



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 02:16 PM UTC

PDB ID : 7A5P / pdb_00007a5p
EMDB ID : EMD-11570
Title : Human C Complex Spliceosome - Medium-resolution PERIPHERY
Authors : Bertram, K.; Kastner, B.
Deposited on : 2020-08-21
Resolution : 5.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

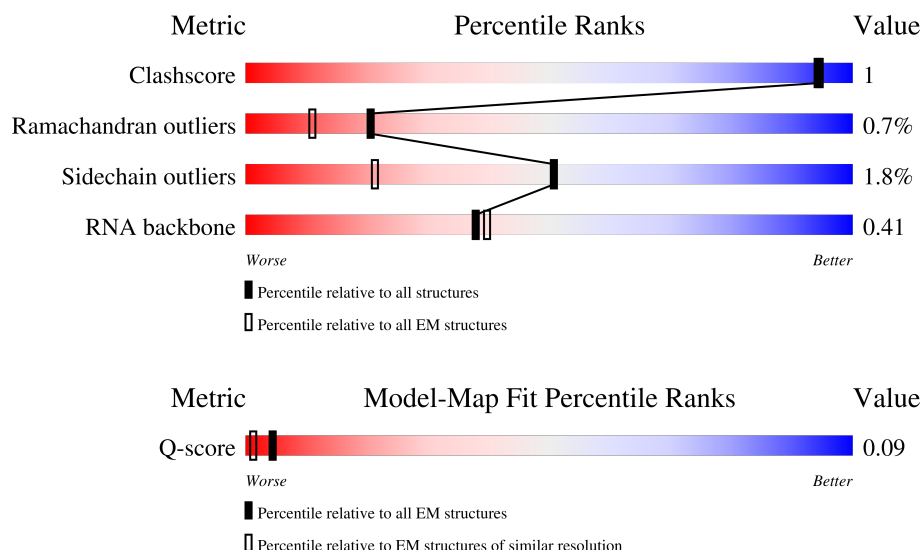
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 5.00 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	10198 (3.30 - 4.30)

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	2	975	
2	5	116	
3	6	106	

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Mol	Chain	Length	Quality of chain
4	8	204	
5	A	2335	
6	C	536	
7	E	579	
8	G	504	
8	H	504	
8	I	504	
8	J	504	
9	K	225	
10	L	802	
11	M	855	
12	N	243	
13	O	848	
14	P	420	
15	S	2752	
16	T	908	
17	U	1485	
18	W	255	
19	X	225	
20	Y	324	
21	a	126	
21	l	126	
22	b	240	
22	m	240	
23	c	119	

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Mol	Chain	Length	Quality of chain
23	n	119	
24	d	118	
24	h	118	
25	e	92	
25	j	92	
26	f	86	
26	i	86	
27	g	76	
27	k	76	
28	o	301	
29	p	654	
30	q	2136	
31	r	1227	
32	s	285	
33	u	323	
34	v	146	
35	w	174	
36	x	258	
37	y	411	
38	z	646	

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 52703 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 RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	155	Total	C	N	O	P	0	0
			2854	1258	396	1045	155		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	40	Total	C	N	O	P	0	0
			718	316	93	269	40		

- Molecule 3 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	16	Total	C	N	O	P	0	0
			296	130	42	108	16		

- Molecule 4 is a protein called UNKNOWN.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	8	76	Total	C	N	O	0	0
			376	224	76	76		

- Molecule 5 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	A	491	Total	C	N	O	0	0
			2485	1496	497	492		

- Molecule 6 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	C	15	Total	C	N	O	0	0
			75	45	15	15		

- Molecule 7 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	E	305	Total	C	N	O	0	0
			1525	915	305	305		

- Molecule 8 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	G	132	Total	C	N	O	0	0
			679	415	132	132		
8	H	135	Total	C	N	O	0	0
			696	426	135	135		
8	I	133	Total	C	N	O	0	0
			684	418	133	133		
8	J	110	Total	C	N	O	0	0
			561	341	110	110		

- Molecule 9 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	K	138	Total	C	N	O	0	0
			689	413	138	138		

- Molecule 10 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	L	115	Total	C	N	O	0	0
			573	343	115	115		

- Molecule 11 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	M	672	Total	C	N	O	0	0
			3387	2043	672	672		

- Molecule 12 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	N	73	Total	C	N	O	0	0
			369	223	73	73		

- Molecule 13 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	O	261	Total	C	N	O	0	0
			1320	798	261	261		

- Molecule 14 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	P	90	Total	C	N	O	0	0
			452	271	90	91		

- Molecule 15 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	S	46	Total	C	N	O	0	0
			229	137	46	46		

- Molecule 16 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	T	253	Total	C	N	O	0	0
			1271	765	253	253		

- Molecule 17 is a protein called Intron-binding protein aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	U	1293	Total	C	N	O	0	0
			6546	3960	1293	1293		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	W	174	Total	C	N	O	0	0
			874	526	174	174		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	89	ASP	CYS	conflict	UNP P09661
W	119	CYS	SER	conflict	UNP P09661

- Molecule 19 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	X	93	Total	C	N	O	0	0
			466	280	93	93		

- Molecule 20 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	Y	29	Total	C	O	P	0	0
			348	145	174	29		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
21	a	72	Total	C	N	O	0	0
			358	214	72	72		
21	l	83	Total	C	N	O	0	0
			415	249	83	83		

- Molecule 22 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	b	66	Total	C	N	O	0	0
			327	195	66	66		
22	m	70	Total	C	N	O	0	0
			351	211	70	70		

- Molecule 23 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	c	81	Total	C	N	O	0	0
			407	245	81	81		
23	n	82	Total	C	N	O	0	0
			412	248	82	82		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	d	81	Total	C	N	O	0	0
			406	244	81	81		
24	h	84	Total	C	N	O	0	0
			421	253	84	84		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	e	79	Total	C	N	O	0	0
			393	235	79	79		
25	j	78	Total	C	N	O	0	0
			388	232	78	78		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	f	74	Total	C	N	O	0	0
			369	221	74	74		
26	i	71	Total	C	N	O	0	0
			352	210	71	71		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	g	74	Total	C	N	O	0	0
			369	221	74	74		
27	k	73	Total	C	N	O	0	0
			364	218	73	73		

- Molecule 28 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	o	77	Total	C	N	O	0	0
			384	230	77	77		

- Molecule 29 is a protein called WD repeat-containing protein 70.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	p	68	Total	C	N	O	0	0
			333	197	68	68		

- Molecule 30 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	q	1896	Total	C	N	O	0	0
			9558	5766	1896	1896		

- Molecule 31 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	r	593	Total	C	N	O	0	0
			2982	1796	593	593		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	855	ASN	GLY	conflict	UNP Q92620

- Molecule 32 is a protein called Pre-mRNA-splicing factor ISY1 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	s	76	Total	C	N	O	0	0
			376	224	76	76		

- Molecule 33 is a protein called Splicing factor YJU2.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	u	43	Total	C	N	O	0	0
			216	129	43	44		

- Molecule 34 is a protein called Protein mago nashi homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	v	144	Total	C	N	O	0	0
			723	435	144	144		

- Molecule 35 is a protein called RNA-binding protein 8A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	w	91	Total	C	N	O	0	0
			453	271	91	91		

- Molecule 36 is a protein called Protein FRG1.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	x	125	Total	C	N	O	0	0
			621	371	125	125		

- Molecule 37 is a protein called Eukaryotic initiation factor 4A-III.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	y	390	Total 1951	C 1171	N 390	O 390	0	0

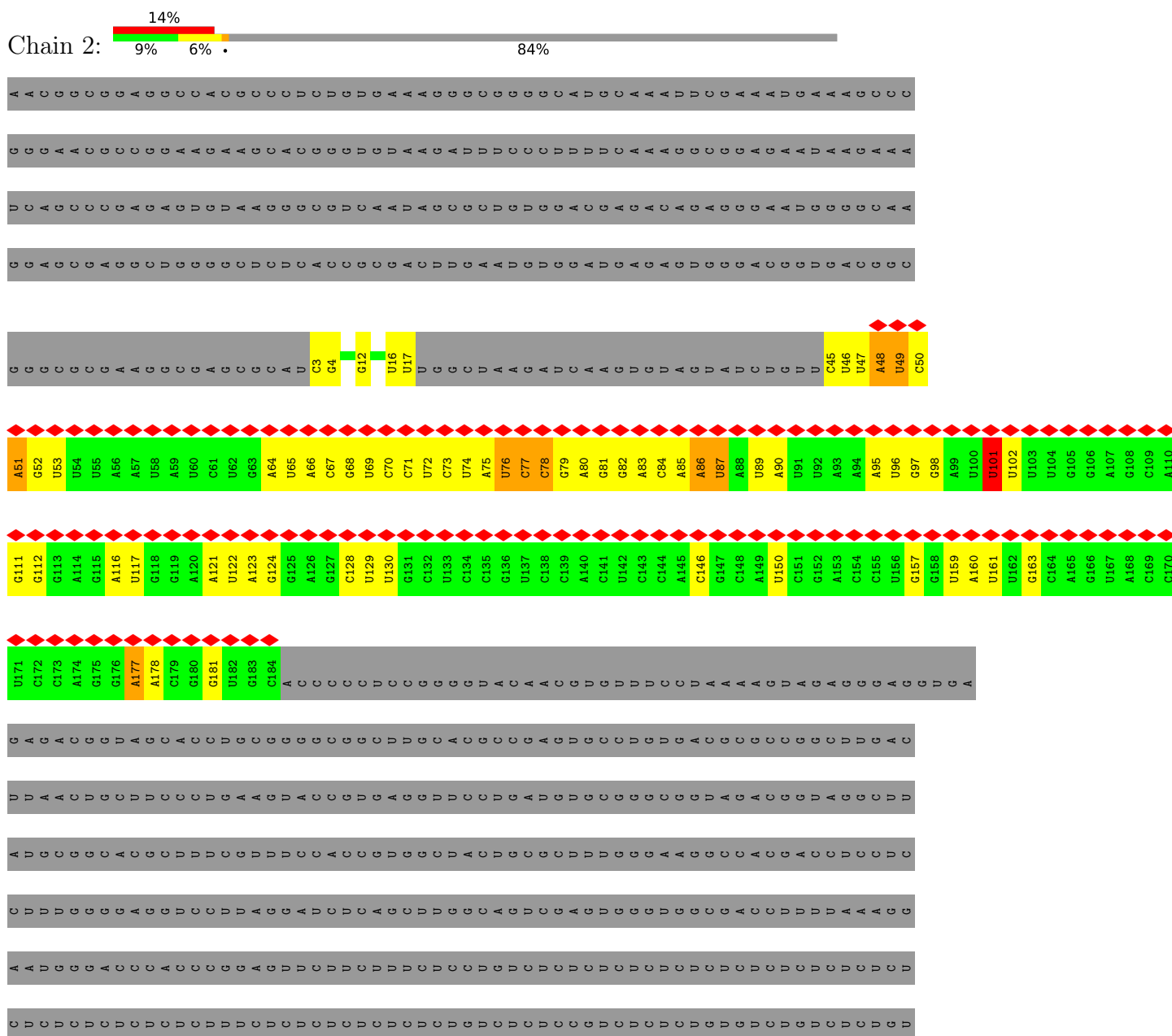
- Molecule 38 is a protein called Peptidylprolyl isomerase domain and WD repeat-containing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	z	460	Total 2301	C 1381	N 460	O 460	0	0

3 Residue-property plots [i](#)

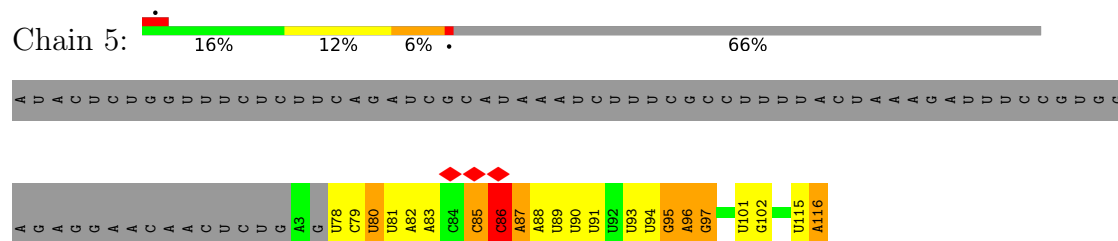
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: U2 snRNA

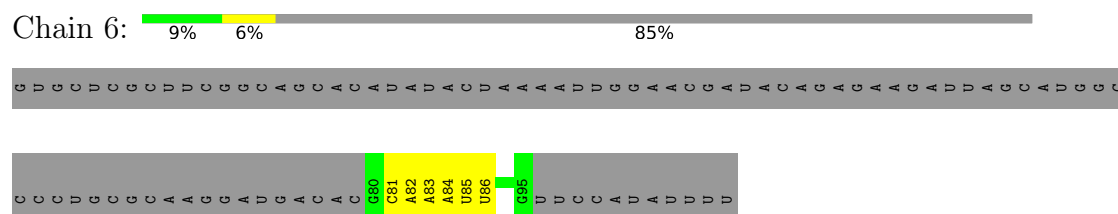




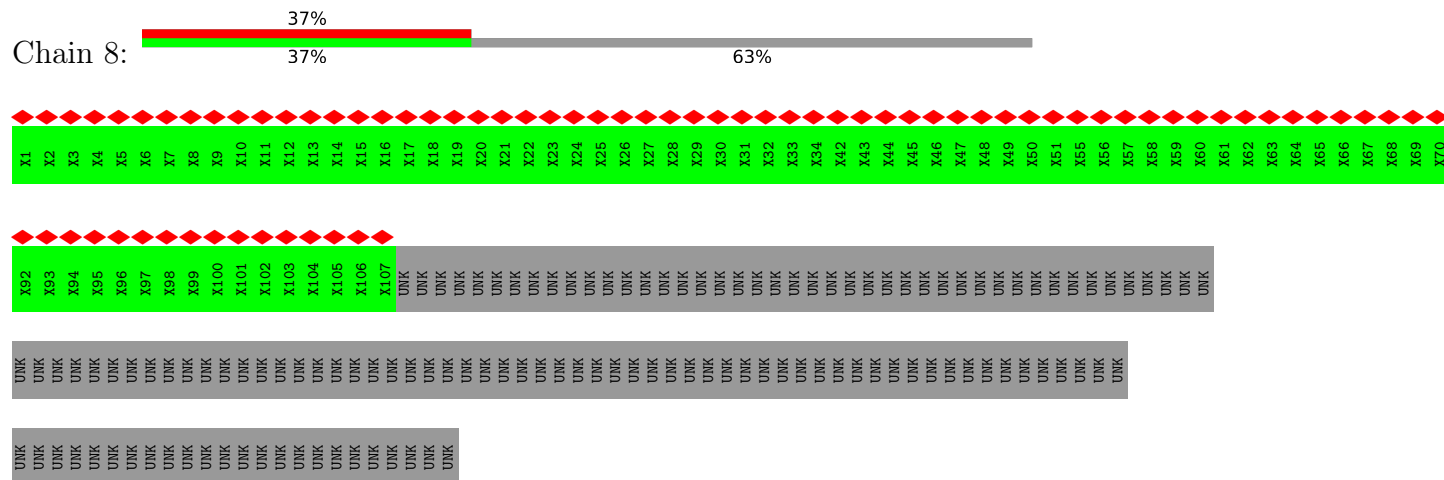
- Molecule 2: U5 snRNA



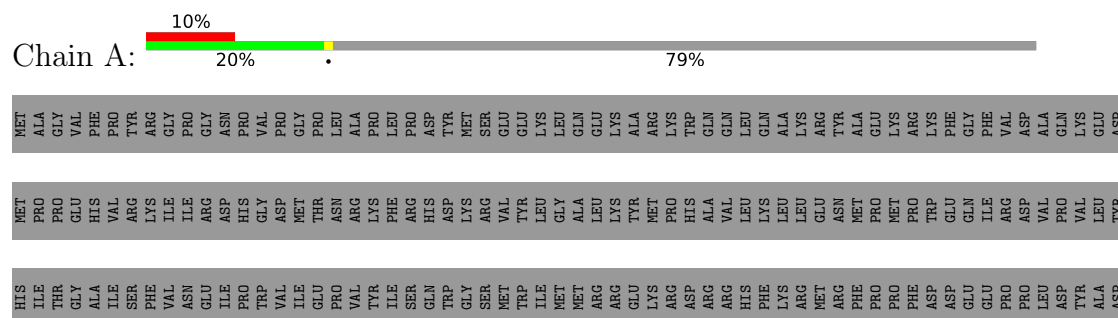
- Molecule 3: U6 snRNA



- Molecule 4: UNKNOWN

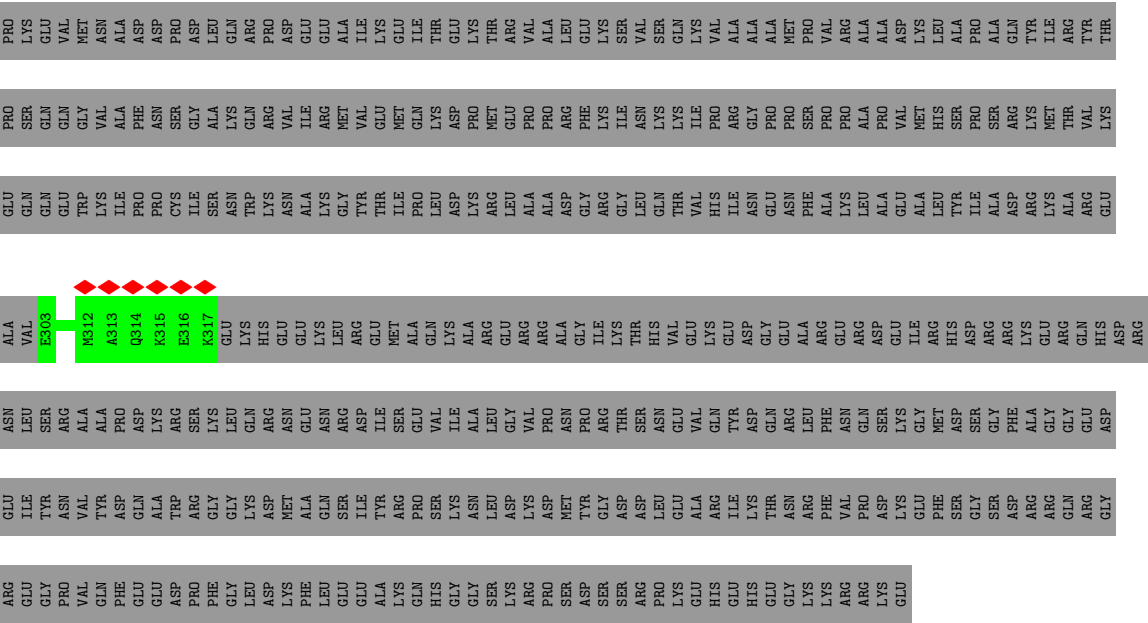


- Molecule 5: Pre-mRNA-processing-splicing factor 8

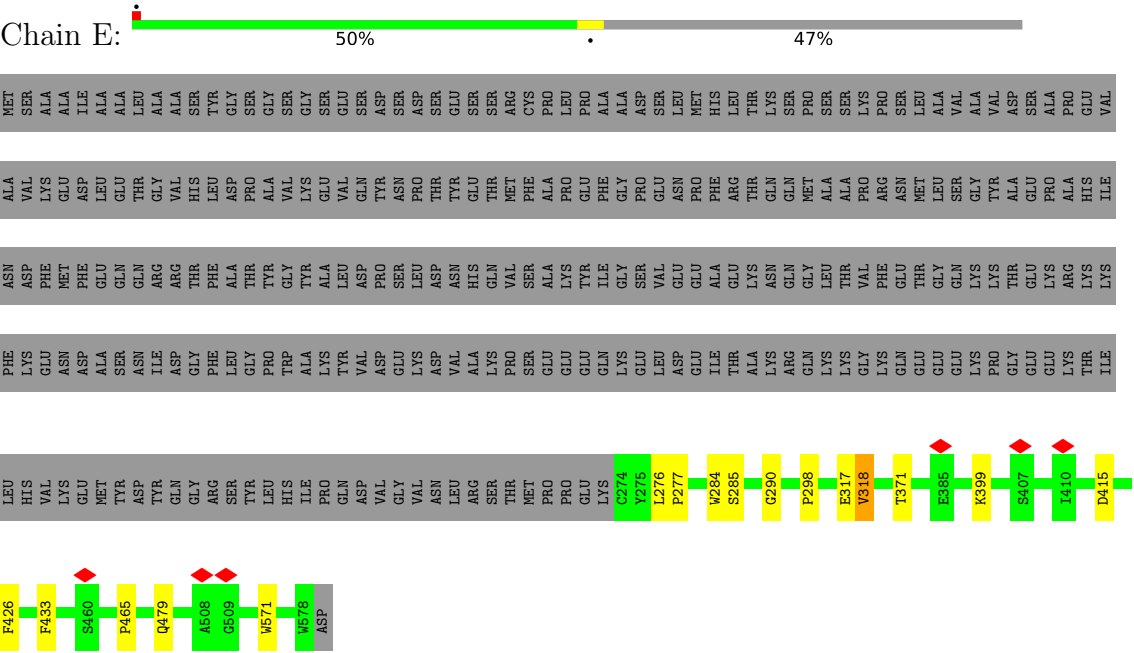






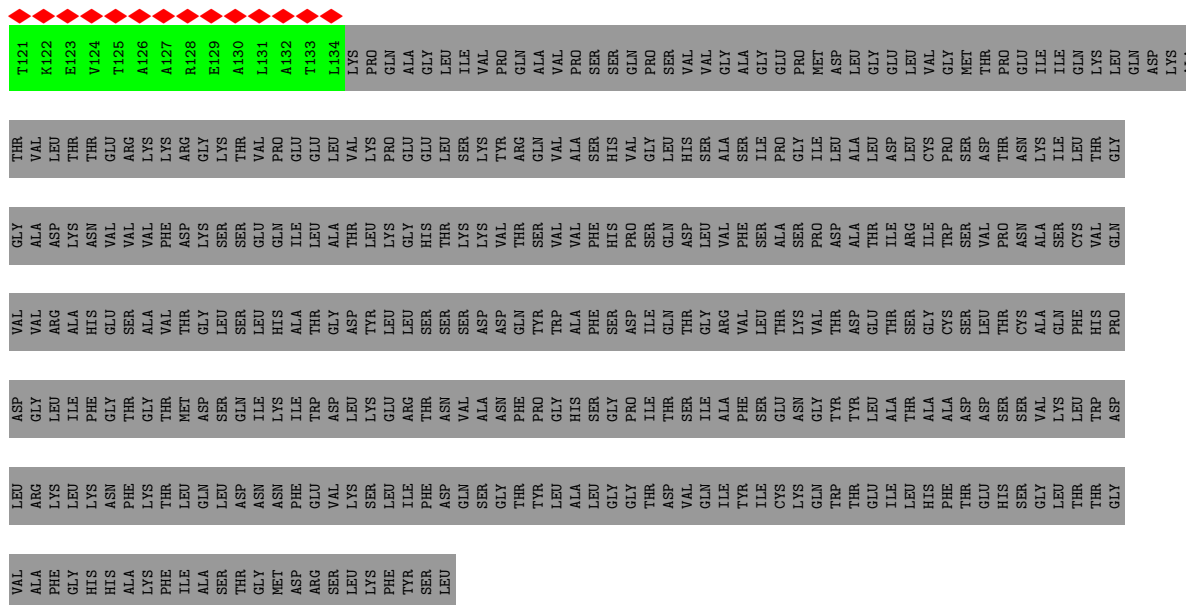


• Molecule 7: Pre-mRNA-processing factor 17

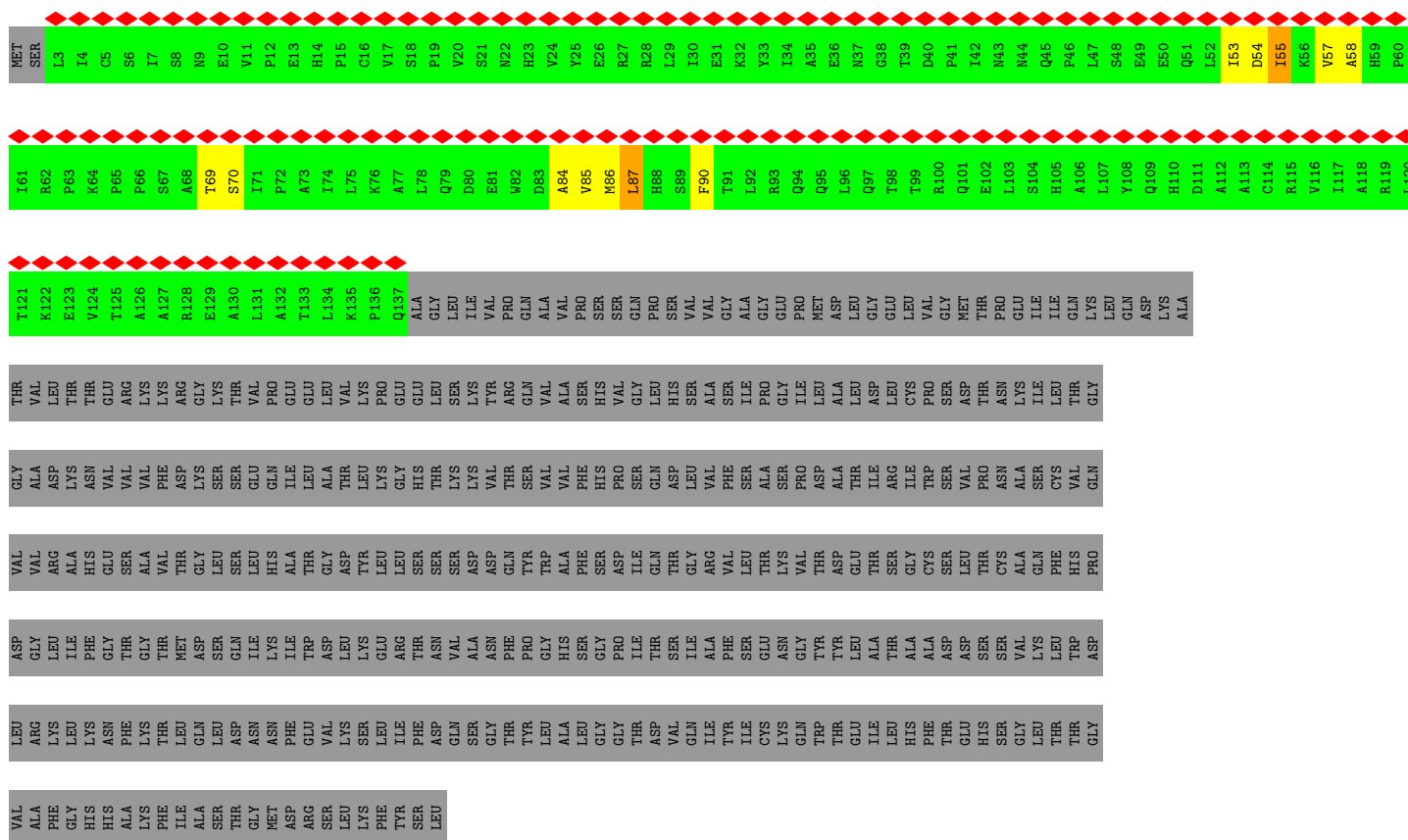


• Molecule 8: Pre-mRNA-processing factor 19





- Molecule 8: Pre-mRNA-processing factor 19



- Molecule 8: Pre-mRNA-processing factor 19



MET	SER	L3	I4	C5	S6	I7	S8	N9	E10	V11	P12	E13	H14	P15	C16	V17	S18	P19	V20	S21	N22	H23	V24	Y25	E26	R27	L28	R29	L30	E31	K32	Y33	I34	A35	E36	N37	G38	T39	D40	P41	I42	N43	N44	Q45	P46	L47	S48	E49	E50	Q51	L52	D54	I55	K56	V57	A58	H59	P60																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
I61	R62	P63	K64	P65	P66	S67	A68	T69	S70	I71	P72	A73	I74	L75	K76	A77	L78	Q79	D80	E81	W82	G83	A84	V85	M86	L87	H88	S89	F90	T91	L92	R93	Q94	Q95	L96	Q97	T98	T99	R100	Q101	E102	N103	N104	H105	A106	L107	Y108	Q109	H110	D111	A112	I113	C114	R115	V116	I117	A118	R119	L120																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
T121	K122	E123	V124	T125	A126	A127	R128	E129	A130	L131	A132	T133	L134	K135	PRO	GLN	ALA	GLY	LEU	ILE	VAL	PRO	GLN	ALA	VAL	SER	SER	GLN	VAL	VAL	GLY	ALA	GLU	PRO	MET	ASP	LEU	GLY	LEU	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GL

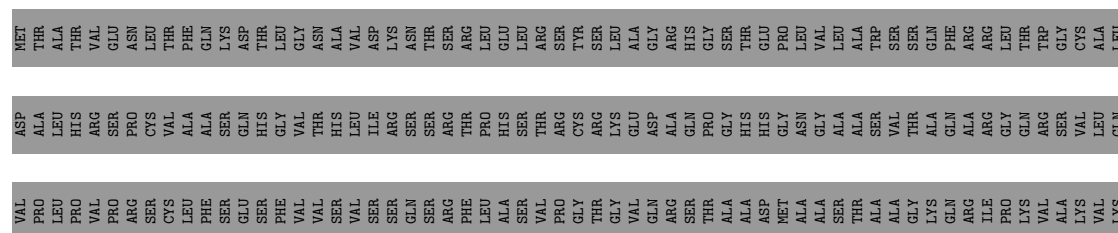
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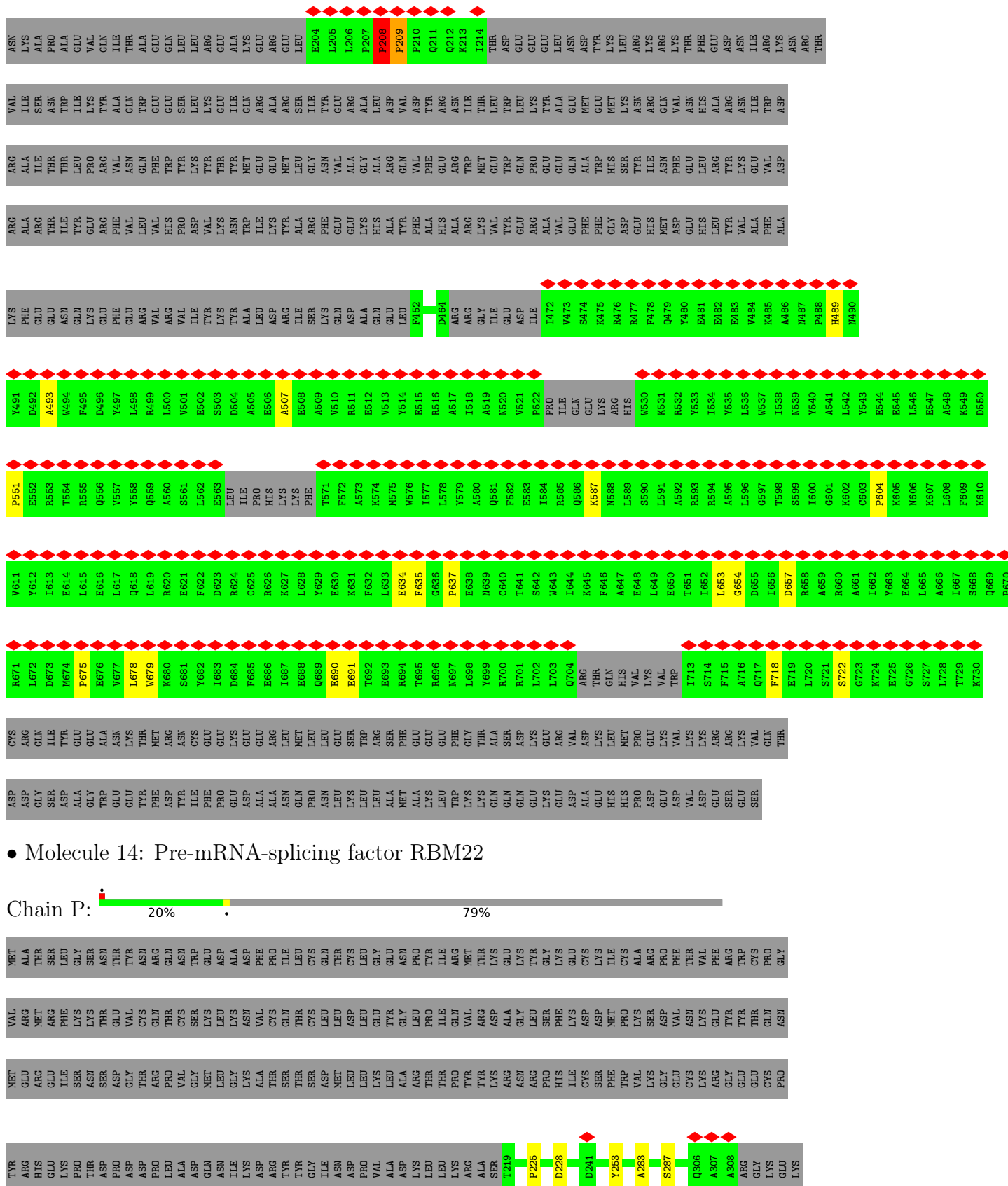


THR	VAL	GLY	ALA	ASP	LYS	VAL	VAL	PHE	ASP	GLY	GLN	ILE	LEU	ALA	THR	LEU	LYS	GLY	HIS	THR	LYS	VAL	THR	SER	PRO	VAL	GLY	ILE	ALA	PHE	VAL	THR	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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● Molecule 11: Pre-mRNA-splicing factor SYF1

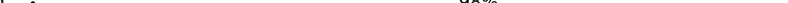
Chain M:





[illegible]

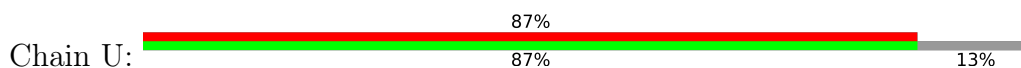
- Molecule 15: Serine/arginine repetitive matrix protein 2

Chain S: 

[illegible]

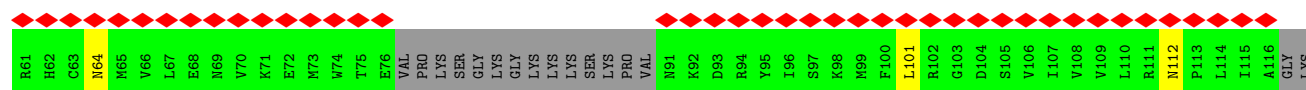


- Molecule 17: Intron-binding protein aquarium

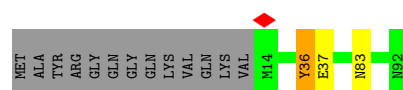
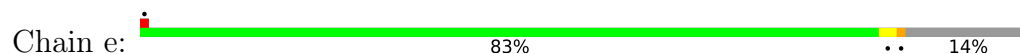
[illegible]

I541	I542	N542	L543	N544	V545	R546	D547	H548	I549	K550	D551	E552	W553	E554	G555	L556	R557	K558	H559	D560	V561	C562	F563	L564	I565	T566	V567	R568	P569	T570	K571	P572	Y573	G574	T575	K576	F577	D578	R579	R580	R581	P582	F583	I584	E585	Q586	V587	G588	L589	V590	Y591	V592	R593	G594	C595	E596	I597	Q598	G599	M600
L601	D602	D603	K604	G605	R606	V607	I608	E609	ASP	GLY	PRO	GLU	P614	R615	P616	N617	L618	R619	G620	E621	S622	R623	T624	F625	R626	V627	F628	L629	D630	P631	N632	Q633	Y634	Q635	Q636	D637	M638	T639	N640	T641	I642	Q643	N644	G645	A646	E647	D648	V649	Y650	E651	T652	F653	N654	I655	I656	M657	R658	K660		
P661	K662	E663	N664	N665	F666	K667	A668	V669	L670	E671	T672	I673	R674	N675	L676	M677	N678	T679	D680	C681	V682	G683	P684	D685	W686	L687	F688	H689	D690	I691	L692	G693	Y694	G695	D696	P697	S698	L699	A700	H701	I702	S703	K704	M705	P706	N707	Q708	I709	A710	T711	L712	F713	F714	N715	D716	T717	F718	L719	S720	
I721	E722	H723	L724	K725	A726	S727	F728	P729	G730	H731	N732	K733	V734	V735	T736	F737	E738	D739	P740	L741	L742	Q743	I744	P745	P746	F747	R748	I749	T750	F751	L692	G693	ARG	SER	GLY	LYS	GLY	LYS	ARG	ASP	ALA	VAL	GLU	ASP	GLU	GLU	ASP	THR	GLU	E773	A774	K775	L776	L777	I778	V779	E780			
F781	H782	F783	I784	N785	F786	R787	G788	P789	F790	F791	V792	N793	Q794	F795	K796	R797	N798	T799	I800	Q801	F802	T803	H804	T805	Q806	I807	E808	A809	I810	R811	A812	G813	M814	Q815	P816	G817	L818	T819	M820	V821	V822	G823	P824	P825	G826	T827	G828	K829	T830	D831	V832	L833	V834	Q835	I836	S838	N839	I840		
Y841	H842	N843	F844	P845	E846	Q847	R848	T849	L850	I851	V852	T853	H854	S855	N856	Q857	A858	L859	N860	Q861	L862	F863	E864	K865	I866	M867	A868	L869	D870	I871	D872	E873	R874	H875	L876	L877	R878	L879	G880	H881	GLY	GLU	GLU	GLU	LEU	GLU	THR	GLU	LYS	ASP	F892	S893	R894	Y895	G896	R897	V898	N899	Y900	
Y901	L902	A903	R904	R905	L906	E907	L908	L909	E910	E911	V912	K913	R914	L915	Q916	K917	S918	L919	G920	V921	P922	G923	D924	A925	S926	Y927	T928	C929	E930	T931	A932	G933	Y934	F935	F936	L937	Y938	Q939	V940	M941	S942	R943	W944	E945	E946	Y947	I948	S949	K950	V951	K952	N953	LYS	GLY	SER	THR	LEU	P959	D960	
V961	T962	E963	V964	F965	T966	F967	F968	P969	F970	H971	E972	Y973	F974	A975	N976	A977	P978	Q979	P980	I981	F982	K983	G984	R985	S986	Y987	E988	E989	D990	M991	E992	I993	A994	E995	G996	C997	F998	R999	H1000	I1001	K1002	K1003	I1004	F1005	T1006	Q1007	L1008	E1009	I1010	F1011	R1012	A1013	I1014	S1015	L1016	L1017	R1018	S1019	G1020	
L1021	D1022	R1023	S1024	K1025	Y1026	L1027	L1028	V1029	K1030	E1031	A1032	K1033	I1034	I1035	A1036	M1037	T1038	C1039	T1040	H1041	A1042	A1043	I1044	K1045	R1046	H1047	D1048	L1049	V1050	K1051	L1052	G1053	F1054	K1055	Y1056	D1057	N1058	I1059	L1060	M1061	E1062	E1063	A1064	A1065	Q1066	I1067	L1068	E1069	T1070	E1071	T1072	F1073	I1074	P1075	L1076	L1077	Q1078	N1080		
P1081	Q1082	D1083	G1084	F1085	S1086	R1087	L1088	K1089	R1090	W1091	I1092	M1093	I1094	G1095	D1096	H1097	H1098	Q1099	L1100	P1101	P1102	V1103	I1104	K1105	F1106	S1107	A1108	F1109	Q1110	K1111	Y1112	S1113	M1114	M1115	E1116	Q1117	S1118	L1119	F1120	T1121	R1122	F1123	V1124	R1125	V1126	G1127	V1128	P1129	T1130	V1131	D1132	L1133	D1134	A1135	Q1136	G1137	R1138	A1139	R1140	
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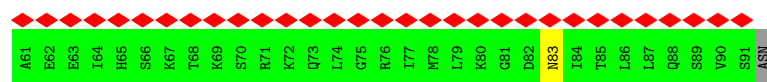
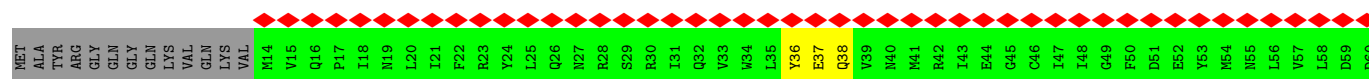
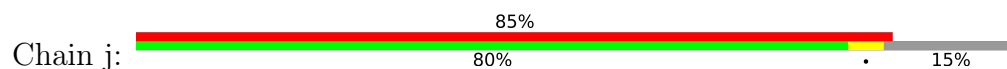
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| MET | LER | LEU | ASN | LYS | PRO | LYS | SER | GLU | MET | THR | PRO | GLU | GLU | LEU | GLN | LYS | R19 | R20 | R21 | R22 | R23 | R24 | R25 | R26 | R27 | R28 | R29 | R30 | R31 | R32 | R33 | R34 | R35 | R36 | R37 | R38 | R39 | R40 | R41 | R42 | R43 | R44 | R45 | R46 | R47 | R48 | R49 | R50 | R51 | R52 | R53 | R54 | R55 | R56 | R57 | R58 | R59 | R60 |
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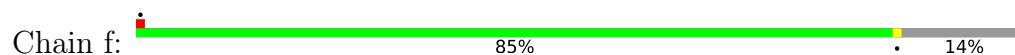
- Molecule 25: Small nuclear ribonucleoprotein E



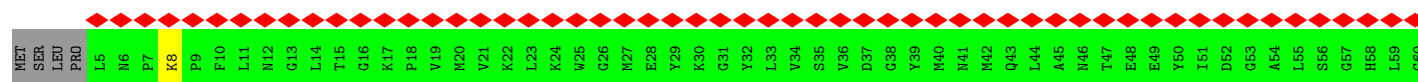
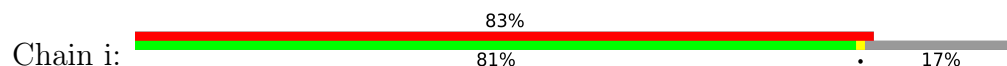
- Molecule 25: Small nuclear ribonucleoprotein E



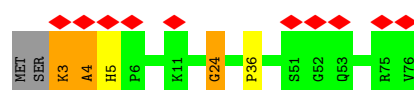
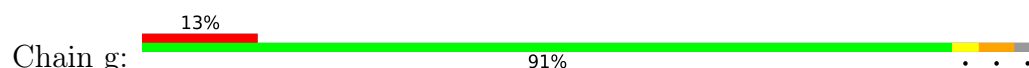
- Molecule 26: Small nuclear ribonucleoprotein F



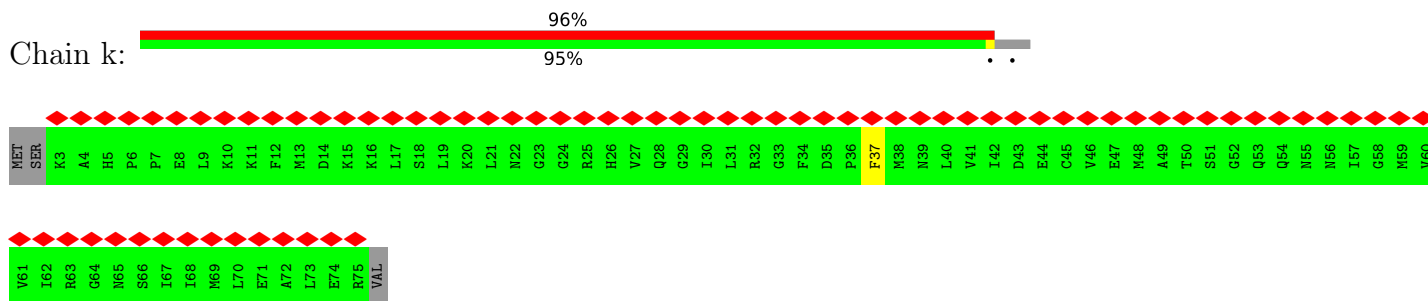
- Molecule 26: Small nuclear ribonucleoprotein F



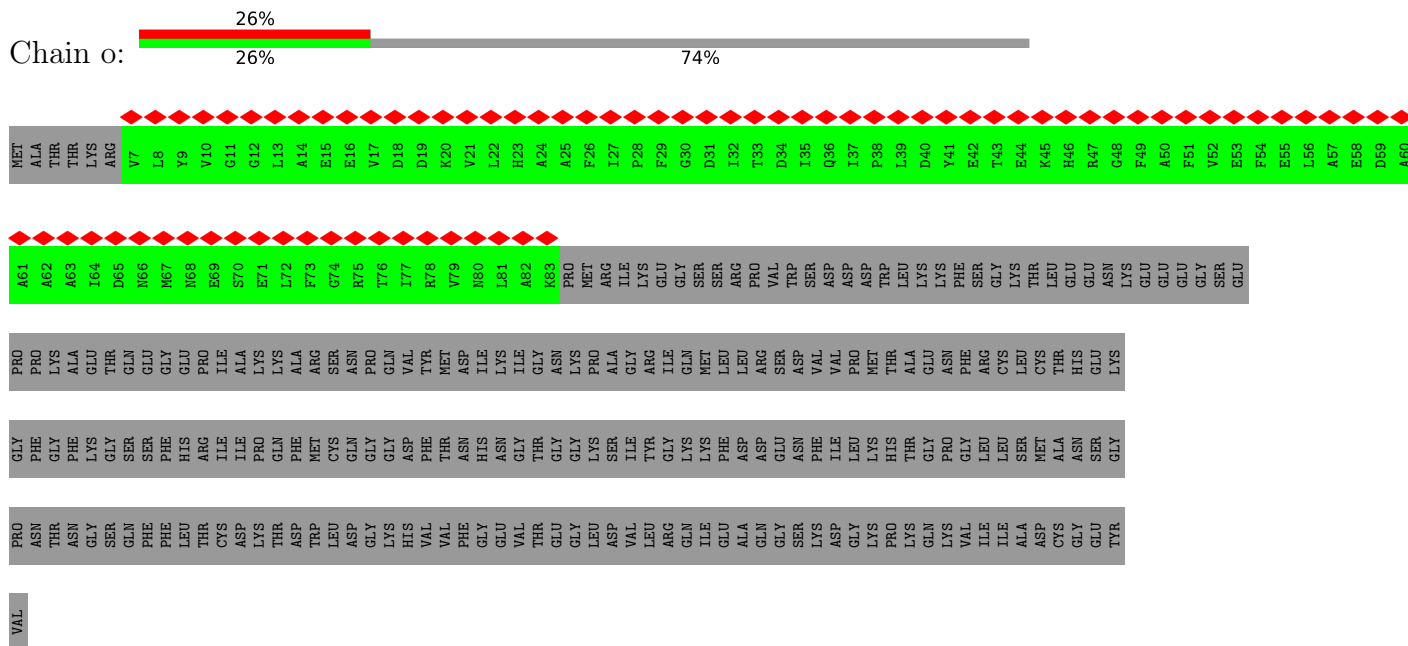
- Molecule 27: Small nuclear ribonucleoprotein G



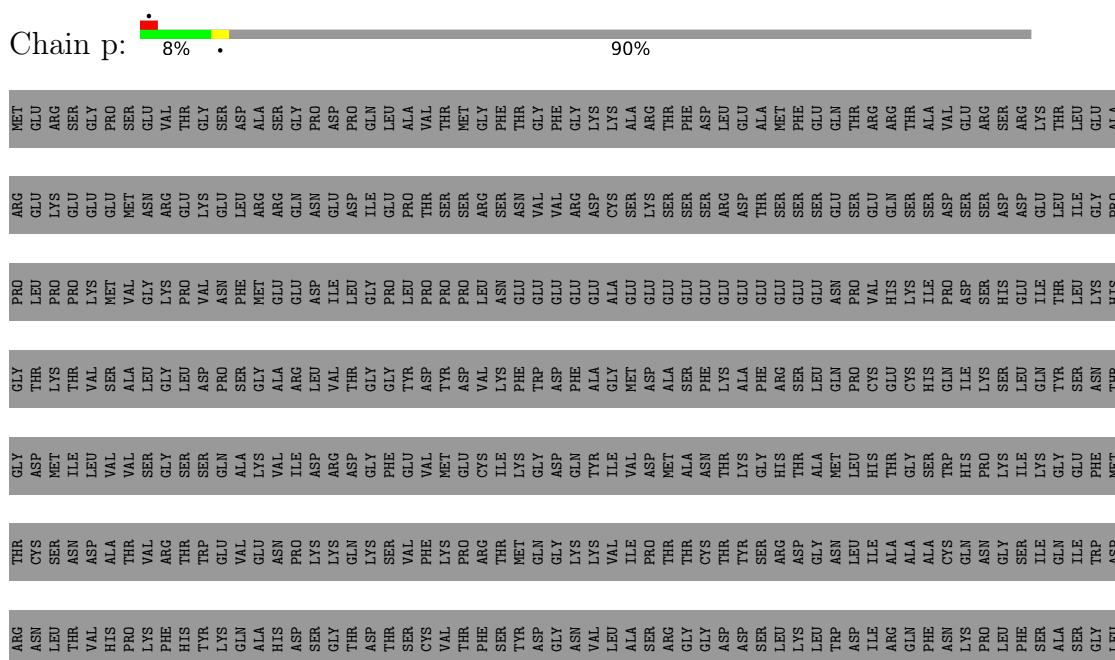
- Molecule 27: Small nuclear ribonucleoprotein G



- Molecule 28: Peptidyl-prolyl cis-trans isomerase E



- Molecule 29: WD repeat-containing protein 70



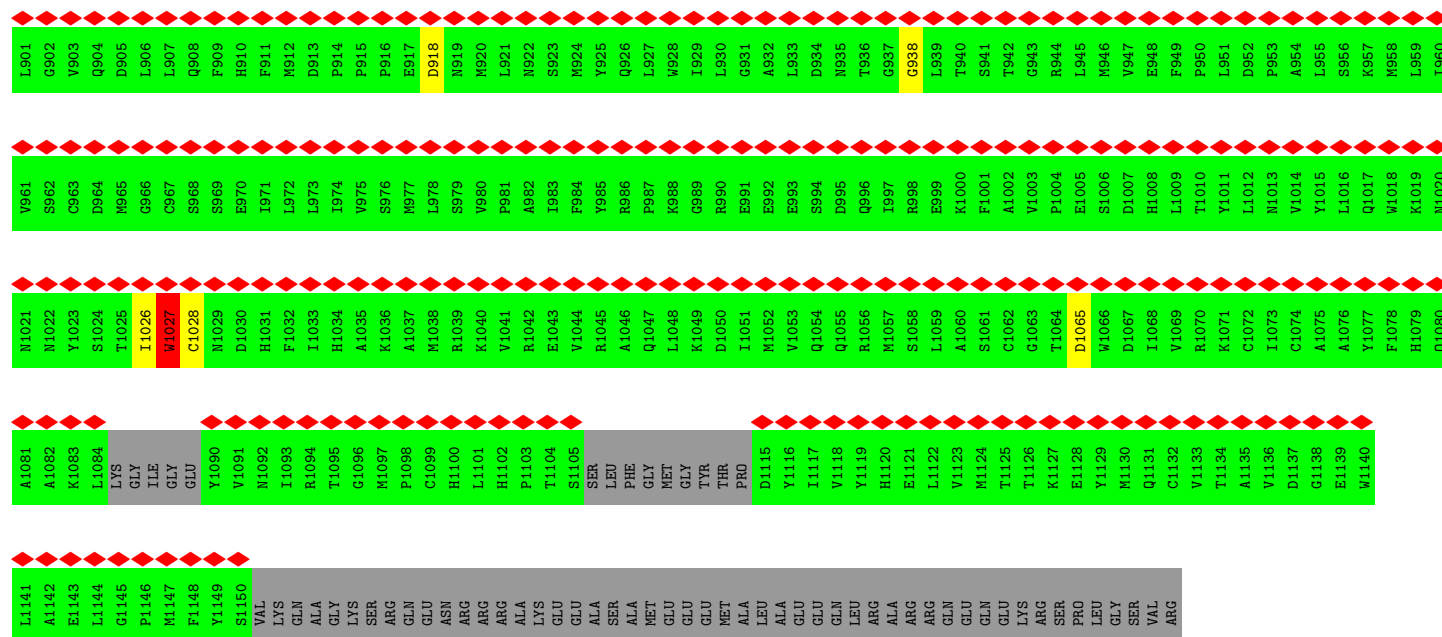
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V2095	V2095	V2035	T1975	I1915	Y1855	D1795	H1735	A1675	N1615	P1555	S1495	L1435
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P2097	P2097	V2037	K1977	S1917	E1857	L1797	M1737	V1677	V1617	K1557	A1497	R1437
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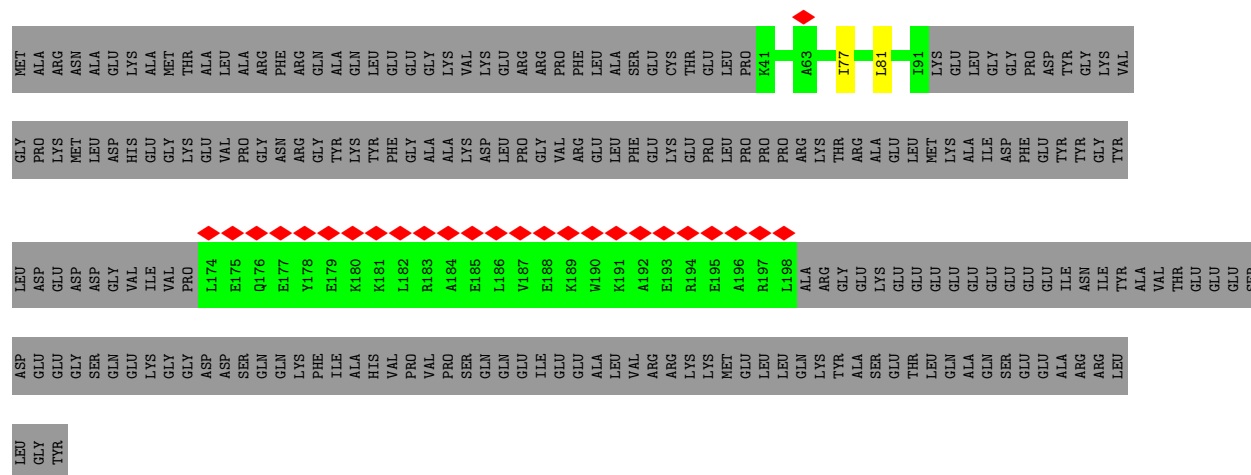
Chain r:

Category	Percentage
Red	48%
Green	47%
Grey	52%

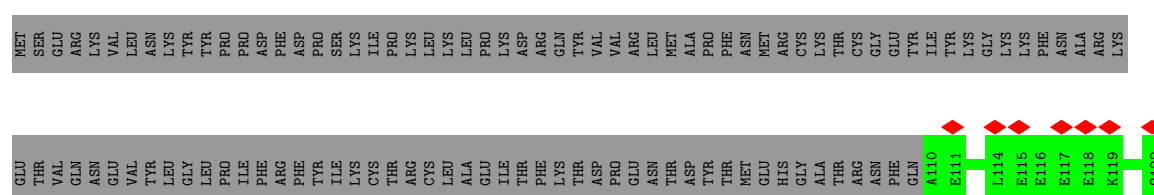


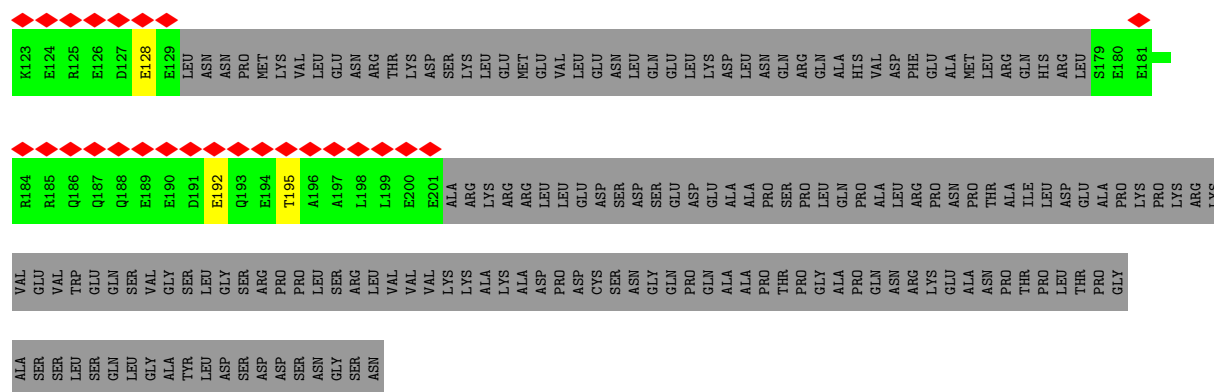


• Molecule 32: Pre-mRNA-splicing factor ISY1 homolog

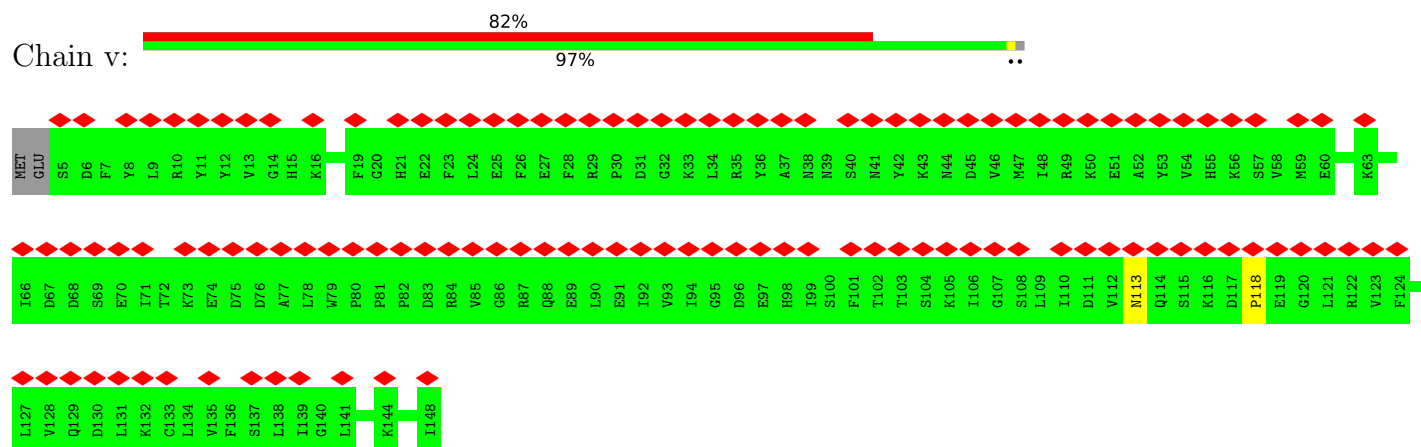


• Molecule 33: Splicing factor YJU2

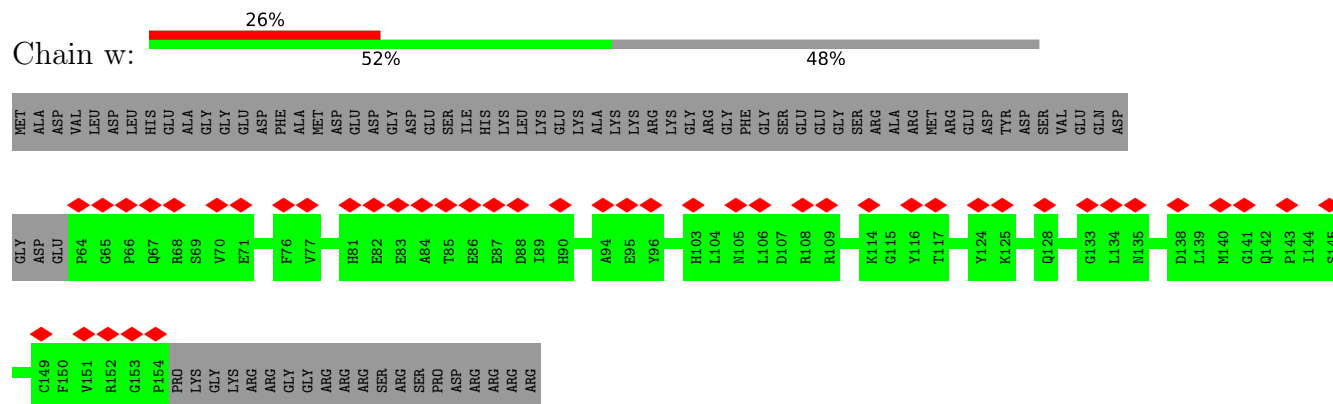




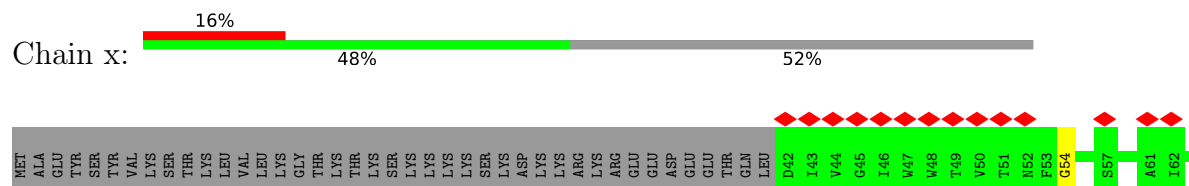
• Molecule 34: Protein mago nashi homolog



• Molecule 35: RNA-binding protein 8A



• Molecule 36: Protein FRG1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69000	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.109	Depositor
Minimum map value	-0.033	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	466.39996, 466.39996, 466.39996	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	2	0.30	0/3166	0.66	1/4915 (0.0%)
2	5	1.34	7/794 (0.9%)	1.07	10/1228 (0.8%)
3	6	0.20	0/328	0.58	0/508
5	A	0.29	0/2500	0.72	9/3491 (0.3%)
6	C	0.13	0/74	0.38	0/102
7	E	0.35	0/1534	0.88	3/2142 (0.1%)
8	G	0.53	1/688 (0.1%)	0.96	6/969 (0.6%)
8	H	0.49	0/706	1.02	5/995 (0.5%)
8	I	0.41	0/693	0.89	1/976 (0.1%)
8	J	0.44	0/565	0.93	3/792 (0.4%)
9	K	0.38	0/686	0.80	3/953 (0.3%)
10	L	0.20	0/572	0.50	0/796
11	M	0.30	1/3406 (0.0%)	0.61	4/4767 (0.1%)
12	N	0.64	0/371	1.14	1/519 (0.2%)
13	O	0.38	0/1325	0.95	5/1850 (0.3%)
14	P	0.33	0/454	0.98	5/633 (0.8%)
15	S	0.37	0/228	0.92	2/317 (0.6%)
16	T	0.15	0/1278	0.45	0/1788
17	U	0.26	0/6574	0.58	5/9159 (0.1%)
18	W	0.26	0/879	0.73	0/1229
19	X	0.38	0/468	0.72	0/653
20	Y	0.40	0/375	1.10	0/572
21	a	0.33	0/359	0.62	0/499
21	l	0.64	1/417 (0.2%)	0.79	1/581 (0.2%)
22	b	0.25	0/326	0.67	0/451
22	m	0.23	0/352	0.72	0/489
23	c	0.24	0/409	0.63	0/571
23	n	0.30	0/414	0.64	0/578
24	d	0.24	0/406	0.62	0/565
24	h	0.42	0/421	0.85	0/586
25	e	0.33	0/393	0.70	0/547
25	j	0.28	0/388	0.72	0/540
26	f	0.36	0/372	0.65	0/517
26	i	0.53	1/354 (0.3%)	0.68	0/491

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	g	0.70	2/371 (0.5%)	0.99	4/516 (0.8%)
27	k	0.43	0/366	0.74	1/509 (0.2%)
28	o	0.22	0/385	0.56	0/536
29	p	0.72	0/332	1.55	4/459 (0.9%)
30	q	0.27	0/9636	0.73	23/13498 (0.2%)
31	r	0.39	3/3001 (0.1%)	0.81	13/4192 (0.3%)
32	s	0.20	0/374	0.62	0/518
33	u	0.52	0/214	1.10	2/296 (0.7%)
34	v	0.27	0/728	0.63	0/1017
35	w	0.19	0/456	0.50	0/633
36	x	0.29	0/622	0.63	0/860
37	y	0.23	0/1962	0.64	0/2741
38	z	0.39	1/2313 (0.0%)	0.82	6/3222 (0.2%)
All	All	0.37	17/53035 (0.0%)	0.74	117/74766 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	5	1	0
5	A	0	5
7	E	0	3
8	G	0	3
8	H	0	4
8	I	0	1
8	J	0	1
9	K	0	1
11	M	0	2
12	N	0	1
13	O	0	3
17	U	0	2
24	d	0	1
24	h	0	1
25	e	0	1
26	f	0	1
27	g	0	1
29	p	0	3
30	q	0	12
31	r	0	5
33	u	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
37	y	0	1
38	z	0	5
All	All	1	58

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	86	C	P-O5'	25.29	1.97	1.59
2	5	86	C	P-OP1	16.32	1.81	1.49
2	5	86	C	C5'-C4'	10.20	1.66	1.51
2	5	86	C	C4'-C3'	-9.08	1.39	1.52
2	5	86	C	C3'-C2'	8.21	1.65	1.52
31	r	833	PRO	CA-CB	-8.12	1.42	1.53
11	M	161	LEU	C-N	-7.50	1.27	1.33
21	l	39	MET	N-CA	7.36	1.55	1.46
27	g	4	ALA	C-N	-6.35	1.23	1.33
27	g	3	LYS	CA-C	-6.04	1.40	1.52
2	5	85	C	O3'-P	-5.83	1.52	1.61
31	r	581	GLY	CA-C	-5.82	1.48	1.52
26	i	8	LYS	N-CA	5.75	1.51	1.46
8	G	65	PRO	C-N	5.66	1.47	1.33
31	r	938	GLY	CA-C	-5.56	1.48	1.52
38	z	584	GLY	C-O	-5.22	1.18	1.23
2	5	86	C	C3'-O3'	-5.01	1.34	1.42

All (117) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	86	C	C5'-C4'-C3'	13.56	136.34	116.00
8	J	43	ASN	CB-CA-C	-10.97	92.58	110.79
2	5	86	C	O4'-C4'-C3'	10.21	114.21	104.00
2	5	86	C	OP2-P-O3'	-9.81	78.56	108.00
2	5	85	C	OP1-P-O3'	-9.79	78.64	108.00
2	5	86	C	C4'-C3'-O3'	9.33	127.00	113.00
27	g	5	HIS	N-CA-C	8.97	119.92	109.60
29	p	616	SER	N-CA-C	8.12	127.75	109.81
30	q	957	VAL	N-CA-C	8.04	126.06	109.34
7	E	298	PRO	CA-C-N	7.88	136.59	121.54
7	E	298	PRO	C-N-CA	7.88	136.59	121.54
31	r	1028	CYS	CB-CA-C	-7.79	102.12	109.83
2	5	86	C	O5'-P-OP2	7.78	131.33	108.00
30	q	128	PRO	N-CA-C	7.72	128.37	112.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	86	C	C2'-C3'-O3'	-7.59	102.32	113.70
2	5	86	C	P-O5'-C5'	-7.53	109.61	120.90
8	I	77	ALA	CB-CA-C	-7.42	99.17	110.90
30	q	2124	VAL	CA-C-N	7.38	134.99	121.70
30	q	2124	VAL	C-N-CA	7.38	134.99	121.70
31	r	1065	ASP	CA-C-N	7.25	134.75	121.70
31	r	1065	ASP	C-N-CA	7.25	134.75	121.70
27	g	4	ALA	CA-C-N	7.22	130.98	120.51
27	g	4	ALA	C-N-CA	7.22	130.98	120.51
31	r	887	GLN	CA-C-N	7.05	133.88	122.67
31	r	887	GLN	C-N-CA	7.05	133.88	122.67
2	5	86	C	OP1-P-OP2	-7.02	98.53	119.60
13	O	691	GLU	N-CA-C	7.01	119.02	107.73
14	P	253	TYR	CA-C-N	-6.95	111.54	122.73
14	P	253	TYR	C-N-CA	-6.95	111.54	122.73
7	E	318	VAL	N-CA-C	6.95	123.79	109.34
38	z	88	MET	N-CA-C	-6.91	98.03	108.46
8	G	68	ALA	CA-C-N	6.88	134.69	121.54
8	G	68	ALA	C-N-CA	6.88	134.69	121.54
30	q	146	GLU	CA-C-N	-6.84	111.05	121.86
30	q	146	GLU	C-N-CA	-6.84	111.05	121.86
8	H	53	ILE	CB-CA-C	-6.80	101.49	112.03
31	r	884	PRO	CA-N-CD	-6.72	102.58	112.00
38	z	221	LEU	CA-C-N	6.72	134.38	121.54
38	z	221	LEU	C-N-CA	6.72	134.38	121.54
27	g	4	ALA	N-CA-CB	-6.71	100.94	113.89
2	5	86	C	OP1-P-O3'	6.54	127.61	108.00
30	q	1054	GLU	N-CA-C	-6.53	102.26	108.07
30	q	148	LEU	N-CA-C	-6.45	104.60	113.18
17	U	1276	VAL	N-CA-C	6.43	122.71	109.34
11	M	722	GLU	N-CA-CB	-6.42	101.30	110.81
30	q	1584	ILE	N-CA-C	6.42	122.70	109.34
5	A	1773	SER	CA-C-N	6.39	133.74	121.54
5	A	1773	SER	C-N-CA	6.39	133.74	121.54
5	A	1943	LEU	CA-C-N	6.33	132.17	122.29
5	A	1943	LEU	C-N-CA	6.33	132.17	122.29
31	r	884	PRO	CA-C-N	6.23	130.37	121.71
31	r	884	PRO	C-N-CA	6.23	130.37	121.71
30	q	1053	GLU	CA-C-N	6.13	130.94	122.06
30	q	1053	GLU	C-N-CA	6.13	130.94	122.06
11	M	719	THR	N-CA-C	6.09	128.07	111.00
30	q	128	PRO	N-CA-CB	-6.09	96.85	103.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	z	574	ARG	O-C-N	-6.05	117.58	121.88
29	p	597	THR	N-CA-CB	-5.97	103.29	111.65
15	S	83	GLU	CA-C-N	5.91	132.82	121.54
15	S	83	GLU	C-N-CA	5.91	132.82	121.54
13	O	654	GLY	N-CA-C	5.87	127.09	113.18
14	P	225	PRO	N-CA-C	5.85	117.83	110.70
30	q	697	ALA	N-CA-CB	-5.82	100.66	110.49
9	K	115	GLU	CB-CA-C	-5.79	98.90	110.42
13	O	634	GLU	CA-C-N	5.78	128.02	120.28
13	O	634	GLU	C-N-CA	5.78	128.02	120.28
8	G	56	LYS	CB-CA-C	-5.75	99.18	110.11
30	q	174	ASN	CA-C-N	-5.75	113.51	122.37
30	q	174	ASN	C-N-CA	-5.75	113.51	122.37
9	K	13	VAL	CA-C-N	5.72	130.59	121.66
9	K	13	VAL	C-N-CA	5.72	130.59	121.66
14	P	228	ASP	CA-C-N	5.72	132.46	121.54
14	P	228	ASP	C-N-CA	5.72	132.46	121.54
21	l	39	MET	N-CA-CB	5.69	120.11	110.49
12	N	162	PRO	N-CA-C	5.59	123.98	112.47
38	z	190	ILE	CA-C-N	5.58	132.20	121.54
38	z	190	ILE	C-N-CA	5.58	132.20	121.54
8	G	65	PRO	CA-C-N	-5.58	112.87	119.84
8	G	65	PRO	C-N-CA	-5.58	112.87	119.84
11	M	122	ASP	CA-C-N	5.45	131.95	121.54
11	M	122	ASP	C-N-CA	5.45	131.95	121.54
8	J	99	THR	CA-C-N	-5.44	113.56	122.54
8	J	99	THR	C-N-CA	-5.44	113.56	122.54
30	q	531	ILE	N-CA-C	5.42	120.61	109.34
8	G	65	PRO	CB-CA-C	5.41	117.52	110.92
13	O	209	PRO	CA-N-CD	-5.39	104.45	112.00
27	k	37	PHE	N-CA-CB	-5.39	102.47	110.61
29	p	568	VAL	N-CA-C	5.38	120.53	109.34
33	u	128	GLU	CA-C-N	5.37	131.36	121.70
33	u	128	GLU	C-N-CA	5.37	131.36	121.70
17	U	456	ASN	CA-C-N	5.35	135.92	126.45
17	U	456	ASN	C-N-CA	5.35	135.92	126.45
1	2	101	U	N1-C1'-C2'	5.34	120.01	112.00
17	U	498	GLU	CA-C-N	5.29	131.65	121.54
17	U	498	GLU	C-N-CA	5.29	131.65	121.54
31	r	738	GLY	CA-C-N	5.25	129.27	120.86
31	r	738	GLY	C-N-CA	5.25	129.27	120.86
8	H	69	THR	CA-C-N	5.25	131.57	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	69	THR	C-N-CA	5.25	131.57	121.54
29	p	616	SER	N-CA-CB	-5.25	101.03	110.37
5	A	1946	ASN	CA-C-N	5.14	131.35	121.54
5	A	1946	ASN	C-N-CA	5.14	131.35	121.54
5	A	1961	ILE	CA-C-N	5.12	129.55	121.56
5	A	1961	ILE	C-N-CA	5.12	129.55	121.56
5	A	1774	ASN	N-CA-CB	-5.10	101.88	110.49
30	q	355	GLU	CA-C-N	5.09	131.27	121.54
30	q	355	GLU	C-N-CA	5.09	131.27	121.54
30	q	1438	ARG	CA-C-N	5.08	127.79	120.38
30	q	1438	ARG	C-N-CA	5.08	127.79	120.38
30	q	175	LEU	CB-CA-C	5.06	119.35	110.64
30	q	606	THR	CA-C-N	5.05	131.19	121.54
30	q	606	THR	C-N-CA	5.05	131.19	121.54
8	H	86	MET	CA-C-N	-5.03	114.63	122.37
8	H	86	MET	C-N-CA	-5.03	114.63	122.37
31	r	832	ASN	CA-C-N	5.02	126.12	119.84
31	r	832	ASN	C-N-CA	5.02	126.12	119.84
31	r	1027	TRP	N-CA-CB	-5.02	102.01	110.49

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	5	86	C	C4'

All (58) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	A	1757	GLU	Mainchain,Peptide
5	A	1759	THR	Peptide
5	A	1760	GLU	Mainchain
5	A	1773	SER	Peptide
7	E	284	TRP	Peptide
7	E	317	GLU	Peptide
7	E	371	THR	Peptide
8	G	56	LYS	Peptide
8	G	62	ARG	Mainchain
8	G	69	THR	Mainchain
8	H	54	ASP	Peptide
8	H	55	ILE	Mainchain
8	H	57	VAL	Peptide
8	H	87	LEU	Peptide

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Mol	Chain	Res	Type	Group
8	I	56	LYS	Peptide
8	J	43	ASN	Peptide
9	K	77	GLN	Peptide
11	M	386	ASP	Peptide
11	M	85	ARG	Peptide
12	N	194	ASP	Peptide
13	O	653	LEU	Peptide
13	O	678	LEU	Peptide
13	O	690	GLU	Peptide
17	U	1275	LEU	Peptide
17	U	714	PHE	Peptide
24	d	112	ASN	Peptide
25	e	36	TYR	Peptide
26	f	3	LEU	Peptide
27	g	24	GLY	Peptide
24	h	112	ASN	Peptide
29	p	567	PRO	Peptide
29	p	598	ASP	Peptide
29	p	615	ASP	Peptide
30	q	128	PRO	Peptide
30	q	144	LYS	Peptide
30	q	146	GLU	Peptide
30	q	147	LYS	Peptide
30	q	1583	ASP	Peptide
30	q	162	GLY	Peptide
30	q	2098	ALA	Mainchain
30	q	532	ASN	Peptide
30	q	584	GLN	Peptide
30	q	696	LYS	Peptide
30	q	701	PHE	Peptide
30	q	956	LEU	Peptide
31	r	1026	ILE	Peptide
31	r	1027	TRP	Mainchain,Peptide
31	r	607	GLU	Mainchain
31	r	882	THR	Peptide
33	u	195	THR	Peptide
37	y	382	LYS	Peptide
38	z	355	ALA	Peptide
38	z	582	ASN	Mainchain
38	z	88	MET	Mainchain,Peptide
38	z	89	HIS	Peptide

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	2	2854	0	1442	18	0
2	5	718	0	363	12	0
3	6	296	0	149	1	0
4	8	376	0	82	0	0
5	A	2485	0	1164	10	0
6	C	75	0	35	0	0
7	E	1525	0	724	5	0
8	G	679	0	356	2	0
8	H	696	0	367	3	0
8	I	684	0	358	3	0
8	J	561	0	285	0	0
9	K	689	0	315	5	0
10	L	573	0	264	0	0
11	M	3387	0	1651	4	0
12	N	369	0	171	0	0
13	O	1320	0	635	4	0
14	P	452	0	229	1	0
15	S	229	0	95	1	0
16	T	1271	0	594	0	0
17	U	6546	0	3178	0	0
18	W	874	0	421	0	0
19	X	466	0	220	1	0
20	Y	348	0	176	0	0
21	a	358	0	168	1	0
21	l	415	0	198	1	0
22	b	327	0	143	1	0
22	m	351	0	161	2	0
23	c	407	0	186	1	0
23	n	412	0	188	0	0
24	d	406	0	179	0	0
24	h	421	0	185	1	0
25	e	393	0	169	2	0
25	j	388	0	167	2	0
26	f	369	0	182	0	0
26	i	352	0	171	0	0
27	g	369	0	178	4	0
27	k	364	0	176	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	o	384	0	198	0	0
29	p	333	0	153	2	0
30	q	9558	0	4623	12	0
31	r	2982	0	1461	3	0
32	s	376	0	172	1	0
33	u	216	0	96	1	0
34	v	723	0	335	1	0
35	w	453	0	227	0	0
36	x	621	0	315	1	0
37	y	1951	0	928	0	0
38	z	2301	0	1090	6	0
All	All	52703	0	25323	94	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 1.

All (94) 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)
2:5:86:C:P	2:5:86:C:O5'	1.97	1.22
5:A:1853:PRO:CB	36:x:54:GLY:O	1.98	1.10
38:z:201:GLY:HA3	38:z:222:HIS:HA	1.59	0.84
38:z:377:GLY:HA2	38:z:393:GLY:HA2	1.69	0.74
2:5:86:C:P	2:5:86:C:C5'	2.82	0.66
1:2:101:U:H5''	1:2:102:U:H5'	1.77	0.66
25:e:36:TYR:N	25:e:83:ASN:O	2.24	0.66
8:G:66:PRO:HG3	8:I:63:PRO:HD2	1.81	0.63
1:2:102:U:O2	22:m:74:GLY:N	2.29	0.63
2:5:96:A:O2'	25:e:37:GLU:O	2.18	0.60
8:H:87:LEU:HA	8:H:90:PHE:H	1.67	0.59
38:z:206:TYR:HA	38:z:214:PRO:HD2	1.84	0.59
5:A:1928:SER:HA	5:A:1932:ALA:HB3	1.85	0.59
14:P:283:ALA:O	14:P:287:SER:N	2.36	0.58
2:5:87:A:OP2	27:g:36:PRO:HB2	2.03	0.58
1:2:48:A:H4'	1:2:49:U:H3'	1.85	0.58
27:g:3:LYS:O	27:g:4:ALA:HB3	2.04	0.57
1:2:51:A:OP1	22:m:5:LYS:N	2.39	0.56
30:q:424:ALA:HB3	30:q:888:PRO:HG2	1.87	0.55
1:2:150:U:H3	1:2:181:G:H1	1.54	0.55
15:S:77:MET:O	15:S:81:GLY:N	2.40	0.55
8:H:84:ALA:C	9:K:112:ALA:HA	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:M:723:MET:N	33:u:192:GLU:HA	2.23	0.54
5:A:1787:ARG:HB3	5:A:1787:ARG:HH21	1.71	0.54
1:2:161:U:O2	1:2:163:G:N2	2.40	0.53
13:O:718:PHE:O	13:O:722:SER:N	2.32	0.53
30:q:1992:GLU:HA	30:q:1995:ALA:HB3	1.90	0.53
30:q:109:THR:HA	30:q:172:LEU:HA	1.90	0.52
5:A:2229:LYS:O	5:A:2257:GLU:N	2.42	0.52
11:M:564:PHE:O	11:M:569:GLY:N	2.43	0.51
13:O:208:PRO:HB2	13:O:209:PRO:HD2	1.91	0.51
30:q:128:PRO:O	30:q:130:ASP:N	2.44	0.51
1:2:77:C:H4'	1:2:78:C:H4'	1.93	0.50
38:z:436:PRO:HG2	38:z:453:LYS:H	1.76	0.50
30:q:134:GLY:HA2	30:q:697:ALA:HB1	1.93	0.50
5:A:1958:LYS:C	5:A:1960:THR:H	2.20	0.50
9:K:116:HIS:O	9:K:120:ARG:N	2.42	0.50
11:M:720:ILE:C	11:M:722:GLU:H	2.21	0.49
34:v:113:ASN:HA	34:v:118:PRO:HB3	1.95	0.48
30:q:163:GLN:C	30:q:165:ASP:H	2.20	0.48
30:q:1351:PRO:HG3	30:q:1516:PRO:HA	1.95	0.48
2:5:96:A:H2'	2:5:97:G:C8	2.48	0.48
8:G:69:THR:HA	8:I:65:PRO:HD2	1.96	0.48
31:r:833:PRO:HB3	31:r:918:ASP:C	2.39	0.48
5:A:1963:GLU:O	5:A:1966:HIS:N	2.47	0.48
23:c:74:LEU:HA	23:c:75:PRO:HD3	1.75	0.47
1:2:76:U:H4'	1:2:77:C:H5'	1.96	0.47
30:q:822:PRO:HG2	30:q:859:PRO:HD3	1.96	0.47
25:j:36:TYR:N	25:j:83:ASN:O	2.46	0.46
32:s:77:ILE:O	32:s:81:LEU:N	2.46	0.46
1:2:101:U:O2	21:l:40:ASN:N	2.49	0.46
2:5:96:A:H2'	2:5:97:G:H8	1.82	0.45
9:K:108:ASN:O	9:K:112:ALA:N	2.49	0.45
13:O:604:PRO:HB2	13:O:635:PHE:CB	2.47	0.45
9:K:109:ASN:O	9:K:112:ALA:HB3	2.17	0.45
5:A:1787:ARG:O	5:A:1803:ILE:N	2.41	0.44
25:j:36:TYR:O	25:j:38:GLN:N	2.50	0.44
1:2:12:G:H1	3:6:86:U:H3	1.64	0.44
5:A:1928:SER:O	5:A:1930:TYR:N	2.44	0.44
2:5:86:C:H5'	27:g:4:ALA:O	2.17	0.44
24:h:64:ASN:HA	24:h:101:LEU:O	2.18	0.44
29:p:609:HIS:O	29:p:612:ALA:N	2.51	0.43
5:A:1963:GLU:O	5:A:1965:HIS:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:3:C:H2'	1:2:4:G:H8	1.82	0.43
13:O:489:HIS:H	13:O:493:ALA:HB2	1.82	0.43
5:A:1942:ALA:C	5:A:1944:HIS:H	2.27	0.43
1:2:89:U:H2'	1:2:90:A:H8	1.84	0.43
2:5:95:G:O6	21:a:67:LYS:HA	2.19	0.43
1:2:163:G:O2'	19:X:50:LYS:O	2.25	0.43
31:r:832:ASN:HA	31:r:833:PRO:HD2	1.87	0.43
11:M:386:ASP:O	11:M:388:PHE:N	2.52	0.42
1:2:86:A:O2'	1:2:87:U:O4'	2.32	0.42
30:q:626:PRO:HG3	30:q:893:MET:HA	2.00	0.42
30:q:2014:TYR:HA	30:q:2015:PRO:HD3	1.91	0.42
1:2:159:U:H2'	1:2:160:A:H8	1.84	0.42
2:5:78:U:O2'	2:5:80:U:OP1	2.38	0.42
2:5:89:U:H5	22:b:37:HIS:HA	1.85	0.42
30:q:163:GLN:O	30:q:165:ASP:N	2.52	0.42
1:2:3:C:H2'	1:2:4:G:C8	2.55	0.42
7:E:426:PHE:HA	7:E:433:PHE:HA	2.01	0.42
1:2:177:A:H2	1:2:178:A:H62	1.67	0.42
2:5:116:A:N1	27:g:24:GLY:N	2.65	0.42
8:H:85:VAL:HA	9:K:112:ALA:HA	2.00	0.42
7:E:290:GLY:HA3	7:E:571:TRP:HA	2.02	0.41
31:r:886:ILE:C	31:r:888:ARG:H	2.27	0.41
7:E:276:LEU:HA	7:E:277:PRO:HD3	1.79	0.41
7:E:399:LYS:HA	7:E:415:ASP:HA	2.01	0.41
7:E:465:PRO:HD2	7:E:479:GLN:O	2.21	0.41
8:I:40:ASP:N	8:I:45:GLN:O	2.45	0.41
38:z:437:THR:HA	38:z:451:PHE:O	2.21	0.40
30:q:577:LYS:O	30:q:581:SER:N	2.55	0.40
38:z:91:ASP:HA	38:z:443:PHE:O	2.22	0.40
1:2:45:C:H2'	29:p:554:ASP:HA	2.03	0.40
2:5:101:U:H2'	2:5:102:G:C8	2.56	0.40

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	
5	A	483/2335 (21%)	418 (86%)	58 (12%)	7 (1%)	9	38
6	C	13/536 (2%)	13 (100%)	0	0	100	100
7	E	303/579 (52%)	275 (91%)	26 (9%)	2 (1%)	18	55
8	G	130/504 (26%)	115 (88%)	10 (8%)	5 (4%)	2	18
8	H	133/504 (26%)	115 (86%)	15 (11%)	3 (2%)	5	27
8	I	131/504 (26%)	122 (93%)	8 (6%)	1 (1%)	16	53
8	J	106/504 (21%)	102 (96%)	4 (4%)	0	100	100
9	K	130/225 (58%)	119 (92%)	7 (5%)	4 (3%)	3	21
10	L	111/802 (14%)	110 (99%)	1 (1%)	0	100	100
11	M	662/855 (77%)	590 (89%)	71 (11%)	1 (0%)	43	77
12	N	71/243 (29%)	58 (82%)	10 (14%)	3 (4%)	2	17
13	O	249/848 (29%)	214 (86%)	27 (11%)	8 (3%)	3	20
14	P	88/420 (21%)	70 (80%)	18 (20%)	0	100	100
15	S	44/2752 (2%)	41 (93%)	3 (7%)	0	100	100
16	T	251/908 (28%)	245 (98%)	6 (2%)	0	100	100
17	U	1281/1485 (86%)	1258 (98%)	21 (2%)	2 (0%)	43	77
18	W	172/255 (68%)	162 (94%)	10 (6%)	0	100	100
19	X	91/225 (40%)	87 (96%)	4 (4%)	0	100	100
21	a	70/126 (56%)	68 (97%)	2 (3%)	0	100	100
21	l	81/126 (64%)	80 (99%)	1 (1%)	0	100	100
22	b	62/240 (26%)	61 (98%)	1 (2%)	0	100	100
22	m	66/240 (28%)	65 (98%)	1 (2%)	0	100	100
23	c	79/119 (66%)	78 (99%)	1 (1%)	0	100	100
23	n	80/119 (67%)	79 (99%)	1 (1%)	0	100	100
24	d	77/118 (65%)	75 (97%)	2 (3%)	0	100	100
24	h	80/118 (68%)	77 (96%)	3 (4%)	0	100	100
25	e	77/92 (84%)	75 (97%)	2 (3%)	0	100	100
25	j	76/92 (83%)	75 (99%)	0	1 (1%)	9	40
26	f	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
26	i	69/86 (80%)	68 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	g	72/76 (95%)	72 (100%)	0	0	100	100
27	k	71/76 (93%)	71 (100%)	0	0	100	100
28	o	75/301 (25%)	74 (99%)	1 (1%)	0	100	100
29	p	66/654 (10%)	38 (58%)	20 (30%)	8 (12%)	0	4
30	q	1888/2136 (88%)	1796 (95%)	80 (4%)	12 (1%)	21	58
31	r	581/1227 (47%)	544 (94%)	33 (6%)	4 (1%)	18	55
32	s	72/285 (25%)	68 (94%)	4 (6%)	0	100	100
33	u	39/323 (12%)	36 (92%)	3 (8%)	0	100	100
34	v	142/146 (97%)	141 (99%)	1 (1%)	0	100	100
35	w	89/174 (51%)	88 (99%)	1 (1%)	0	100	100
36	x	117/258 (45%)	109 (93%)	8 (7%)	0	100	100
37	y	388/411 (94%)	382 (98%)	6 (2%)	0	100	100
38	z	448/646 (69%)	411 (92%)	34 (8%)	3 (1%)	18	55
All	All	9386/22759 (41%)	8815 (94%)	507 (5%)	64 (1%)	20	55

All (64) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	A	1758	PRO
5	A	1760	GLU
5	A	1762	TYR
7	E	318	VAL
8	G	57	VAL
8	H	55	ILE
12	N	195	LYS
13	O	551	PRO
17	U	1276	VAL
29	p	563	LYS
29	p	568	VAL
29	p	571	PRO
29	p	616	SER
29	p	617	PRO
30	q	128	PRO
30	q	129	ARG
30	q	163	GLN
30	q	164	THR
30	q	531	ILE

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Mol	Chain	Res	Type
30	q	957	VAL
30	q	1584	ILE
30	q	2098	ALA
31	r	1027	TRP
38	z	89	HIS
5	A	1773	SER
5	A	1774	ASN
7	E	285	SER
8	G	69	THR
8	H	58	ALA
8	I	57	VAL
12	N	162	PRO
13	O	657	ASP
25	j	37	GLU
29	p	599	ASP
30	q	146	GLU
30	q	585	ILE
8	G	65	PRO
9	K	66	MET
31	r	884	PRO
5	A	1761	PRO
5	A	1802	PRO
8	H	70	SER
9	K	78	PRO
13	O	587	LYS
13	O	637	PRO
13	O	675	PRO
29	p	579	THR
30	q	145	ASN
30	q	697	ALA
8	G	62	ARG
12	N	144	PRO
13	O	208	PRO
13	O	679	TRP
17	U	715	ASN
38	z	189	ALA
38	z	582	ASN
11	M	51	PRO
13	O	507	ALA
29	p	575	GLY
31	r	883	VAL
9	K	65	ILE

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Mol	Chain	Res	Type
31	r	833	PRO
8	G	63	PRO
9	K	77	GLN

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	
5	A	20/2108 (1%)	19 (95%)	1 (5%)	22	43
7	E	10/502 (2%)	10 (100%)	0	100	100
8	G	10/435 (2%)	8 (80%)	2 (20%)	1	7
8	H	11/435 (2%)	11 (100%)	0	100	100
8	I	10/435 (2%)	10 (100%)	0	100	100
8	J	6/435 (1%)	6 (100%)	0	100	100
9	K	1/196 (0%)	1 (100%)	0	100	100
10	L	1/709 (0%)	1 (100%)	0	100	100
11	M	24/749 (3%)	24 (100%)	0	100	100
12	N	3/209 (1%)	2 (67%)	1 (33%)	0	2
13	O	11/751 (2%)	10 (91%)	1 (9%)	9	28
14	P	4/361 (1%)	4 (100%)	0	100	100
16	T	8/838 (1%)	8 (100%)	0	100	100
17	U	68/1297 (5%)	68 (100%)	0	100	100
18	W	6/218 (3%)	6 (100%)	0	100	100
19	X	3/195 (2%)	3 (100%)	0	100	100
21	a	2/101 (2%)	2 (100%)	0	100	100
21	l	3/101 (3%)	3 (100%)	0	100	100
22	b	1/177 (1%)	1 (100%)	0	100	100
22	m	3/177 (2%)	3 (100%)	0	100	100
23	c	3/101 (3%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	n	3/101 (3%)	3 (100%)	0	100	100
24	d	2/110 (2%)	2 (100%)	0	100	100
24	h	2/110 (2%)	2 (100%)	0	100	100
25	e	1/84 (1%)	1 (100%)	0	100	100
25	j	1/84 (1%)	1 (100%)	0	100	100
26	f	4/74 (5%)	4 (100%)	0	100	100
26	i	3/74 (4%)	3 (100%)	0	100	100
27	g	3/66 (4%)	3 (100%)	0	100	100
27	k	3/66 (4%)	3 (100%)	0	100	100
28	o	2/252 (1%)	2 (100%)	0	100	100
30	q	82/1908 (4%)	81 (99%)	1 (1%)	63	74
31	r	25/1075 (2%)	25 (100%)	0	100	100
33	u	1/289 (0%)	1 (100%)	0	100	100
34	v	6/134 (4%)	6 (100%)	0	100	100
35	w	4/143 (3%)	4 (100%)	0	100	100
36	x	5/223 (2%)	5 (100%)	0	100	100
37	y	12/361 (3%)	12 (100%)	0	100	100
38	z	18/572 (3%)	17 (94%)	1 (6%)	19	41
All	All	385/16256 (2%)	378 (98%)	7 (2%)	51	67

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	A	1787	ARG
8	G	63	PRO
8	G	65	PRO
12	N	162	PRO
13	O	208	PRO
30	q	128	PRO
38	z	283	PRO

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
1	2	153/975 (15%)	53 (34%)	0
2	5	38/116 (32%)	18 (47%)	0
20	Y	27/324 (8%)	18 (66%)	0
3	6	15/106 (14%)	5 (33%)	0
All	All	233/1521 (15%)	94 (40%)	0

All (94) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	16	U
1	2	17	U
1	2	46	U
1	2	47	U
1	2	48	A
1	2	49	U
1	2	50	C
1	2	51	A
1	2	52	G
1	2	53	U
1	2	64	A
1	2	65	U
1	2	66	A
1	2	67	C
1	2	68	G
1	2	69	U
1	2	70	C
1	2	71	C
1	2	72	U
1	2	73	C
1	2	74	U
1	2	75	A
1	2	76	U
1	2	77	C
1	2	78	C
1	2	79	G
1	2	80	A
1	2	81	G
1	2	82	G
1	2	83	A
1	2	84	C
1	2	85	A
1	2	86	A
1	2	87	U

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Mol	Chain	Res	Type
1	2	95	A
1	2	96	U
1	2	97	G
1	2	98	G
1	2	101	U
1	2	111	G
1	2	112	G
1	2	116	A
1	2	117	U
1	2	121	A
1	2	122	U
1	2	123	A
1	2	124	G
1	2	128	C
1	2	129	U
1	2	130	U
1	2	146	C
1	2	157	G
1	2	177	A
2	5	79	C
2	5	80	U
2	5	81	U
2	5	82	A
2	5	83	A
2	5	85	C
2	5	86	C
2	5	87	A
2	5	88	A
2	5	90	U
2	5	91	U
2	5	93	U
2	5	94	U
2	5	95	G
2	5	96	A
2	5	97	G
2	5	115	U
2	5	116	A
3	6	81	C
3	6	82	A
3	6	83	A
3	6	84	A
3	6	85	U

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Mol	Chain	Res	Type
20	Y	83	G
20	Y	84	U
20	Y	85	U
20	Y	86	A
20	Y	87	C
20	Y	88	C
20	Y	91	C
20	Y	94	C
20	Y	128	C
20	Y	131	G
20	Y	133	U
20	Y	134	U
20	Y	135	U
20	Y	136	C
20	Y	137	C
20	Y	138	U
20	Y	139	U
20	Y	140	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	8	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	70:UNK	C	92:UNK	N	23.10
1	8	34:UNK	C	42:UNK	N	21.26
1	8	51:UNK	C	55:UNK	N	10.71

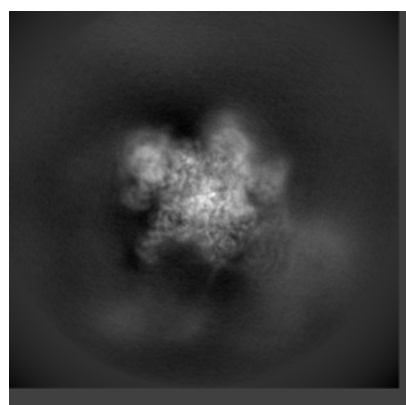
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11570. These allow visual inspection of the internal detail of the map and identification of artifacts.

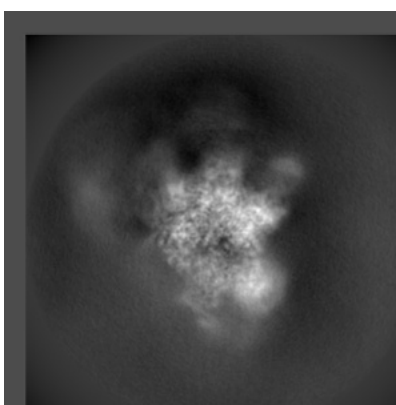
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

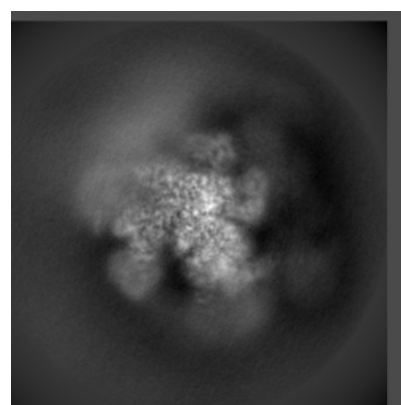
6.1.1 Primary map



X



Y

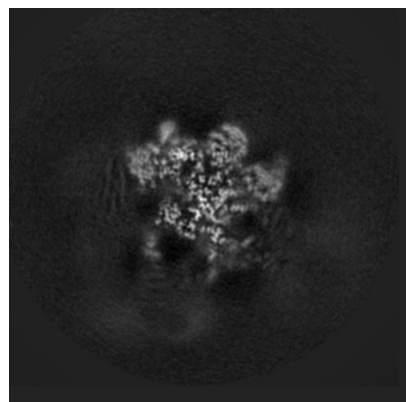


Z

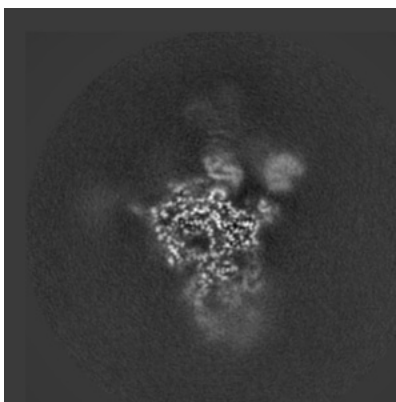
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

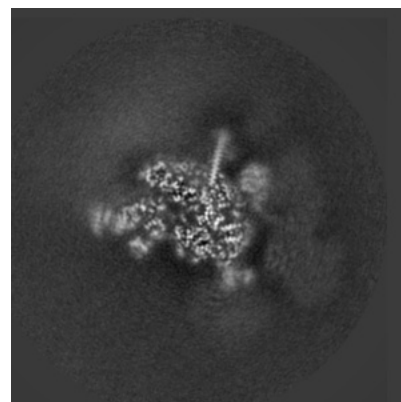
6.2.1 Primary map



X Index: 220



Y Index: 220

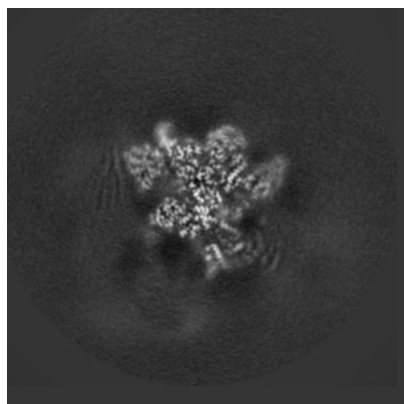


Z Index: 220

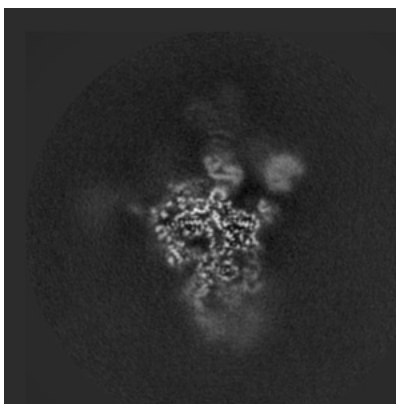
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

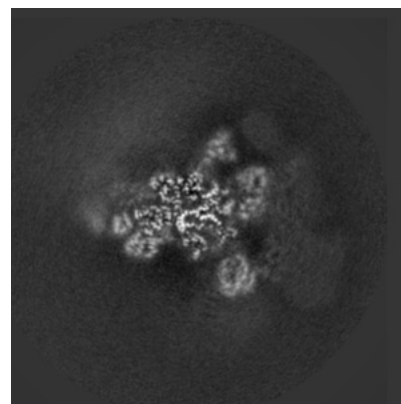
6.3.1 Primary map



X Index: 215



Y Index: 219

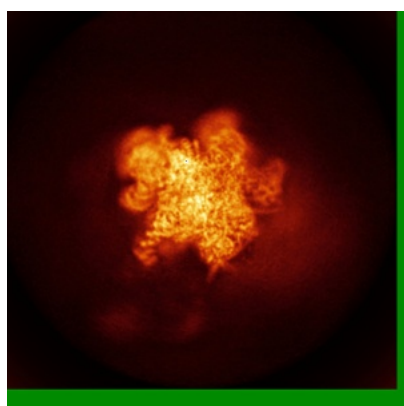


Z Index: 231

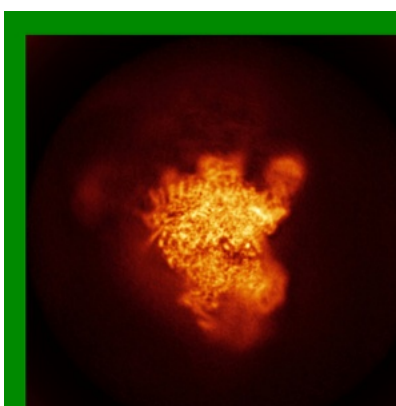
The images above show the largest variance slices of the map in three orthogonal directions.

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

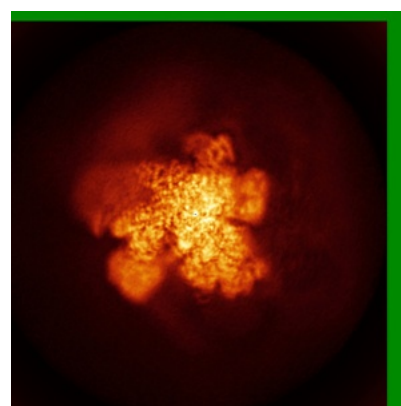
6.4.1 Primary map



X



Y



Z

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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

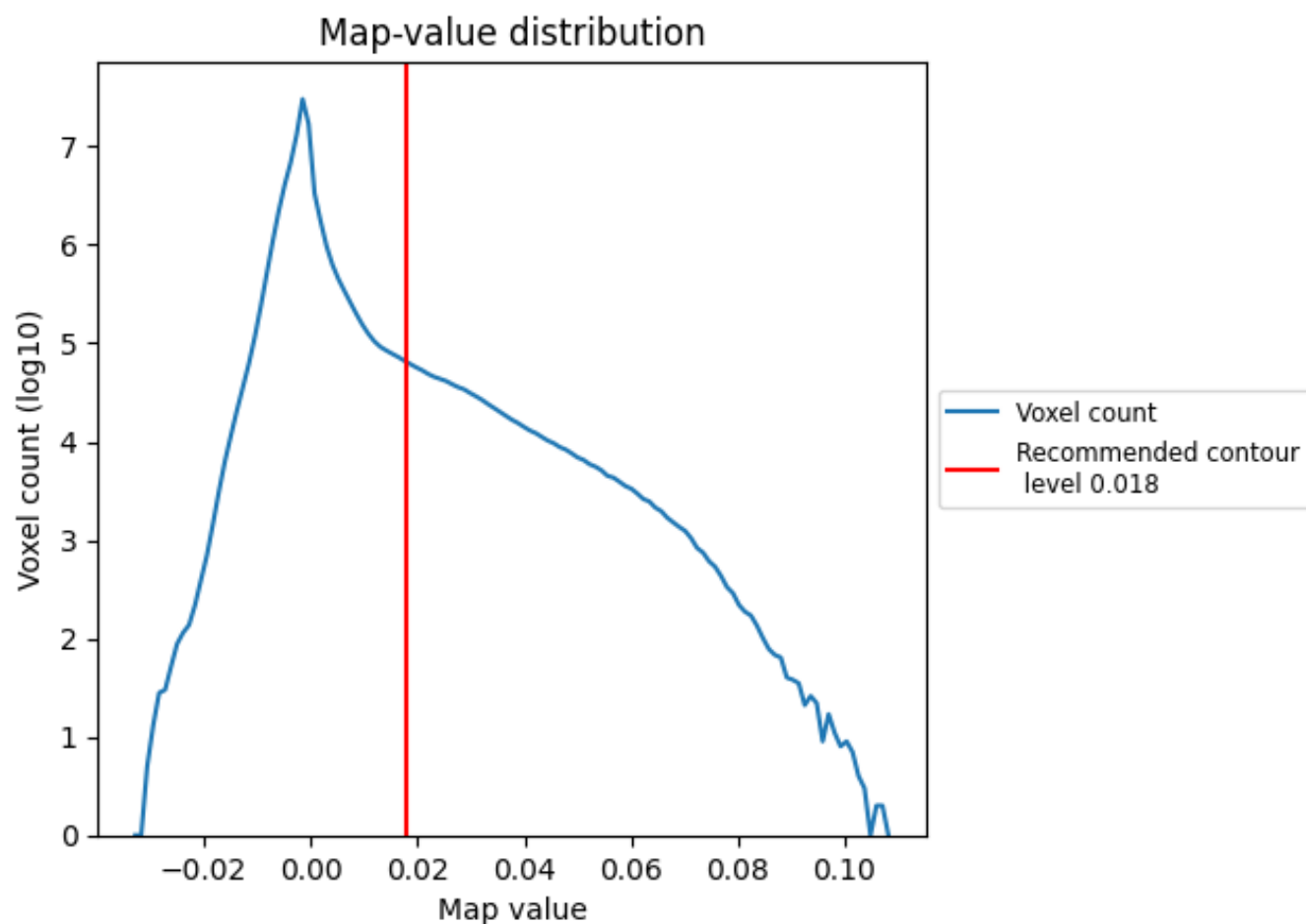
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

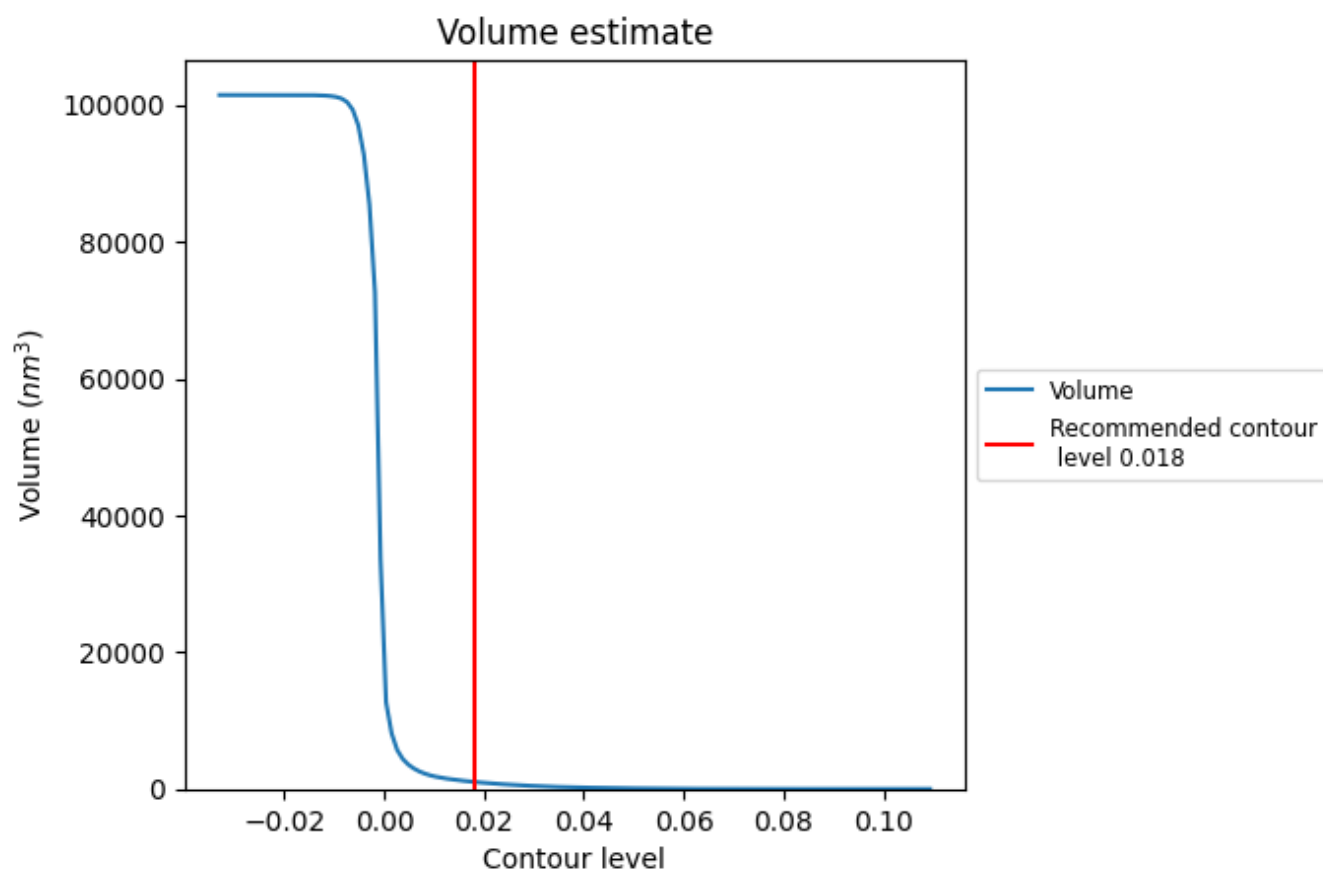
This section contains the results of statistical analysis of the map.

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.

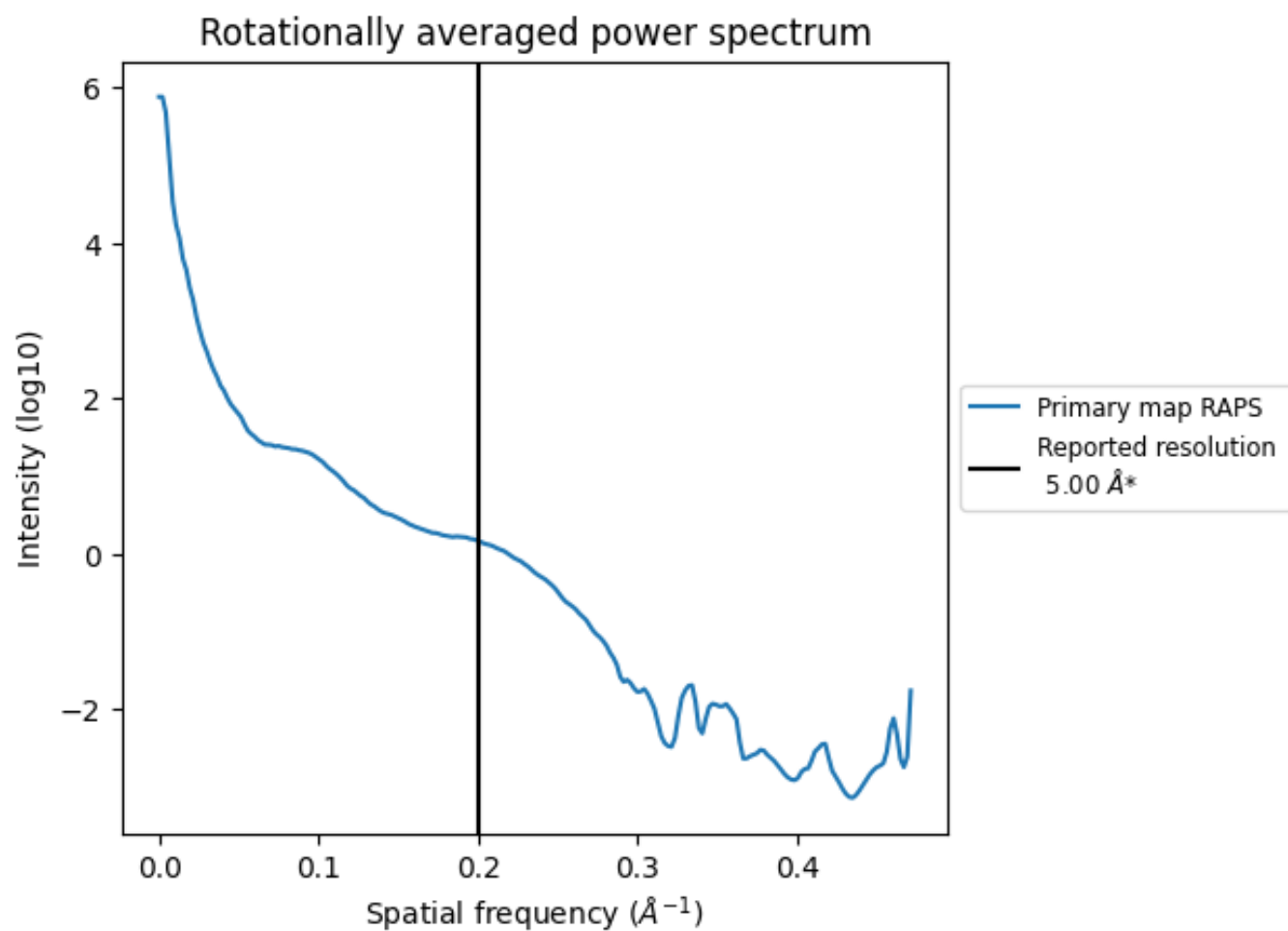
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1034 nm³; this corresponds to an approximate mass of 934 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 0.200 Å⁻¹

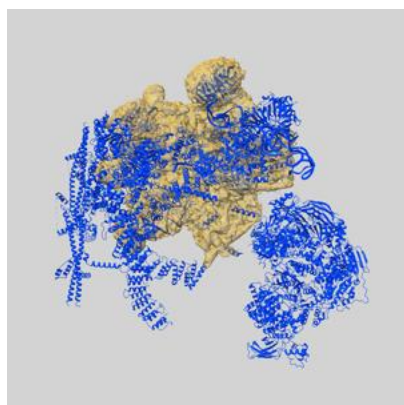
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

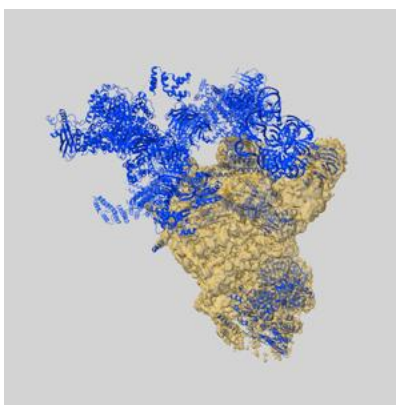
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11570 and PDB model 7A5P. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

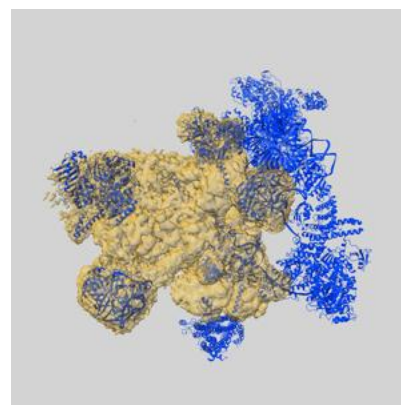
9.1 Map-model overlay [i](#)



X



Y



Z

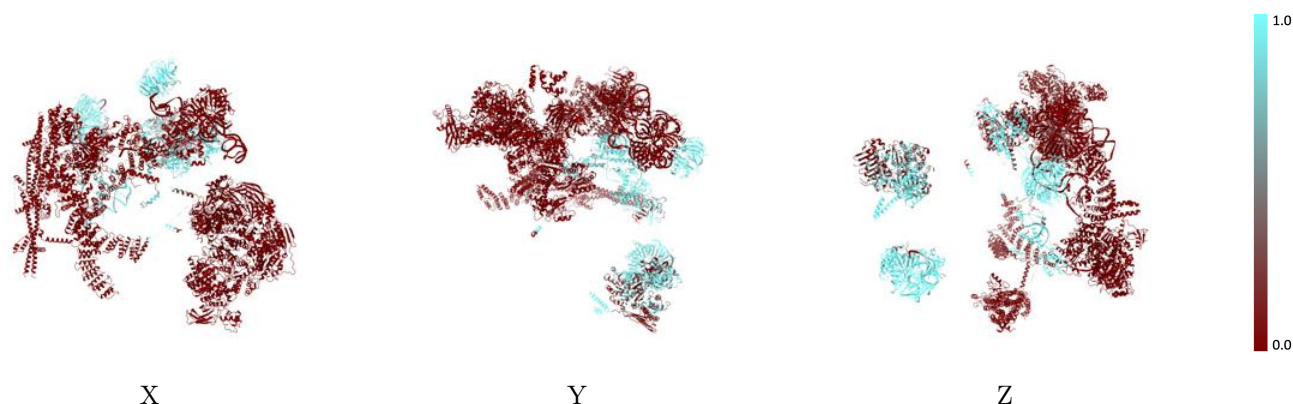
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



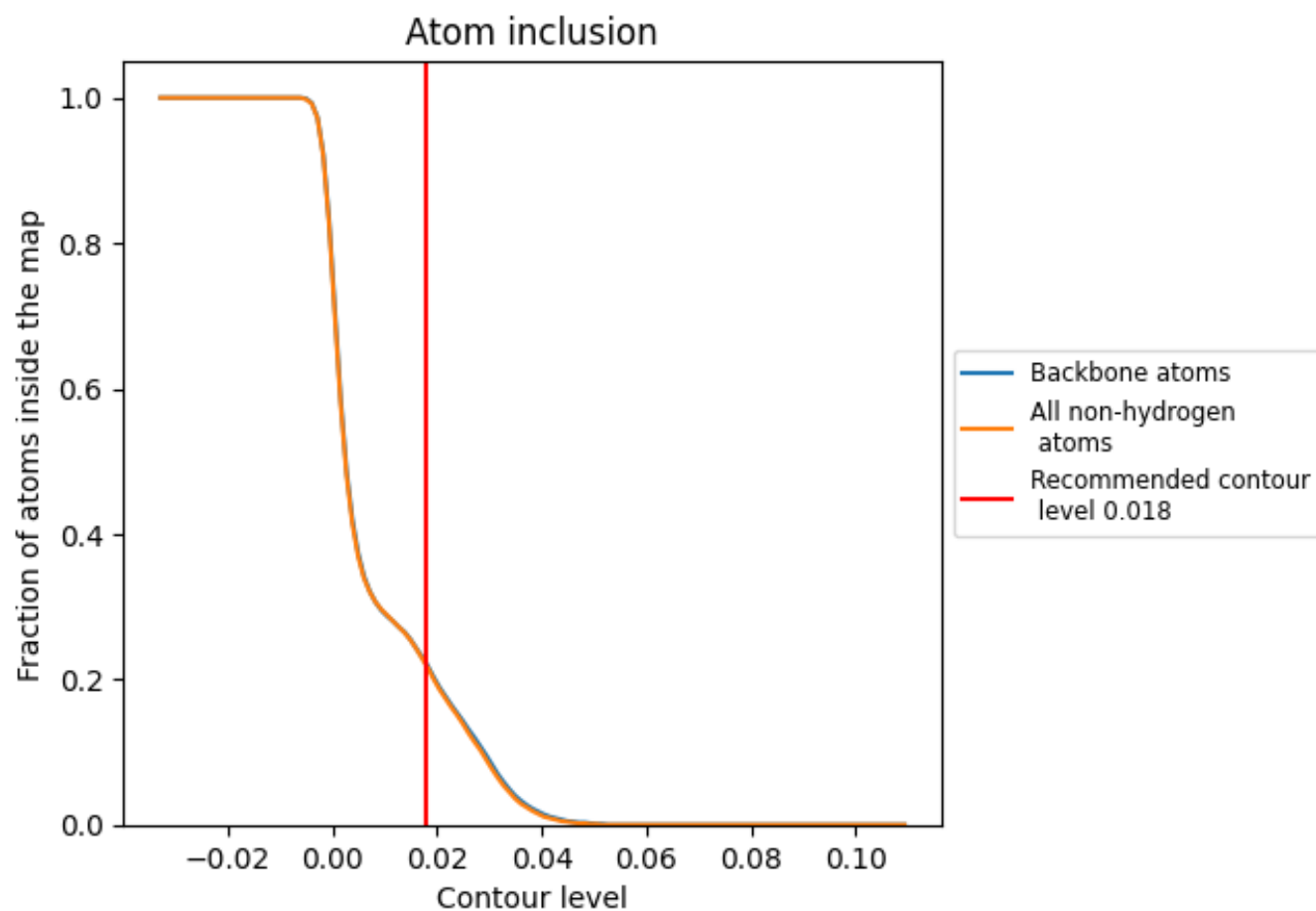
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.018).

9.4 Atom inclusion ⓘ



At the recommended contour level, 22% of all backbone atoms, 22% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2180	 0.0900
2	 0.1120	 0.0670
5	 0.9250	 0.1000
6	 0.8450	 0.1020
8	 0.0000	 0.0250
A	 0.4880	 0.1660
C	 0.6000	 0.1890
E	 0.9660	 0.1410
G	 0.0000	 0.0170
H	 0.0000	 -0.0120
I	 0.0000	 0.0270
J	 0.0000	 0.0530
K	 0.0020	 0.0950
L	 0.0870	 0.1010
M	 0.0010	 0.0910
N	 0.8100	 0.2420
O	 0.0530	 0.0600
P	 0.9230	 0.2320
S	 1.0000	 0.2050
T	 0.6450	 0.1840
U	 0.0000	 0.0620
W	 0.0070	 0.0270
X	 0.0000	 0.1030
Y	 0.4450	 0.1130
a	 0.9410	 0.1320
b	 0.9450	 0.1530
c	 0.9560	 0.2580
d	 0.9460	 0.1890
e	 0.9870	 0.1260
f	 0.9810	 0.0910
g	 0.8810	 0.0980
h	 0.0070	 0.1890
i	 0.0000	 0.1530
j	 0.0000	 0.1070
k	 0.0000	 0.0930



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Chain	Atom inclusion	Q-score
l	 0.0000	 0.1030
m	 0.0000	 0.1420
n	 0.0610	 0.1550
o	 0.0000	 0.1650
p	 0.6880	 0.2740
q	 0.0000	 0.0070
r	 0.0010	 0.1540
s	 0.6570	 0.2240
u	 0.2640	 0.1360
v	 0.1770	 0.0500
w	 0.4550	 0.0820
x	 0.6230	 0.1030
y	 0.4940	 0.1930
z	 0.3290	 0.0870