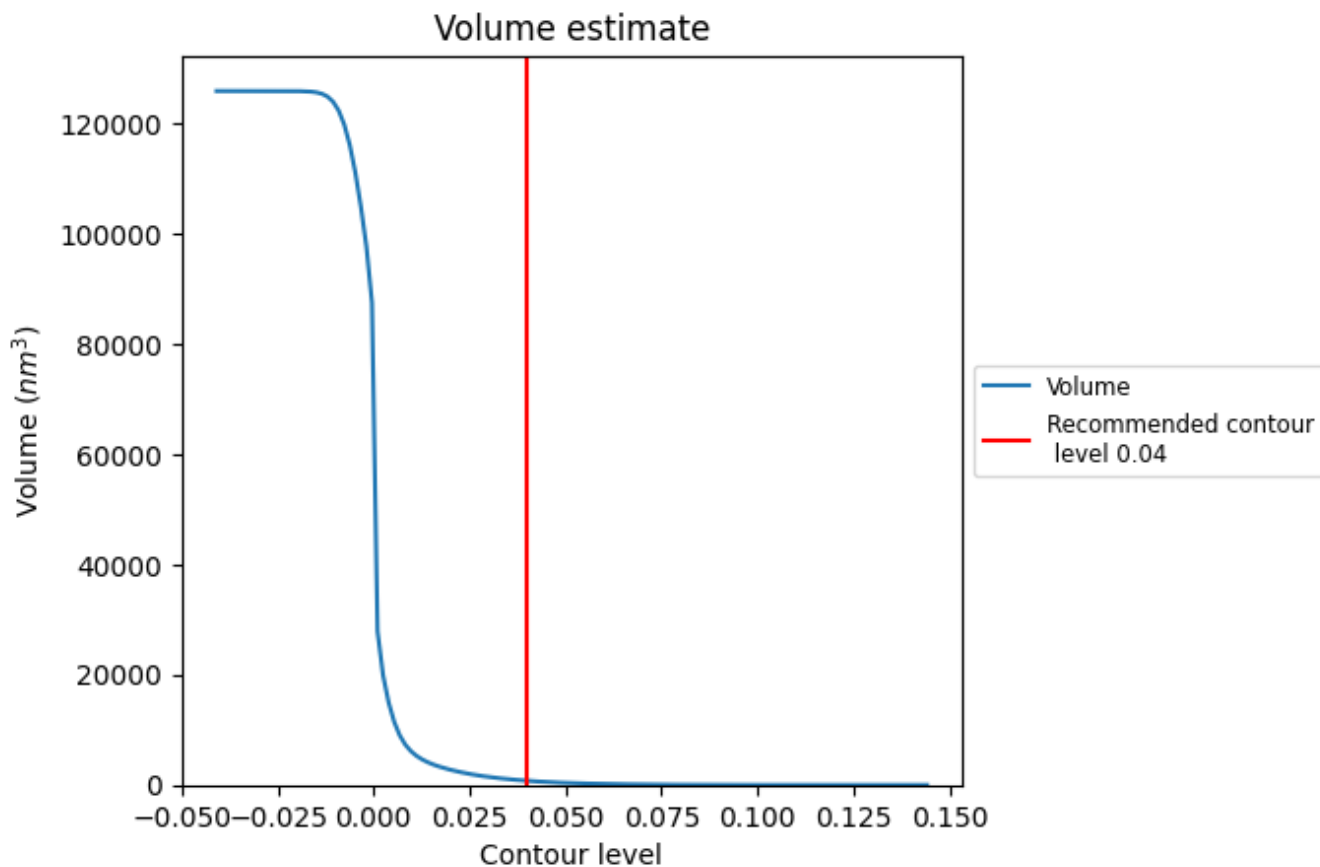
This section contains the results of statistical analysis of the map.

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.

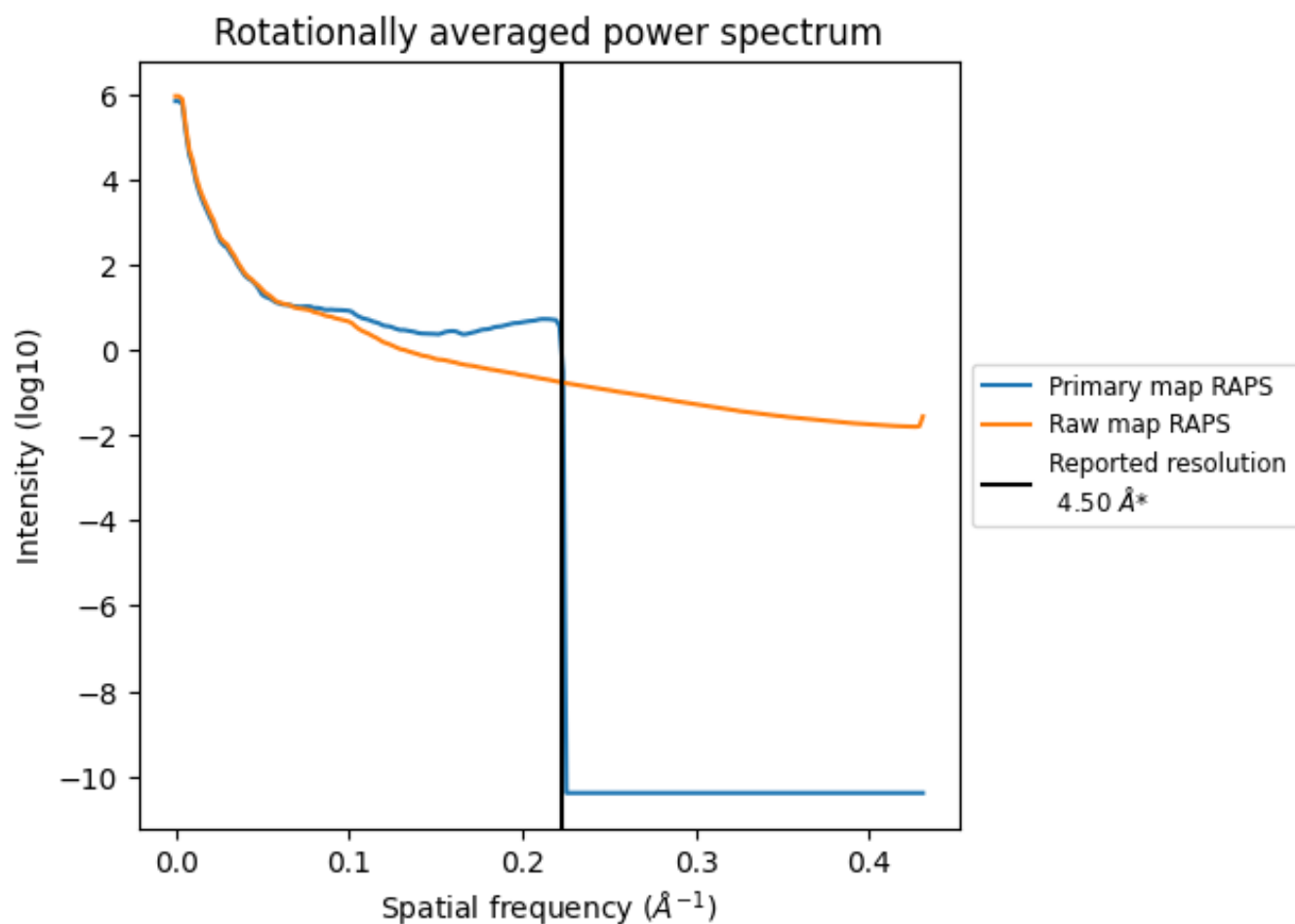
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 761 nm^3 ; this corresponds to an approximate mass of 688 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

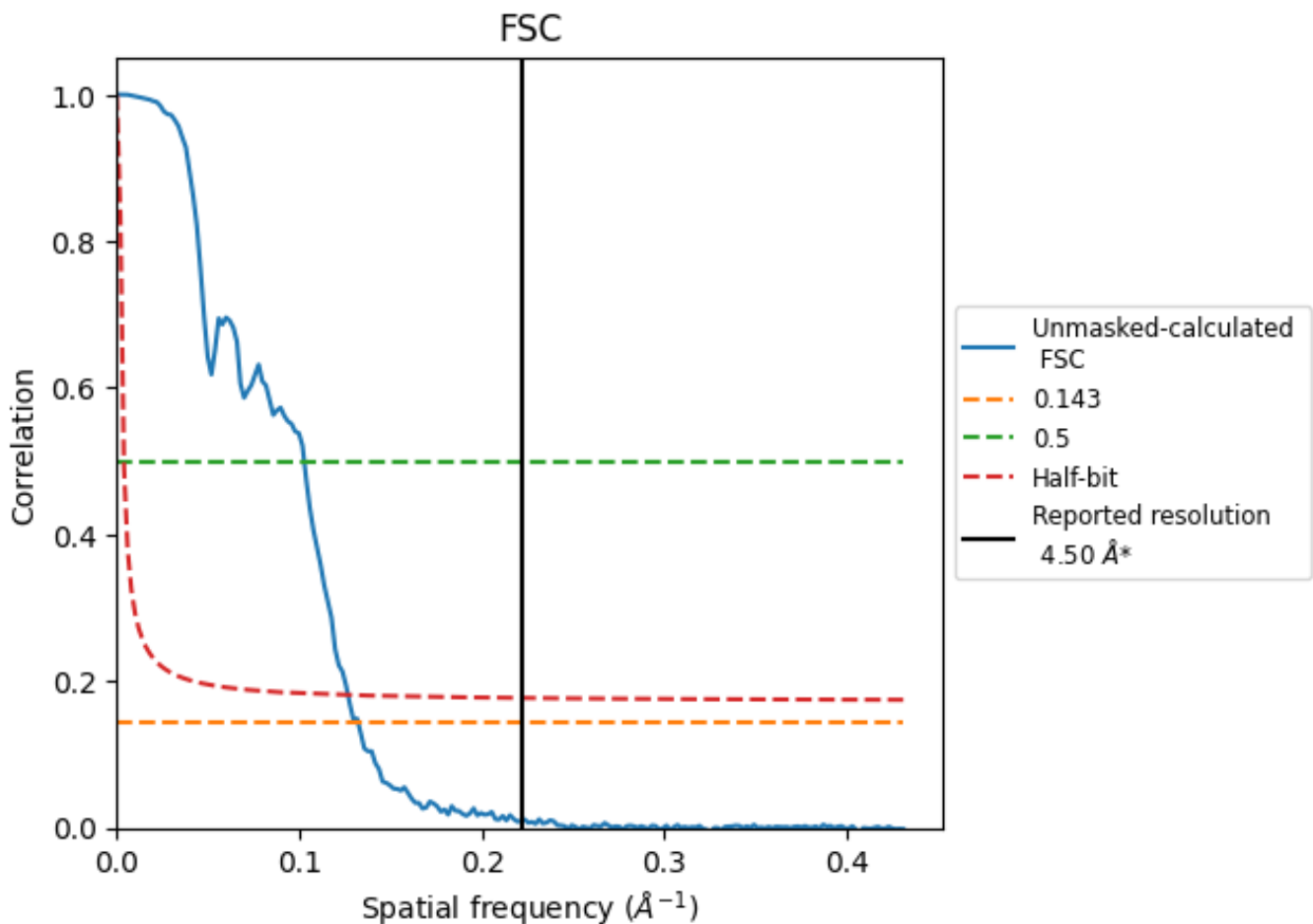


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.222 \AA^{-1}

8.2 Resolution estimates [i](#)

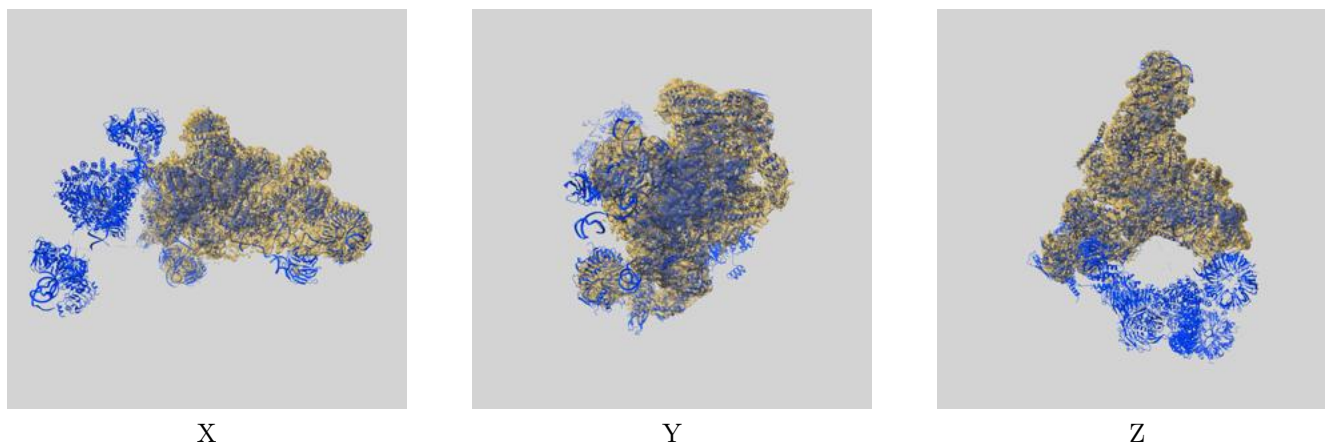
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.56	9.74	7.89

*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 7.56 differs from the reported value 4.5 by more than 10 %

9 Map-model fit [i](#)

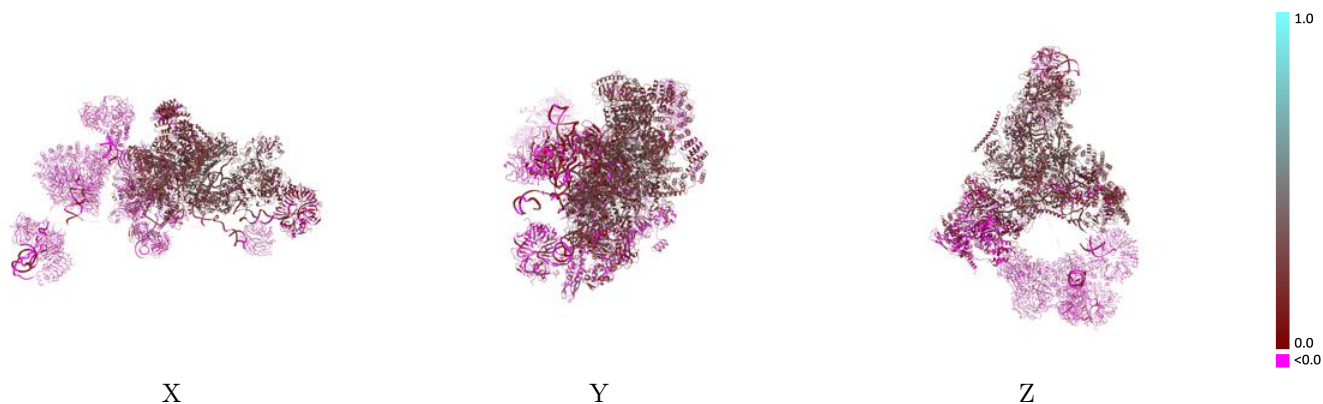
This section contains information regarding the fit between EMDB map EMD-3766 and PDB model 5O9Z. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



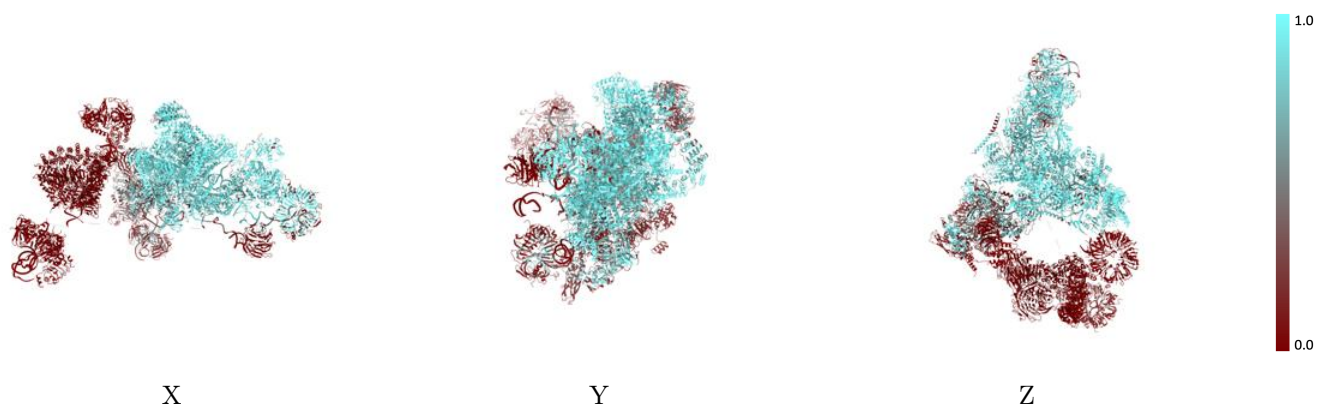
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



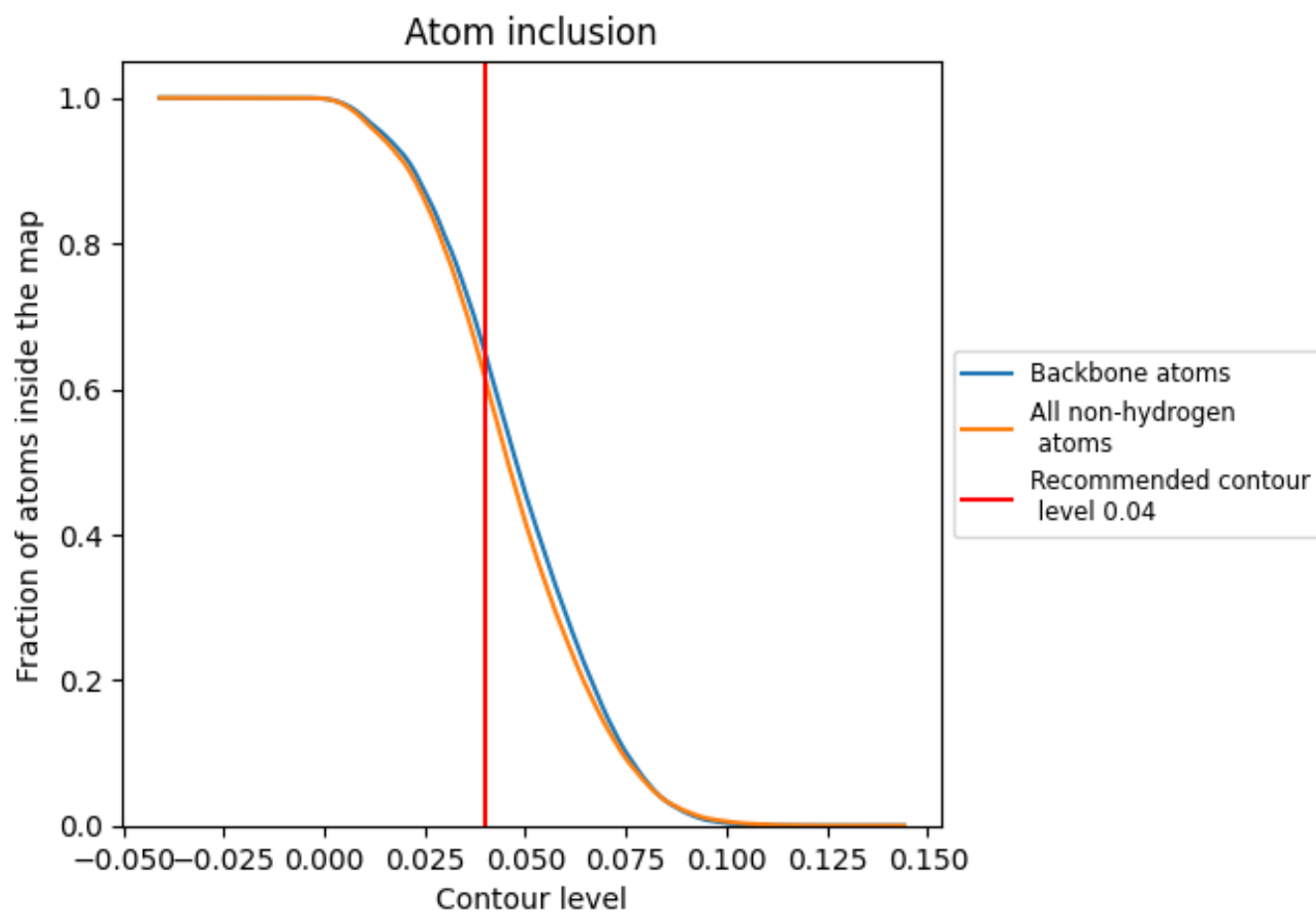
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 61% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6147	 0.1700
1	 0.0000	 -0.0190
2	 0.0033	 0.0020
4	 0.5472	 0.1530
5	 0.7514	 0.1460
6	 0.5125	 0.1590
A	 0.8732	 0.2930
B	 0.9022	 0.2720
C	 0.4551	 0.1010
D	 0.0795	 0.0160
E	 0.8719	 0.2380
F	 0.9357	 0.2270
G	 0.8541	 0.2100
H	 0.8559	 0.2640
I	 0.8641	 0.2710
J	 0.9084	 0.3400
K	 0.5333	 0.1580
L	 0.0022	 0.0000
M	 0.8448	 0.1800
N	 0.8881	 0.2410
O	 0.9104	 0.3320
P	 0.8668	 0.2450
Q	 0.8439	 0.2290
R	 0.0000	 -0.0450
S	 0.0000	 -0.0040
T	 0.0000	 0.0150
U	 0.0000	 0.0180
V	 0.0000	 -0.0160
W	 0.0000	 0.0150
X	 0.0000	 -0.0380
Y	 0.4815	 0.1140
Z	 0.0000	 0.0200
a	 0.6463	 0.0580
b	 0.5220	 0.0720
c	 0.6753	 0.1070



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Chain	Atom inclusion	Q-score
d	 0.6977	 0.1330
e	 0.7256	 0.1590
f	 0.6740	 0.1190
g	 0.4968	 0.0860
h	 0.3127	 0.0490
i	 0.1808	 0.0130
j	 0.1778	 -0.0180
k	 0.1126	 -0.0050
l	 0.2011	 -0.0270
m	 0.1994	 0.0790
n	 0.2379	 -0.0190
o	 0.0000	 0.0070
p	 0.0000	 -0.0560
q	 0.0000	 0.0160
r	 0.0000	 0.0060
s	 0.0000	 0.0340
t	 0.0000	 0.0120
u	 0.0000	 0.0350
v	 0.0000	 0.0080
w	 0.0009	 0.0070
x	 0.0000	 0.0850
y	 0.0000	 -0.0320
z	 0.0000	 0.0070