



## wwPDB EM Validation Summary Report ⓘ

May 18, 2026 – 07:19 pm BST

PDB ID : 9R8V / pdb\_00009r8v  
EMDB ID : EMD-53843  
Title : Cryo-EM structure of the human pre-Bact-OTS complex (whole map)  
Authors : Zhang, Z.; Kumar, V.; Zhong, J.; Dybkov, O.; Kastner, B.; Urlaub, H.;  
Luhmann, R.  
Deposited on : 2025-05-17  
Resolution : 8.50 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](mailto: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>.

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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

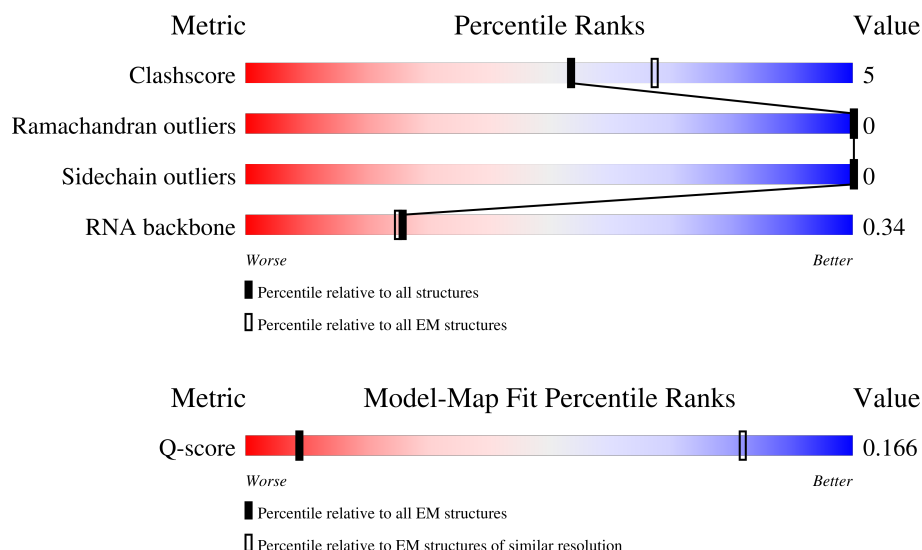
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 8.50 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.





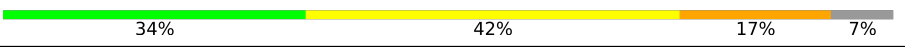
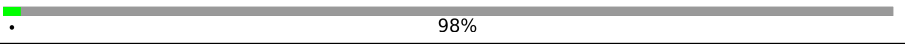


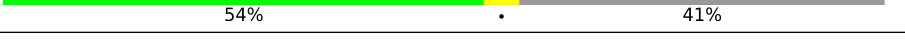
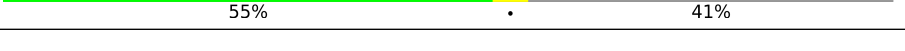
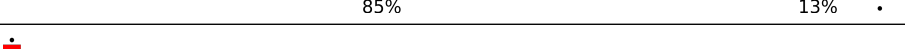
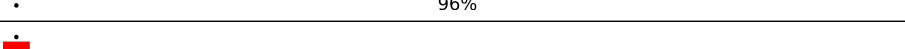
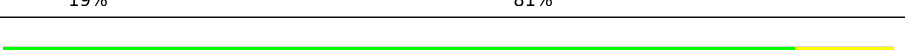

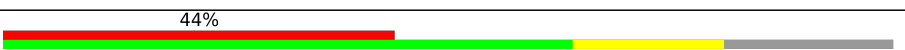








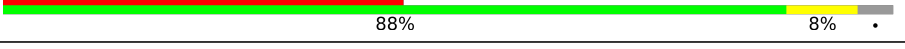



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	328 ( 8.00 - 9.00 )

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  $\geq 3$ , 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	2769	
2	B	2136	
3	2	188	

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Mol	Chain	Length	Quality of chain
4	6	106	
5	7	793	
6	5	117	
7	L	802	
8	C	972	
9	E	357	
10	G	514	
11	I	312	
12	Q	144	
13	R	229	
14	X	641	
15	q	73	
16	r	199	
17	22	118	
17	52	118	
18	2B	225	
19	2f	86	
19	5f	86	
20	2b	240	
20	5b	240	
21	23	126	
21	53	126	
22	2g	76	
22	5g	76	
23	2e	92	

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Mol	Chain	Length	Quality of chain
23	5e	92	
24	21	119	
24	51	119	
25	2A	255	
26	B4	424	
27	9	501	
28	8	464	
29	B2	895	
30	B5	86	
31	B3	1217	
32	B1	1304	
33	B6	125	
34	BL	563	
35	SR	1029	
36	DH	795	
37	Z	410	
38	x	557	
38	y	557	
39	v	513	
39	w	513	
40	P	500	
41	t	520	
42	62	95	
43	63	102	
44	64	139	

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Mol	Chain	Length	Quality of chain
45	65	91	
46	66	80	
47	67	103	
48	68	96	
49	S1	536	
50	A6	248	
51	T	1098	
52	K	439	
53	P7	579	
54	5A	110	

## 2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 80644 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	2207	Total	C	N	O	0	0
			11189	6775	2207	2207		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	1722	Total	C	N	O	0	0
			8688	5244	1722	1722		

- Molecule 3 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	101	Total	C	N	O	P	0	0
			2135	955	362	718	100		

- Molecule 4 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	99	Total	C	N	O	P	0	0
			2104	940	386	679	99		

- Molecule 5 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	7	123	Total	C	N	O	0	0
			621	375	123	123		

- Molecule 6 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	109	Total	C	N	O	P	0	0
			2296	1028	383	776	109		

- Molecule 7 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	L	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 8 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	C	843	Total	C	N	O	0	0
			4260	2574	843	843		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	E	302	Total	C	N	O	0	0
			1506	902	302	302		

- Molecule 10 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	G	302	Total	C	N	O	0	0
			1508	904	302	302		

- Molecule 11 is a protein called Pre-mRNA-splicing factor 38A.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	I	184	Total	C	N	O	0	0
			925	557	184	184		

- Molecule 12 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	Q	142	Total	C	N	O	0	0
			713	429	142	142		

- Molecule 13 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	R	9	Total	C	N	O	0	0
			45	27	9	9		

- Molecule 14 is a protein called WW domain-binding protein 11.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	X	124	Total	C	N	O	0	0
			630	382	124	124		

- Molecule 15 is a protein called Ubiquitin-like protein 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	q	73	Total	C	N	O	0	0
			360	214	73	73		

- Molecule 16 is a protein called Zinc finger matrin-type protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	r	89	Total	C	N	O	0	0
			442	264	89	89		

- Molecule 17 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	22	95	Total	C	N	O	0	0
			482	292	95	95		
17	52	78	Total	C	N	O	0	0
			393	237	78	78		

- Molecule 18 is a protein called U2 small nuclear ribonucleoprotein B''.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	2B	92	Total	C	N	O	0	0
			461	277	92	92		

- Molecule 19 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	2f	72	Total	C	N	O	0	0
			359	215	72	72		
19	5f	71	Total	C	N	O	0	0
			352	210	71	71		

- Molecule 20 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.



Mol	Chain	Residues	Atoms				AltConf	Trace
20	2b	82	Total	C	N	O	0	0
			413	249	82	82		
20	5b	64	Total	C	N	O	0	0
			319	191	64	64		

- Molecule 21 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	23	83	Total	C	N	O	0	0
			415	249	83	83		
21	53	78	Total	C	N	O	0	0
			390	234	78	78		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
22	2g	73	Total	C	N	O	0	0
			364	218	73	73		
22	5g	69	Total	C	N	O	0	0
			344	206	69	69		

- Molecule 23 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	2e	81	Total	C	N	O	0	0
			403	241	81	81		
23	5e	78	Total	C	N	O	0	0
			388	232	78	78		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	21	80	Total	C	N	O	0	0
			402	242	80	80		
24	51	94	Total	C	N	O	0	0
			474	286	94	94		

- Molecule 25 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	2A	162	Total	C	N	O	0	0
			816	492	162	162		

- Molecule 26 is a protein called Splicing factor 3B subunit 4.

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

- Molecule 27 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	9	383	Total	C	N	O	0	0
			1920	1154	383	383		

- Molecule 28 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	8	144	Total	C	N	O	0	0
			729	441	144	144		

- Molecule 29 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	B2	172	Total	C	N	O	0	0
			891	547	172	172		

- Molecule 30 is a protein called Splicing factor 3B subunit 5.

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

- Molecule 31 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	B3	1168	Total	C	N	O	0	0
			5880	3544	1168	1168		

- Molecule 32 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	B1	937	Total	C	N	O	0	0
			4725	2851	937	937		

- Molecule 33 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	B6	93	Total	C	N	O	0	0
			470	284	93	93		

- Molecule 34 is a protein called Beta-catenin-like protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	BL	484	Total	C	N	O	0	0
			2418	1450	484	484		

- Molecule 35 is a protein called U2 snRNP-associated SURP motif-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	SR	112	Total	C	N	O	0	0
			563	339	112	112		

- Molecule 36 is a protein called ATP-dependent RNA helicase DHX15.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	DH	675	Total	C	N	O	4	0
			3431	2081	675	675		

- Molecule 37 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Z	44	Total	C	N	O	P	0	0
			931	417	161	309	44		

- Molecule 38 is a protein called Protein Red.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	x	39	Total	C	N	O	0	0
			197	119	39	39		
38	y	67	Total	C	N	O	0	0
			338	204	67	67		

- Molecule 39 is a protein called WD40 repeat-containing protein SMU1.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	v	484	Total	C	N	O	0	0
			2419	1451	484	484		
39	w	496	Total	C	N	O	0	0
			2478	1486	496	496		

- Molecule 40 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	P	234	Total	C	N	O	0	0
			1180	712	234	234		

- Molecule 41 is a protein called RING-type E3 ubiquitin-protein ligase PPIL2.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	t	95	Total	C	N	O	0	0
			482	292	95	95		

- Molecule 42 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	62	90	Total	C	N	O	0	0
			360	180	90	90		

- Molecule 43 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	63	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 44 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	64	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 45 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	65	72	Total	C	N	O	0	0
			288	144	72	72		

- Molecule 46 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	66	70	Total	C	N	O	0	0
			280	140	70	70		

- Molecule 47 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	67	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 48 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	68	61	Total	C	N	O	0	0
			244	122	61	61		

- Molecule 49 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	S1	93	Total	C	N	O	0	0
			475	289	93	93		

- Molecule 50 is a protein called Serine/arginine-rich splicing factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	A6	74	Total	C	N	O	0	0
			368	220	74	74		

- Molecule 51 is a protein called Transcription elongation regulator 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	T	407	Total	C	N	O	0	0
			2044	1230	407	407		

- Molecule 52 is a protein called Microfibrillar-associated protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	K	214	Total	C	N	O	0	0
			1066	638	214	214		

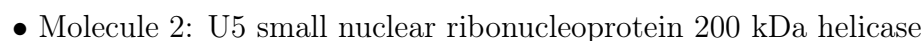
- Molecule 53 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	P7	18	Total	C	N	O	0	0
			92	56	18	18		

- Molecule 54 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	5A	100	Total 498	C 298	N 100	O 100	0	0



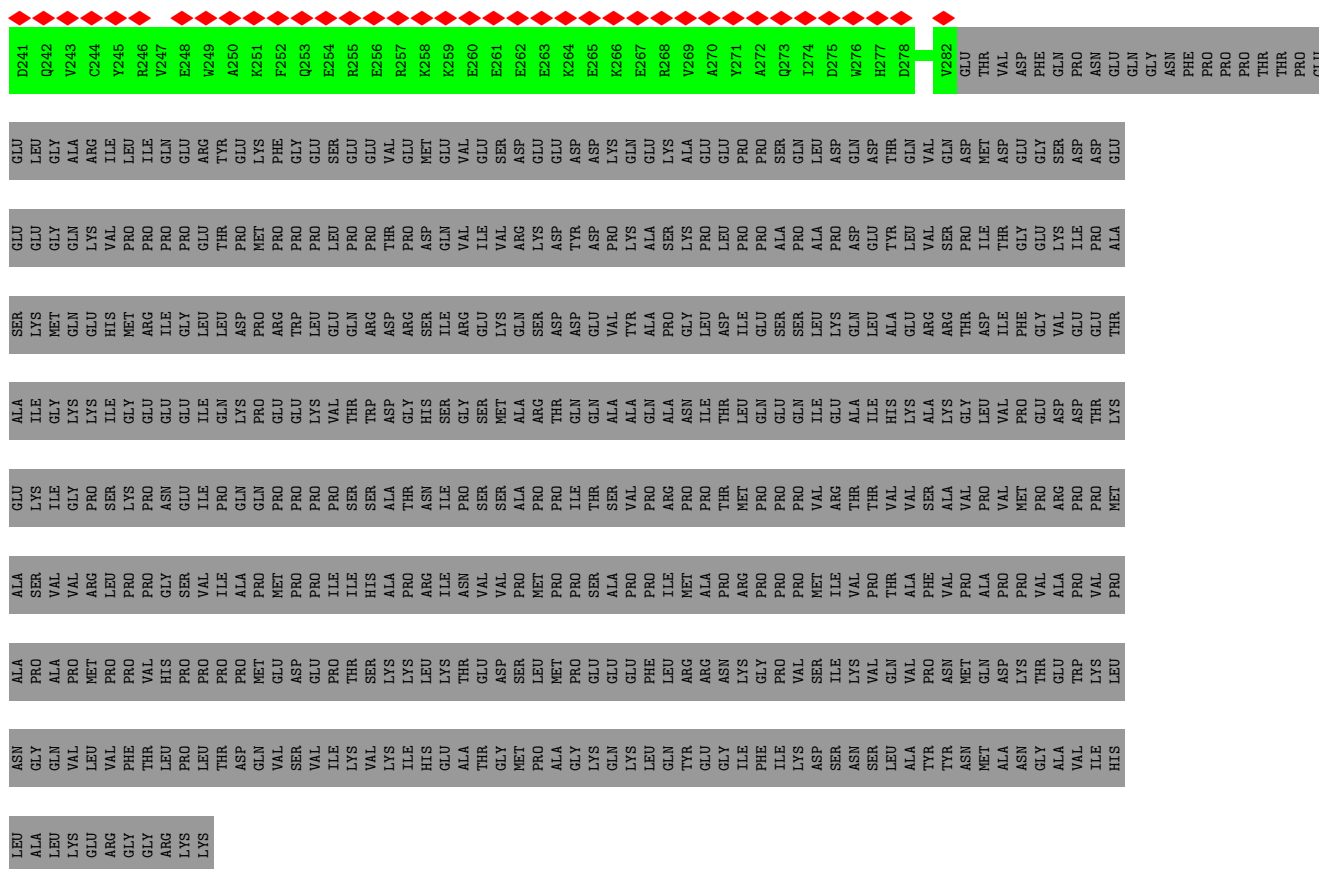


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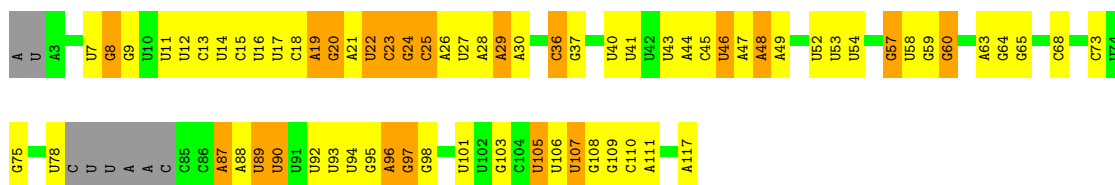




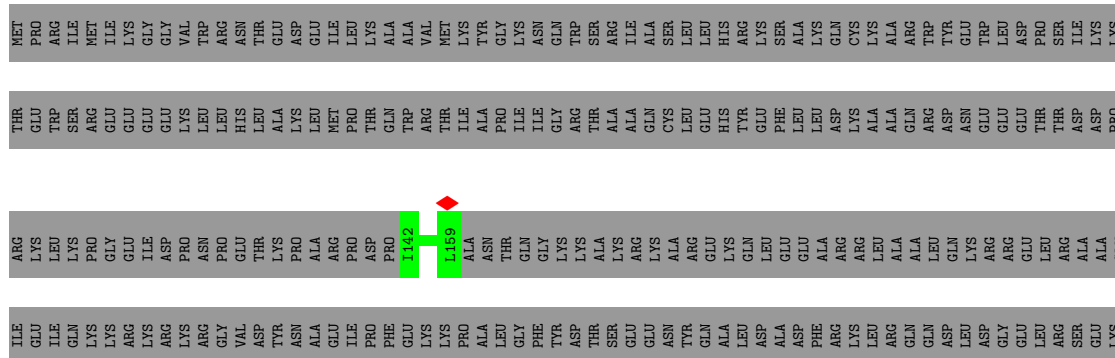




- Molecule 6: U5 snRNA

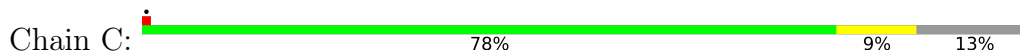


- Molecule 7: Cell division cycle 5-like protein

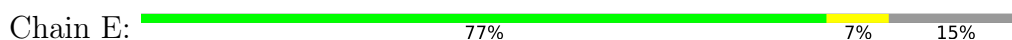


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- Molecule 8: 116 kDa U5 small nuclear ribonucleoprotein component

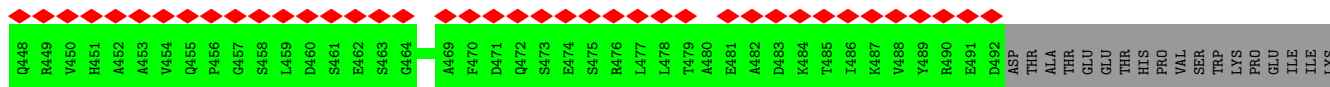
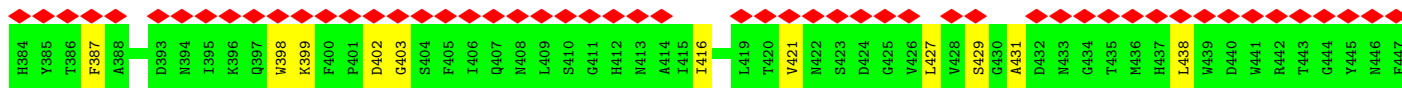
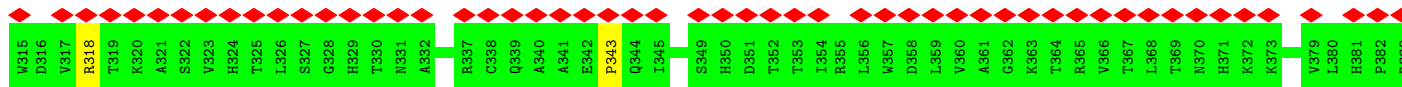
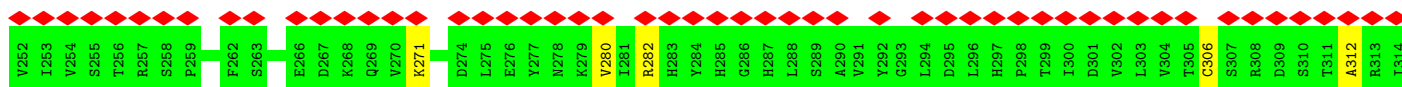
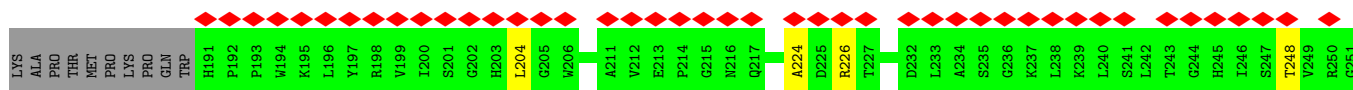
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- Molecule 9: U5 small nuclear ribonucleoprotein 40 kDa protein.

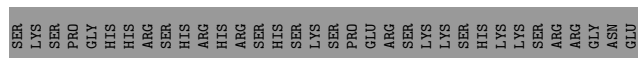
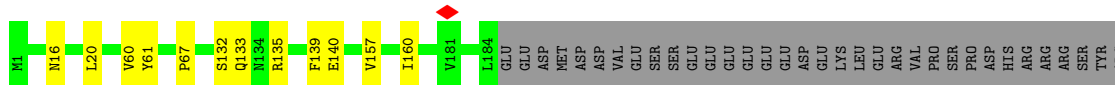





Chain G:  47% 54% 41%



Chain I:  55% 1% 41%



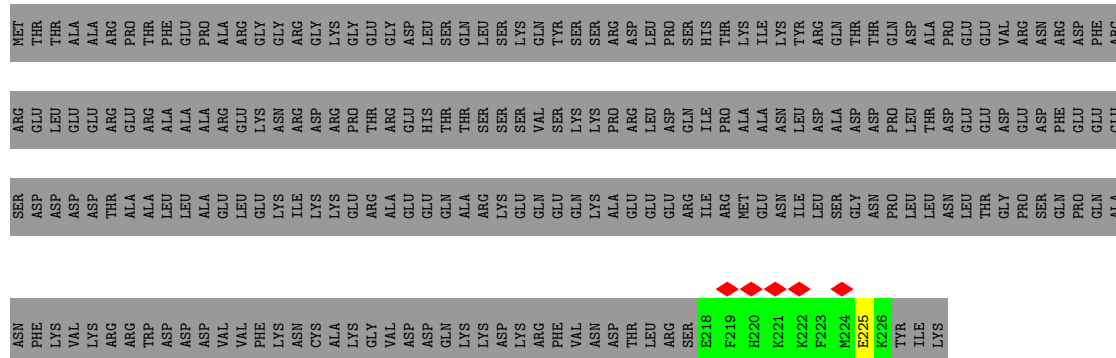
- Molecule 12: Protein BUD31 homolog

Chain Q:  85% 13%



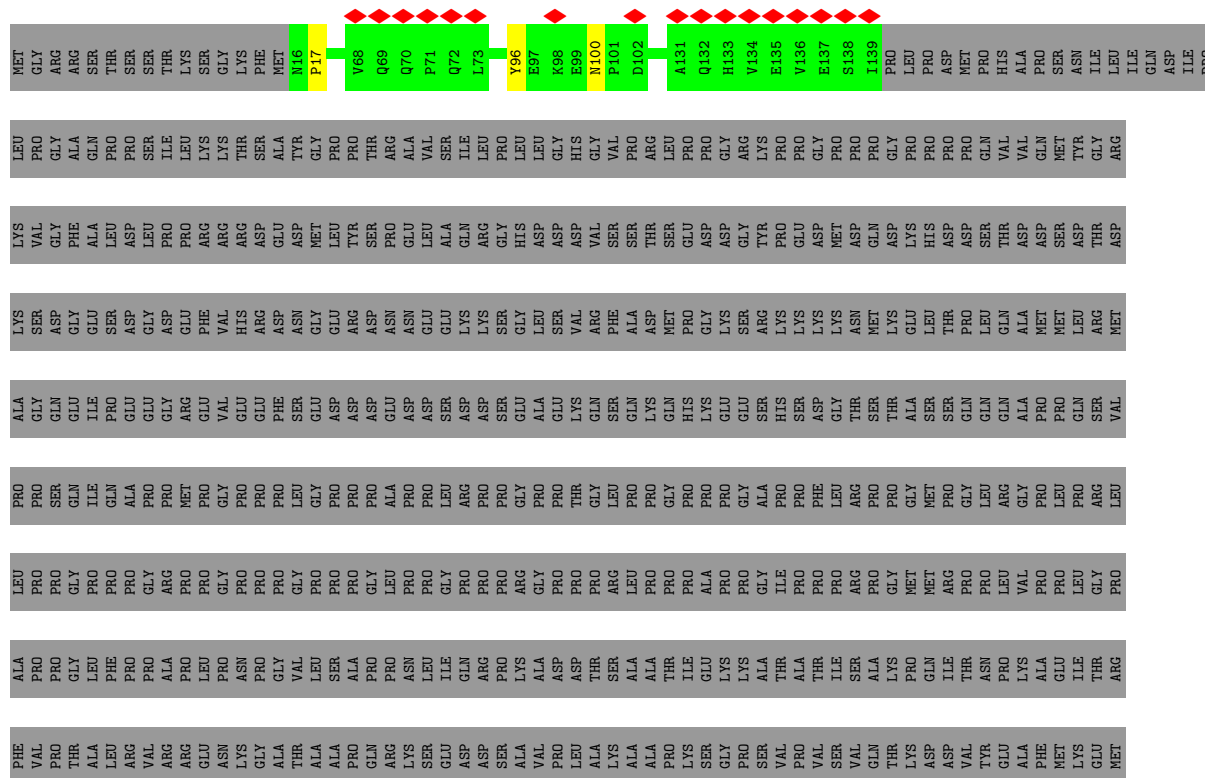
- Molecule 13: Spliceosome-associated protein CWC15 homolog

Chain R:  96%



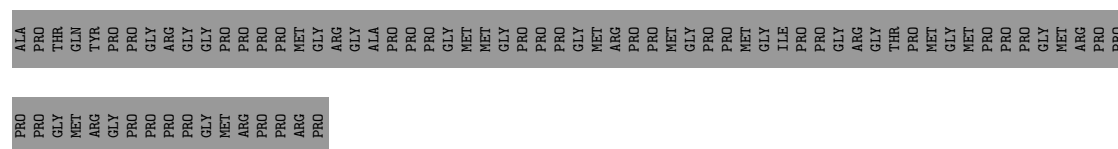
- Molecule 14: WW domain-binding protein 11

Chain X:  19% 81%

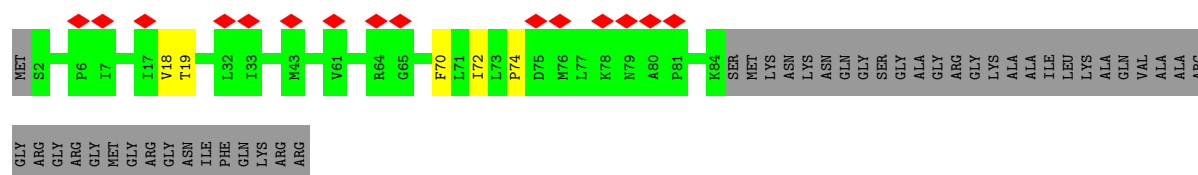




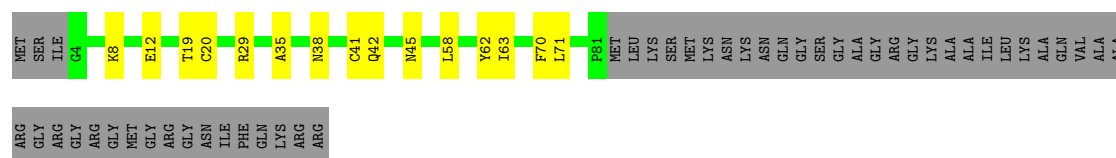




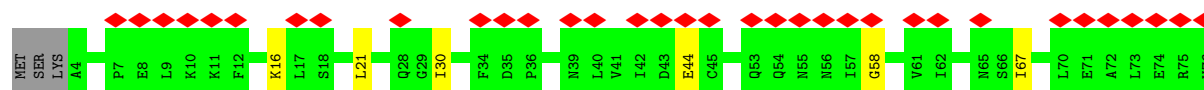
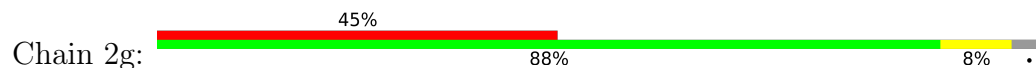
- Molecule 21: Small nuclear ribonucleoprotein Sm D3



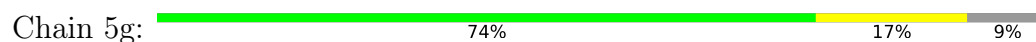
- Molecule 21: Small nuclear ribonucleoprotein Sm D3



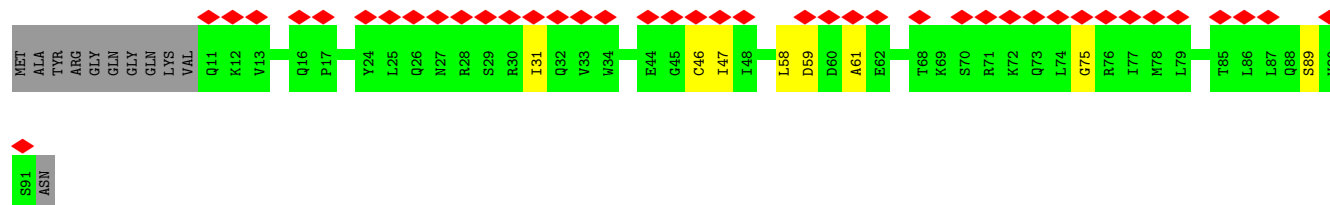
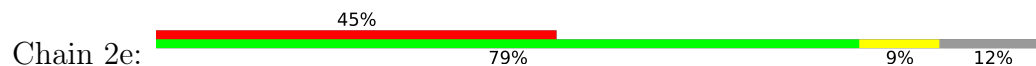
- Molecule 22: Small nuclear ribonucleoprotein G



- Molecule 22: Small nuclear ribonucleoprotein G



- Molecule 23: Small nuclear ribonucleoprotein E

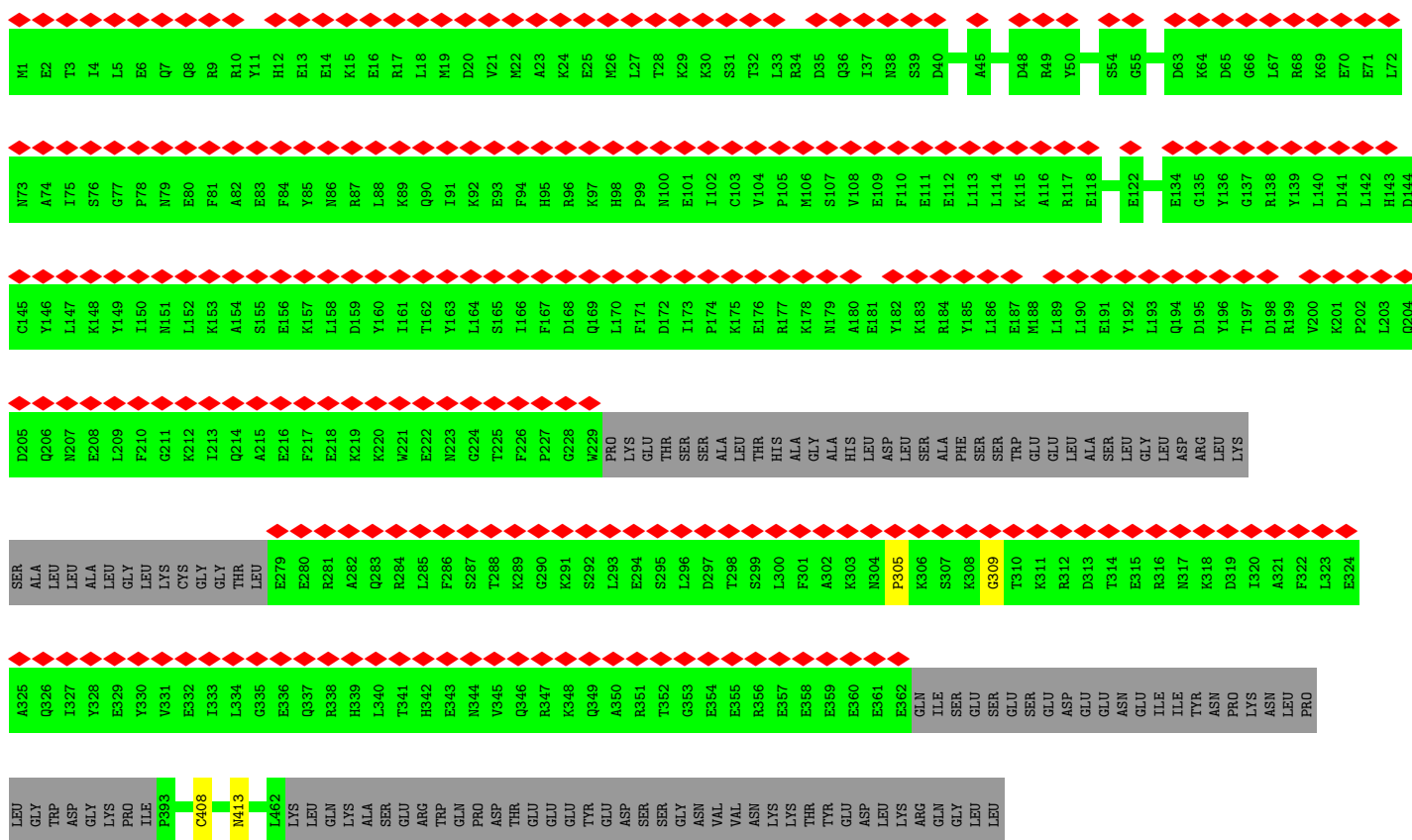
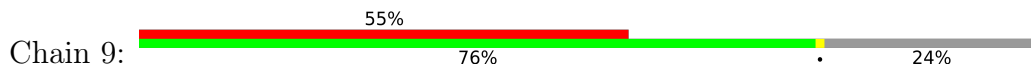




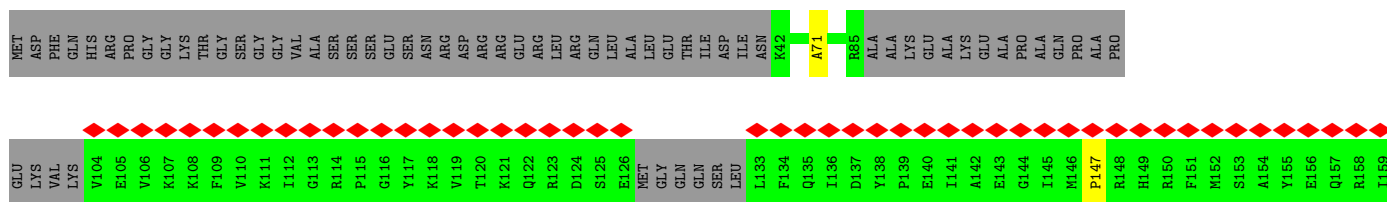
- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |   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

[illegible]

- Molecule 27: Splicing factor 3A subunit 3




- Molecule 28: Splicing factor 3A subunit 2






HIS  
ALA  
ALA  
LYS  
GLN  
LYS  
GLN  
LYS  
LYS  
ARG  
GLN  
LYS  
ALA  
GLN  
PRO  
GLN  
ASP  
LYS  
SER  
ARG  
GLY  
GLY  
SER  
LYS  
LYS  
TYR  
LYS  
GLU  
PHE  
LYS  
PHE

- Molecule 30: Splicing factor 3B subunit 5

Chain B5:  80% 20%

MET  
THR  
ASP  
ARG  
TYR  
THR  
ILE  
HIS  
SER  
GLN  
LEU  
E12  
A80  
ASP  
LYS  
PRO  
GLU  
GLU  
ASN

- Molecule 31: Splicing factor 3B subunit 3

Chain B3:  5% 84% 12%

W1  
F2  
L3  
Y4  
N5  
G13  
I14  
S15  
H19  
I30  
R34  
Y4  
L53  
S84  
I89  
K101  
I102  
H103  
K109  
S110  
G111  
P117  
I132  
E136  
L140  
L166  
V167  
M181  
E186  
M187  
E212  
L249  
I250  
T257  
Y258  
R273  
A303  
G308  
D309

I310  
F311  
K312  
I313  
T317  
V322  
L327  
K328  
Y329  
F330  
D331  
V332  
V333  
V341  
L347  
D368  
M377  
F387  
P406  
I407  
L408  
Q422  
V425  
A426  
C427  
G428  
L435  
R436  
R439  
S445  
E446  
R463  
R464  
H465  
I466  
E467  
D468  
D471  
S477  
F478  
A481  
T482

G488  
E489  
V491  
V494  
T495  
D513  
A529  
ASP  
LYS  
VAL  
ASN  
GLU  
TRP  
LYS  
THR  
PRO  
GLY  
LYS  
K542  
G560  
G561  
E562  
S571  
T578  
E582  
M583  
S584  
A585  
D586  
V587  
V588  
C589  
M590  
N594  
V595  
P596  
P597  
G598  
E599  
F604  
L605  
A606  
V607  
G608  
L609  
V610  
D611

V614  
R615  
I616  
I617  
S618  
S622  
D623  
C624  
L625  
Q626  
L628  
S629  
A632  
L640  
C641  
I642  
M645  
GLY  
THR  
GLU  
LYS  
GLN  
LEU  
GLY  
ARG  
GLY  
SER  
ILE  
GLY  
F662  
L663  
Y664  
L665  
M666  
I667  
R676  
T677  
V678  
V682  
T683  
T691  
ARG  
TYR  
LEU  
GLY  
SER  
R697  
P698

R703  
G708  
Q709  
Q726  
F729  
A742  
S743  
A746  
V755  
A756  
L765  
A766  
L767  
E768  
K769  
F779  
N796  
L797  
I798  
D803  
A806  
E825  
A826  
ALA  
GLY  
GLY  
ASP  
ARG  
GLU  
L834  
A835  
A836  
E837  
M838  
A839  
A840  
A841  
A863  
V868  
M869  
N870  
T876

A887  
W893  
V905  
G908  
A909  
P910  
G923  
F924  
V925  
Y928  
F939  
P949  
A950  
A951  
I952  
I961  
G962  
I990  
I993  
Q994  
V1000  
I1001  
V1002  
V1005  
I1010  
I1011  
V1012  
R1013  
I1022  
D1026  
G1046  
G1051  
C1054  
E1068  
ASP  
PRO  
THR  
GLY  
ASN  
LYS  
ALA

LEU  
TRP  
D1078  
A1089  
G1098  
Q1105  
K1106  
T1107  
T1108  
G1112  
G1113  
L1117  
V1118  
S1123  
F1132  
P1153  
G1176  
F1217

- Molecule 32: Splicing factor 3B subunit 1

Chain B1:  70% 28%

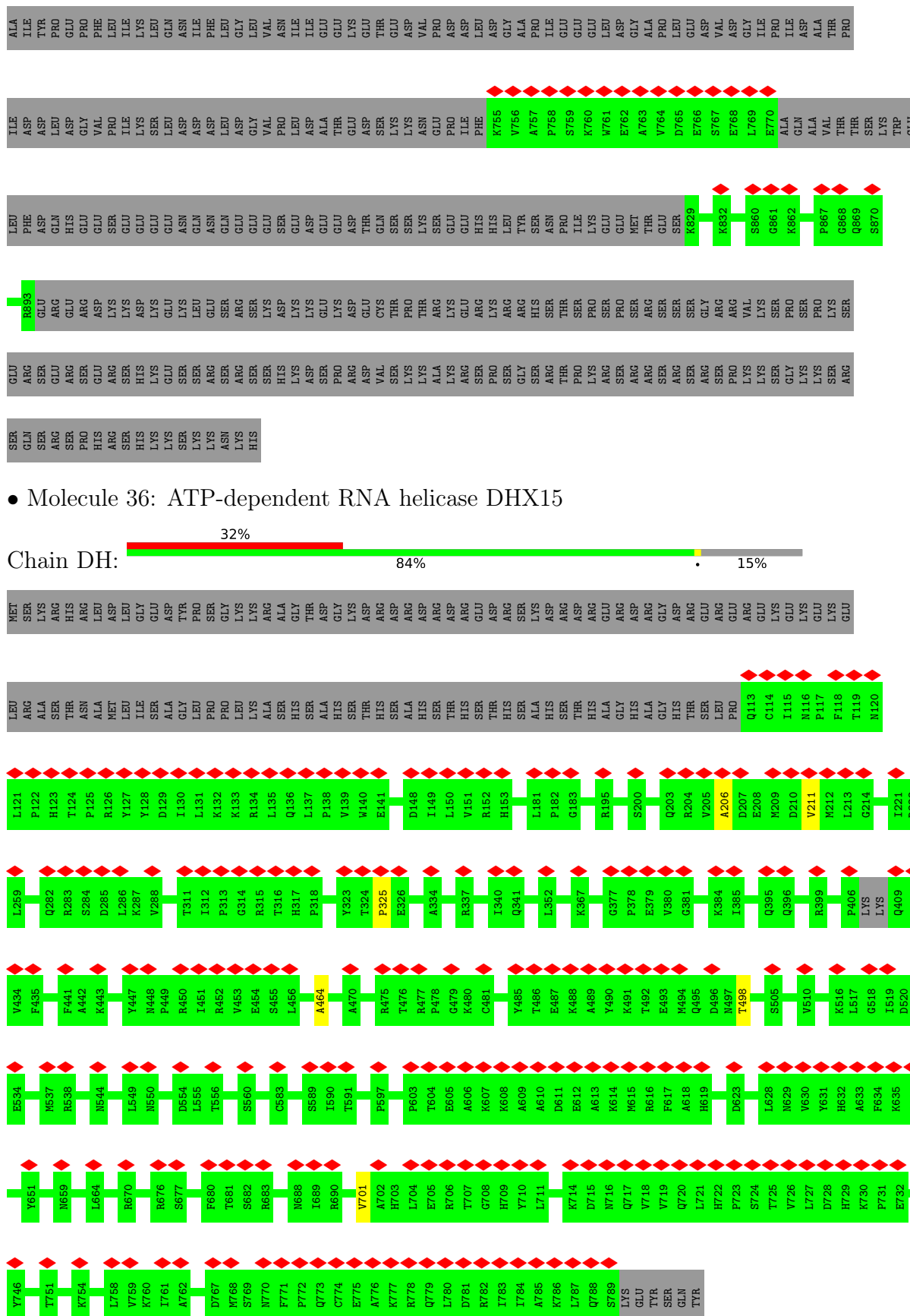
MET  
ALA  
LYS  
ILE  
ALA  
LYS  
THR  
HIS  
GLU  
ASP  
LEU  
GLU  
GLN  
ILE  
ARG  
GLU  
ILE  
GLN  
GLY  
LYS  
PRO  
LYS  
LYS  
ALA  
ALA  
LEU  
ASP  
GLU  
GLU  
ALA  
G30  
D34  
S35  
T36  
G37  
Y38  
Y39  
G46  
S47  
E62  
LEU  
GLU  
ASP  
PHE  
ASP  
ASP  
ASP  
TYR  
SER  
SER  
SER  
SER  
THR  
THR  
LEU  
LEU  
GLY  
GLN  
LYS

LYS  
PRO  
TYR  
HIS  
ALA  
PRO  
VAL  
ALA  
LEU  
LEU  
ASN  
ASP  
I94  
F104  
ALA  
GLU  
HIS  
ARG  
PRO  
PRO  
LYS  
LYS  
ILE  
ALA  
ASP  
ARG  
GLU  
GLU  
ASP  
TYR  
LYS  
HIS  
T36  
ARG  
ARG  
THR  
MET  
ILE  
ILE  
SER  
PRO  
PRO  
GLU  
ARG  
LEU  
ASP  
PHE  
ASP  
ASP  
GLY  
GLY  
LYS  
LYS  
THR  
SER  
PRO  
ASP  
PRO  
LYS  
MET  
ASN

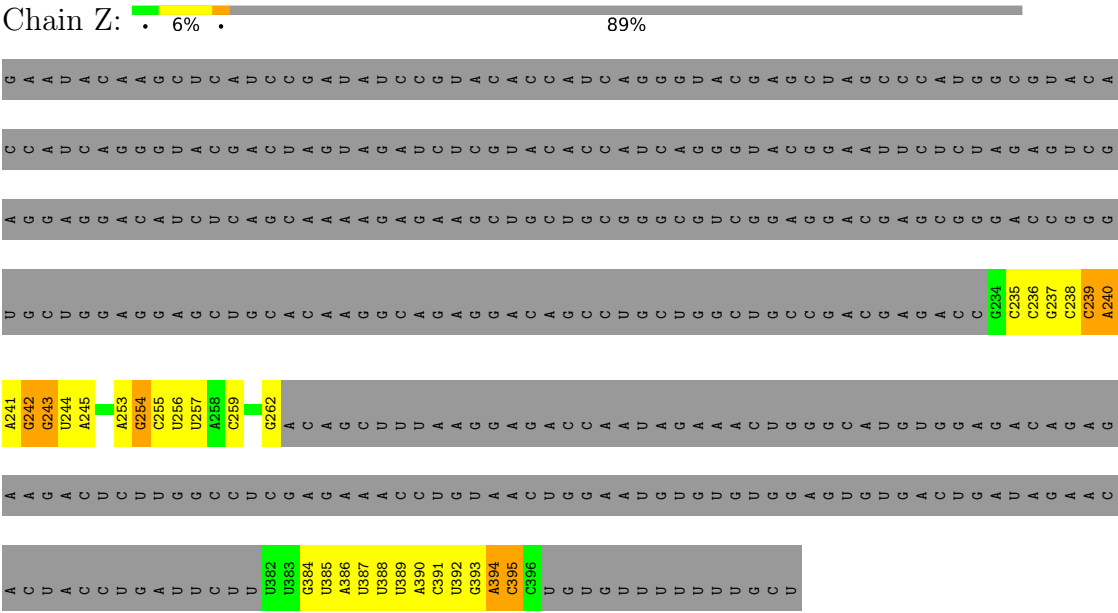




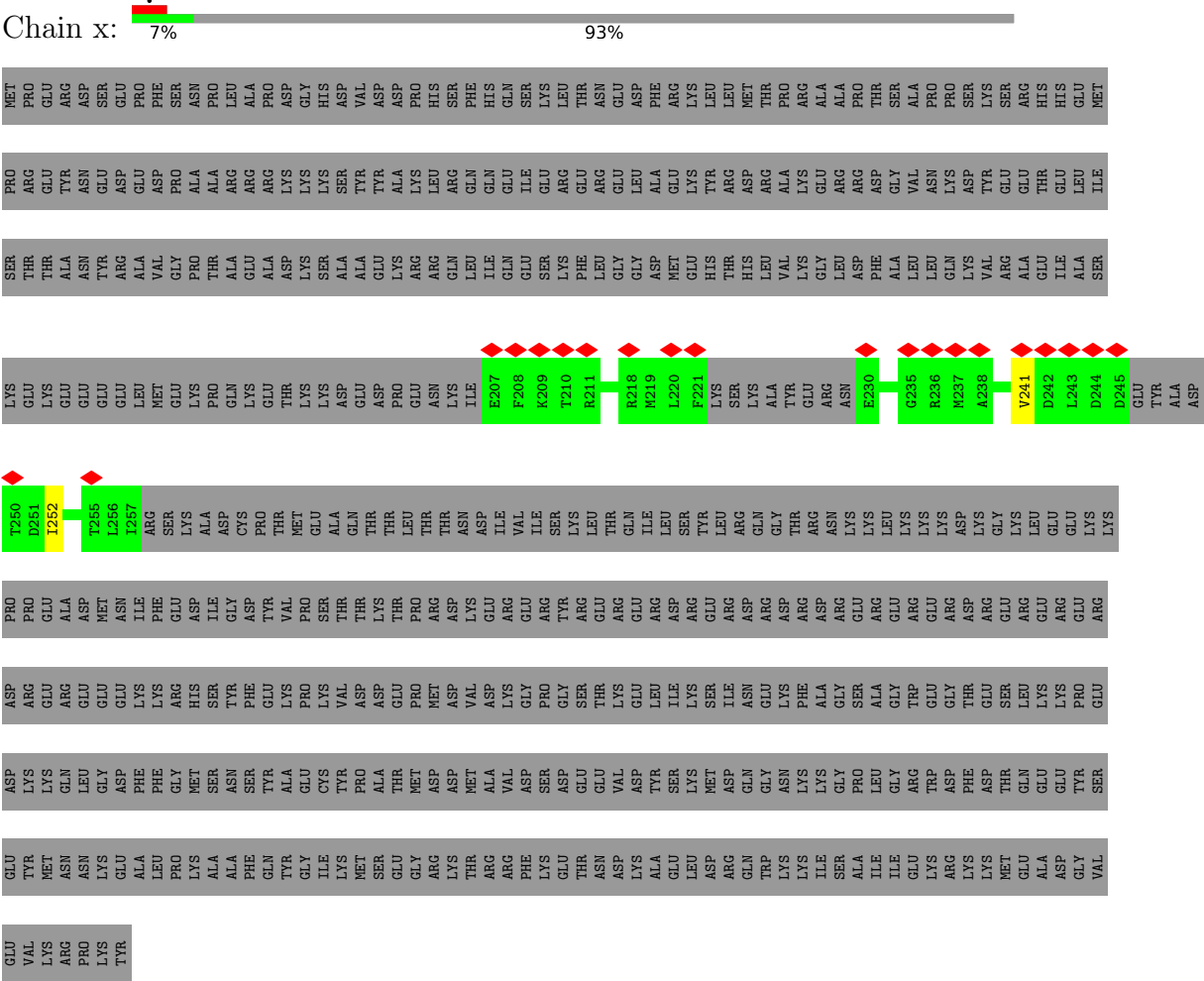
VAL	LYS	LEU	ILE	HIS	ALA	GLN	SER	LEU	ALA	ARG	MET
THR	LEU	GLN	PRO	PRO	SER	ARG	LEU	LEU	ALA	GLU	ALA
ASN	GLU	GLY	THR	ILE	GLY	ARG	LEU	VAL	ALA	SER	ASP
SER	ILE	ASP	GLU	TYR	ILE	SER	ILE	VAL	PHE	LEU	THR
LEU	LEU	PRO	ASN	PRO	MET	ASP	GLU	ASP	GLY	CYS	LYS
ALA	ARG	THR	LEU	PRO	THR	TRP	THR	THR	SER	ASP	PRO
LYS	GLY	LYS	LEU	SER	PRO	ALA	LYS	LYS	ASP	PRO	GLY
VAL	THR	TRP	ALA	MET	ARG	SER	GLN	ARG	GLY	HIS	GLN
ASN	PRO	THR	ILE	GLU	ASP	GLU	PRO	ARG	K131	ASN	LYS
ALA	ARG	GLU	HIS	HIS	GLU	GLU	LEU	ASN	V132	LEU	ALA
SER	LYS	ASP	ARG	THR	GLU	GLU	LYS	ARG	K133	SER	SER
TYR	ASN	PHE	MET	PRO	ARG	ARG	GLY	SER	T134	ARG	SER
THR	ASP	ARG	ILE	PRO	ALA	SER	GLY	LYS	F135	PRO	LYS
ARG	ILE	MET	GLU	PRO	ARG	GLY	GLU	GLU		LEU	THR
LYS	GLY	PHE	PHE	PRO	GLU	VAL	LYS	LYS		LEU	ARG
PHE	ASP	LYS	VAL	SER	ARG	ASP	GLU	GLU		GLU	SER
PHE	ALA	ASN	VAL	PRO	ASN	ASP	LYS	LYS	R137	ASN	SER
GLU	MET	GLY	ARG	GLY	CYS	ASP	LYS	LYS	G138	LYS	ASP
THR	VAL	SER	GLU	LEU	PHE	TYR	LYS	LYS	G139	LEU	VAL
LYS	PHE	PHE	GLY	PRO	GLY	ALA	SER	SER	V140	LYS	HIS
LEU	CYS	TRP	PRO	PHE	VAL	PRO	ASN	ALA	V141	ALA	SER
CYS	LEU	ARG	MET	ASN	ALA	GLY	LEU	LEU	N142	PHE	SER
GLN	ASN	PRO	PHE	ALA	PHE	SER	GLU	GLU	A143	SER	GLY
ILE	ASN	PRO	GLU	GLN	MET	HIS	LEU	LEU	A144	ILE	SER
PHE	GLU	ALA	ALA	PRO	ASN	ASP	PHE	PHE	A145	GLY	SER
SER	GLU	LEU	MET	ARG	ARG	VAL	LYS	LYS	E146	MET	ALA
ASP	ALA	ASN	ILE	GLU	ASP	GLY	GLU	GLU	E147	SER	ALA
LEU	ALA	PRO	MET	LEU	ALA	ASP	GLU	LEU	H148	THR	ASP
ASN	GLU	THR	ARG	LYS	GLU	SER	LYS	LYS	E149	ALA	SER
THR	ILE	THR	ILE	ASN	ALA	THR	ILE	GLN	T150	THR	GLY
ARG	ASP	MET	ASN	ASN	LYS	ASN	GLU	GLU	D151	LEU	PRO
ILE	ILE	GLU	PRO	ALA	ASN	TYR	GLU	GLU	E152	SER	SER
GLN	THR	GLU	PRO	LEU	LEU	GLY	ARG	GLU	K153	LYS	ASP
GLY	GLU	GLN	PHE	PRO	ASN	ASN	GLU	GLU	R154	GLU	ASP
LEU	LEU	THR	PHE	PRO	LYS	ILE	ARG	HIS	G155	GLN	MET
GLN	SER	GLU	LEU	PRO	MET	ASN	LYS	GLU	K156	GLU	PRO
THR	ILE	PHE	PHE	LYS	ILE	PRO	LYS	THR	I157	GLU	ARG
ASN	LYS	VAL	GLN	ASN	SER	GLN	LYS	LYS	Y158	LEU	THR
PHE	THR	GLU	ASN	GLU	PHE	ASN	GLY	GLY	K159	LYS	ARG
LYS	PRO	GLU	THR	ASP	GLU	GLU	ARG	ARG	P160	LYS	PRO
GLN	LEU	PRO	PRO	PHE	MET	GLU	LEU	LEU	SER	GLU	LYS
ARG	PRO	SER	ALA	GLU	LYS	MET	SER	SER	ARG	ASP	SER
VAL	LYS	SER	HIS	LYS	LEU	LEU	ARG	ARG	LYS	GLU	PRO
THR	LYS	LYS	VAL	THR	GLY	CYS	PHE	PHE	ALA	LYS	ARG
ILE	ILE	GLY	TYR	LEU	TRP	GLN	GLU	GLU	ALA	ALA	HIS
CYS	ALA	ALA	TYR	SER	LYS	PHE	PRO	PRO	ASP	ALA	ASN
PHE	ARG	LEU	ARG	GLN	VAL	GLY	THR	GLN	ALA	GLU	TYR
ARG	LEU	LYS	TRP	ALA	ALA	ARG	SER	GLN	LYS	GLU	ASN
ALA	TYR	GLU	LYS	ILE	VAL	ARG	ILE	ARG	ASN	ILE	ILE
TRP	LEU	GLU	LEU	VAL	PRO	PHE	SER	PHE	PRO	GLY	GLY
ASP	VAL	GLN									



- Molecule 37: pre-mRNA

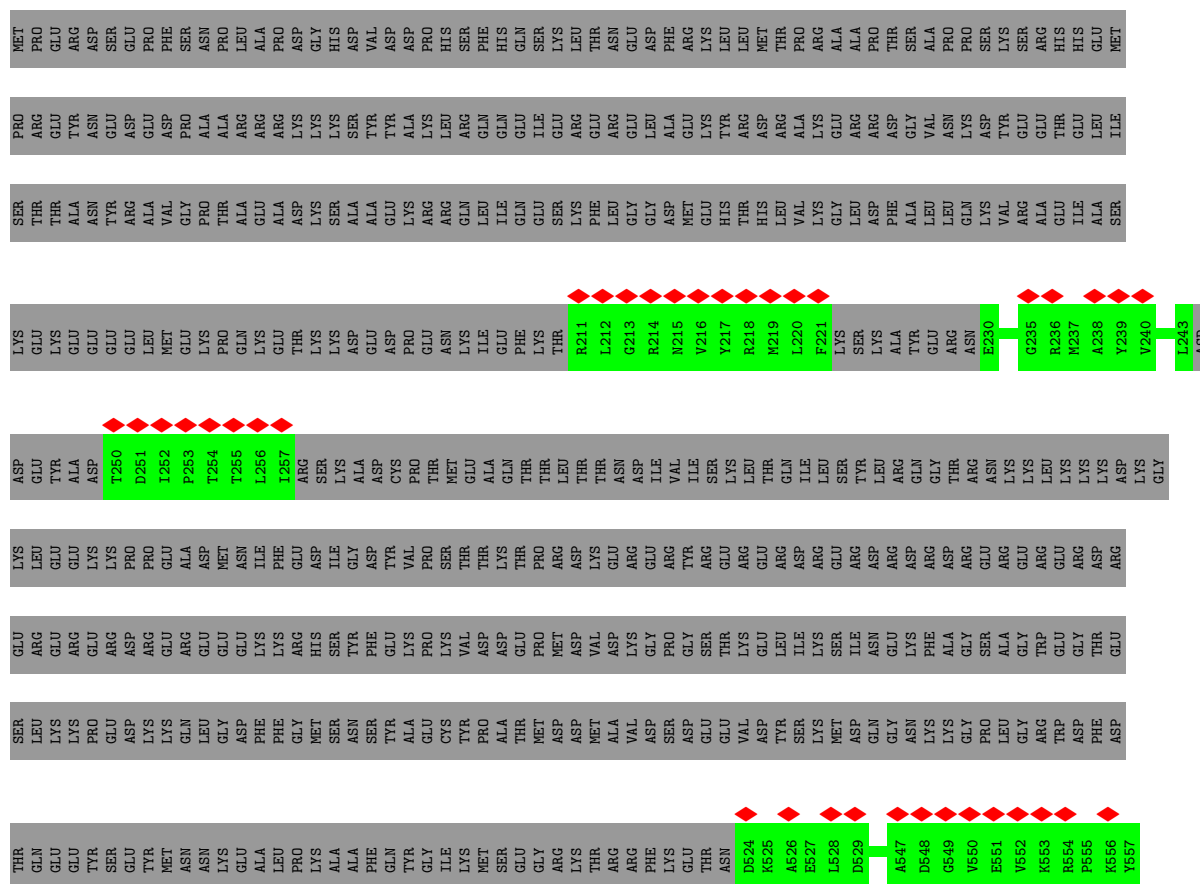


• Molecule 38: Protein Red

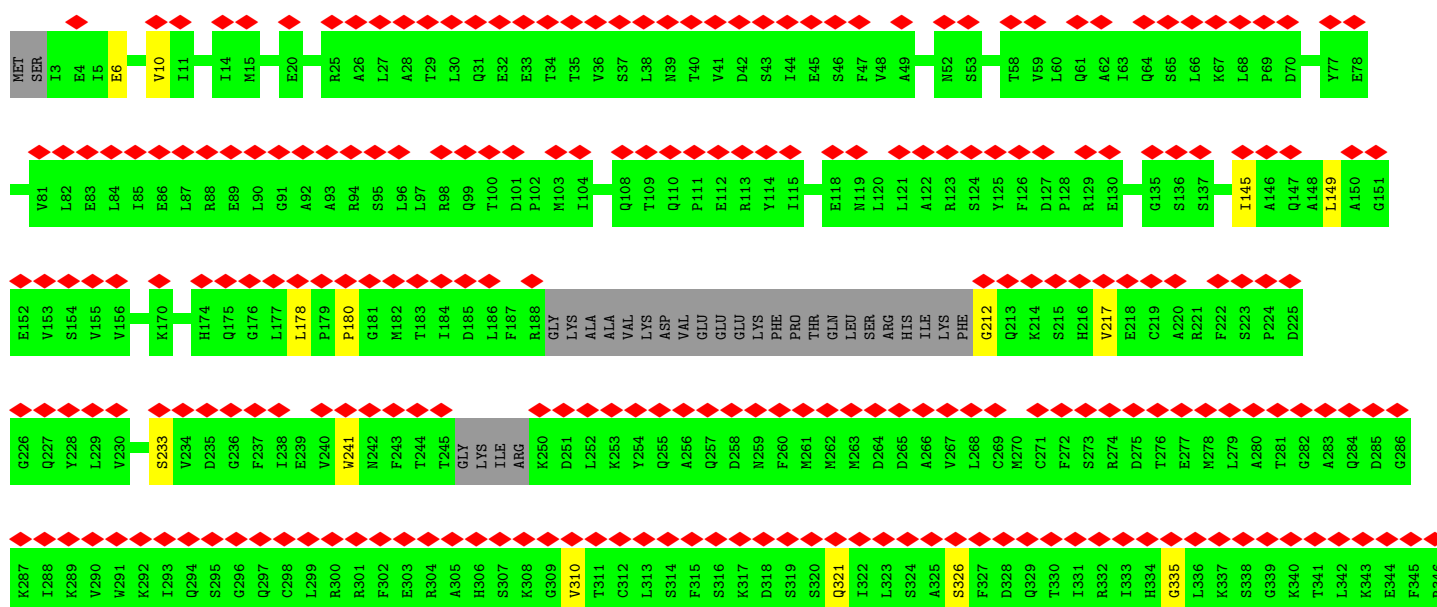
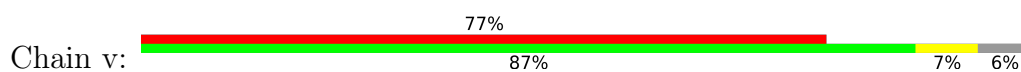


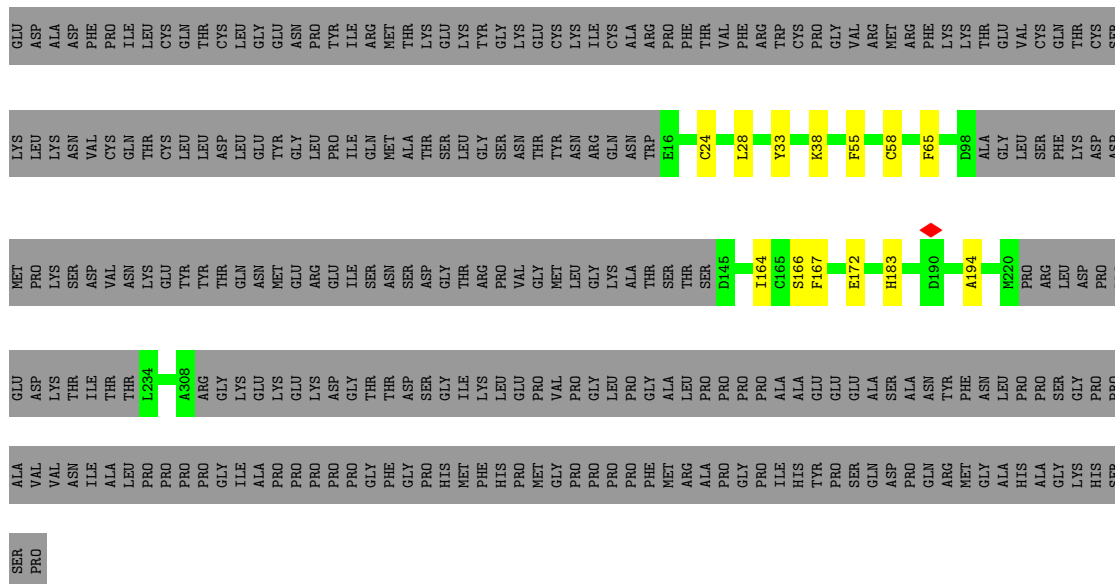
• Molecule 38: Protein Red





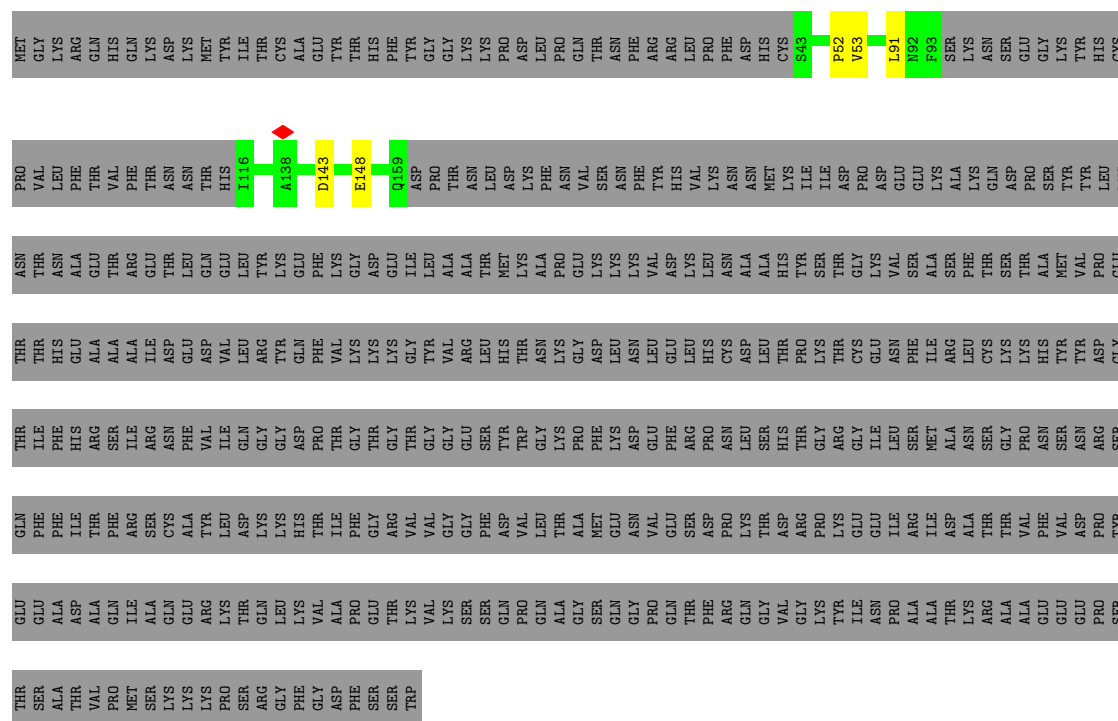
• Molecule 39: WD40 repeat-containing protein SMU1





- Molecule 41: RING-type E3 ubiquitin-protein ligase PPIL2

Chain t:  17% 82%



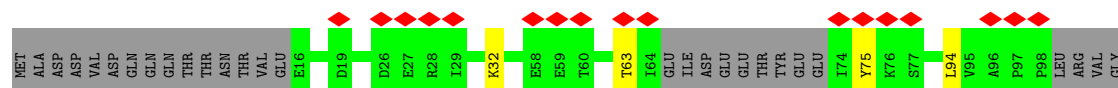
- Molecule 42: U6 snRNA-associated Sm-like protein LSm2

Chain 62:  9% 93% 5%



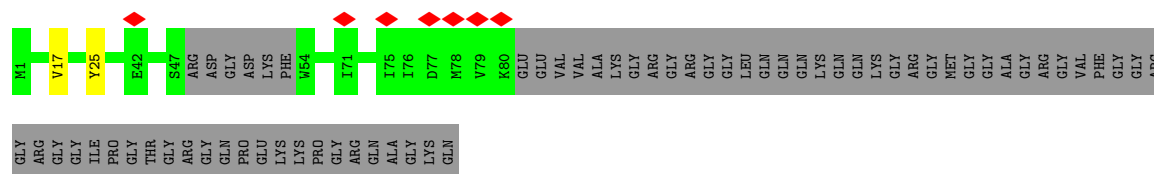
- Molecule 43: U6 snRNA-associated Sm-like protein LSm3

Chain 63:  17% 69% 27%



- Molecule 44: U6 snRNA-associated Sm-like protein LSm4

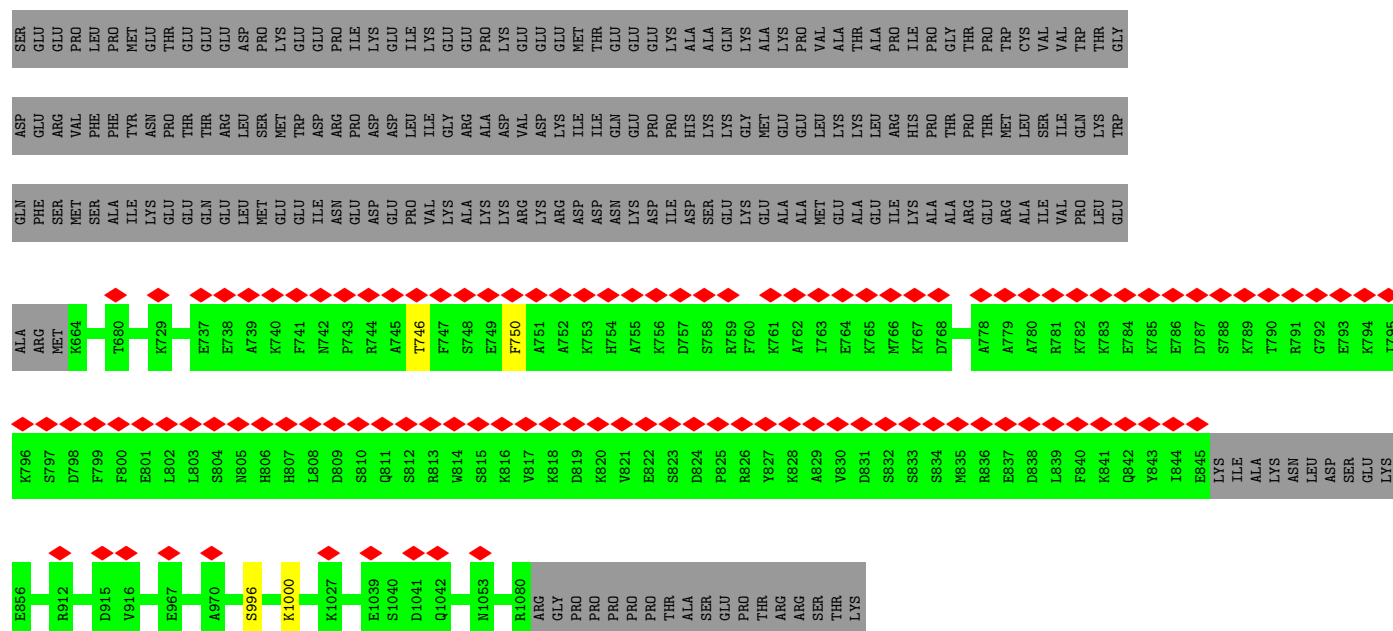
Chain 64:  5% 52% 47%



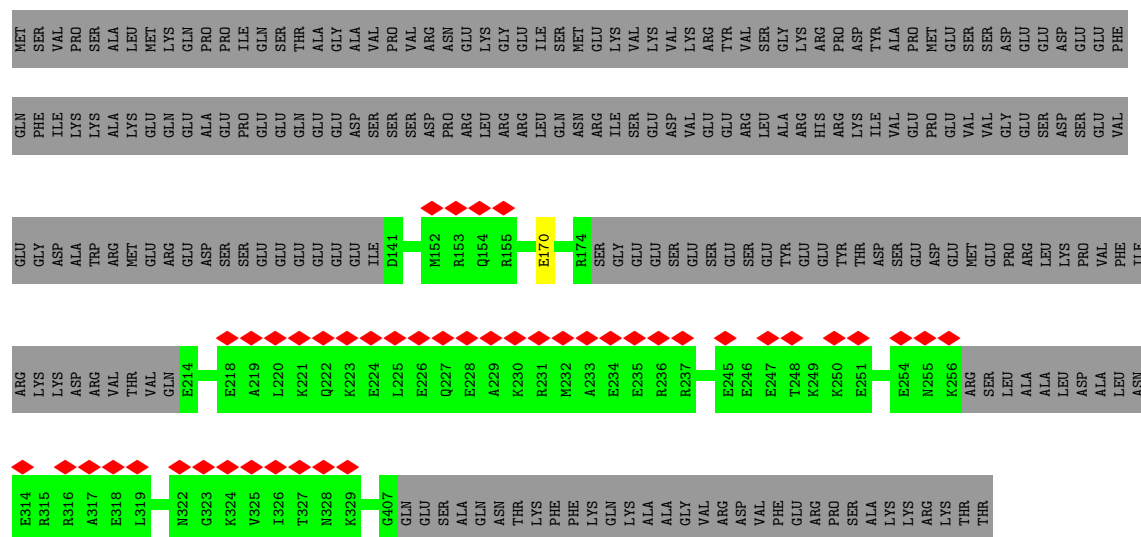
- Chain 65:



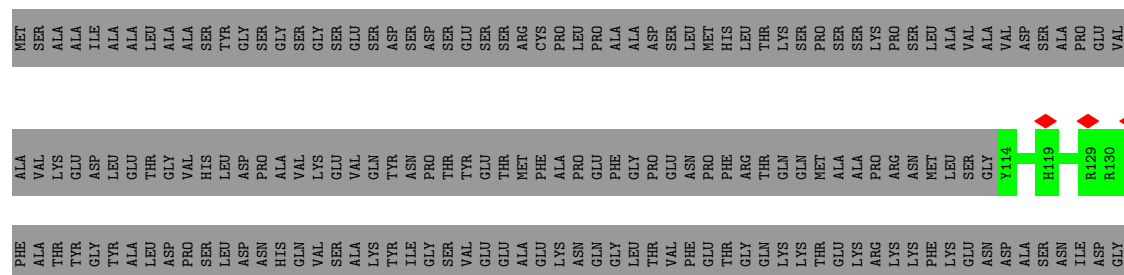




• Molecule 52: Microfibrillar-associated protein 1



• Molecule 53: Pre-mRNA-processing factor 17



[illegible]

- Molecule 54: PHD finger-like domain-containing protein 5A

Chain 5A:  85% 5% 9%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55345	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS TITAN THEMIS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	39	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.013	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.0021	Depositor
Map size (Å)	648.0, 648.0, 648.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.7, 2.7, 2.7	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	0.08	0/11308	0.22	0/15866
2	B	0.08	0/8766	0.22	0/12286
3	2	0.05	0/2378	0.12	0/3692
4	6	0.06	0/2354	0.14	0/3664
5	7	0.07	0/624	0.19	0/874
6	5	0.08	0/2559	0.19	0/3977
7	L	0.06	0/89	0.21	0/123
8	C	0.08	0/4308	0.23	0/6037
9	E	0.08	0/1515	0.27	0/2113
10	G	0.08	0/1517	0.23	0/2117
11	I	0.07	0/931	0.21	0/1302
12	Q	0.10	0/718	0.26	0/1003
13	R	0.03	0/44	0.16	0/60
14	X	0.08	0/634	0.19	0/890
15	q	0.07	0/359	0.24	0/498
16	r	0.08	0/442	0.23	0/615
17	22	0.08	0/485	0.20	0/677
17	52	0.06	0/394	0.20	0/548
18	2B	0.05	0/463	0.17	0/646
19	2f	0.08	0/362	0.20	0/502
19	5f	0.07	0/354	0.22	0/491
20	2b	0.06	0/416	0.21	0/581
20	5b	0.07	0/319	0.21	0/442
21	23	0.08	0/417	0.24	0/581
21	53	0.07	0/392	0.23	0/546
22	2g	0.06	0/366	0.22	0/509
22	5g	0.11	0/346	0.25	0/481
23	2e	0.06	0/403	0.19	0/561
23	5e	0.05	0/388	0.21	0/540
24	21	0.06	0/404	0.20	0/564
24	51	0.08	0/477	0.20	0/667
25	2A	0.08	0/821	0.24	0/1149
26	B4	0.08	0/394	0.19	0/549
27	9	0.07	0/1928	0.19	0/2692

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
28	8	0.07	0/734	0.22	0/1025
29	B2	0.09	0/909	0.24	0/1278
30	B5	0.06	0/349	0.18	0/487
31	B3	0.07	0/5933	0.22	0/8297
32	B1	0.08	0/4768	0.22	0/6674
33	B6	0.06	0/474	0.19	0/663
34	BL	0.06	0/2428	0.17	0/3392
35	SR	0.04	0/564	0.15	0/785
36	DH	0.07	0/3480	0.21	0/4882
37	Z	0.06	0/1038	0.14	0/1611
38	x	0.09	0/196	0.21	0/270
38	y	0.05	0/337	0.14	0/466
39	v	0.08	0/2431	0.22	0/3392
39	w	0.07	0/2491	0.21	0/3477
40	P	0.07	0/1189	0.22	0/1661
41	t	0.09	0/486	0.27	0/679
42	62	0.04	0/359	0.10	0/447
43	63	0.04	0/294	0.12	0/364
44	64	0.05	0/294	0.09	0/364
45	65	0.05	0/286	0.10	0/354
46	66	0.05	0/279	0.12	0/347
47	67	0.04	0/258	0.09	0/319
48	68	0.04	0/242	0.07	0/299
49	S1	0.08	0/478	0.19	0/668
50	A6	0.06	0/369	0.18	0/513
51	T	0.08	0/2048	0.18	0/2867
52	K	0.07	0/1065	0.21	0/1483
53	P7	0.05	0/92	0.14	0/128
54	5A	0.07	0/501	0.25	0/697
All	All	0.07	0/82047	0.21	0/115732

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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	11189	0	5462	86	0
2	B	8688	0	4221	46	0
3	2	2135	0	1084	20	0
4	6	2104	0	1061	27	0
5	7	621	0	288	1	0
6	5	2296	0	1163	34	0
7	L	90	0	41	0	0
8	C	4260	0	2118	49	0
9	E	1506	0	737	13	0
10	G	1508	0	738	11	0
11	I	925	0	438	7	0
12	Q	713	0	337	10	0
13	R	45	0	17	1	0
14	X	630	0	293	3	0
15	q	360	0	159	4	0
16	r	442	0	187	3	0
17	22	482	0	220	10	0
17	52	393	0	176	6	0
18	2B	461	0	218	4	0
19	2f	359	0	179	4	0
19	5f	352	0	171	8	0
20	2b	413	0	194	9	0
20	5b	319	0	144	6	0
21	23	415	0	198	3	0
21	53	390	0	188	10	0
22	2g	364	0	176	3	0
22	5g	344	0	168	11	0
23	2e	403	0	173	5	0
23	5e	388	0	167	10	0
24	21	402	0	184	3	0
24	51	474	0	217	11	0
25	2A	816	0	386	2	0
26	B4	391	0	197	0	0
27	9	1920	0	902	2	0
28	8	729	0	356	4	0
29	B2	891	0	481	4	0
30	B5	347	0	171	0	0
31	B3	5880	0	2937	80	0
32	B1	4725	0	2384	15	0
33	B6	470	0	233	9	0
34	BL	2418	0	1115	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	SR	563	0	261	1	0
36	DH	3431	0	1710	5	0
37	Z	931	0	473	20	0
38	x	197	0	90	1	0
38	y	338	0	160	0	0
39	v	2419	0	1155	19	0
39	w	2478	0	1181	12	0
40	P	1180	0	579	9	0
41	t	482	0	235	4	0
42	62	360	0	95	1	0
43	63	296	0	76	2	0
44	64	296	0	77	1	0
45	65	288	0	78	3	0
46	66	280	0	81	0	0
47	67	260	0	75	1	0
48	68	244	0	71	1	0
49	S1	475	0	245	3	0
50	A6	368	0	175	3	0
51	T	2044	0	917	2	0
52	K	1066	0	485	1	0
53	P7	92	0	46	0	0
54	5A	498	0	241	5	0
All	All	80644	0	38785	576	0

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

The worst 5 of 576 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)
39:v:447:CYS:HA	39:v:458:TYR:O	1.72	0.88
1:A:2046:THR:O	1:A:2053:GLU:HA	1.78	0.82
12:Q:133:GLU:HA	12:Q:138:GLY:HA2	1.65	0.78
8:C:830:PRO:HA	8:C:904:TRP:HA	1.66	0.78
8:C:835:GLU:O	8:C:897:SER:HA	1.85	0.77

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	2197/2769 (79%)	2127 (97%)	70 (3%)	0	100	100
2	B	1720/2136 (80%)	1644 (96%)	76 (4%)	0	100	100
5	7	121/793 (15%)	119 (98%)	2 (2%)	0	100	100
7	L	16/802 (2%)	16 (100%)	0	0	100	100
8	C	841/972 (86%)	809 (96%)	32 (4%)	0	100	100
9	E	300/357 (84%)	273 (91%)	27 (9%)	0	100	100
10	G	300/514 (58%)	285 (95%)	15 (5%)	0	100	100
11	I	182/312 (58%)	175 (96%)	7 (4%)	0	100	100
12	Q	140/144 (97%)	136 (97%)	4 (3%)	0	100	100
13	R	7/229 (3%)	7 (100%)	0	0	100	100
14	X	122/641 (19%)	120 (98%)	2 (2%)	0	100	100
15	q	71/73 (97%)	71 (100%)	0	0	100	100
16	r	87/199 (44%)	80 (92%)	7 (8%)	0	100	100
17	22	91/118 (77%)	91 (100%)	0	0	100	100
17	52	74/118 (63%)	71 (96%)	3 (4%)	0	100	100
18	2B	90/225 (40%)	89 (99%)	1 (1%)	0	100	100
19	2f	70/86 (81%)	70 (100%)	0	0	100	100
19	5f	69/86 (80%)	63 (91%)	6 (9%)	0	100	100
20	2b	80/240 (33%)	79 (99%)	1 (1%)	0	100	100
20	5b	60/240 (25%)	58 (97%)	2 (3%)	0	100	100
21	23	81/126 (64%)	78 (96%)	3 (4%)	0	100	100
21	53	76/126 (60%)	73 (96%)	3 (4%)	0	100	100
22	2g	71/76 (93%)	67 (94%)	4 (6%)	0	100	100
22	5g	67/76 (88%)	63 (94%)	4 (6%)	0	100	100
23	2e	79/92 (86%)	78 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	5e	76/92 (83%)	74 (97%)	2 (3%)	0	100	100
24	21	78/119 (66%)	73 (94%)	5 (6%)	0	100	100
24	51	92/119 (77%)	88 (96%)	4 (4%)	0	100	100
25	2A	160/255 (63%)	154 (96%)	6 (4%)	0	100	100
26	B4	76/424 (18%)	75 (99%)	1 (1%)	0	100	100
27	9	377/501 (75%)	367 (97%)	10 (3%)	0	100	100
28	8	138/464 (30%)	134 (97%)	4 (3%)	0	100	100
29	B2	166/895 (18%)	157 (95%)	9 (5%)	0	100	100
30	B5	67/86 (78%)	64 (96%)	3 (4%)	0	100	100
31	B3	1156/1217 (95%)	1107 (96%)	49 (4%)	0	100	100
32	B1	929/1304 (71%)	899 (97%)	30 (3%)	0	100	100
33	B6	91/125 (73%)	90 (99%)	1 (1%)	0	100	100
34	BL	482/563 (86%)	478 (99%)	4 (1%)	0	100	100
35	SR	106/1029 (10%)	106 (100%)	0	0	100	100
36	DH	675/795 (85%)	660 (98%)	15 (2%)	0	100	100
38	x	33/557 (6%)	31 (94%)	2 (6%)	0	100	100
38	y	59/557 (11%)	59 (100%)	0	0	100	100
39	v	478/513 (93%)	461 (96%)	17 (4%)	0	100	100
39	w	492/513 (96%)	469 (95%)	23 (5%)	0	100	100
40	P	228/500 (46%)	222 (97%)	6 (3%)	0	100	100
41	t	91/520 (18%)	86 (94%)	5 (6%)	0	100	100
42	62	88/95 (93%)	85 (97%)	3 (3%)	0	100	100
43	63	70/102 (69%)	59 (84%)	11 (16%)	0	100	100
44	64	70/139 (50%)	66 (94%)	4 (6%)	0	100	100
45	65	68/91 (75%)	64 (94%)	4 (6%)	0	100	100
46	66	68/80 (85%)	63 (93%)	5 (7%)	0	100	100
47	67	61/103 (59%)	59 (97%)	2 (3%)	0	100	100
48	68	57/96 (59%)	53 (93%)	4 (7%)	0	100	100
49	S1	87/536 (16%)	86 (99%)	1 (1%)	0	100	100
50	A6	72/248 (29%)	69 (96%)	3 (4%)	0	100	100
51	T	403/1098 (37%)	395 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	K	208/439 (47%)	202 (97%)	6 (3%)	0	100	100
53	P7	16/579 (3%)	16 (100%)	0	0	100	100
54	5A	98/110 (89%)	90 (92%)	8 (8%)	0	100	100
All	All	14428/26414 (55%)	13903 (96%)	525 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	124/2511 (5%)	124 (100%)	0	100	100
2	B	79/1908 (4%)	79 (100%)	0	100	100
5	7	4/709 (1%)	4 (100%)	0	100	100
8	C	49/866 (6%)	49 (100%)	0	100	100
9	E	10/300 (3%)	10 (100%)	0	100	100
10	G	10/441 (2%)	10 (100%)	0	100	100
11	I	7/293 (2%)	7 (100%)	0	100	100
12	Q	6/130 (5%)	6 (100%)	0	100	100
14	X	5/554 (1%)	5 (100%)	0	100	100
16	r	1/181 (1%)	1 (100%)	0	100	100
17	22	5/110 (4%)	5 (100%)	0	100	100
17	52	3/110 (3%)	3 (100%)	0	100	100
18	2B	3/195 (2%)	3 (100%)	0	100	100
19	2f	4/74 (5%)	4 (100%)	0	100	100
19	5f	3/74 (4%)	3 (100%)	0	100	100
20	2b	4/177 (2%)	4 (100%)	0	100	100
20	5b	2/177 (1%)	2 (100%)	0	100	100
21	23	3/101 (3%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	53	3/101 (3%)	3 (100%)	0	100	100
22	2g	3/66 (4%)	3 (100%)	0	100	100
22	5g	3/66 (4%)	3 (100%)	0	100	100
23	2e	1/84 (1%)	1 (100%)	0	100	100
23	5e	1/84 (1%)	1 (100%)	0	100	100
24	21	3/101 (3%)	3 (100%)	0	100	100
24	51	4/101 (4%)	4 (100%)	0	100	100
25	2A	6/218 (3%)	6 (100%)	0	100	100
26	B4	4/336 (1%)	4 (100%)	0	100	100
27	9	11/446 (2%)	11 (100%)	0	100	100
28	8	8/382 (2%)	8 (100%)	0	100	100
29	B2	21/776 (3%)	21 (100%)	0	100	100
30	B5	3/77 (4%)	3 (100%)	0	100	100
31	B3	59/1051 (6%)	59 (100%)	0	100	100
32	B1	47/1104 (4%)	47 (100%)	0	100	100
33	B6	5/109 (5%)	5 (100%)	0	100	100
34	BL	11/510 (2%)	11 (100%)	0	100	100
35	SR	4/934 (0%)	4 (100%)	0	100	100
36	DH	39/704 (6%)	39 (100%)	0	100	100
38	x	2/498 (0%)	2 (100%)	0	100	100
38	y	3/498 (1%)	3 (100%)	0	100	100
39	v	15/450 (3%)	15 (100%)	0	100	100
39	w	15/450 (3%)	15 (100%)	0	100	100
40	P	12/435 (3%)	12 (100%)	0	100	100
41	t	6/456 (1%)	6 (100%)	0	100	100
49	S1	6/459 (1%)	6 (100%)	0	100	100
50	A6	2/203 (1%)	2 (100%)	0	100	100
51	T	6/956 (1%)	6 (100%)	0	100	100
52	K	2/395 (0%)	2 (100%)	0	100	100
53	P7	1/502 (0%)	1 (100%)	0	100	100
54	5A	4/95 (4%)	4 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	632/21558 (3%)	632 (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 ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	2	96/188 (51%)	28 (29%)	1 (1%)
37	Z	42/410 (10%)	17 (40%)	0
4	6	96/106 (90%)	33 (34%)	1 (1%)
6	5	107/117 (91%)	43 (40%)	2 (1%)
All	All	341/821 (41%)	121 (35%)	4 (1%)

5 of 121 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	2	8	C
3	2	11	G
3	2	20	G
3	2	30	A
3	2	37	U

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	2	106	G
4	6	67	G
6	5	64	G
6	5	96	A

## 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 ⓘ

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.

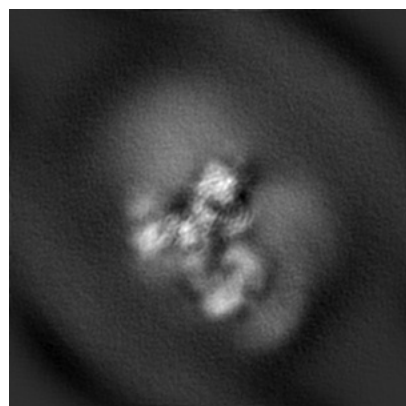
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53843. These allow visual inspection of the internal detail of the map and identification of artifacts.

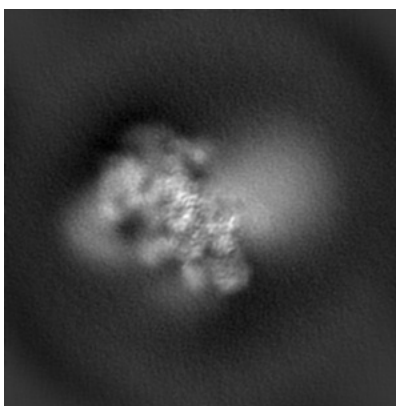
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

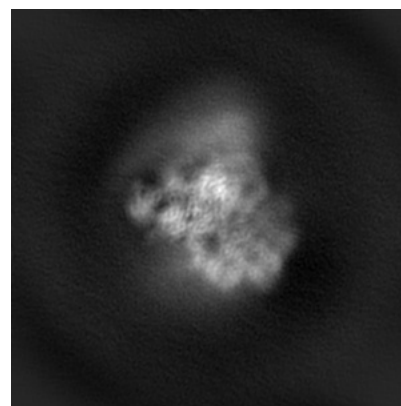
#### 6.1.1 Primary map



X

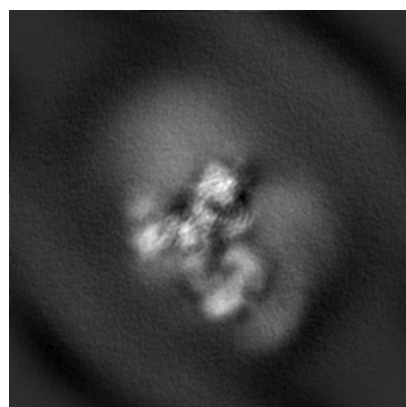


Y

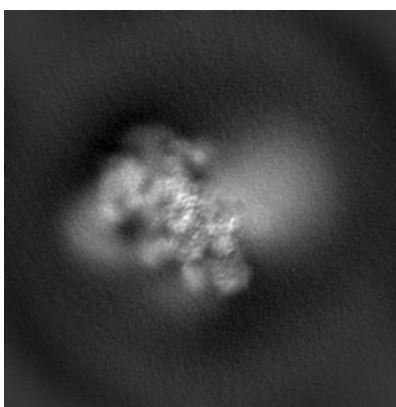


Z

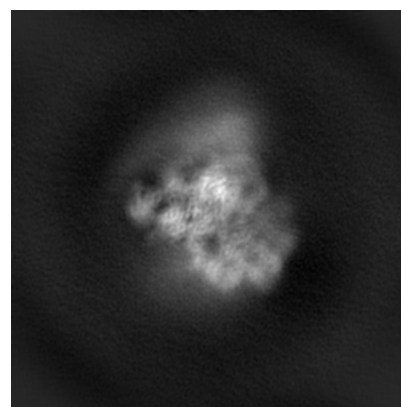
#### 6.1.2 Raw map



X



Y

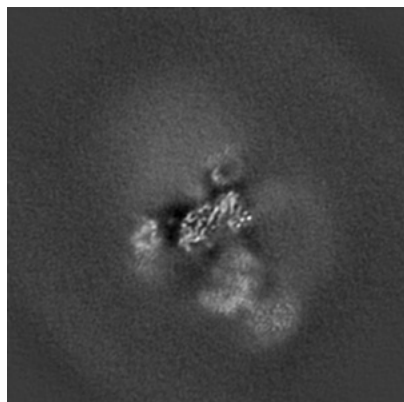


Z

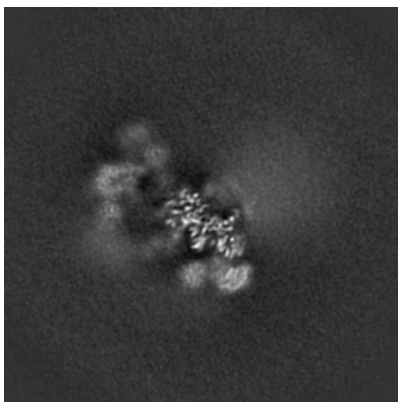
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

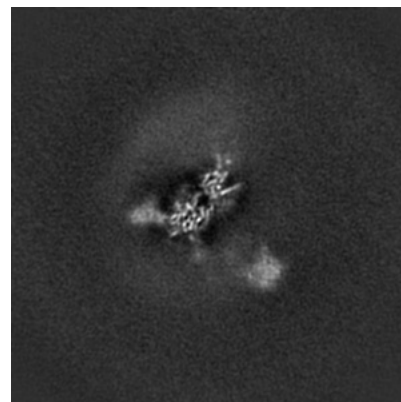
### 6.2.1 Primary map



X Index: 120

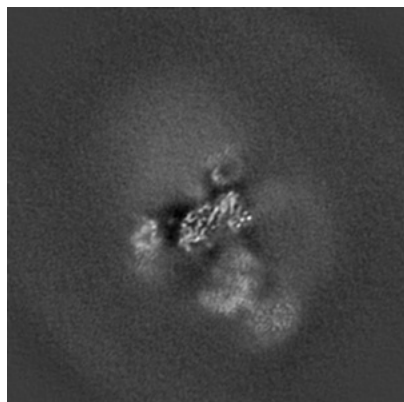


Y Index: 120

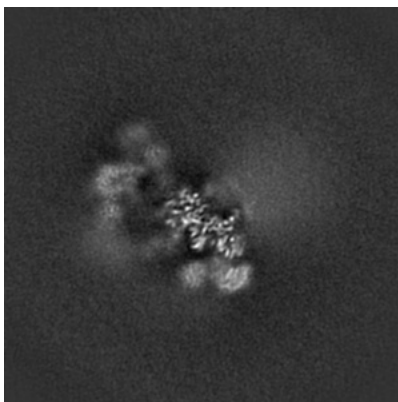


Z Index: 120

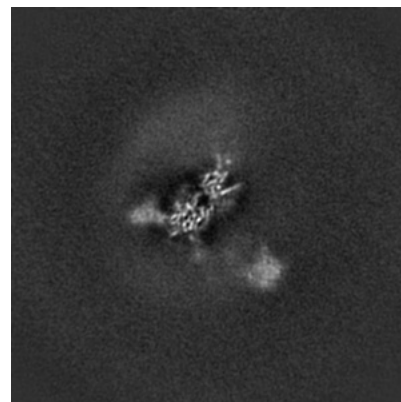
### 6.2.2 Raw map



X Index: 120



Y Index: 120

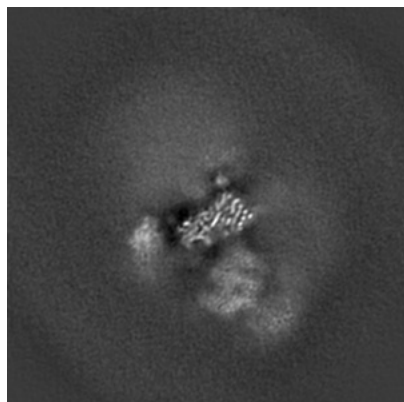


Z Index: 120

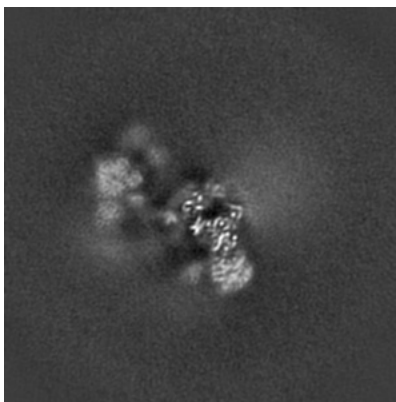
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

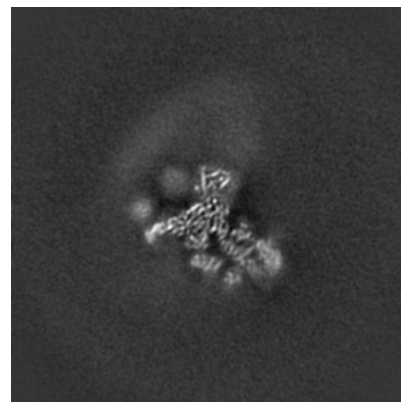
### 6.3.1 Primary map



X Index: 122

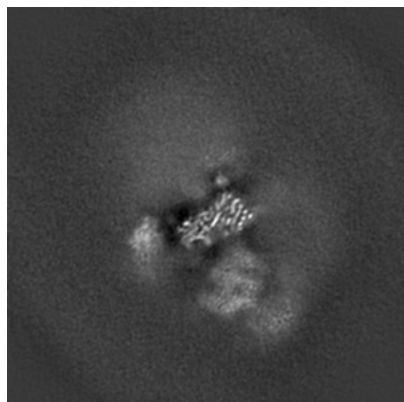


Y Index: 124

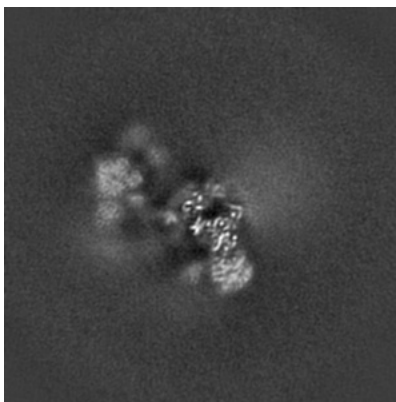


Z Index: 109

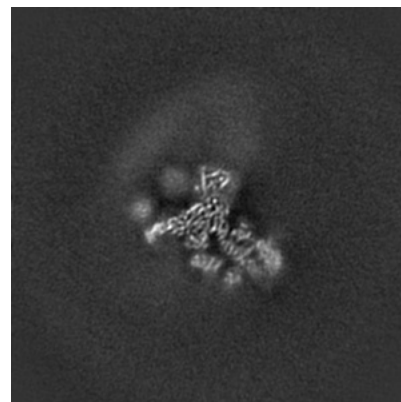
### 6.3.2 Raw map



X Index: 122



Y Index: 124

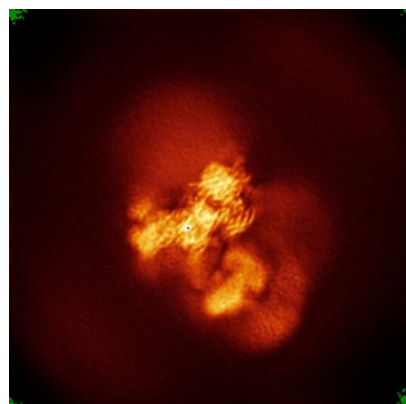


Z Index: 109

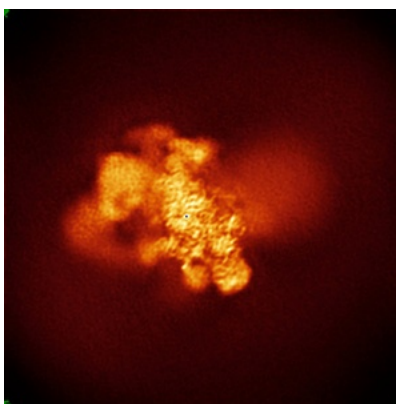
The images above show the largest variance slices of the map in three orthogonal directions.

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

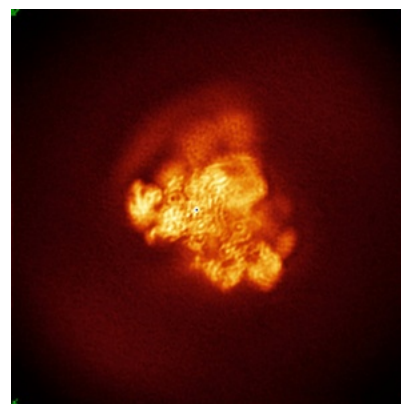
### 6.4.1 Primary map



X

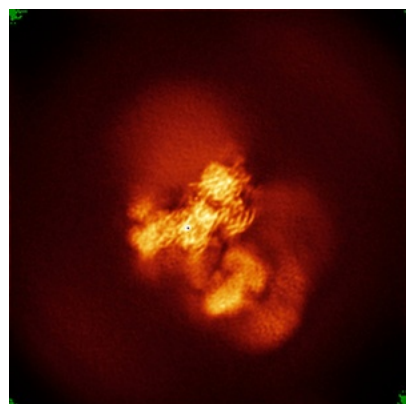


Y

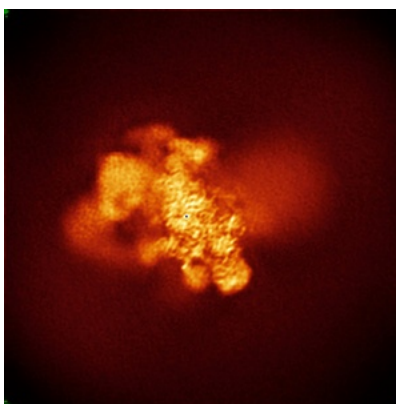


Z

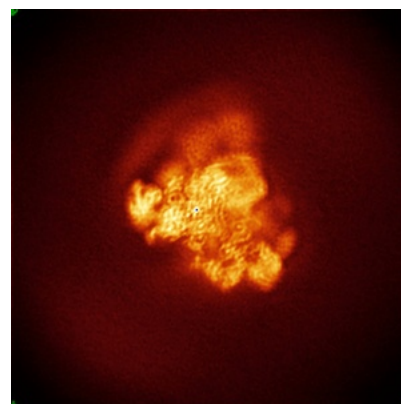
### 6.4.2 Raw map



X



Y



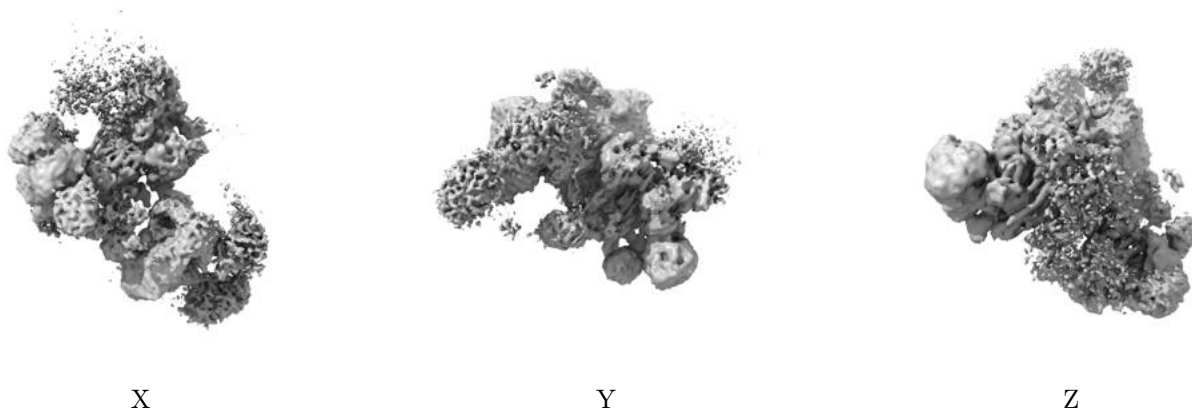
Z

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.



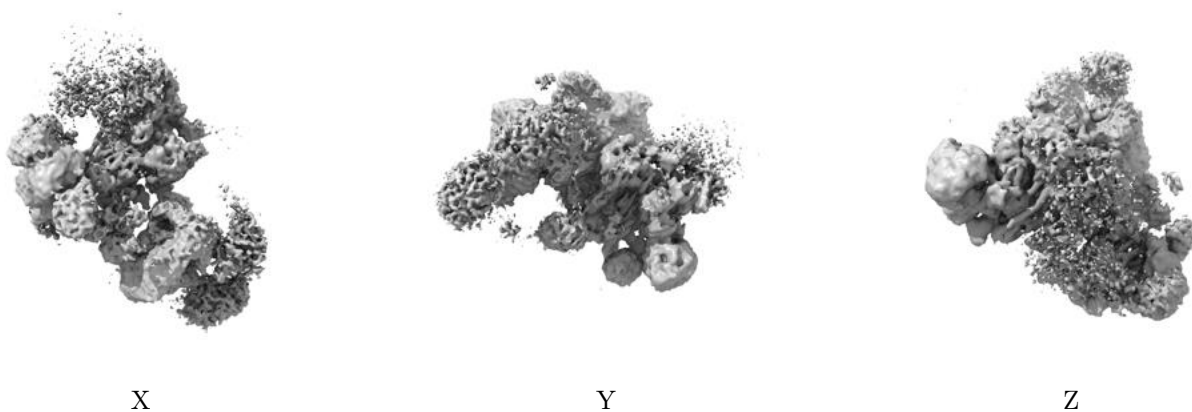
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0021. 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.

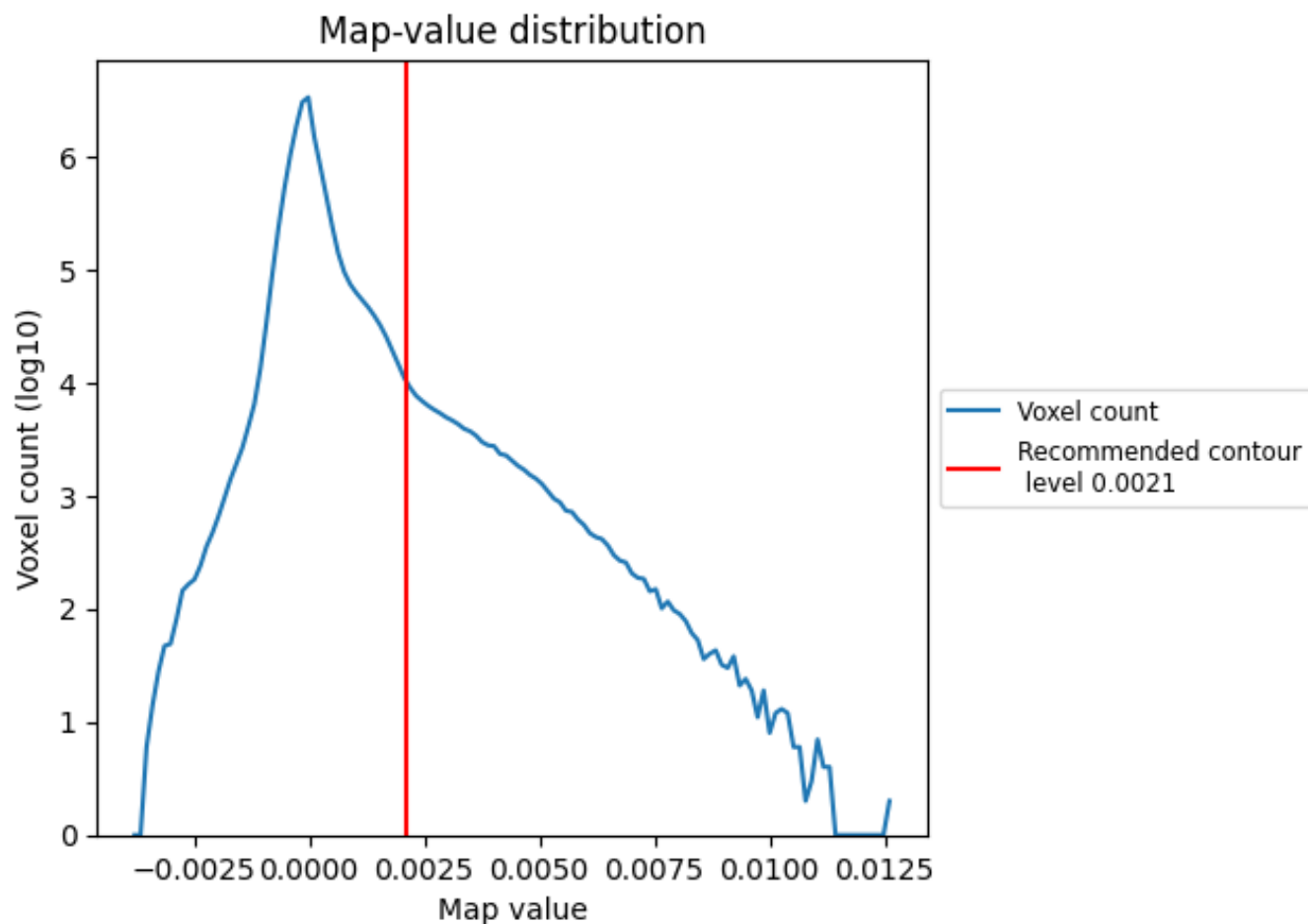
## 6.6 Mask visualisation [i](#)

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.

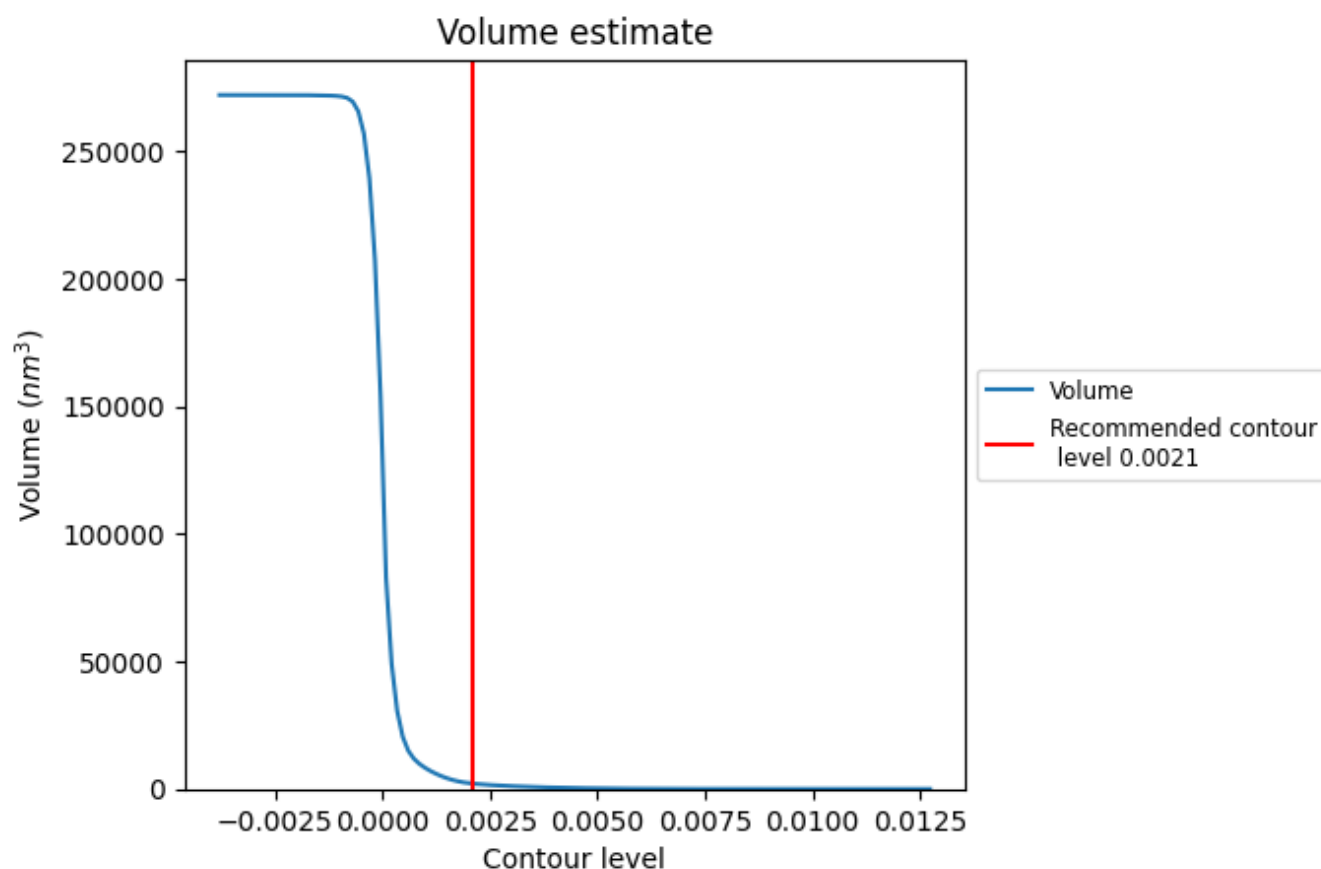
### 7.1 Map-value distribution [i](#)



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.



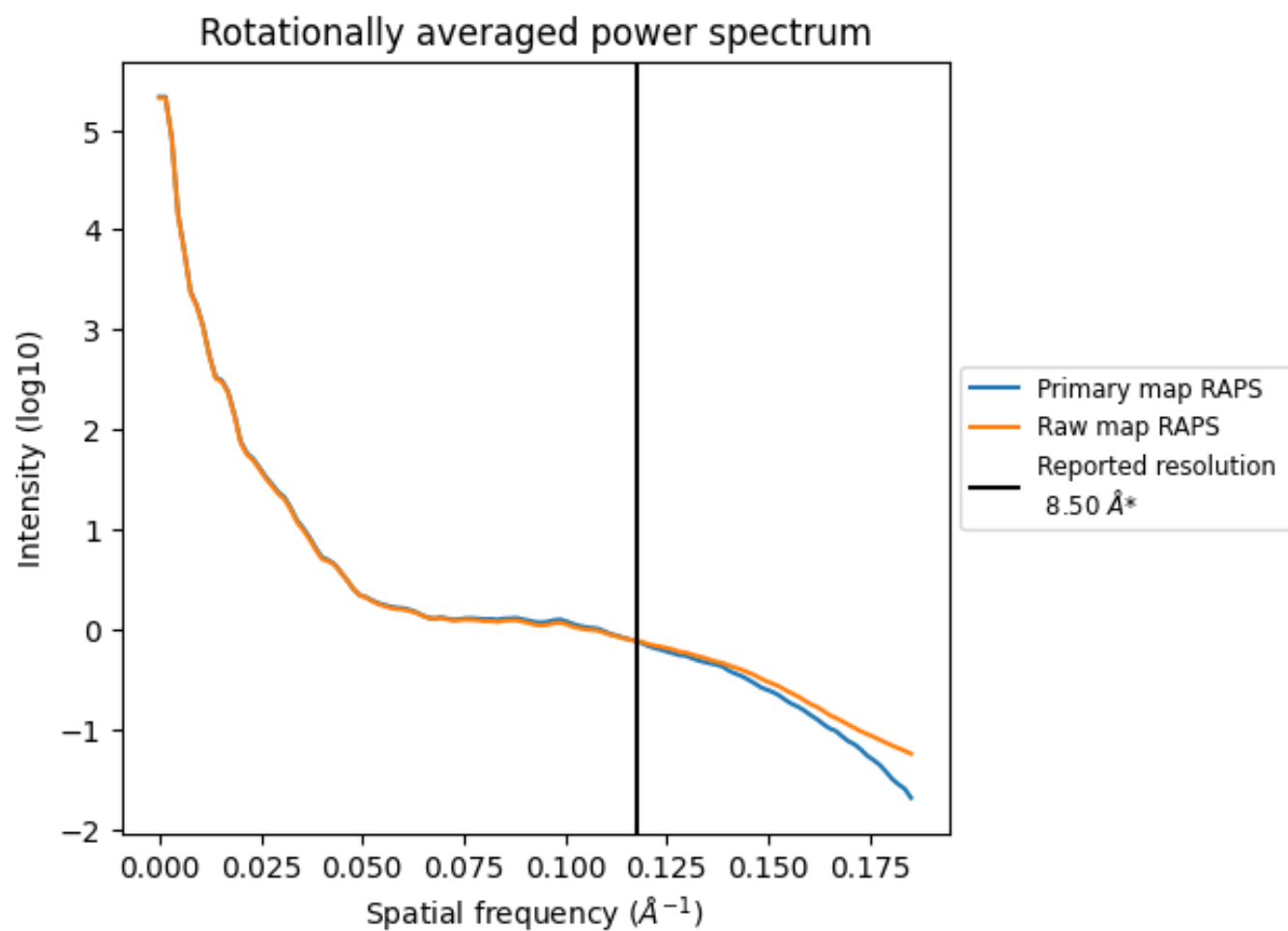
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2103  $\text{nm}^3$ ; this corresponds to an approximate mass of 1900 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 ⓘ

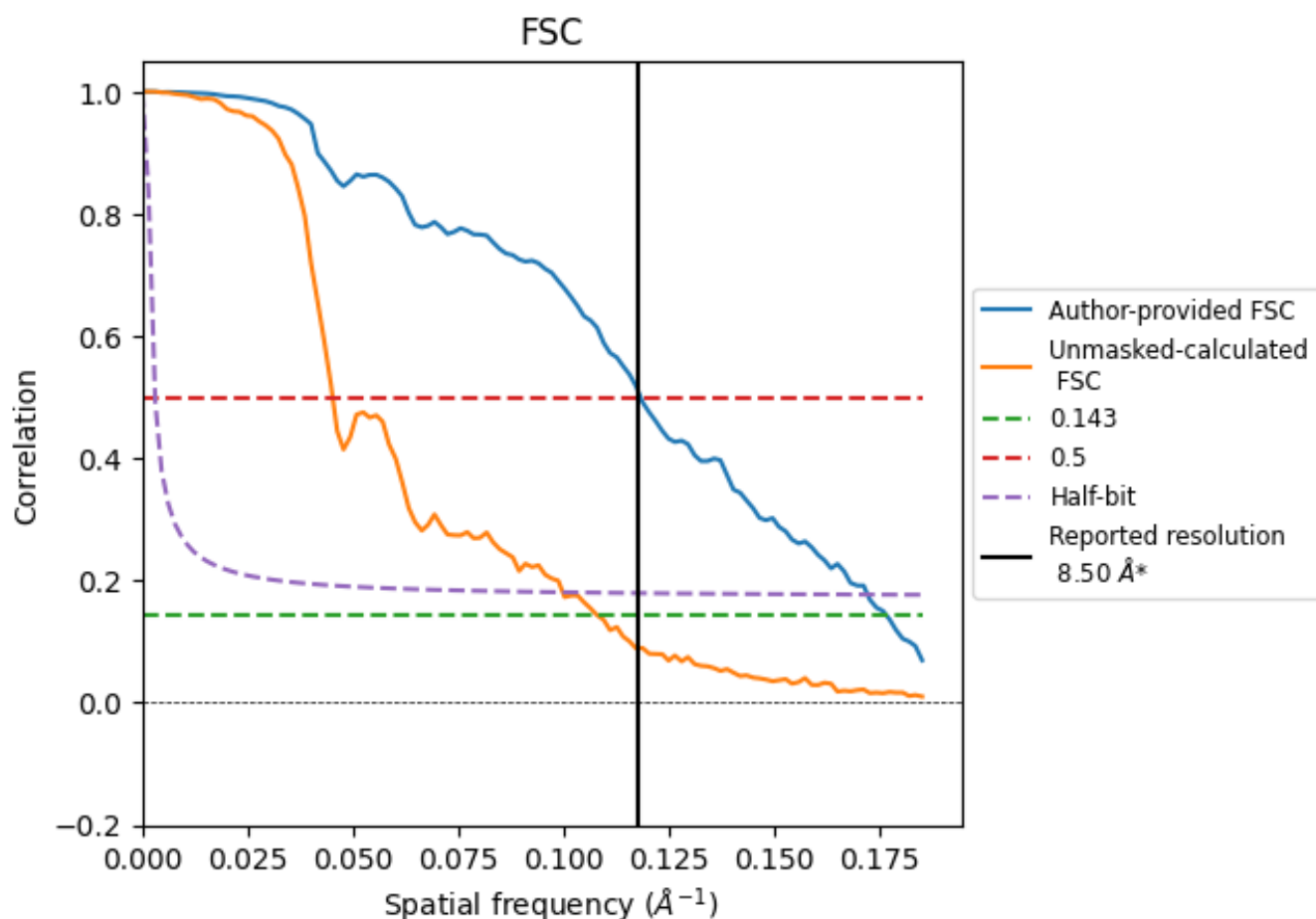


\*Reported resolution corresponds to spatial frequency of 0.118  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.118 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

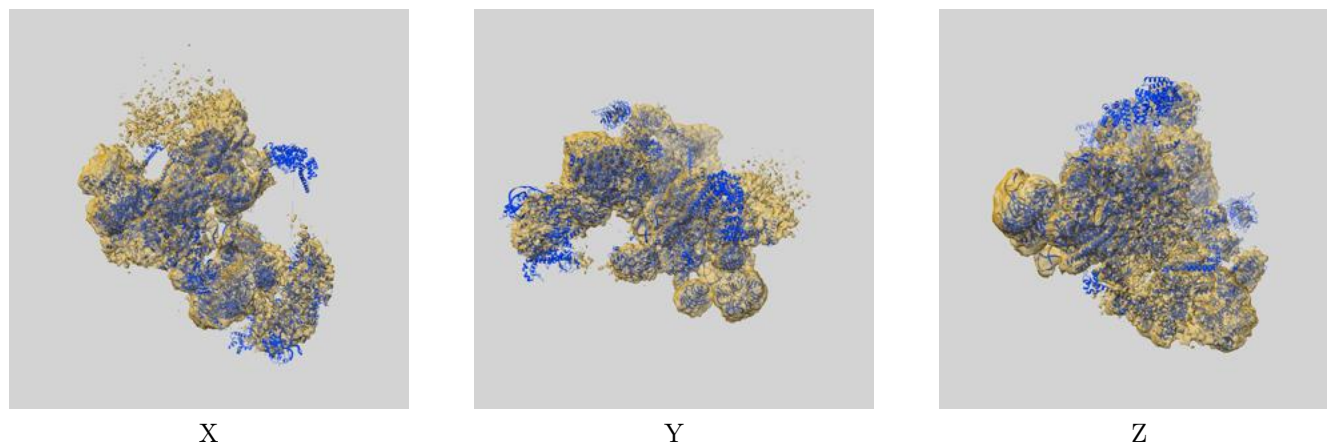
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.50	-	-
Author-provided FSC curve	5.66	8.45	5.80
Unmasked-calculated*	9.25	22.12	10.01

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 5.66 differs from the reported value 8.5 by more than 10 %

## 9 Map-model fit [i](#)

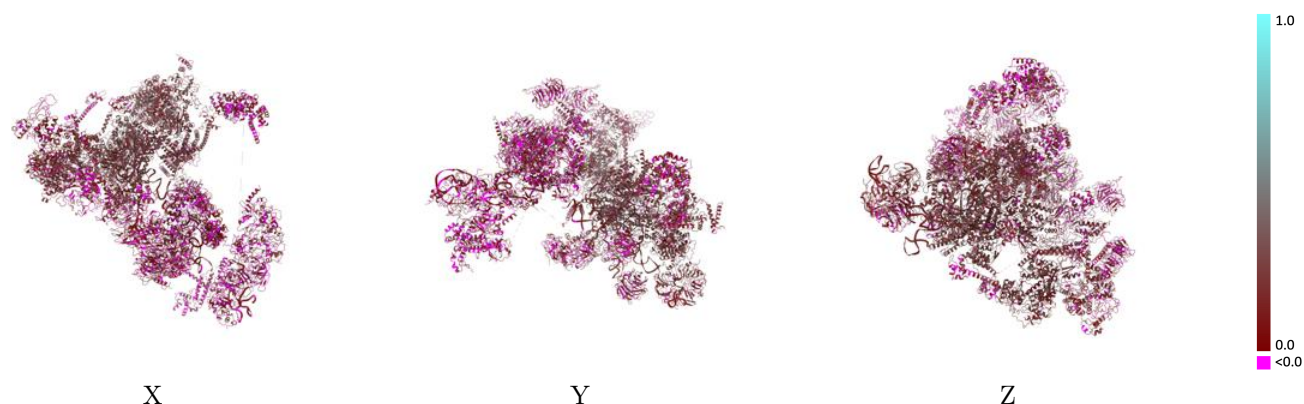
This section contains information regarding the fit between EMDB map EMD-53843 and PDB model 9R8V. Per-residue inclusion information can be found in section [3](#) on page [15](#).

### 9.1 Map-model overlay [i](#)



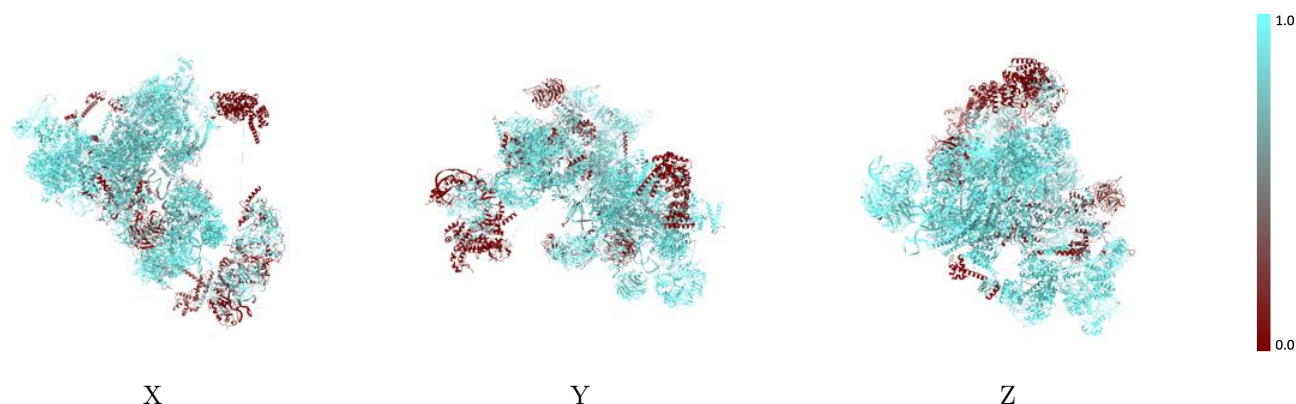
The images above show the 3D surface view of the map at the recommended contour level 0.0021 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



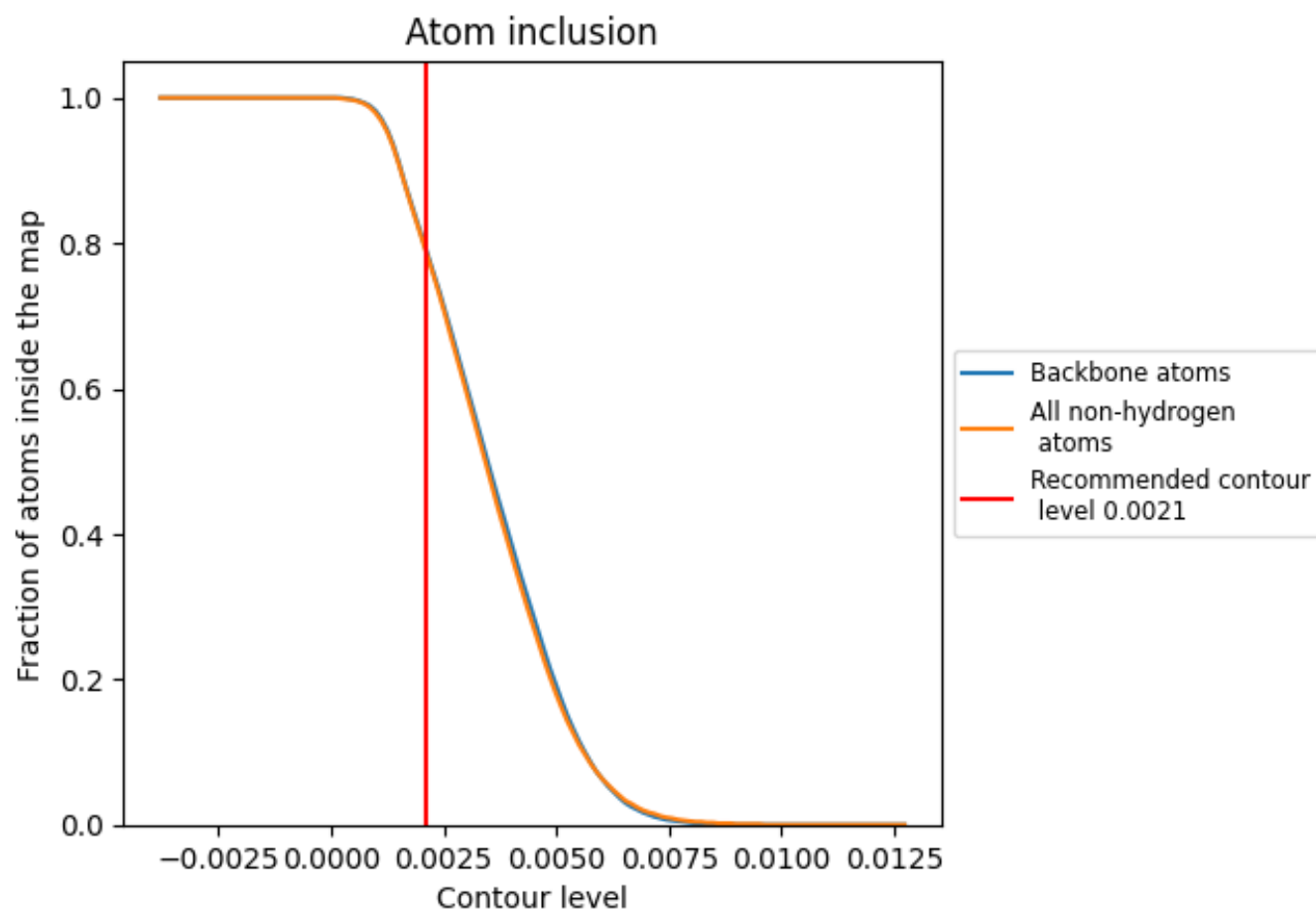
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0021).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 79% 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 (0.0021) and Q-score for the entire model and for each chain.



























































Chain	Atom inclusion	Q-score
All	 0.7900	 0.1660
2	 0.6580	 0.0900
21	 0.7510	 0.1140
22	 0.4440	 0.0980
23	 0.7950	 0.1140
2A	 0.4410	 0.1120
2B	 0.1350	 0.0920
2b	 0.9640	 0.1150
2e	 0.4690	 0.0860
2f	 0.2280	 0.0770
2g	 0.4920	 0.0800
5	 0.9880	 0.1950
51	 0.9750	 0.1710
52	 1.0000	 0.1580
53	 1.0000	 0.2760
5A	 0.9800	 0.1380
5b	 1.0000	 0.2460
5e	 0.9920	 0.1890
5f	 1.0000	 0.1790
5g	 1.0000	 0.1940
6	 0.9270	 0.1890
62	 0.8440	 0.1440
63	 0.7300	 0.0770
64	 0.8720	 0.1750
65	 0.5870	 0.1380
66	 0.7680	 0.1740
67	 0.7350	 0.0810
68	 0.9300	 0.1540
7	 0.0400	 0.0810
8	 0.3040	 0.1210
9	 0.2860	 0.0720
A	 0.9110	 0.2480
A6	 0.4750	 0.1020
B	 0.9920	 0.1980
B1	 0.9540	 0.1130



*Continued on next page...*



*Continued from previous page...*

Chain	Atom inclusion	Q-score
B2	 0.9780	 0.1190
B3	 0.9400	 0.1280
B4	 1.0000	 0.1110
B5	 0.9940	 0.1530
B6	 0.9450	 0.1150
BL	 0.0190	 0.1000
C	 0.9810	 0.2460
DH	 0.5930	 0.1280
E	 0.9980	 0.1060
G	 0.1980	 0.0820
I	 0.9800	 0.2630
K	 0.7620	 0.2300
L	 0.9670	 0.2510
P	 0.9920	 0.1970
P7	 0.7930	 0.2020
Q	 0.9920	 0.2280
R	 0.5330	 0.2310
S1	 0.9090	 0.2600
SR	 0.5560	 0.1530
T	 0.7170	 0.1920
X	 0.8410	 0.2220
Z	 0.9890	 0.1860
q	 0.9610	 0.2520
r	 0.9680	 0.2500
t	 0.9480	 0.2100
v	 0.1870	 0.0880
w	 0.7820	 0.1180
x	 0.4870	 0.0860
y	 0.4380	 0.1450