



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:05 AM UTC

PDB ID : 8QZS / pdb_00008qzs
EMDB ID : EMD-18781
Title : Cryo-EM structure of the cross-exon B-like complex
Authors : Zhang, Z.; Kumar, V.; Dybkov, O.; Will, C.L.; Zhong, J.; Ludwig, S.; Urlaub, H.; Kastner, B.; Stark, H.; Luehrmann, R.
Deposited on : 2023-10-29
Resolution : 4.10 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:

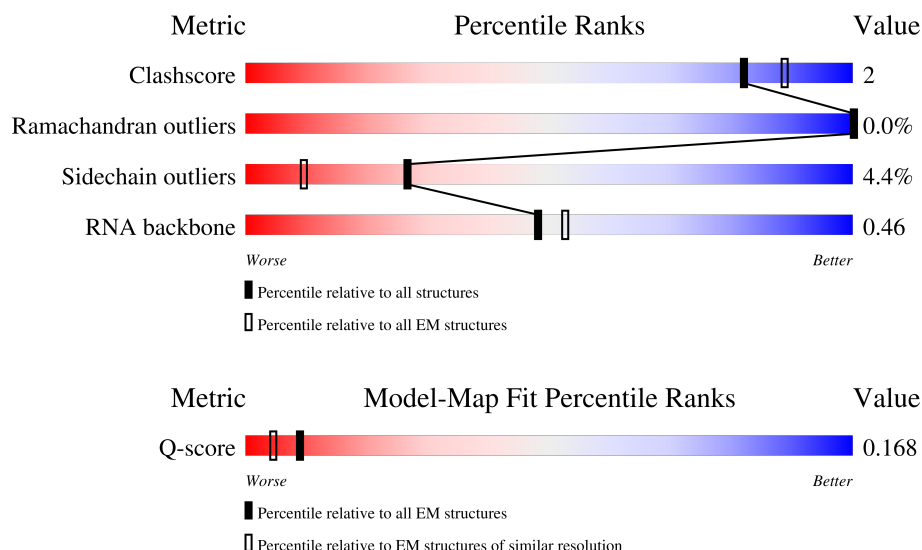
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.10 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.



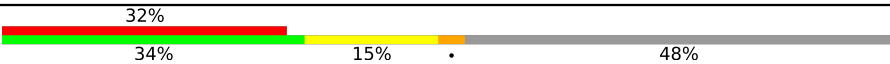
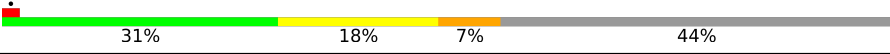
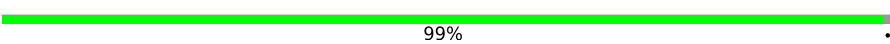
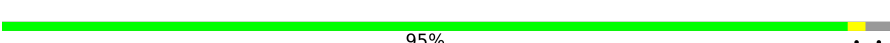
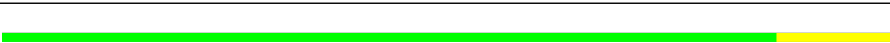
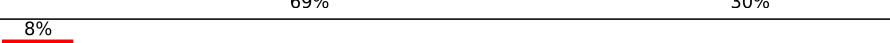
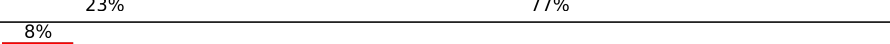
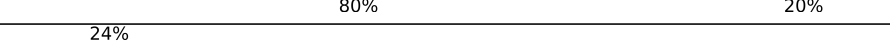
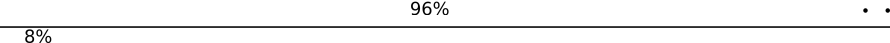
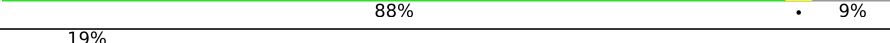
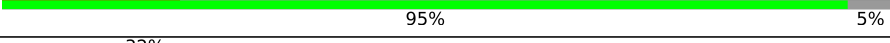
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6458 (3.60 - 4.60)

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	
2	B	2136	
3	5	117	

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Mol	Chain	Length	Quality of chain
4	2	188	
5	6	106	
6	4	144	
7	C	972	
8	D	142	
9	E	357	
10	I	312	
11	M	128	
12	U	565	
13	W	177	
14	X	376	
15	Z	15	
16	7	793	
17	r	199	
18	B4	424	
19	8	464	
20	9	501	
21	B2	895	
22	B5	86	
23	B3	1217	
24	BP	110	
25	B1	1304	
26	B6	125	
27	62	95	
28	63	102	

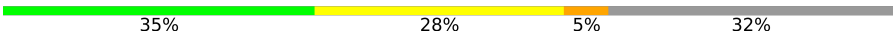
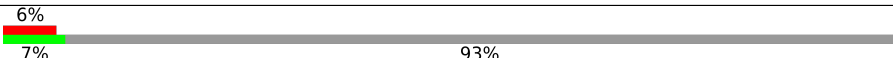
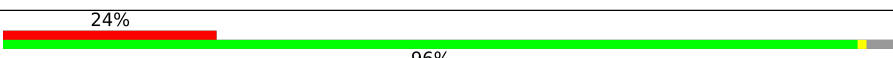
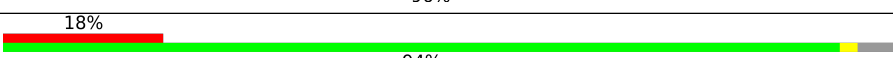
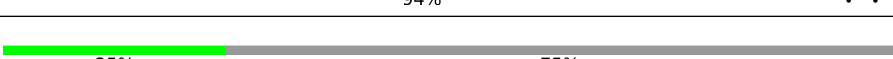
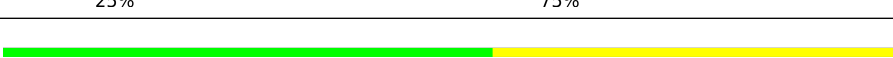
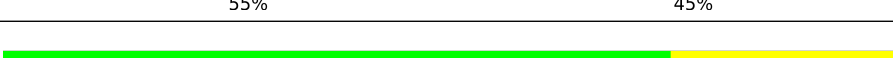
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Mol	Chain	Length	Quality of chain
29	64	139	
30	65	91	
31	66	80	
32	67	103	
33	68	96	
34	22	118	
34	42	118	
34	52	118	
35	2f	86	
35	4f	86	
35	5f	86	
36	2e	92	
36	4e	92	
36	5e	92	
37	2g	76	
37	4g	76	
37	5g	76	
38	23	126	
38	43	126	
38	53	126	
39	2b	240	
39	4b	240	
39	5b	240	
40	21	119	
40	41	119	

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Mol	Chain	Length	Quality of chain
40	51	119	
41	2B	225	
42	2A	255	
43	x	557	
43	y	557	
44	v	513	
44	w	513	
45	K	439	
46	z1	11	
47	z2	4	
48	J	683	
49	L	499	
50	F	522	
51	N	941	
52	S	800	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 86145 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
1	A	2247	Total	C	N	O	0	0
			11389	6895	2247	2247		

- Molecule 2 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

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

- Molecule 3 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	109	Total	C	N	O	P	0	0
			2296	1028	383	776	109		

- Molecule 4 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	2	98	Total	C	N	O	P	0	0
			2071	926	349	698	98		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	97	A	G	conflict	GB 36516

- Molecule 5 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	59	Total	C	N	O	P	0	0
			1251	558	230	404	59		

- Molecule 6 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	4	136	Total	C	N	O	P	0	0
			2881	1288	498	959	136		

- Molecule 7 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	C	836	Total	C	N	O	0	0
			4223	2551	836	836		

- Molecule 8 is a protein called Thioredoxin-like protein 4A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	D	141	Total	C	N	O	0	0
			708	426	141	141		

- Molecule 9 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	E	299	Total	C	N	O	0	0
			1196	598	299	299		

- Molecule 10 is a protein called Pre-mRNA-splicing factor 38A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	I	183	Total	C	N	O	0	0
			920	554	183	183		

- Molecule 11 is a protein called NHP2-like protein 1, N-terminally processed.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	M	124	Total	C	N	O	0	0
			627	379	124	124		

- Molecule 12 is a protein called Ubiquitin carboxyl-terminal hydrolase 39.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	U	456	Total	C	N	O	0	0
			2308	1396	456	456		

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

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

- Molecule 14 is a protein called WW domain-binding protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	X	80	Total	C	N	O	0	0
			403	243	80	80		

- Molecule 15 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Z	15	Total	C	N	O	P	0	0
			314	141	51	107	15		

- Molecule 16 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	7	204	Total	C	N	O	0	0
			1028	620	204	204		

- Molecule 17 is a protein called Zinc finger matrin-type protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	r	114	Total	C	N	O	0	0
			568	340	114	114		

- Molecule 18 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	B4	78	Total	C	N	O	0	0
			391	235	78	78		

- Molecule 19 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	8	144	Total	C	N	O	0	0
			729	441	144	144		

- Molecule 20 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	9	350	Total	C	N	O	0	0
			1755	1055	350	350		

- Molecule 21 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	B2	208	Total	C	N	O	0	0
			1072	656	208	208		

- Molecule 22 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	B5	69	Total	C	N	O	0	0
			347	209	69	69		

- Molecule 23 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	B3	1186	Total	C	N	O	0	0
			5969	3597	1186	1186		

- Molecule 24 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	BP	100	Total	C	N	O	0	0
			498	298	100	100		

- Molecule 25 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	B1	870	Total	C	N	O	0	0
			4383	2643	870	870		

- Molecule 26 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	B6	90	Total	C	N	O	0	0
			455	275	90	90		

- Molecule 27 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	62	90	Total	C	N	O	0	0
			360	180	90	90		

- Molecule 28 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	63	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 29 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	64	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 30 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	65	72	Total	C	N	O	0	0
			288	144	72	72		

- Molecule 31 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	66	70	Total	C	N	O	0	0
			280	140	70	70		

- Molecule 32 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	67	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 33 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	68	61	Total	C	N	O	0	0
			244	122	61	61		

- Molecule 34 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	42	74	Total	C	N	O	0	0
			300	152	74	74		
34	52	98	Total	C	N	O	S	0
			796	498	144	148	6	0
34	22	95	Total	C	N	O		0
			482	292	95	95		0

- Molecule 35 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	4f	71	Total	C	N	O	0	0
			292	150	71	71		
35	5f	73	Total	C	N	O	S	0
			567	367	94	101	5	0
35	2f	72	Total	C	N	O		0
			359	215	72	72		0

- Molecule 36 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	4e	78	Total	C	N	O	0	0
			314	158	78	78		
36	5e	77	Total	C	N	O	S	0
			638	405	113	115	5	0
36	2e	81	Total	C	N	O		0
			403	241	81	81		0

- Molecule 37 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	4g	73	Total	C	N	O	0	0
			298	152	73	73		
37	5g	74	Total	C	N	O	S	0
			577	364	104	103	6	0
37	2g	73	Total	C	N	O		0
			364	218	73	73		0

- Molecule 38 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	43	71	Total	C	N	O	0	0
			288	146	71	71		

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Mol	Chain	Residues	Atoms					AltConf	Trace
38	53	84	Total	C	N	O	S	0	0
			657	412	116	123	6		
38	23	83	Total	C	N	O		0	0
			415	249	83	83			

- Molecule 39 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	4b	64	Total	C	N	O		0	0
			256	128	64	64			
39	5b	73	Total	C	N	O	S	0	0
			594	376	108	103	7		
39	2b	82	Total	C	N	O		0	0
			413	249	82	82			

- Molecule 40 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	41	82	Total	C	N	O		0	0
			334	170	82	82			
40	51	81	Total	C	N	O	S	0	0
			641	408	112	118	3		
40	21	80	Total	C	N	O		0	0
			402	242	80	80			

- Molecule 41 is a protein called U2 small nuclear ribonucleoprotein B''.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	2B	92	Total	C	N	O	0	0
			461	277	92	92		

- Molecule 42 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	2A	162	Total	C	N	O	0	0
			816	492	162	162		

- Molecule 43 is a protein called Protein Red.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	x	39	Total	C	N	O	0	0
			197	119	39	39		
43	y	37	Total	C	N	O	0	0
			187	113	37	37		

- Molecule 44 is a protein called WD40 repeat-containing protein SMU1.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	w	495	Total	C	N	O	0	0
			2474	1484	495	495		
44	v	496	Total	C	N	O	0	0
			2478	1486	496	496		

- Molecule 45 is a protein called Microfibrillar-associated protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	K	109	Total	C	N	O	0	0
			543	325	109	109		

- Molecule 46 is a RNA chain called Oligo 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	z1	11	Total	C	N	O	P	0	0
			239	107	46	75	11		

- Molecule 47 is a RNA chain called Oligo 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	z2	4	Total	C	N	O	P	0	0
			90	40	20	26	4		

- Molecule 48 is a protein called U4/U6 small nuclear ribonucleoprotein Prp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	J	224	Total	C	N	O	0	0
			1125	677	224	224		

- Molecule 49 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	L	376	Total	C	N	O	0	0
			1887	1135	376	376		

- Molecule 50 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	F	404	Total	C	N	O	0	0
			2020	1212	404	404		

- Molecule 51 is a protein called Pre-mRNA-processing factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	N	831	Total	C	N	O	0	0
			4192	2530	831	831		

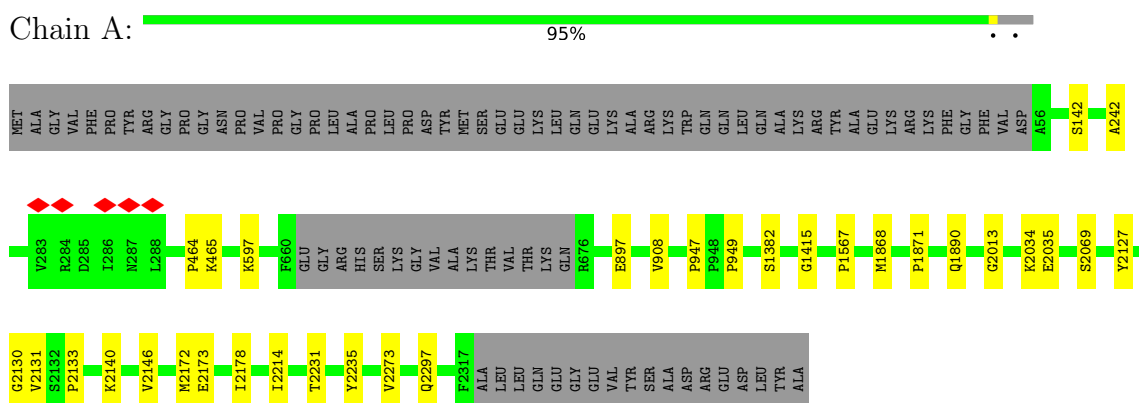
- Molecule 52 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	S	171	Total	C	N	O	0	0
			858	516	171	171		

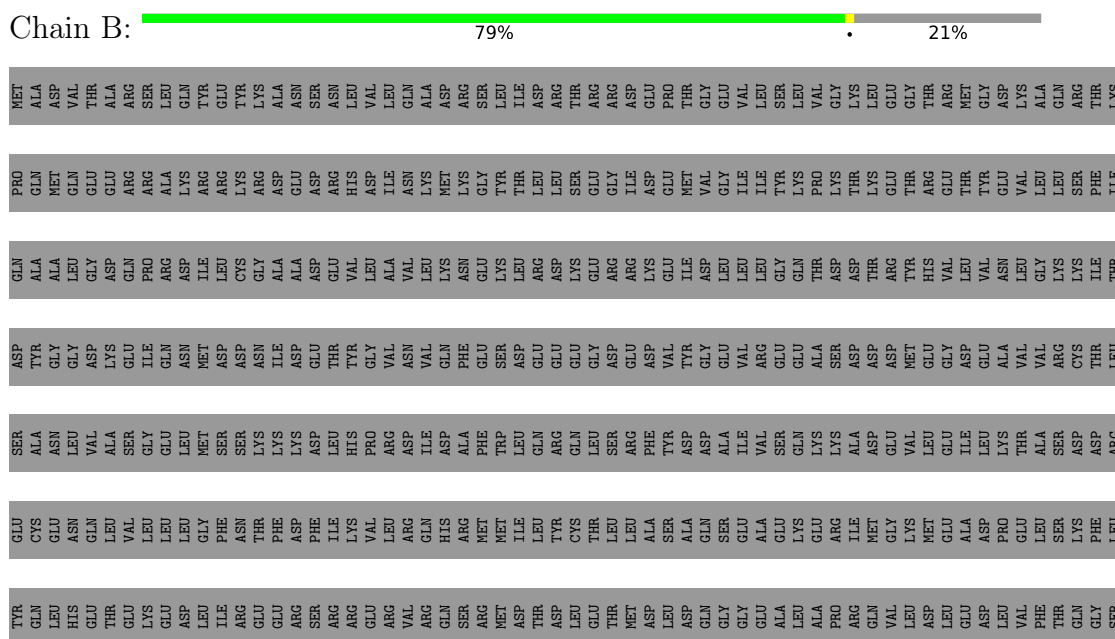
3 Residue-property plots

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 2: U5 small nuclear ribonucleoprotein 200 kDa helicase



- MET
THR
GLU
ALA
D5
E61
P62
V128

[illegible]

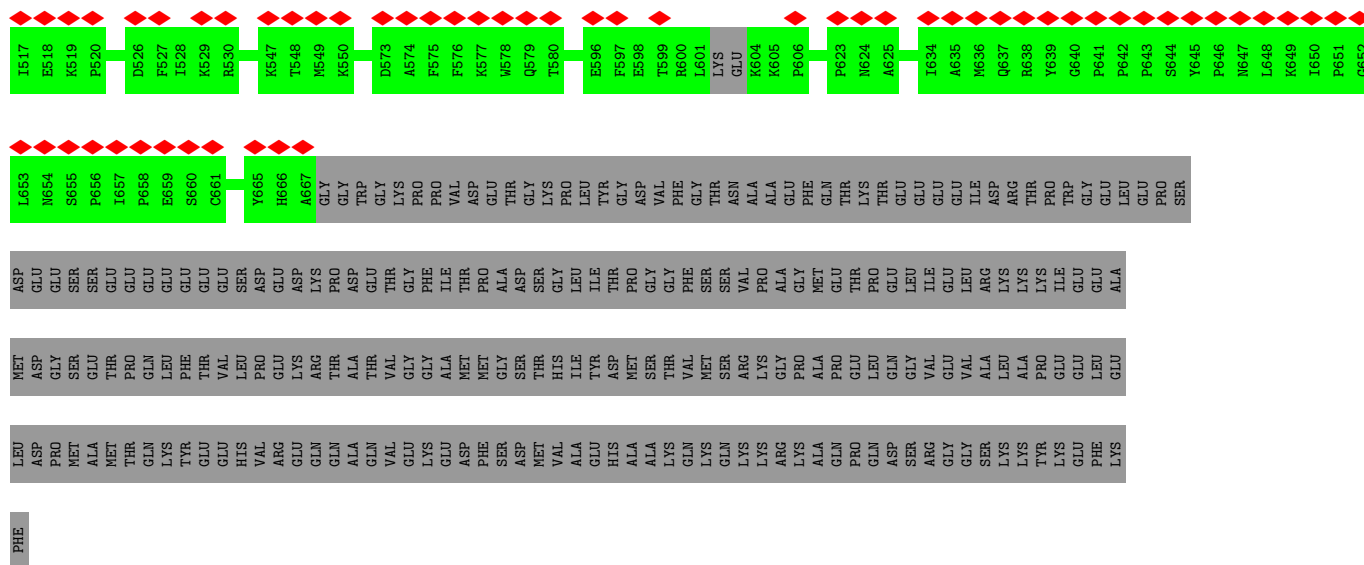
- Molecule 19: Splicing factor 3A subunit 2

[illegible]

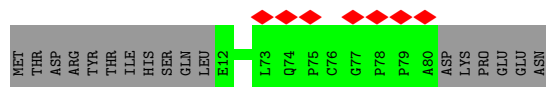
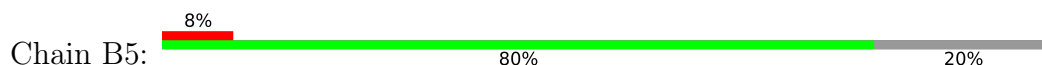
- Molecule 20: Splicing factor 3A subunit 3



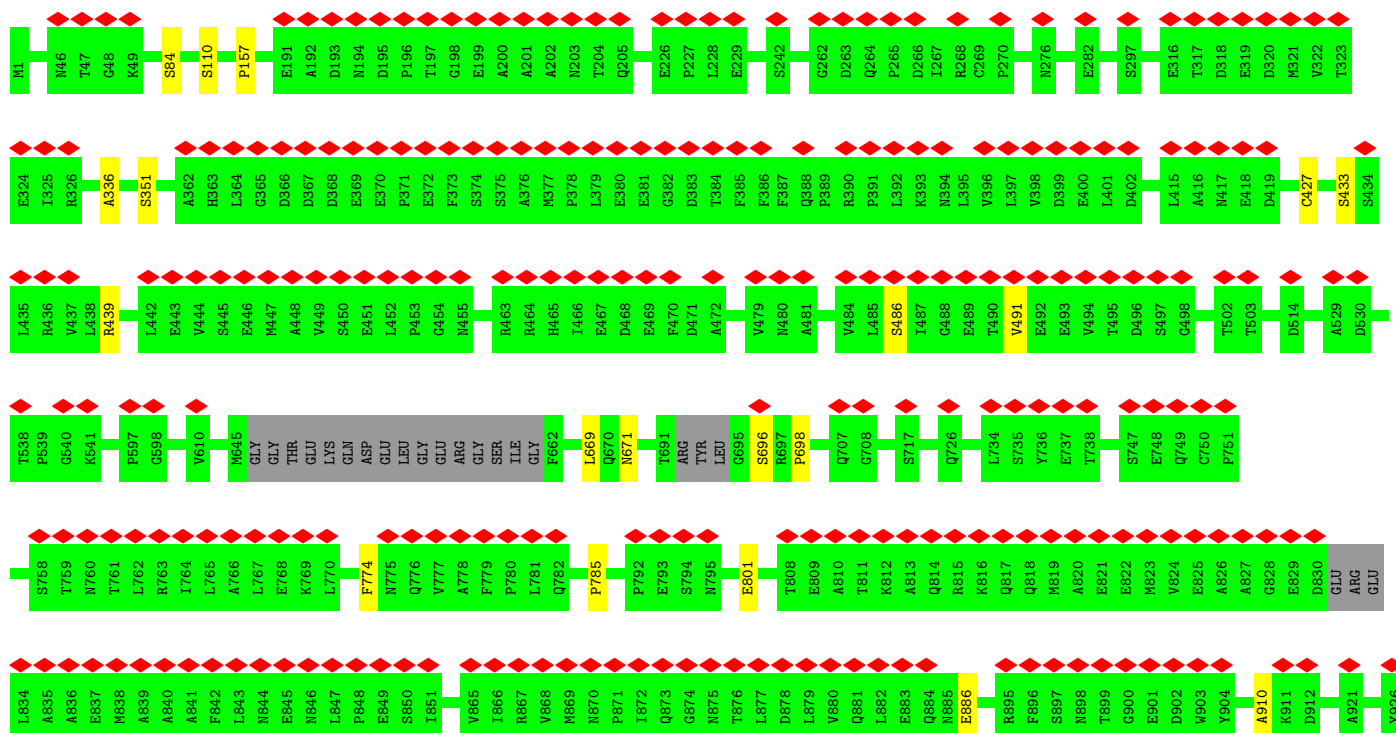
M1	E2	T3	I4	L5	E6	Q7	Q8	R9	R10	V11	H12	E13	E14	K15	E16	R17	L18	M19	D20	V21	M22	A23	K24	E25	M26	L27	T28	K29	K30	S31	L32	L33	K34	D35	Q36	Q37	N38	S39	D40	H41	R42	T43	R44	A45	M46	Q47	D48	R49	Y50	M51	E52	V53	S54	G55	N56	L57	R58	D59	E60
----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

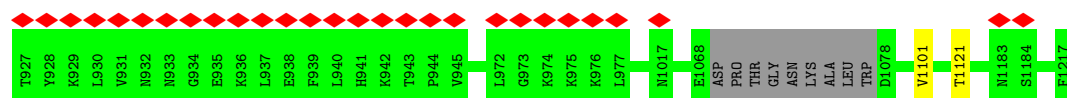


• Molecule 22: Splicing factor 3B subunit 5

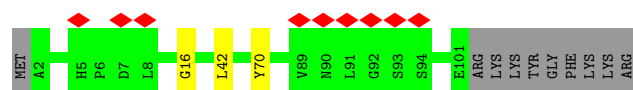
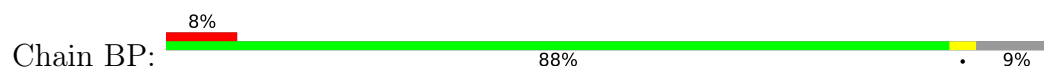


• Molecule 23: Splicing factor 3B subunit 3

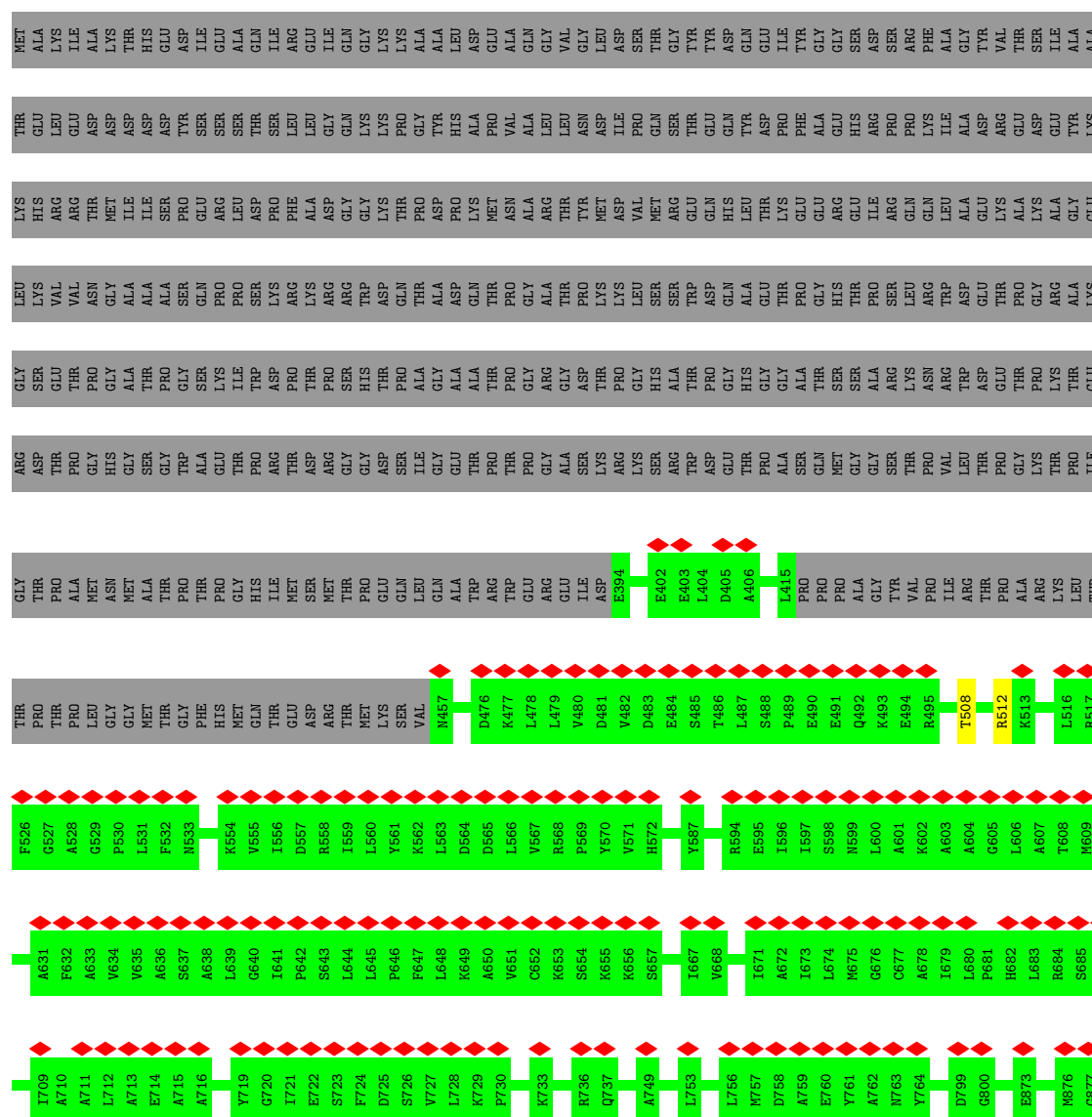


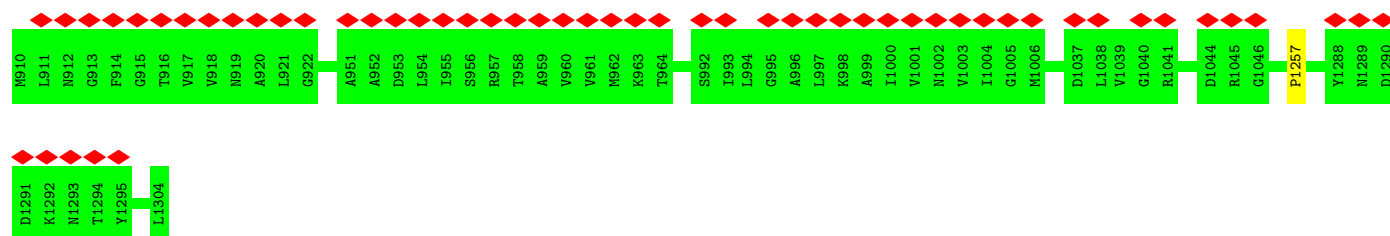


- Molecule 24: PHD finger-like domain-containing protein 5A

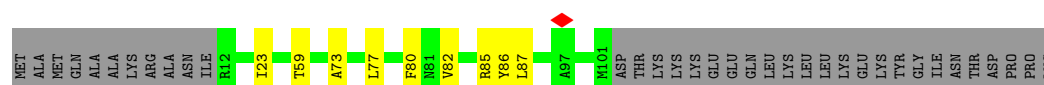


- Molecule 25: Splicing factor 3B subunit 1

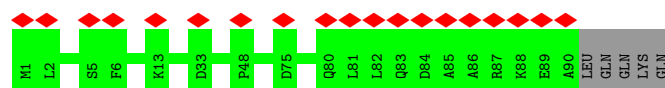




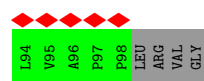
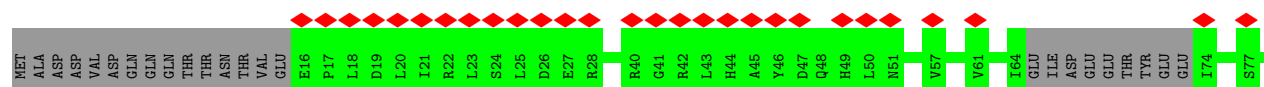
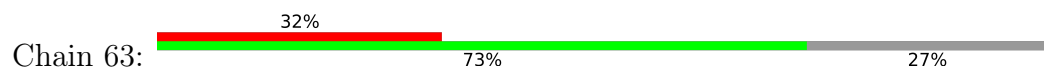
- Molecule 26: Splicing factor 3B subunit 6



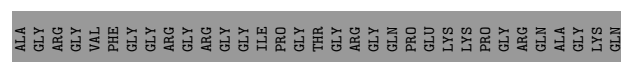
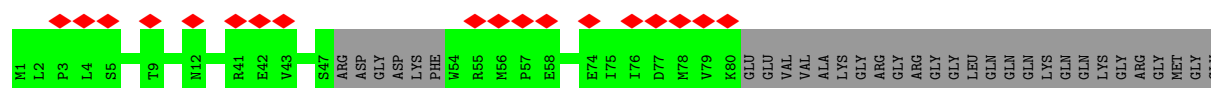
- Molecule 27: U6 snRNA-associated Sm-like protein LSm2



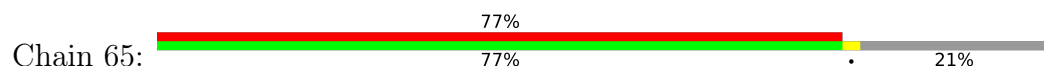
- Molecule 28: U6 snRNA-associated Sm-like protein LSm3

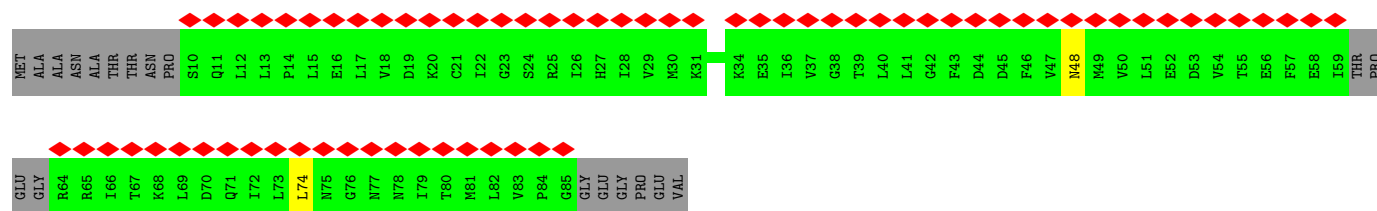


- Molecule 29: U6 snRNA-associated Sm-like protein LSm4

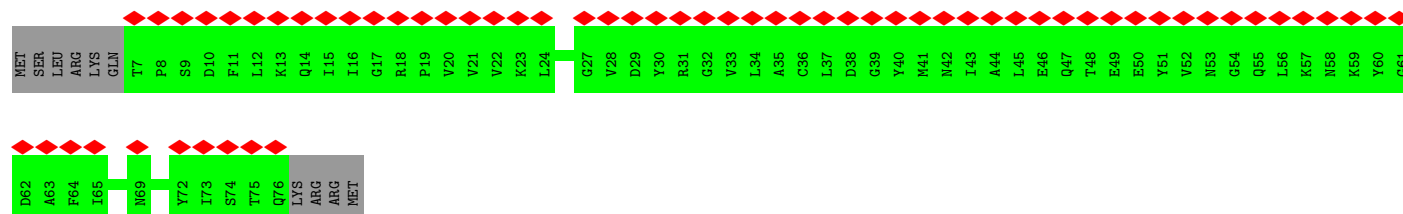
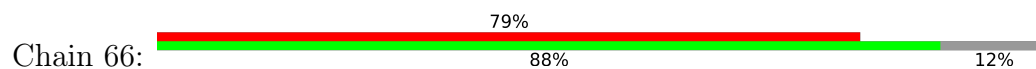


- Molecule 30: U6 snRNA-associated Sm-like protein LSm5

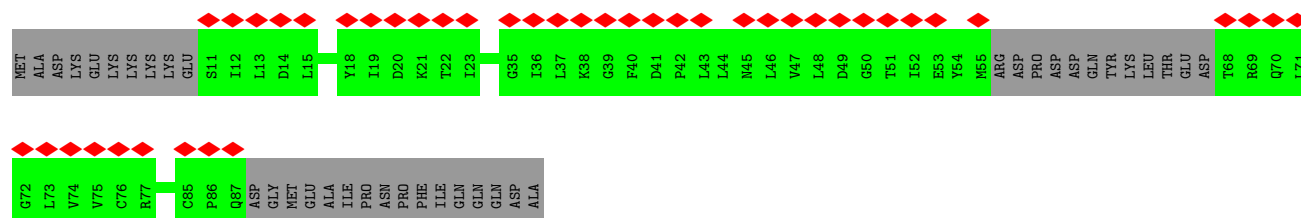
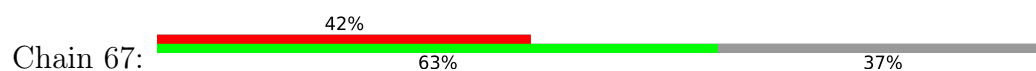




• Molecule 31: U6 snRNA-associated Sm-like protein LSm6



• Molecule 32: U6 snRNA-associated Sm-like protein LSm7



• Molecule 33: U6 snRNA-associated Sm-like protein LSm8

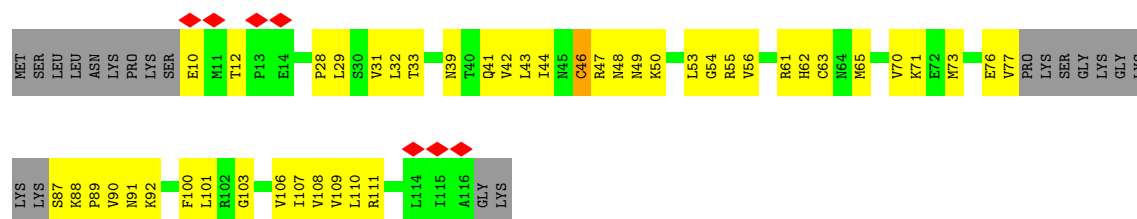


• Molecule 34: Small nuclear ribonucleoprotein Sm D2

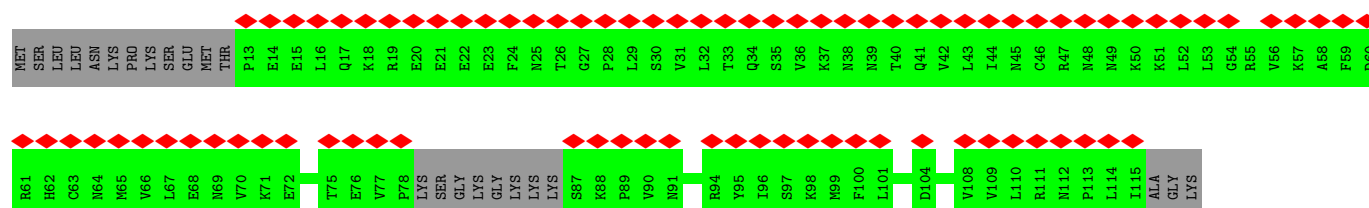
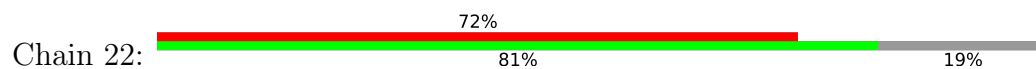


• Molecule 34: Small nuclear ribonucleoprotein Sm D2

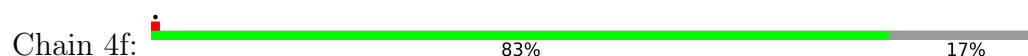




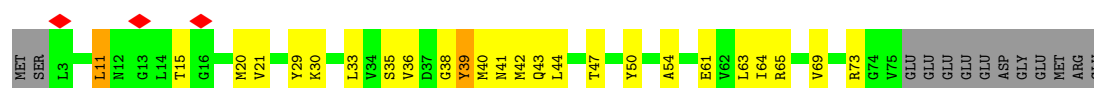
• Molecule 34: Small nuclear ribonucleoprotein Sm D2



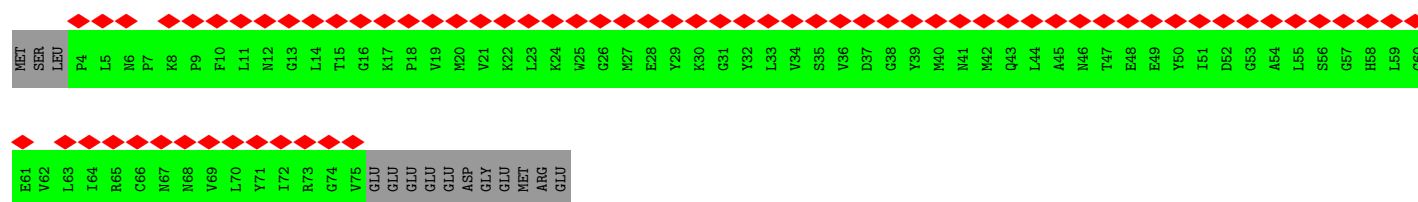
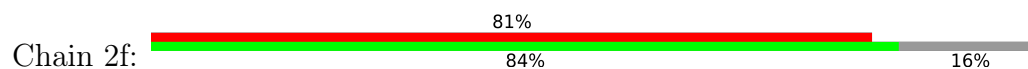
• Molecule 35: Small nuclear ribonucleoprotein F



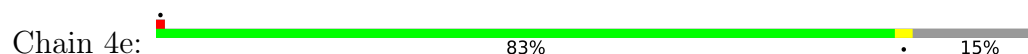
• Molecule 35: Small nuclear ribonucleoprotein F

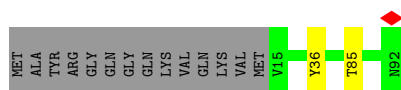


• Molecule 35: Small nuclear ribonucleoprotein F



• Molecule 36: Small nuclear ribonucleoprotein E





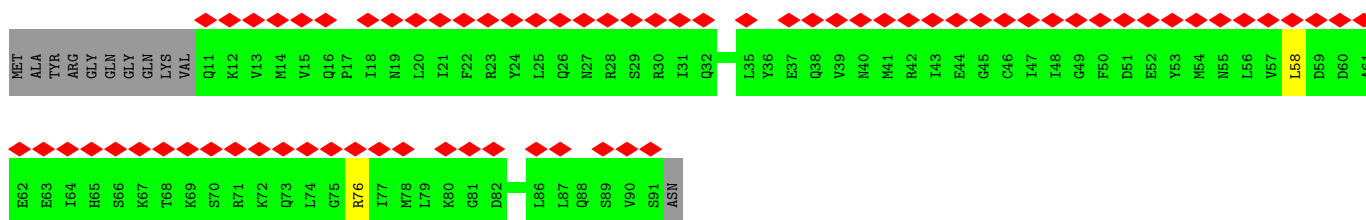
- Molecule 36: Small nuclear ribonucleoprotein E

Chain 5e: 59% 25% 16%



- Molecule 36: Small nuclear ribonucleoprotein E

Chain 2e: 78% 86% 12%



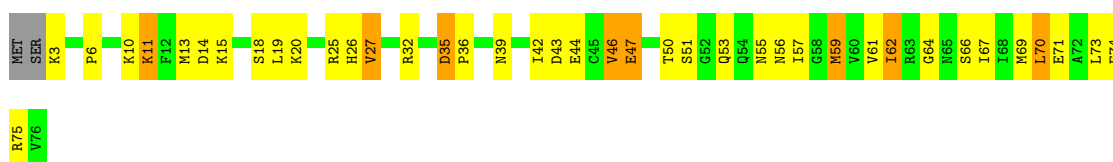
- Molecule 37: Small nuclear ribonucleoprotein G

Chain 4g: 93% 1% 6%



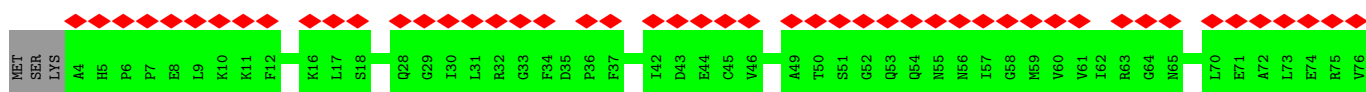
- Molecule 37: Small nuclear ribonucleoprotein G

Chain 5g: 45% 42% 11%



- Molecule 37: Small nuclear ribonucleoprotein G

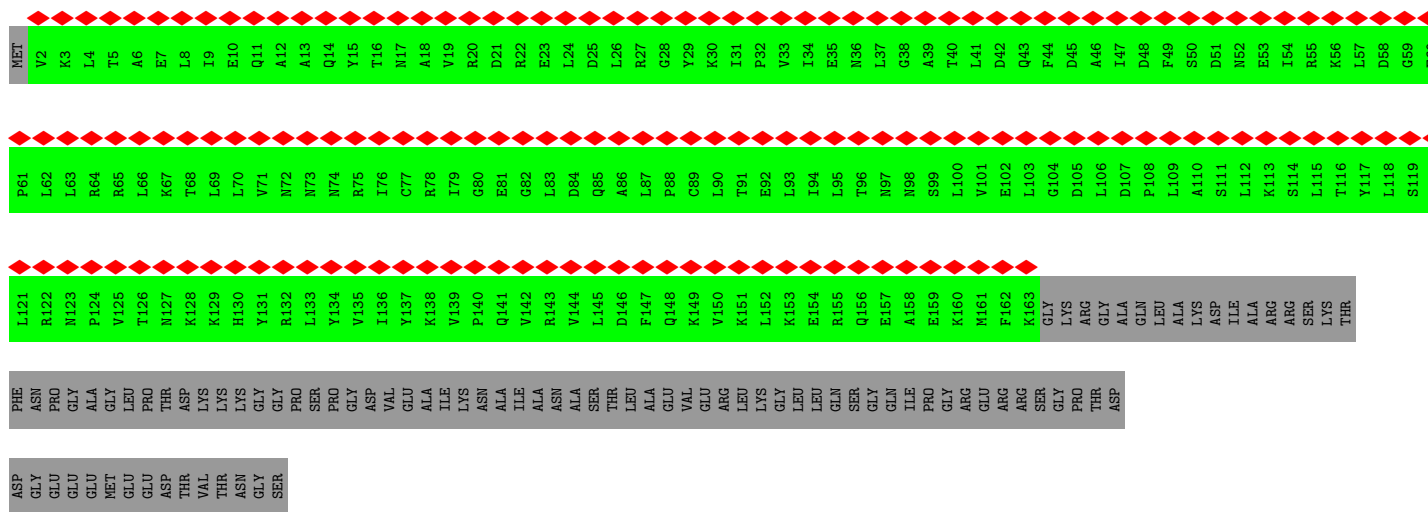
Chain 2g: 64% 96%



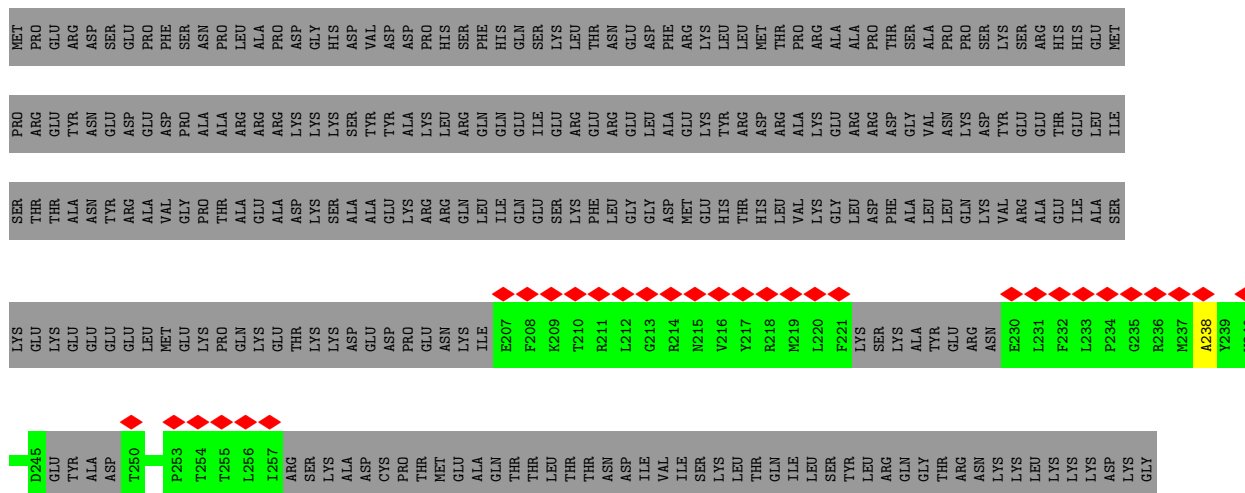
- Molecule 38: Small nuclear ribonucleoprotein Sm D3

Chain 43: 56% 44%

- Molecule 42: U2 small nuclear ribonucleoprotein A'



- Molecule 43: Protein Red



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

- Molecule 43: Protein Red

Chain y: 6% 93%

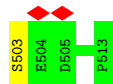
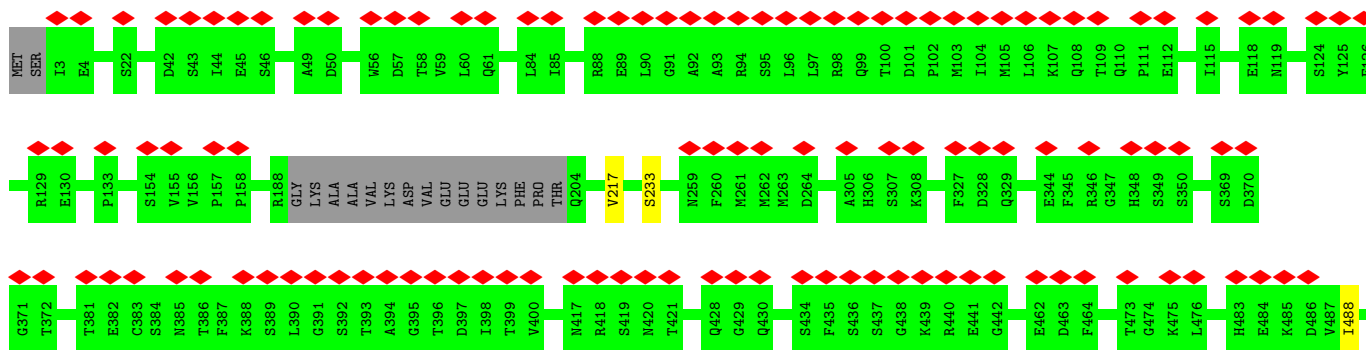
ALA	ALA	ASN	SER	SER	ILE	ASP	LYS	SER	THR	PRO	MET
PHE	PHE	SER	TYR	GLU	GLY	CYS	GLU	THR	THR	ARG	PRO
TYR	TYR	GLU	GLY	VAL	VAL	TYR	GLU	ALA	ALA	TYR	ARG
GLY	GLY	GLY	PRO	PRO	SER	GLY	GLU	ARG	TYR	GLY	SER
ILE	ILE	CYS	LYS	LYS	SER	ALA	GLU	ARG	ARG	ASP	GLY
MET	MET	TYR	VAL	VAL	THR	GLN	LEU	VAL	ALA	GLU	PRO
SER	SER	PRO	ASP	THR	THR	THR	MET	VAL	GLY	ASP	PHE
GLY	GLY	ALA	GLY	GLY	THR	LEU	LYS	PRO	PRO	ALA	ASN
GLY	GLY	MET	PRO	PRO	PRO	THR	PRO	THR	THR	ALA	PRO
ARG	ARG	MET	ASP	THR	THR	THR	GLN	ALA	ALA	ARG	LEU
THR	THR	VAL	ASP	ASP	ASP	ASN	LYS	GLU	GLU	ARG	ALA
ARG	ARG	ALA	LYS	ILE	ILE	ILE	THR	ASP	ASP	LYS	ASP
PHE	PHE	GLY	GLY	GLU	GLU	ILE	LYS	SER	SER	LYS	GLY
LYS	LYS	SER	PRO	GLY	SER	SER	ASP	ALA	ALA	SER	HIS
GLU	GLU	ASP	GLY	TYR	TYR	LEU	GLU	GLU	GLU	VAL	VAL
THR	THR	SER	THR	THR	GLY	GLY	PHE	GLN	GLN	GLY	GLY
ASN	ASN	GLU	GLY	GLU	ARG	GLN	GLY	LYS	LYS	LEU	PRO
ASP	ASP	VAL	LYS	LYS	ARG	ILE	ASN	ARG	ARG	LYS	PRO
LYS	LYS	ASP	GLY	GLU	GLU	LEU	GLY	ASN	ARG	LEU	HIS
ALA	ALA	TYR	ILE	ILE	ASP	LEU	LYS	LYS	GLN	ARG	SER
GLU	GLU	SER	ILE	ASP	ASP	ASP	ILE	ILE	LEU	GLN	PHE
LEU	LEU	LYS	LYS	ASP	TYR	TYR	GLY	ILE	GLN	GLY	GLY
LEU	LEU	MET	MET	GLY	GLY	LEU	PHE	GLN	GLN	ILE	SER
ARG	ARG	ASP	ASP	ILE	ARG	ARG	LYS	LYS	GLY	ILE	LYS
GLN	GLN	ASN	ASN	ASP	ASP	GLN	THR	SER	SER	GLY	LYS
TRP	TRP	GLY	GLY	GLY	ARG	GLY	R211	THR	THR	ARG	LEU
LYS	LYS	ASN	LYS	ASP	THR	THR	F221	PHE	PHE	ARG	THR
ILE	ILE	LYS	ALA	ARG	ARG	ASN	SER	GLY	GLY	GLY	ASN
SER	SER	GLY	GLY	ARG	ARG	LYS	LYS	ASP	ASP	ALA	ASP
ALA	ALA	PRO	SER	GLY	GLY	SER	LYS	LYS	MET	GLU	PHE
ILE	ILE	LEU	ALA	ALA	LEU	LEU	ALA	GLY	GLY	GLU	GLY
ILE	ILE	GLY	GLY	GLY	GLY	GLY	TYR	TYR	GLY	LYS	LYS
GLU	GLU	ARG	TRP	ARG	ARG	LYS	GLY	HIS	TYR	TYR	LEU
LYS	LYS	TRP	GLY	GLY	GLY	LYS	ARG	THR	THR	ARG	LEU
ARG	ARG	ASP	GLY	GLY	ASP	ASP	ASN	HIS	HIS	ASP	MET
LYS	LYS	PHE	THR	THR	ASP	LYS	E230	LEU	LEU	THR	THR
ASP	ASP	ASP	GLY	GLY	GLY	ASP	V240	VAL	VAL	ARG	PRO
MET	MET	THR	SER	SER	ARG	LYS	V241	LYS	LYS	ARG	ARG
GLU	GLU	GLN	LEU	LEU	LEU	LEU	D242	GLY	GLY	GLU	ALA
ALA	ALA	GLY	LYS	LYS	GLY	GLY	D243	LEU	LEU	ARG	ALA
ASP	ASP	GLY	LYS	LYS	ARG	GLY	L243	ASP	ASP	ARG	PRO
GLY	GLY	TYR	PRO	PRO	GLY	LYS	D244	PHE	PHE	PRO	THR
VAL	VAL	SER	GLY	GLY	ASP	LYS	D245	ALA	GLY	VAL	ALA
VAL	VAL	GLY	GLY	ASP	ASP	PRO	E246	LEU	LEU	ASN	PRO
LYS	LYS	TYR	LYS	LYS	GLY	GLY	Y247	GLN	GLN	LYS	PRO
ARG	ARG	ASN	GLN	GLN	ARG	ALA	ALA	LYS	LYS	ASP	SER
PRO	PRO	ASN	LEU	LEU	ARG	ASP	ASP	VAL	VAL	TYR	SER
TYR	TYR	GLY	GLY	GLY	GLY	MET	T250	ARG	ARG	GLY	SER
		LEU	PHE	PHE	LYS	ILE	T257	ILE	ILE	THR	HIS
		ALA	PHE	GLY	ARG	PHE	ARG	ALA	ALA	GLY	HIS
		PRO	GLY	GL	ARG	GLY	SER	ALA	ALA	LEU	GLY
		LYS	MET	ASP	HIS	ASP	LYS	SER	SER	ILE	MET

- Molecule 44: WD40 repeat-containing protein SMU1

Chain w: 18% 94%

[illegible]

- Molecule 44: WD40 repeat-containing protein SMU1



- Molecule 45: Microfibrillar-associated protein 1

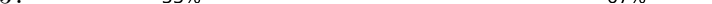


- Molecule 46: Oligo 1

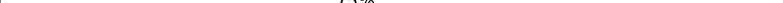


- Molecule 47: Oligo 2

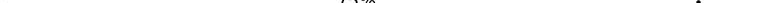
A diagram showing a green box labeled 'A-3' connected to a yellow box labeled 'G1'.

- Chain J:  33% 67%

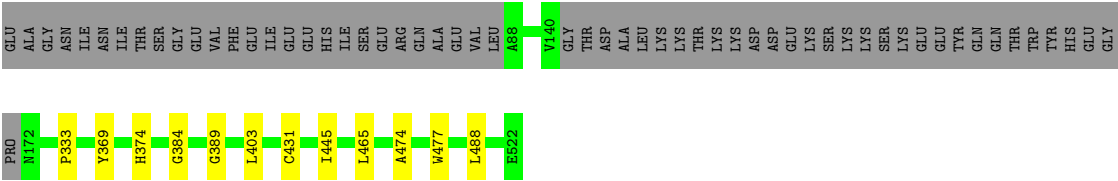
[illegible]

- Chain L:  75% 25%

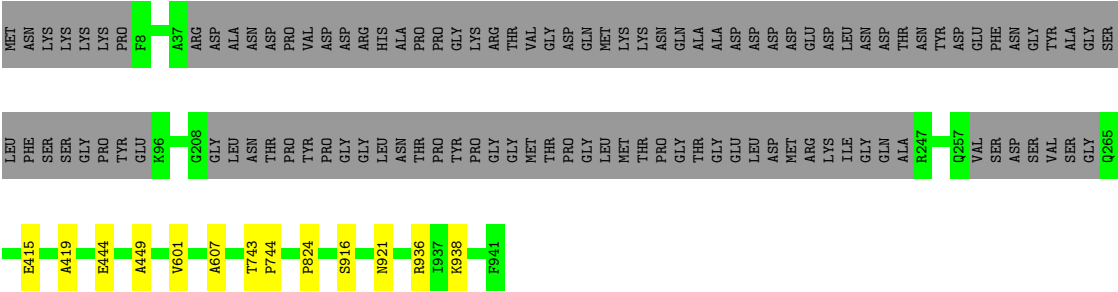
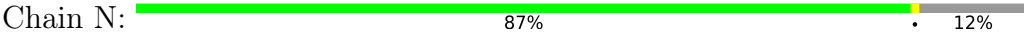
[illegible]

- Chain F:  75% . 23%

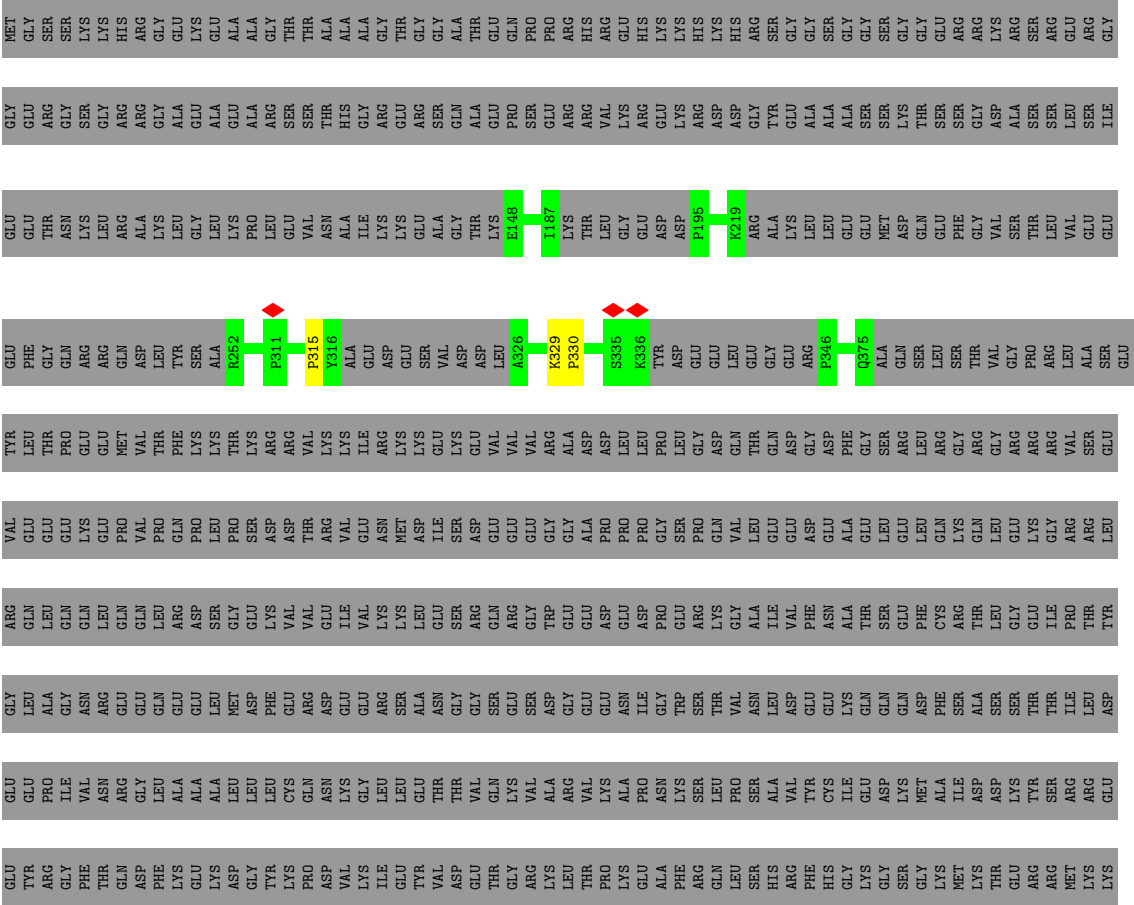
[illegible]



• Molecule 51: Pre-mRNA-processing factor 6



• Molecule 52: U4/U6.U5 tri-snRNP-associated protein 1



LEU
ASP
GLU
GLU
ALA
LEU
LEU
LYS
LYS
MET
SER
SER
SER
ASP
THR
PRO
LEU
GLY
THR
VAL
ALA
LEU
LEU
GLN
GLU
LYS
GLN
LYS
LYS
ALA
GLN
LYS
THR
PRO
TYR
ILE
VAL
LEU
SER
GLY
SER
GLY
LYS
SER
MET
ASN
ALA
ASN
THR
ILE
THR
LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	334084	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.088	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.011	Depositor
Map size (Å)	540.0, 540.0, 540.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	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	0.14	0/11512	0.30	0/16156
2	B	0.18	0/8614	0.37	0/12072
3	5	0.22	0/2559	0.40	3/3977 (0.1%)
4	2	0.17	0/2307	0.39	3/3582 (0.1%)
5	6	0.24	0/1398	0.51	5/2172 (0.2%)
6	4	0.12	0/3214	0.21	0/4998
7	C	0.18	0/4270	0.33	0/5983
8	D	0.12	0/712	0.29	0/995
9	E	0.13	0/1195	0.36	0/1492
10	I	0.09	0/926	0.26	0/1295
11	M	0.12	0/632	0.28	0/885
12	U	0.10	0/2330	0.28	0/3268
13	W	0.15	0/853	0.43	0/1188
14	X	0.11	0/404	0.21	0/565
15	Z	0.15	0/349	0.28	0/540
16	7	0.15	0/1034	0.38	0/1446
17	r	0.10	0/568	0.27	0/790
18	B4	0.17	0/394	0.37	0/549
19	8	0.19	0/734	0.52	0/1025
20	9	0.16	0/1762	0.43	0/2460
21	B2	0.21	0/1092	0.43	0/1536
22	B5	0.12	0/349	0.36	0/487
23	B3	0.18	0/6024	0.42	0/8425
24	BP	0.15	0/501	0.48	0/697
25	B1	0.19	0/4421	0.49	0/6190
26	B6	0.33	0/459	0.47	0/642
27	62	0.14	0/359	0.38	0/447
28	63	0.14	0/294	0.42	0/364
29	64	0.13	0/294	0.43	0/364
30	65	0.13	0/286	0.39	0/354
31	66	0.14	0/279	0.37	0/347
32	67	0.15	0/258	0.32	0/319
33	68	0.14	0/242	0.42	0/299
34	22	0.15	0/485	0.37	0/677

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	42	0.12	0/298	0.31	0/370
34	52	0.46	0/805	0.83	0/1081
35	2f	0.18	0/362	0.43	0/502
35	4f	0.12	0/291	0.31	0/363
35	5f	0.45	0/579	0.89	0/783
36	2e	0.17	0/403	0.40	0/561
36	4e	0.15	0/313	0.33	0/390
36	5e	0.34	0/646	0.75	0/867
37	2g	0.17	0/366	0.41	0/509
37	4g	0.17	0/297	0.37	0/371
37	5g	0.38	0/584	0.78	0/779
38	23	0.19	0/417	0.49	0/581
38	43	0.10	0/287	0.22	0/358
38	53	0.37	0/665	0.55	0/896
39	2b	0.16	0/416	0.44	0/581
39	4b	0.09	0/254	0.22	0/314
39	5b	0.41	0/602	0.62	0/801
40	21	0.15	0/404	0.41	0/564
40	41	0.12	0/333	0.26	0/416
40	51	0.37	0/649	0.78	0/878
41	2B	0.14	0/463	0.31	0/646
42	2A	0.17	0/821	0.46	0/1149
43	x	0.60	0/196	0.72	0/270
43	y	0.45	0/186	0.49	0/256
44	v	0.15	0/2491	0.39	0/3477
44	w	0.29	0/2486	0.48	0/3469
45	K	0.11	0/540	0.29	0/750
46	z1	0.12	0/268	0.21	0/416
47	z2	0.10	0/101	0.26	0/156
48	J	0.12	0/1131	0.27	0/1580
49	L	0.11	0/1899	0.28	0/2654
50	F	0.11	0/2034	0.32	0/2838
51	N	0.11	0/4224	0.29	0/5915
52	S	0.53	0/858	0.69	0/1191
All	All	0.19	0/87779	0.40	11/123318 (0.0%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	6	66	C	P-O3'-C3'	-8.48	107.47	120.20
5	6	67	G	P-O3'-C3'	-8.32	107.72	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	5	75	G	P-O3'-C3'	-8.20	107.90	120.20
3	5	76	A	P-O3'-C3'	-8.17	107.95	120.20
5	6	68	C	P-O3'-C3'	-7.81	108.48	120.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	11389	0	5553	19	0
2	B	8538	0	4146	7	0
3	5	2296	0	1163	34	0
4	2	2071	0	1049	11	0
5	6	1251	0	630	17	0
6	4	2881	0	1461	15	0
7	C	4223	0	2099	9	0
8	D	708	0	328	0	0
9	E	1196	0	337	0	0
10	I	920	0	433	1	0
11	M	627	0	315	1	0
12	U	2308	0	1104	3	0
13	W	844	0	426	9	0
14	X	403	0	200	6	0
15	Z	314	0	160	1	0
16	7	1028	0	487	0	0
17	r	568	0	245	1	0
18	B4	391	0	197	0	0
19	8	729	0	356	4	0
20	9	1755	0	823	1	0
21	B2	1072	0	563	1	0
22	B5	347	0	171	0	0
23	B3	5969	0	2985	14	0
24	BP	498	0	241	2	0
25	B1	4383	0	2195	2	0
26	B6	455	0	227	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	62	360	0	95	0	0
28	63	296	0	76	0	0
29	64	296	0	77	0	0
30	65	288	0	78	1	0
31	66	280	0	81	0	0
32	67	260	0	75	0	0
33	68	244	0	71	1	0
34	22	482	0	220	0	0
34	42	300	0	80	2	0
34	52	796	0	821	46	0
35	2f	359	0	179	0	0
35	4f	292	0	93	0	0
35	5f	567	0	575	29	0
36	2e	403	0	173	1	0
36	4e	314	0	86	1	0
36	5e	638	0	657	21	0
37	2g	364	0	176	0	0
37	4g	298	0	89	1	0
37	5g	577	0	603	21	0
38	23	415	0	198	1	0
38	43	288	0	84	0	0
38	53	657	0	675	17	0
39	2b	413	0	194	1	0
39	4b	256	0	70	0	0
39	5b	594	0	615	14	0
40	21	402	0	184	0	0
40	41	334	0	92	0	0
40	51	641	0	681	17	0
41	2B	461	0	218	1	0
42	2A	816	0	386	0	0
43	x	197	0	90	1	0
43	y	187	0	86	1	0
44	v	2478	0	1181	2	0
44	w	2474	0	1177	7	0
45	K	543	0	238	0	0
46	z1	239	0	119	0	0
47	z2	90	0	45	1	0
48	J	1125	0	551	1	0
49	L	1887	0	934	0	0
50	F	2020	0	1002	6	0
51	N	4192	0	2152	7	0
52	S	858	0	408	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	86145	0	43579	305	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 2.

The worst 5 of 305 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)
13:W:153:LYS:HA	14:X:72:ALA:HB2	1.20	1.10
39:5b:47:GLU:HB3	39:5b:65:ARG:HB3	1.42	1.00
36:5e:58:LEU:O	36:5e:76:ARG:HA	1.63	0.99
7:C:191:PRO:HA	7:C:197:SER:HA	1.45	0.97
13:W:153:LYS:CA	14:X:72:ALA:HB2	2.00	0.92

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2243/2335 (96%)	2208 (98%)	35 (2%)	0	100	100
2	B	1691/2136 (79%)	1643 (97%)	47 (3%)	1 (0%)	48	81
7	C	834/972 (86%)	815 (98%)	18 (2%)	1 (0%)	48	81
8	D	139/142 (98%)	138 (99%)	1 (1%)	0	100	100
9	E	297/357 (83%)	283 (95%)	14 (5%)	0	100	100
10	I	181/312 (58%)	176 (97%)	5 (3%)	0	100	100
11	M	122/128 (95%)	122 (100%)	0	0	100	100
12	U	454/565 (80%)	447 (98%)	7 (2%)	0	100	100
13	W	167/177 (94%)	163 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	X	78/376 (21%)	78 (100%)	0	0	100	100
16	7	200/793 (25%)	197 (98%)	3 (2%)	0	100	100
17	r	110/199 (55%)	109 (99%)	1 (1%)	0	100	100
18	B4	76/424 (18%)	76 (100%)	0	0	100	100
19	8	138/464 (30%)	136 (99%)	2 (1%)	0	100	100
20	9	344/501 (69%)	336 (98%)	8 (2%)	0	100	100
21	B2	204/895 (23%)	200 (98%)	4 (2%)	0	100	100
22	B5	67/86 (78%)	66 (98%)	1 (2%)	0	100	100
23	B3	1176/1217 (97%)	1131 (96%)	45 (4%)	0	100	100
24	BP	98/110 (89%)	96 (98%)	2 (2%)	0	100	100
25	B1	866/1304 (66%)	840 (97%)	26 (3%)	0	100	100
26	B6	88/125 (70%)	86 (98%)	1 (1%)	1 (1%)	11	44
27	62	88/95 (93%)	84 (96%)	4 (4%)	0	100	100
28	63	70/102 (69%)	66 (94%)	4 (6%)	0	100	100
29	64	70/139 (50%)	66 (94%)	4 (6%)	0	100	100
30	65	68/91 (75%)	64 (94%)	4 (6%)	0	100	100
31	66	68/80 (85%)	63 (93%)	5 (7%)	0	100	100
32	67	61/103 (59%)	59 (97%)	2 (3%)	0	100	100
33	68	57/96 (59%)	55 (96%)	2 (4%)	0	100	100
34	22	91/118 (77%)	90 (99%)	1 (1%)	0	100	100
34	42	70/118 (59%)	67 (96%)	3 (4%)	0	100	100
34	52	94/118 (80%)	86 (92%)	6 (6%)	2 (2%)	5	32
35	2f	70/86 (81%)	68 (97%)	2 (3%)	0	100	100
35	4f	69/86 (80%)	66 (96%)	3 (4%)	0	100	100
35	5f	71/86 (83%)	64 (90%)	7 (10%)	0	100	100
36	2e	79/92 (86%)	79 (100%)	0	0	100	100
36	4e	76/92 (83%)	75 (99%)	1 (1%)	0	100	100
36	5e	75/92 (82%)	72 (96%)	3 (4%)	0	100	100
37	2g	71/76 (93%)	70 (99%)	1 (1%)	0	100	100
37	4g	71/76 (93%)	65 (92%)	6 (8%)	0	100	100
37	5g	72/76 (95%)	66 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	23	81/126 (64%)	79 (98%)	2 (2%)	0	100	100
38	43	69/126 (55%)	68 (99%)	1 (1%)	0	100	100
38	53	82/126 (65%)	77 (94%)	5 (6%)	0	100	100
39	2b	80/240 (33%)	80 (100%)	0	0	100	100
39	4b	60/240 (25%)	58 (97%)	2 (3%)	0	100	100
39	5b	69/240 (29%)	67 (97%)	2 (3%)	0	100	100
40	21	78/119 (66%)	76 (97%)	2 (3%)	0	100	100
40	41	80/119 (67%)	78 (98%)	2 (2%)	0	100	100
40	51	79/119 (66%)	75 (95%)	4 (5%)	0	100	100
41	2B	90/225 (40%)	90 (100%)	0	0	100	100
42	2A	160/255 (63%)	157 (98%)	3 (2%)	0	100	100
43	x	33/557 (6%)	29 (88%)	4 (12%)	0	100	100
43	y	31/557 (6%)	28 (90%)	3 (10%)	0	100	100
44	v	492/513 (96%)	484 (98%)	8 (2%)	0	100	100
44	w	489/513 (95%)	478 (98%)	10 (2%)	1 (0%)	43	76
45	K	103/439 (24%)	103 (100%)	0	0	100	100
48	J	220/683 (32%)	217 (99%)	3 (1%)	0	100	100
49	L	372/499 (74%)	364 (98%)	8 (2%)	0	100	100
50	F	400/522 (77%)	386 (96%)	14 (4%)	0	100	100
51	N	823/941 (88%)	799 (97%)	24 (3%)	0	100	100
52	S	161/800 (20%)	160 (99%)	1 (1%)	0	100	100
All	All	15016/23399 (64%)	14624 (97%)	386 (3%)	6 (0%)	100	100

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	52	49	ASN
34	52	91	ASN
44	w	177	LEU
2	B	1292	PRO
7	C	199	LEU

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	A	125/2108 (6%)	125 (100%)	0	100	100
2	B	77/1908 (4%)	77 (100%)	0	100	100
7	C	48/866 (6%)	48 (100%)	0	100	100
8	D	5/130 (4%)	5 (100%)	0	100	100
10	I	7/293 (2%)	7 (100%)	0	100	100
11	M	6/111 (5%)	6 (100%)	0	100	100
12	U	23/511 (4%)	23 (100%)	0	100	100
13	W	10/148 (7%)	10 (100%)	0	100	100
14	X	2/333 (1%)	2 (100%)	0	100	100
16	7	8/709 (1%)	8 (100%)	0	100	100
17	r	2/181 (1%)	2 (100%)	0	100	100
18	B4	4/336 (1%)	4 (100%)	0	100	100
19	8	8/382 (2%)	8 (100%)	0	100	100
20	9	10/446 (2%)	10 (100%)	0	100	100
21	B2	22/776 (3%)	22 (100%)	0	100	100
22	B5	3/77 (4%)	3 (100%)	0	100	100
23	B3	60/1051 (6%)	60 (100%)	0	100	100
24	BP	4/95 (4%)	4 (100%)	0	100	100
25	B1	40/1104 (4%)	40 (100%)	0	100	100
26	B6	5/109 (5%)	5 (100%)	0	100	100
34	22	5/110 (4%)	5 (100%)	0	100	100
34	52	93/110 (84%)	91 (98%)	2 (2%)	45	64
35	2f	4/74 (5%)	4 (100%)	0	100	100
35	5f	61/74 (82%)	59 (97%)	2 (3%)	33	55
36	2e	1/84 (1%)	1 (100%)	0	100	100
36	5e	72/84 (86%)	72 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	2g	3/66 (4%)	3 (100%)	0	100	100
37	5g	64/66 (97%)	43 (67%)	21 (33%)	0	2
38	23	3/101 (3%)	3 (100%)	0	100	100
38	53	73/101 (72%)	73 (100%)	0	100	100
39	2b	4/177 (2%)	4 (100%)	0	100	100
39	5b	67/177 (38%)	66 (98%)	1 (2%)	57	70
40	21	3/101 (3%)	3 (100%)	0	100	100
40	51	76/101 (75%)	53 (70%)	23 (30%)	0	2
41	2B	3/195 (2%)	3 (100%)	0	100	100
42	2A	6/218 (3%)	6 (100%)	0	100	100
43	x	2/498 (0%)	2 (100%)	0	100	100
43	y	2/498 (0%)	2 (100%)	0	100	100
44	v	15/450 (3%)	15 (100%)	0	100	100
44	w	15/450 (3%)	15 (100%)	0	100	100
48	J	8/599 (1%)	8 (100%)	0	100	100
49	L	14/424 (3%)	14 (100%)	0	100	100
50	F	16/442 (4%)	16 (100%)	0	100	100
51	N	36/792 (4%)	36 (100%)	0	100	100
52	S	5/681 (1%)	5 (100%)	0	100	100
All	All	1120/18347 (6%)	1071 (96%)	49 (4%)	27	48

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	5g	3	LYS
37	5g	44	GLU
37	5g	10	LYS
37	5g	27	VAL
37	5g	47	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
34	52	41	GLN

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Mol	Chain	Res	Type
37	5g	28	GLN
37	5g	55	ASN
37	5g	26	HIS
35	5f	46	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	Z	14/15 (93%)	1 (7%)	0
3	5	107/117 (91%)	34 (31%)	3 (2%)
4	2	94/188 (50%)	18 (19%)	4 (4%)
46	z1	10/11 (90%)	5 (50%)	0
47	z2	3/4 (75%)	0	0
5	6	55/106 (51%)	11 (20%)	3 (5%)
6	4	133/144 (92%)	39 (29%)	0
All	All	416/585 (71%)	108 (25%)	10 (2%)

5 of 108 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	5	8	G
3	5	9	G
3	5	10	U
3	5	20	G
3	5	21	A

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	6	45	A
5	6	51	U
5	6	77	C
4	2	37	U
4	2	46	U

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

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](#)

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](#)

There are no chain breaks in this entry.

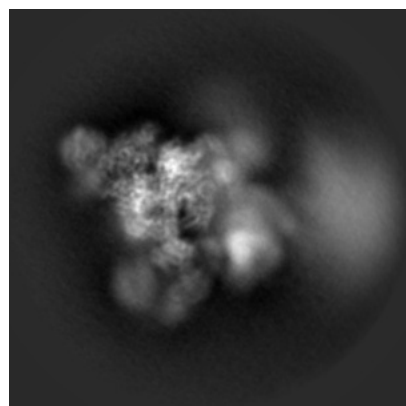
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18781. These allow visual inspection of the internal detail of the map and identification of artifacts.

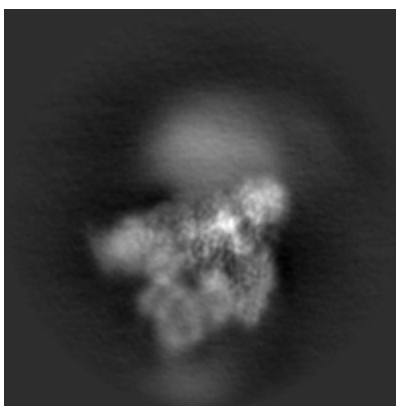
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

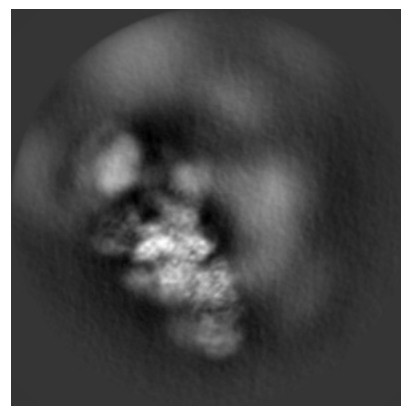
6.1.1 Primary map



X

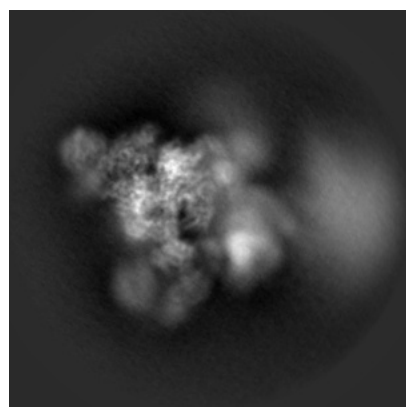


Y

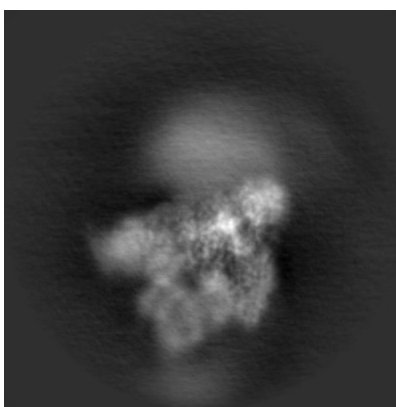


Z

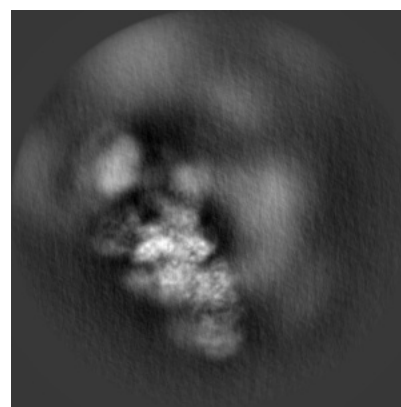
6.1.2 Raw map



X



Y

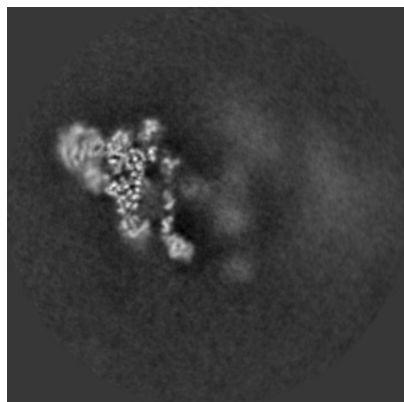


Z

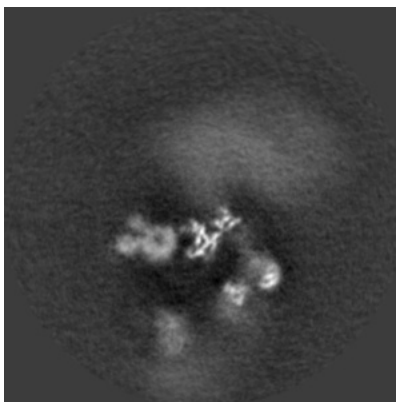
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

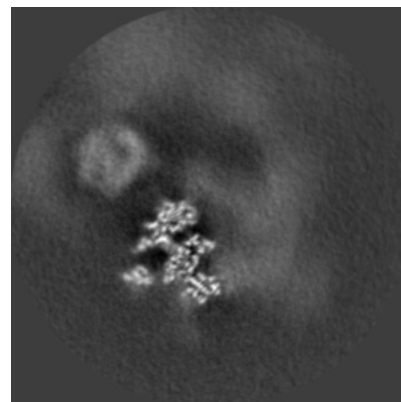
6.2.1 Primary map



X Index: 200

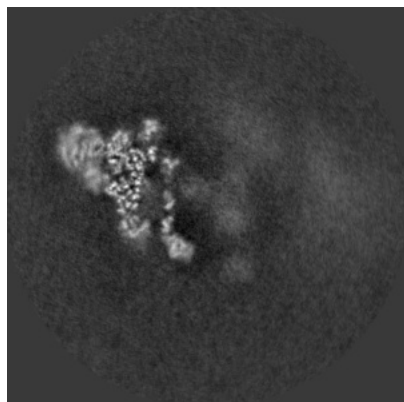


Y Index: 200

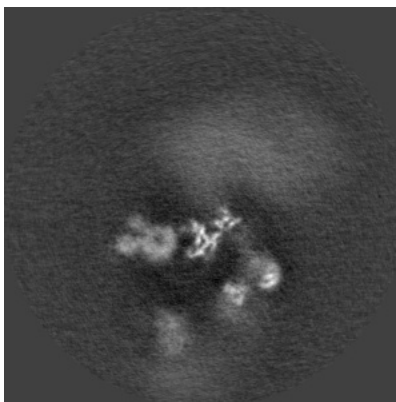


Z Index: 200

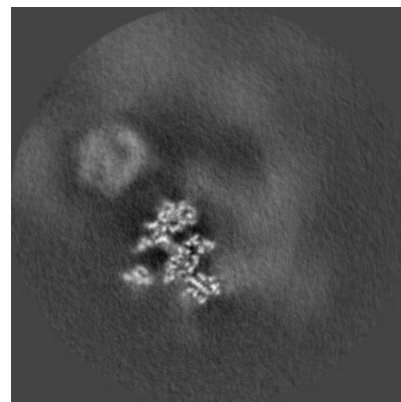
6.2.2 Raw map



X Index: 200



Y Index: 200

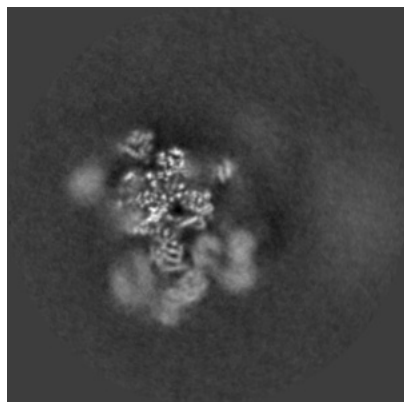


Z Index: 200

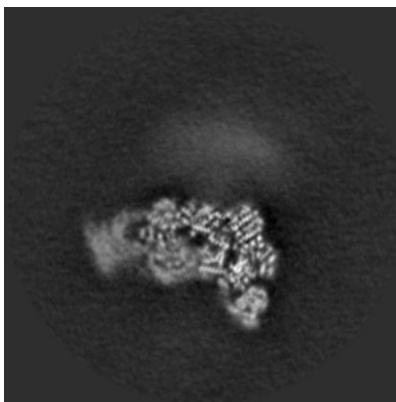
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

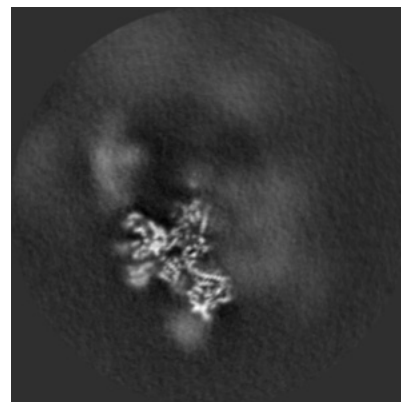
6.3.1 Primary map



X Index: 171

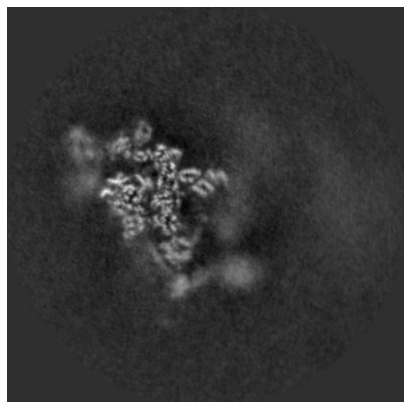


Y Index: 164

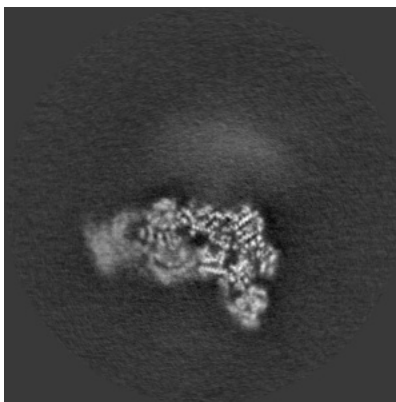


Z Index: 216

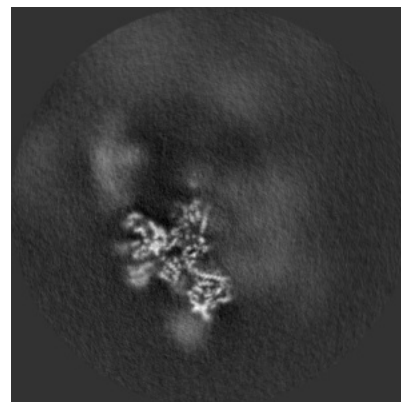
6.3.2 Raw map



X Index: 187



Y Index: 165

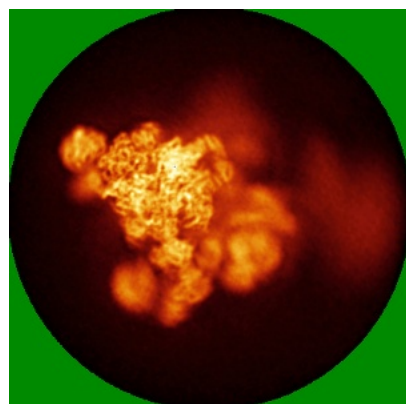


Z Index: 216

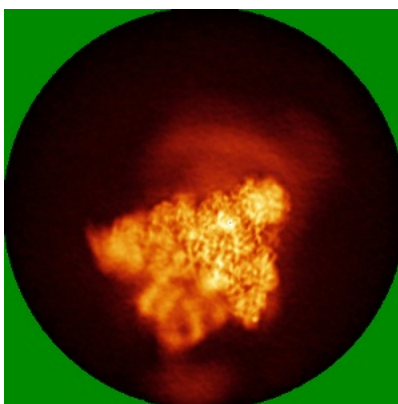
The images above show the largest variance slices of the map in three orthogonal directions.

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

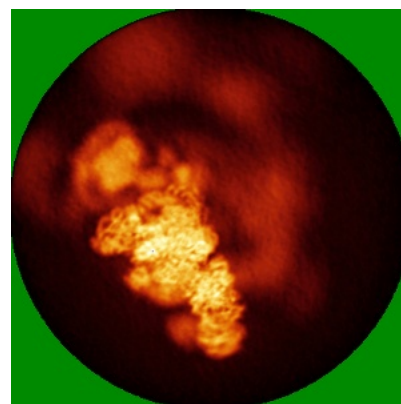
6.4.1 Primary map



X

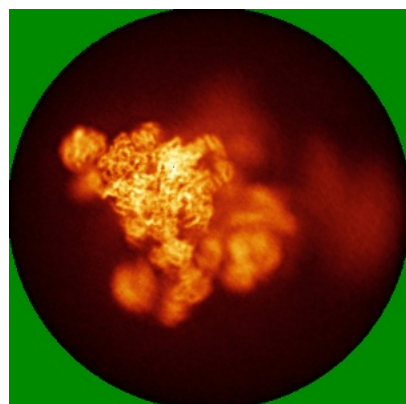


Y

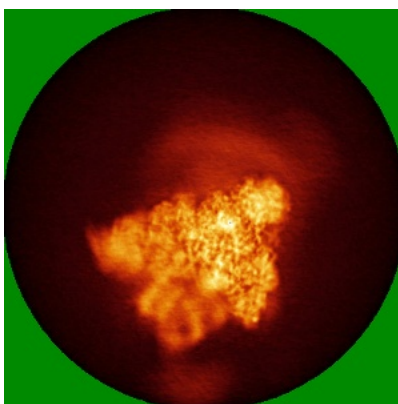


Z

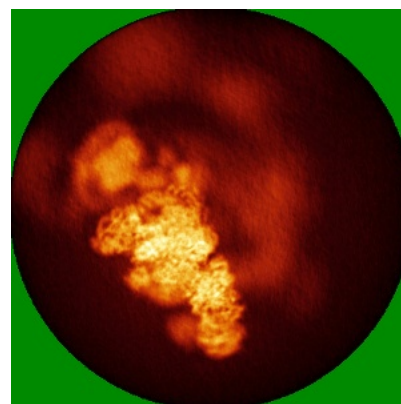
6.4.2 Raw map



X



Y

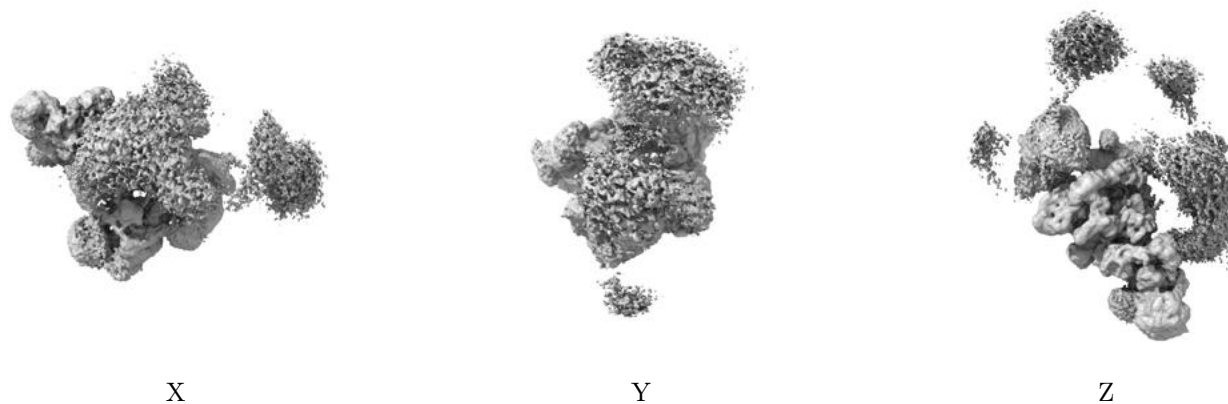


Z

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.

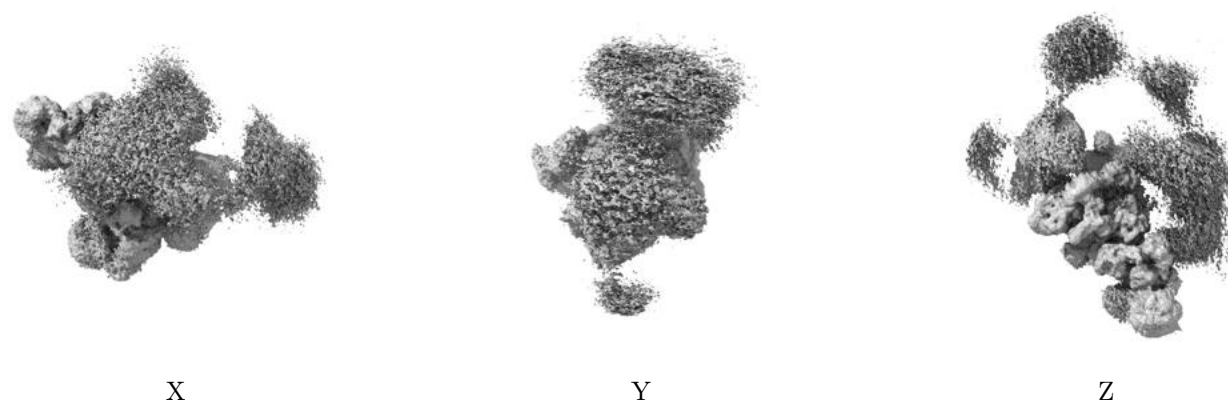
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.011. 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.

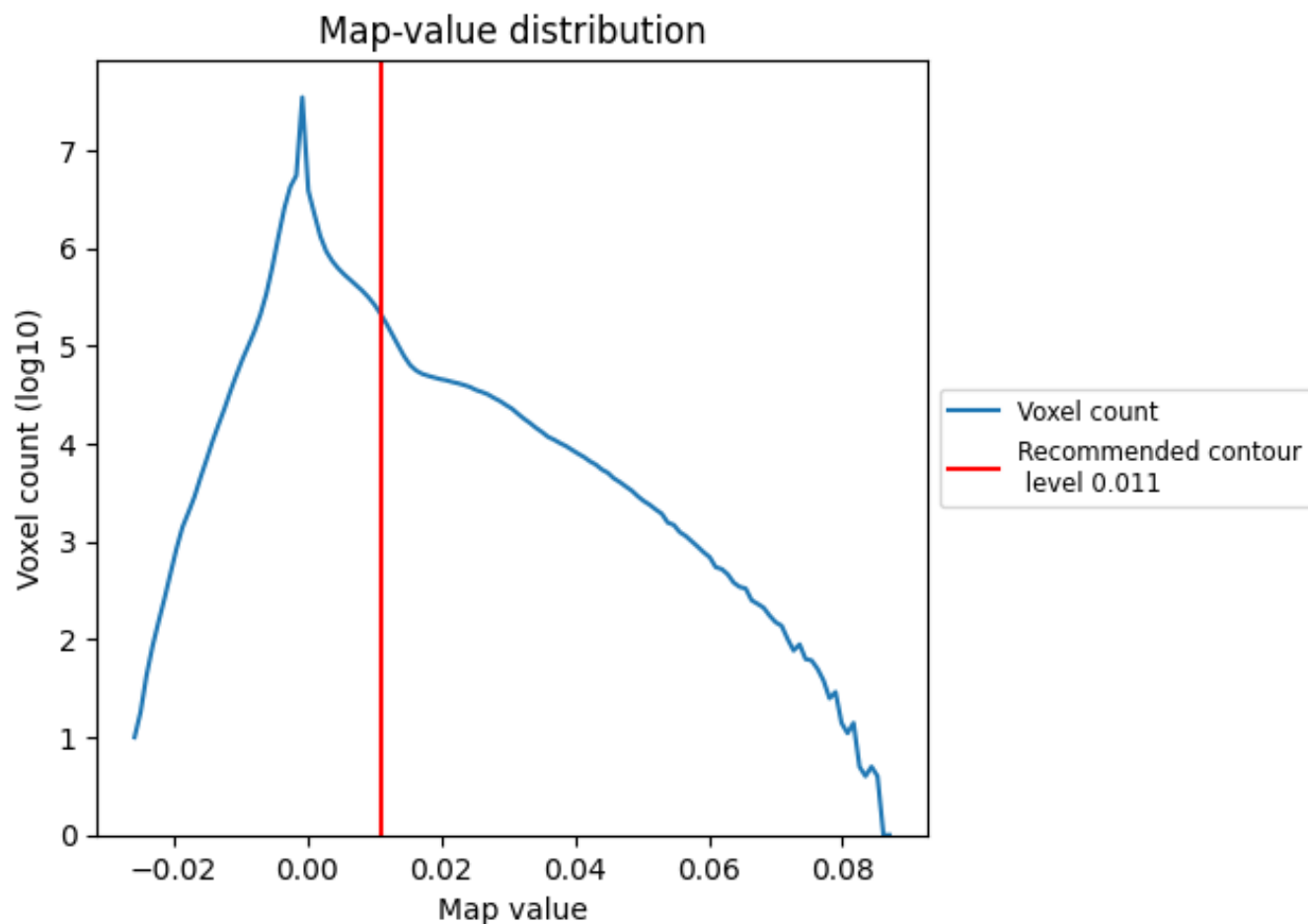
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

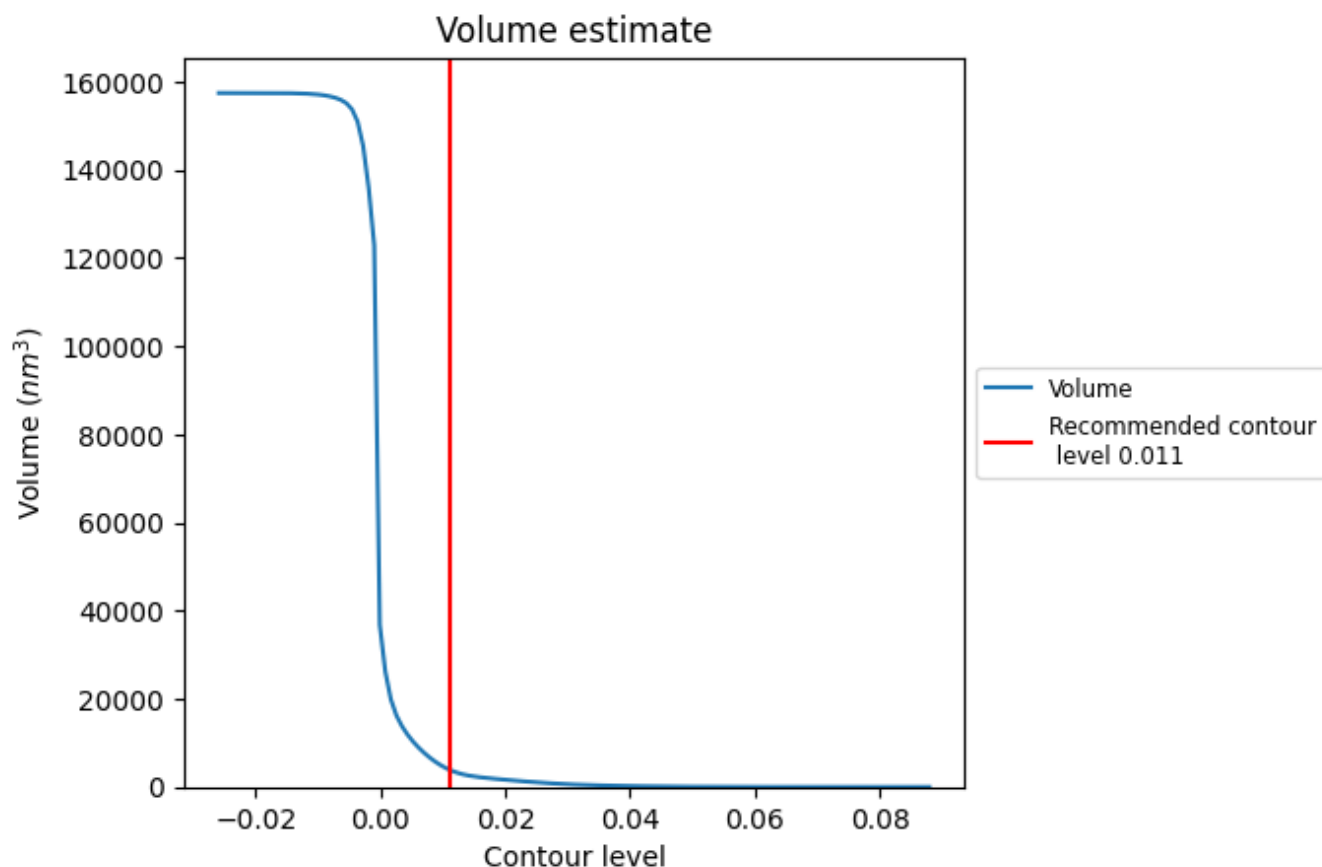
This section contains the results of statistical analysis of the map.

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.

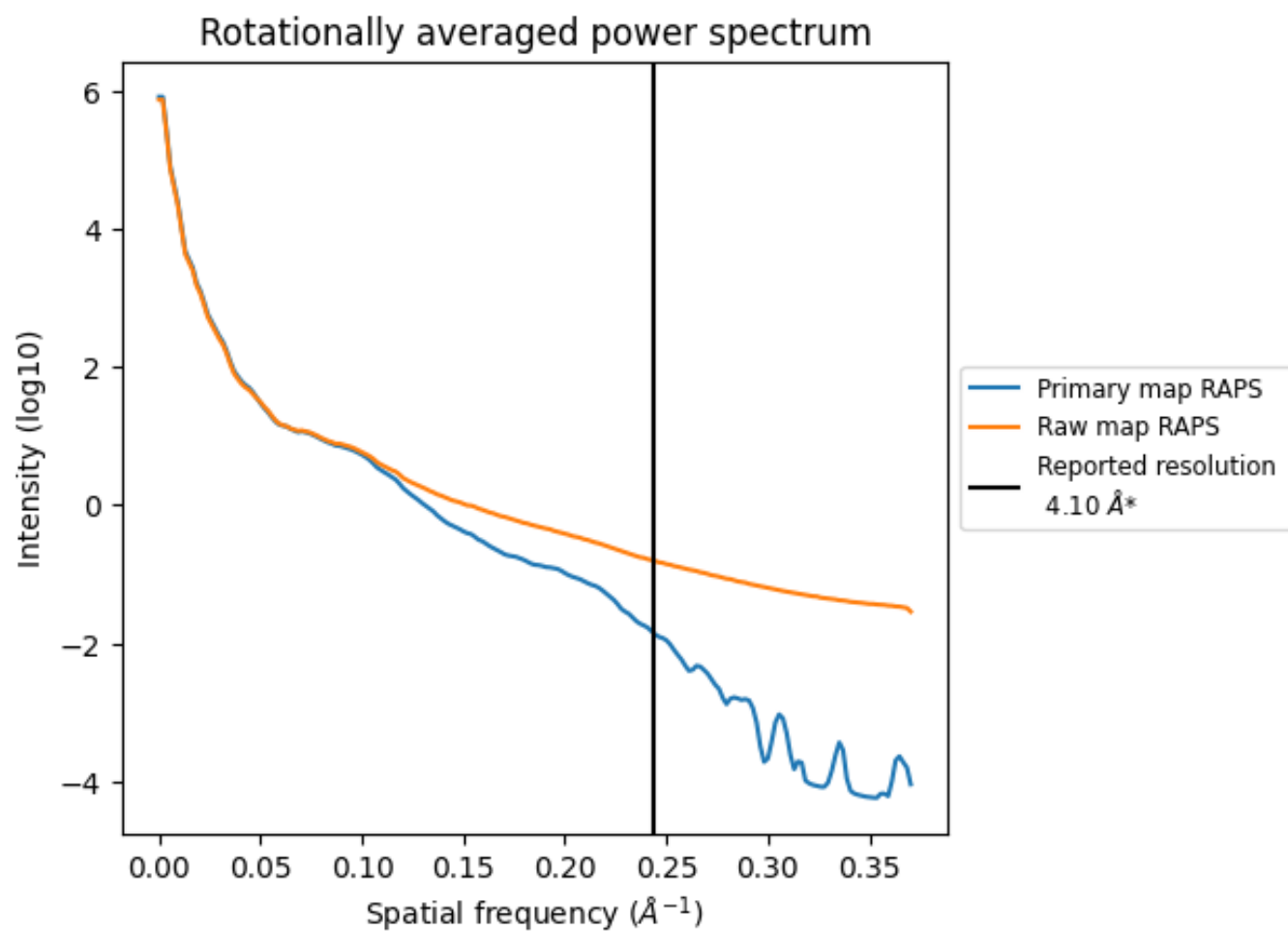
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3969 nm^3 ; this corresponds to an approximate mass of 3585 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 ⓘ

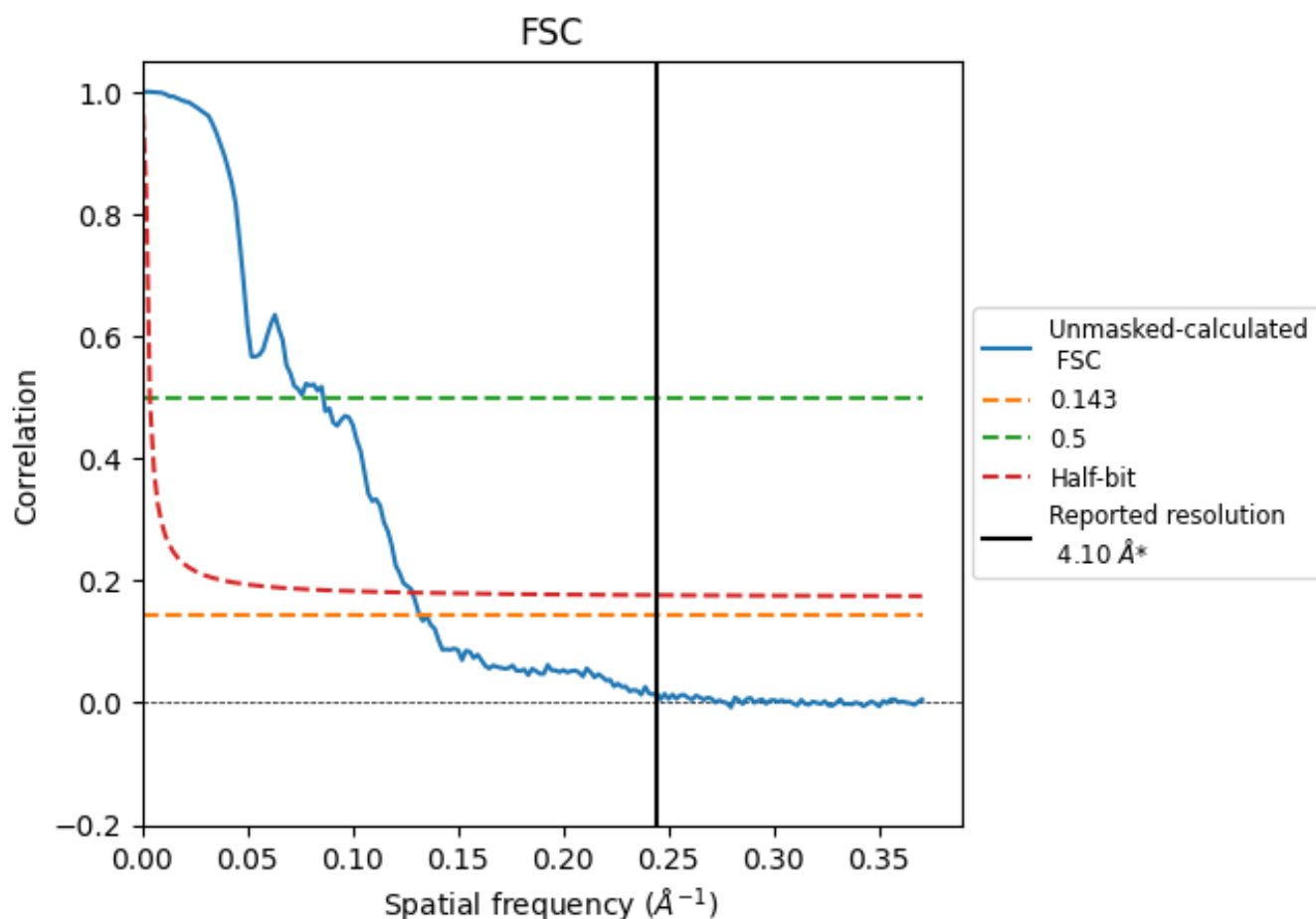


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.59	11.63	7.79

*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 7.59 differs from the reported value 4.1 by more than 10 %

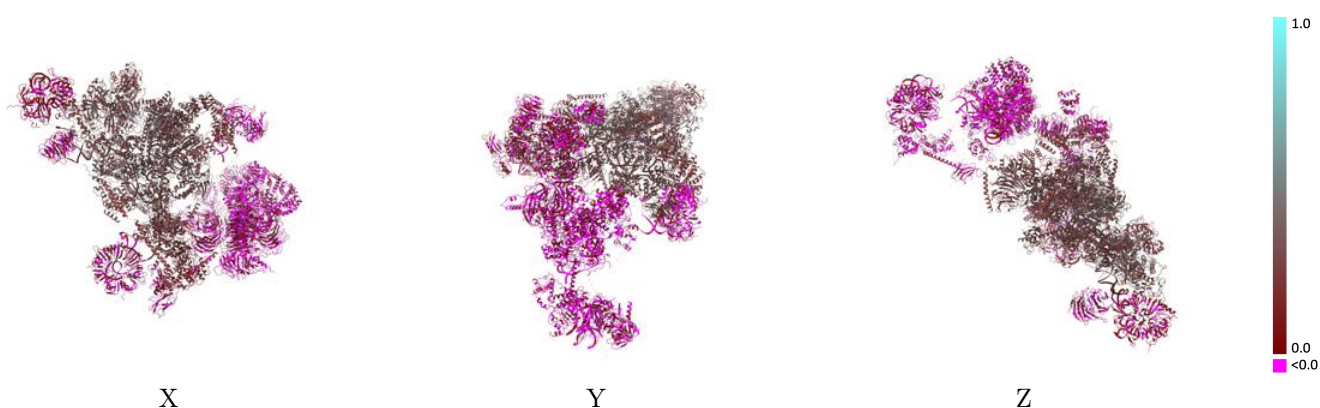
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-18781 and PDB model 8QZS. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

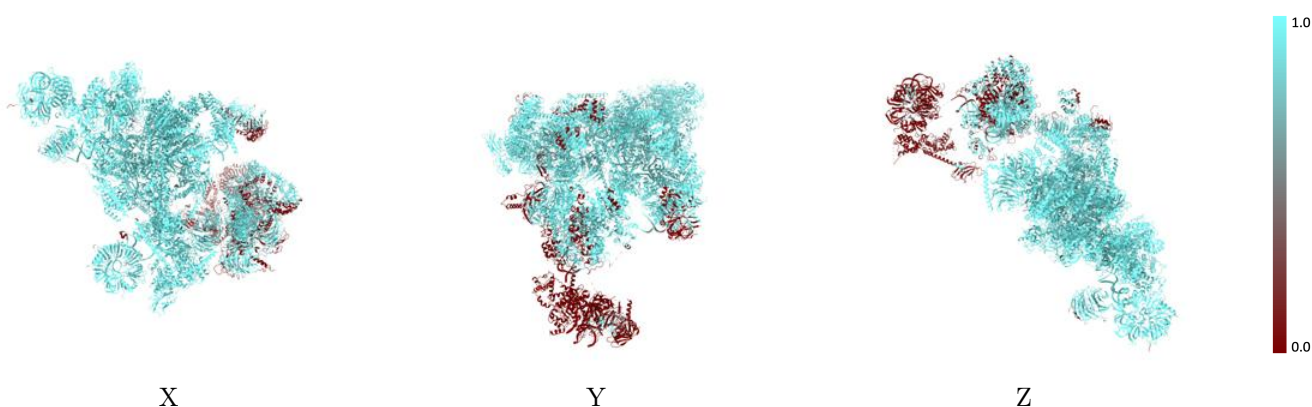
This section was not generated.

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



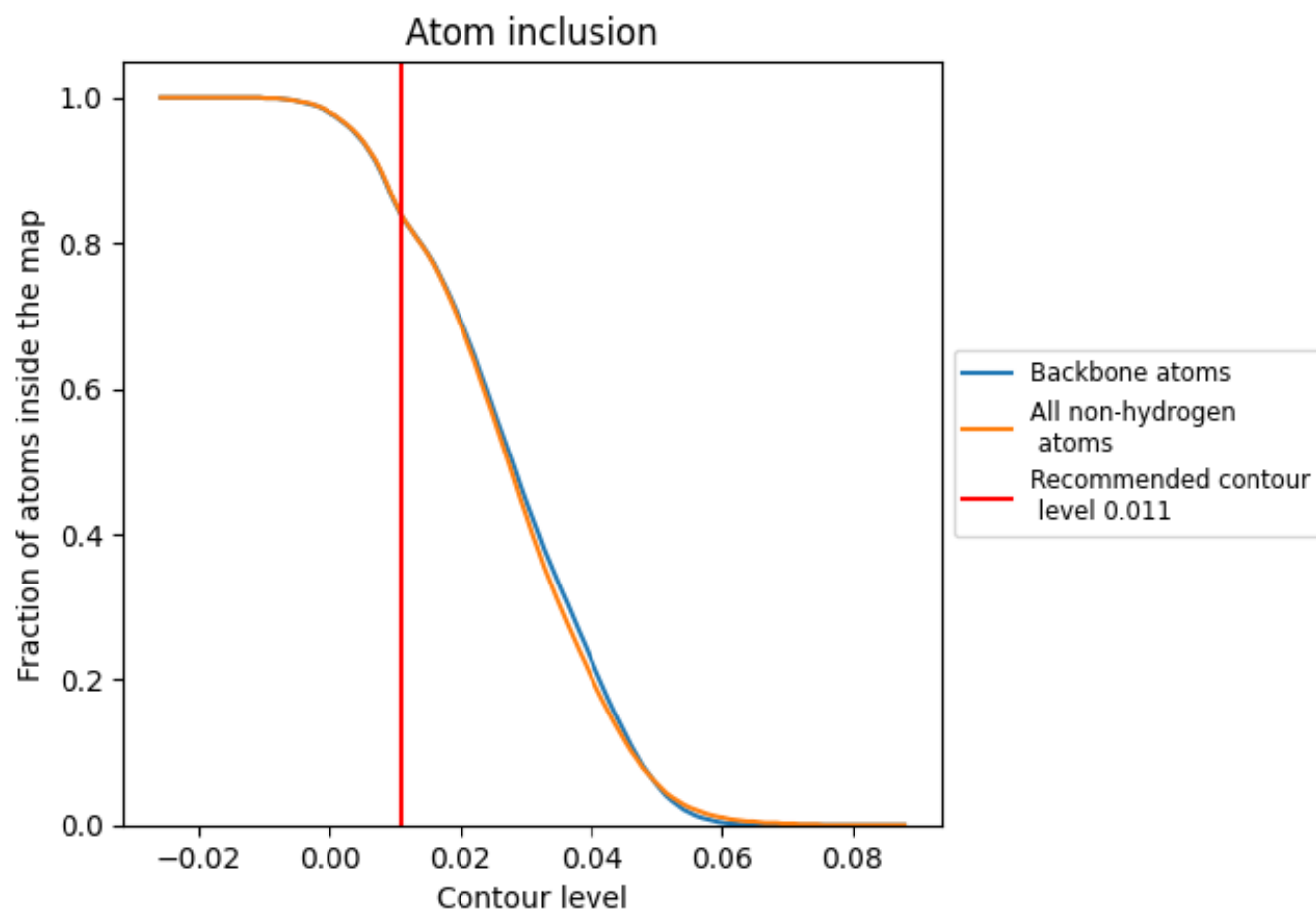
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 84% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8380	 0.1680
2	 0.3540	 -0.0190
21	 0.0900	 0.0130
22	 0.0980	 0.0220
23	 0.1730	 0.0220
2A	 0.0040	 -0.0060
2B	 0.0090	 0.0360
2b	 0.1190	 -0.0180
2e	 0.1090	 -0.0070
2f	 0.0470	 0.0470
2g	 0.3430	 0.0280
4	 0.9500	 0.1680
41	 1.0000	 0.0610
42	 1.0000	 0.0610
43	 0.9970	 0.0530
4b	 0.9920	 0.0540
4e	 0.9840	 0.0580
4f	 0.9830	 0.0330
4g	 0.9730	 0.0790
5	 0.9980	 0.2060
51	 1.0000	 0.0990
52	 0.9230	 0.0950
53	 0.9810	 0.0860
5b	 0.9930	 0.0910
5e	 0.9700	 0.0730
5f	 0.9610	 0.0810
5g	 0.9820	 0.0570
6	 0.9190	 0.2200
62	 0.7610	 0.0080
63	 0.5340	 0.0060
64	 0.6930	 0.0110
65	 0.0210	 -0.0540
66	 0.0790	 -0.0320
67	 0.3000	 0.0020
68	 0.9550	 -0.0080



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Chain	Atom inclusion	Q-score
7	 0.4520	 0.1340
8	 0.3060	 0.0100
9	 0.1180	 0.0150
A	 0.9970	 0.3450
B	 0.9950	 0.2040
B1	 0.7250	 -0.0010
B2	 0.6230	 -0.0080
B3	 0.7530	 0.0100
B4	 0.7750	 0.0500
B5	 0.8700	 0.0380
B6	 0.9870	 0.0020
BP	 0.9020	 -0.0080
C	 1.0000	 0.3320
D	 1.0000	 0.3700
E	 0.9580	 0.0470
F	 1.0000	 0.2960
I	 0.9990	 0.3150
J	 1.0000	 0.3140
K	 0.9820	 0.2080
L	 0.9940	 0.3270
M	 1.0000	 0.3490
N	 0.9990	 0.2840
S	 0.9710	 0.2950
U	 0.9580	 0.3090
W	 1.0000	 0.2400
X	 1.0000	 0.3080
Z	 0.9780	 -0.0170
r	 0.9790	 0.3070
v	 0.7610	 0.0240
w	 0.8150	 0.0420
x	 0.1880	 -0.0090
y	 0.8400	 -0.0060
z1	 1.0000	 0.3250
z2	 1.0000	 0.2400