



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 07:05 AM UTC

PDB ID : 5Y88 / pdb_00005y88
EMDB ID : EMD-6817
Title : Cryo-EM structure of the intron-lariat spliceosome ready for disassembly from *S.cerevisiae* at 3.5 angstrom
Authors : Wan, R.; Yan, C.; Bai, R.; Lei, J.; Shi, Y.
Deposited on : 2017-08-20
Resolution : 3.46 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

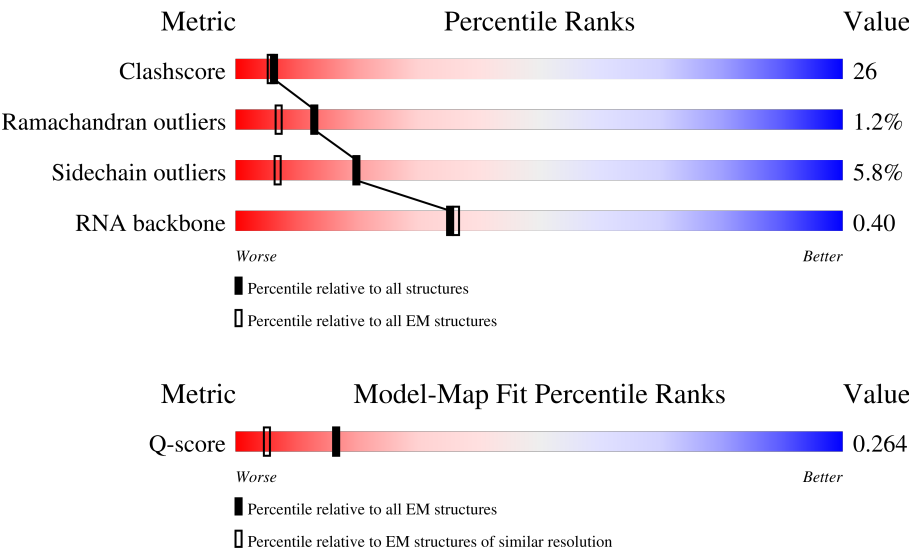
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.46 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	13788 (2.96 - 3.96)

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

Mol	Chain	Length	Quality of chain
1	A	2413	
2	B	214	
3	C	1008	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	112	
5	E	38	
6	F	1175	
7	G	175	
8	H	859	
9	I	687	
10	J	590	
11	K	215	
12	L	157	
13	M	364	
14	N	339	
15	O	451	
16	P	175	
17	Q	379	
18	R	278	
19	S	455	
20	T	283	
21	U	708	
22	V	322	
23	W	767	
24	a	196	
24	h	196	
25	b	94	
25	i	94	
26	c	86	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
26	j	86	
27	d	77	
27	k	77	
28	e	101	
28	l	101	
29	f	146	
29	m	146	
30	g	110	
30	n	110	
31	o	238	
32	p	111	
33	q	503	
33	r	503	
33	s	503	
33	t	503	
34	x	9	

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 72347 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-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1903	Total	C	N	O	S	0	0
			15715	10107	2697	2854	57		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	117	Total	C	N	O	P	0	0
			2465	1104	414	830	117		

- Molecule 3 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	913	Total	C	N	O	S	0	0
			7278	4696	1205	1347	30		

- Molecule 4 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	101	Total	C	N	O	P	0	0
			2150	963	384	702	101		

- Molecule 5 is a RNA chain called Intron lariat.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	28	Total	C	N	O	P	0	0
			587	264	95	200	28		

- Molecule 6 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	82	Total	C	N	O	P	0	0
			1727	772	286	587	82		

- Molecule 7 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	155	Total	C	N	O	S	0	0
			921	582	159	179	1		

- Molecule 8 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	601	Total	C	N	O	S	0	0
			3204	1958	611	634	1		

- Molecule 9 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	541	Total	C	N	O	S	0	0
			3542	2200	667	667	8		

- Molecule 10 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	431	Total	C	N	O	S	0	0
			2944	1824	544	568	8		

- Molecule 11 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	102	Total	C	N	O	S	0	0
			822	504	152	165	1		

- Molecule 12 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	157	Total	C	N	O	S	0	0
			1290	808	240	231	11		

- Molecule 13 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	182	Total	C	N	O	S	0	0
			1298	805	235	243	15		

- Molecule 14 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	261	Total	C	N	O	S	0	0
			2089	1320	369	388	12		

- Molecule 15 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	337	Total	C	N	O	S	0	0
			2646	1669	466	501	10		

- Molecule 16 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	68	Total	C	N	O	S	0	0
			554	348	111	94	1		

- Molecule 17 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	201	Total	C	N	O	S	0	0
			1583	988	290	298	7		

- Molecule 18 is a protein called Protein CWC16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	46	Total	C	N	O	S	0	0
			379	225	73	79	2		

- Molecule 19 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	23	Total	C	N	O	0	0
			195	122	41	32		

- Molecule 20 is a protein called Pre-mRNA-splicing factor CWC23.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	107	Total	C	N	O	0	0
			816	523	144	149		

- Molecule 21 is a protein called Pre-mRNA-splicing factor SPP382.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	488	Total	C	N	O	S	0	0
			2690	1644	514	529	3		

- Molecule 22 is a protein called Pre-mRNA-splicing factor NTR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	91	Total	C	N	O	S	0	0
			619	381	112	124	2		

- Molecule 23 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	708	Total	C	N	O	S	0	0
			3505	2089	708	708			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	80	Total	C	N	O	S	0	0
			631	403	114	111	3		
24	h	78	Total	C	N	O	S	0	0
			610	389	110	108	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	75	Total	C	N	O	S	0	0
			575	379	92	101	3		
25	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	70	Total	C	N	O	S	0	0
			554	355	98	100	1		
26	j	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	69	Total	C	N	O	S	0	0
			529	337	93	97	2		
27	k	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	e	82	Total	C	N	O	S	0	0
			625	399	109	115	2		
28	l	82	Total	C	N	O	S	0	0
			625	399	109	115	2		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	f	82	Total	C	N	O	S	0	0
			644	409	110	123	2		
29	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	94	Total	C	N	O	S	0	0
			741	477	141	119	4		
30	n	65	Total	C	N	O	S	0	0
			528	340	102	84	2		

- Molecule 31 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	o	135	Total	C	N	O	0	0
			841	538	142	161		

- Molecule 32 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	p	81	Total	C	N	O	0	0
			513	332	89	92		

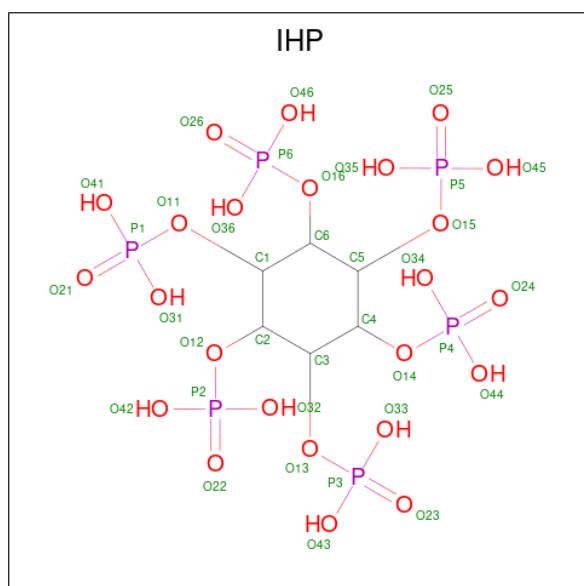
- Molecule 33 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	q	126	Total	C	N	O	S	0	0
			831	526	134	169	2		
33	r	129	Total	C	N	O	S	0	0
			849	536	137	174	2		
33	s	129	Total	C	N	O	S	0	0
			850	537	137	174	2		
33	t	125	Total	C	N	O	S	0	0
			823	521	133	167	2		

- Molecule 34 is a RNA chain called RNA (intron or U6 snRNA).

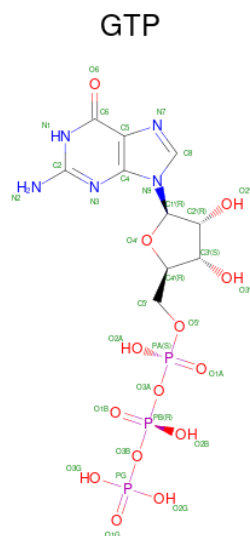
Mol	Chain	Residues	Atoms					AltConf	Trace
34	x	9	Total	C	N	O	P	0	0
			177	81	18	70	8		

- Molecule 35 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



Mol	Chain	Residues	Atoms				AltConf
35	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 36 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
36	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

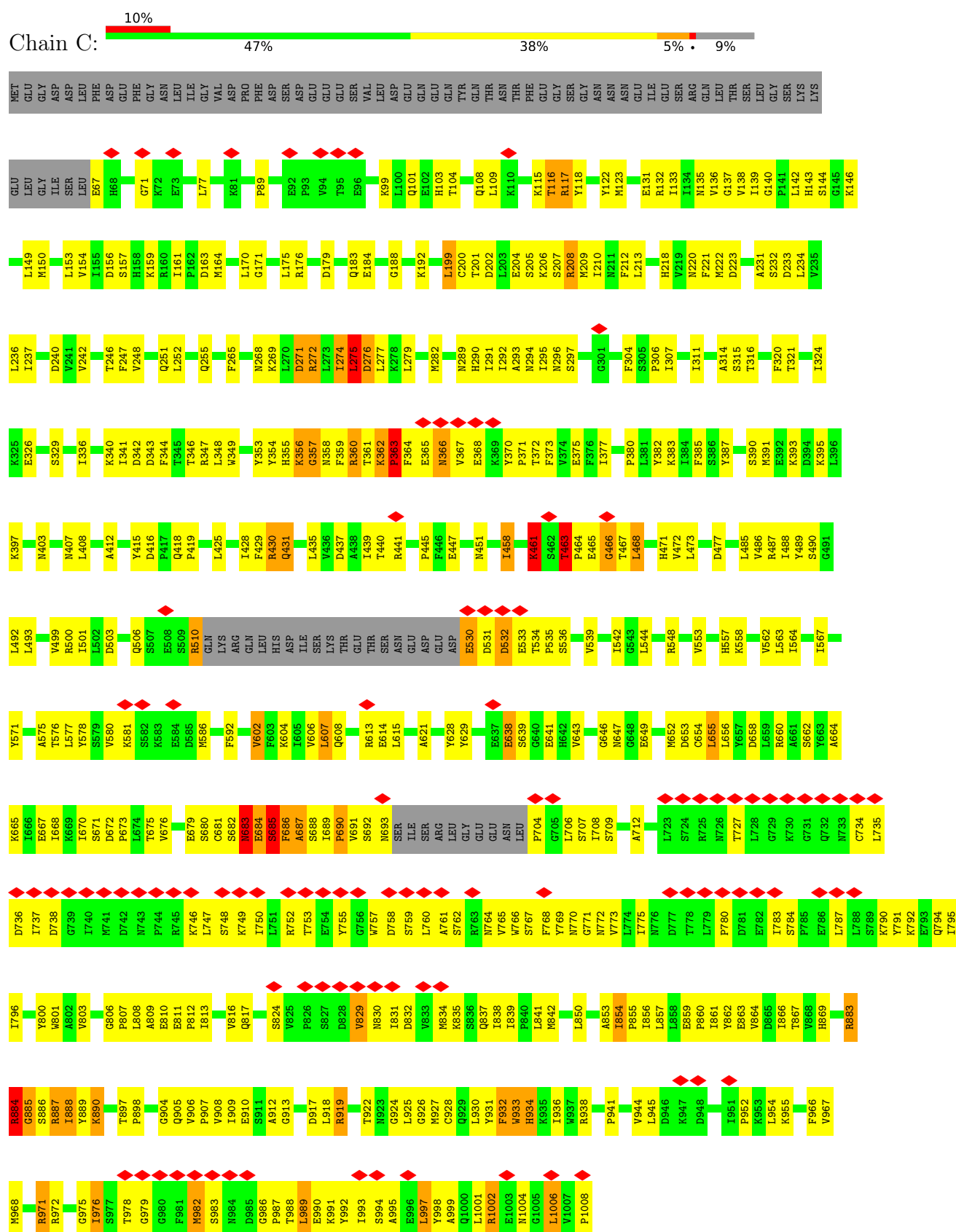
- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
37	C	1	Total Mg 1 1	0
37	D	5	Total Mg 5 5	0

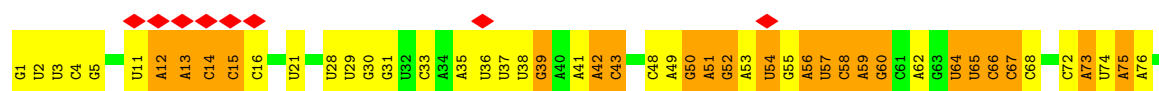
- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
38	L	3	Total Zn 3 3	0
38	M	2	Total Zn 2 2	0
38	N	1	Total Zn 1 1	0

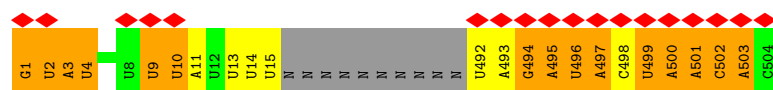




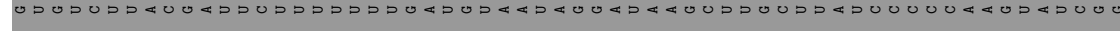
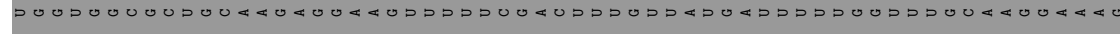
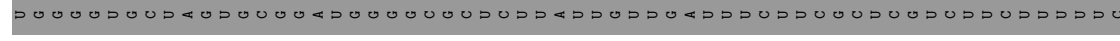
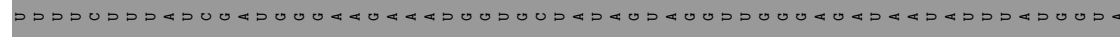
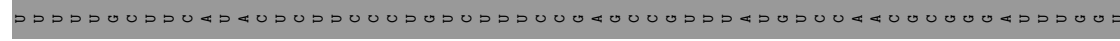
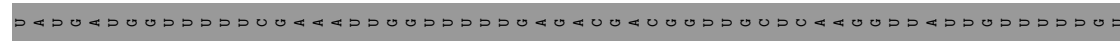
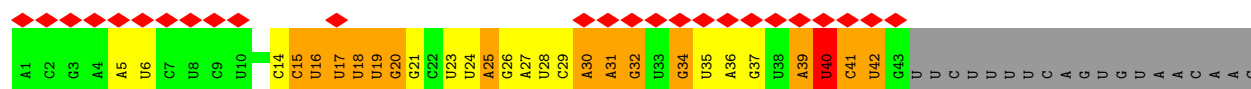
• Molecule 4: U6 snRNA



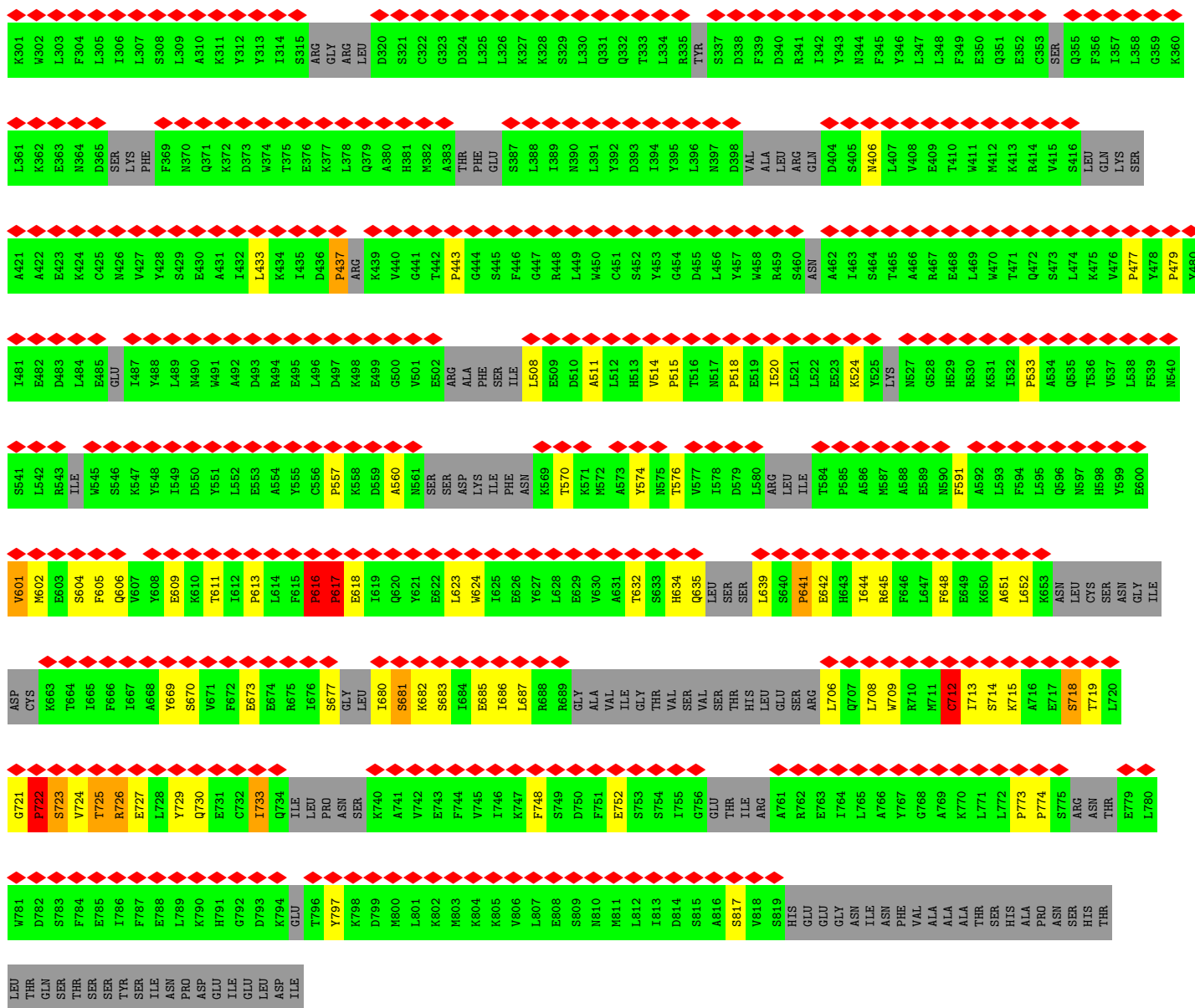
• Molecule 5: Intron lariat



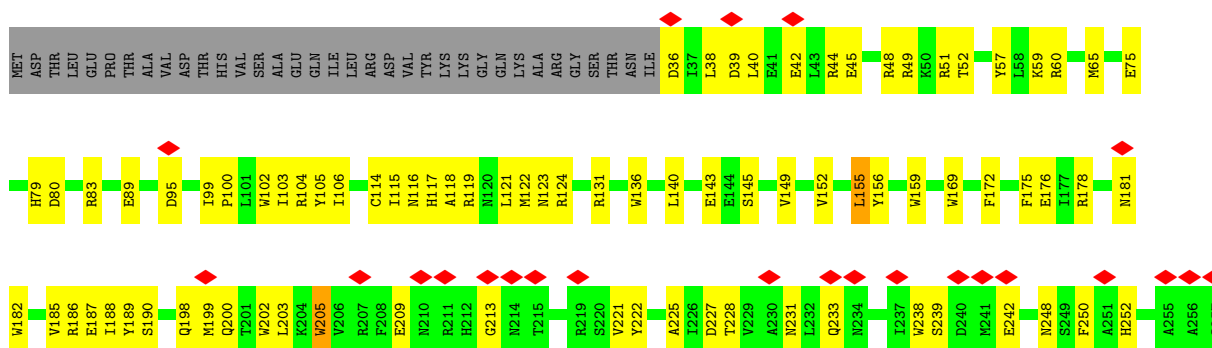
• Molecule 6: U2 snRNA

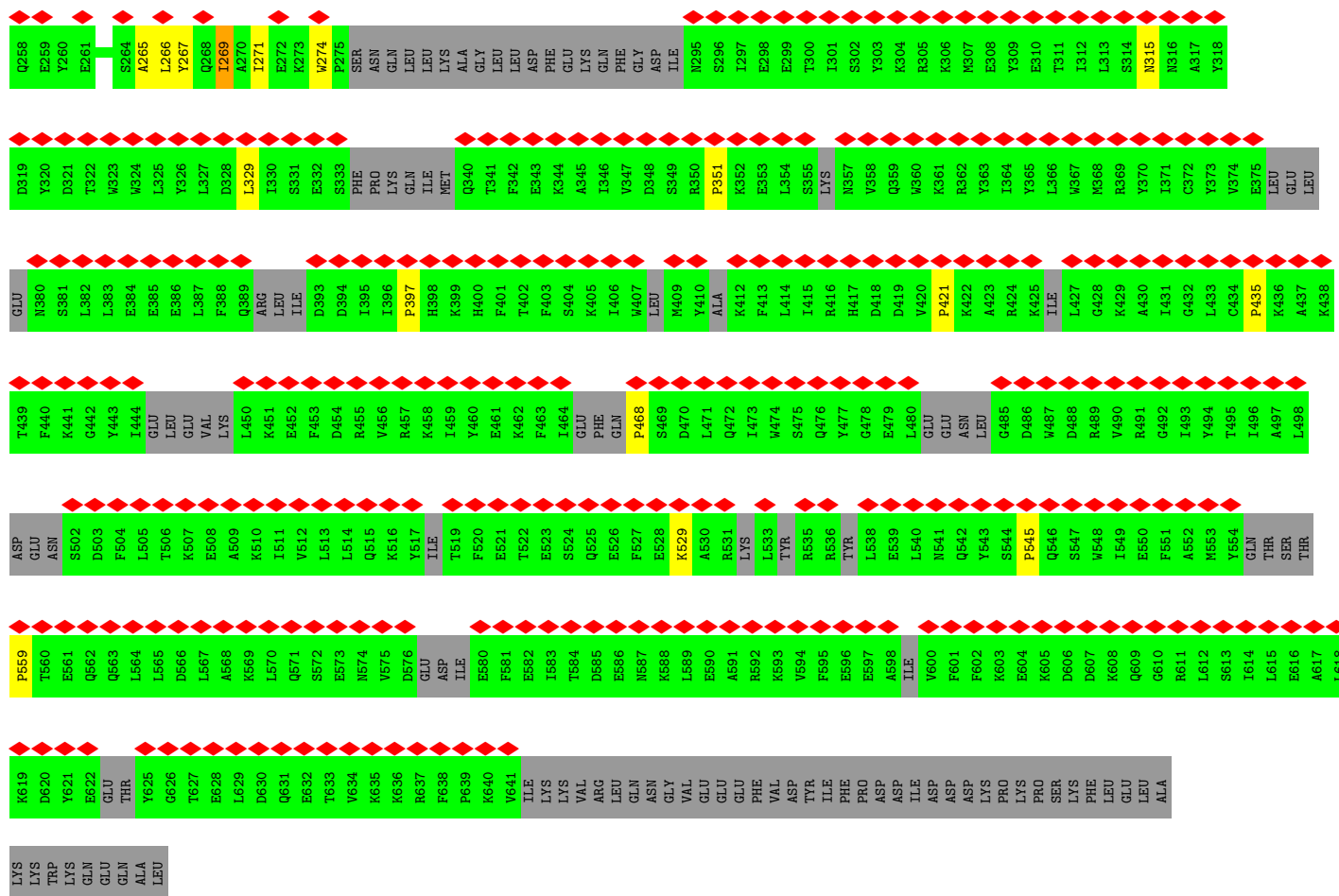




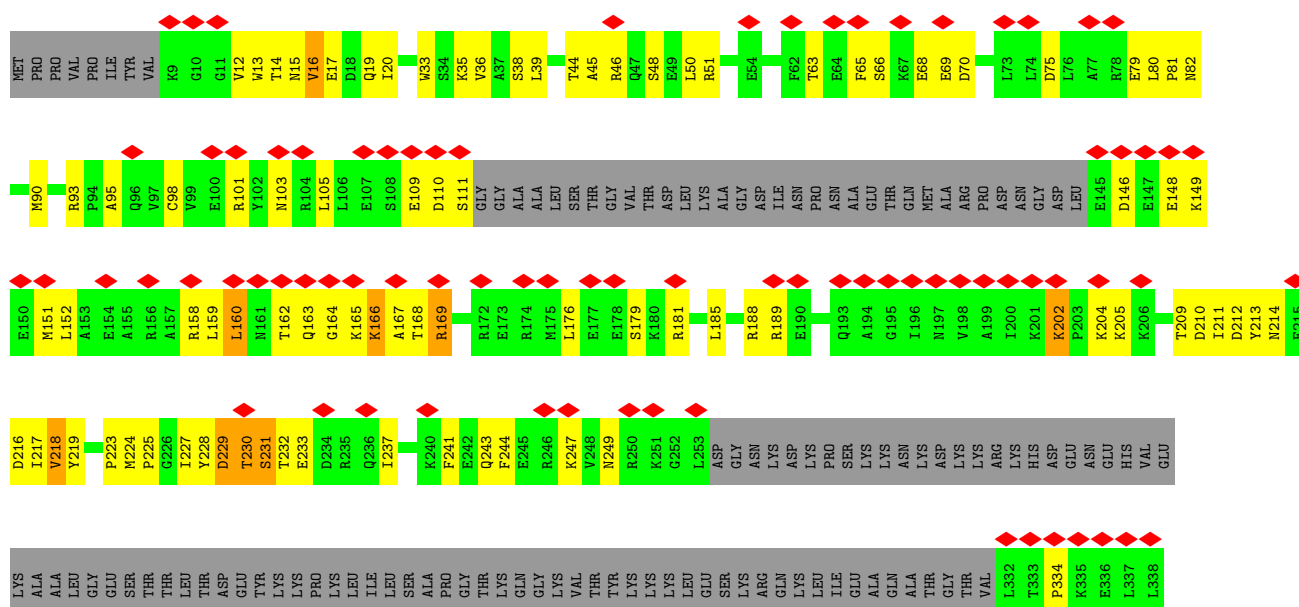


• Molecule 9: Pre-mRNA-splicing factor CLF1



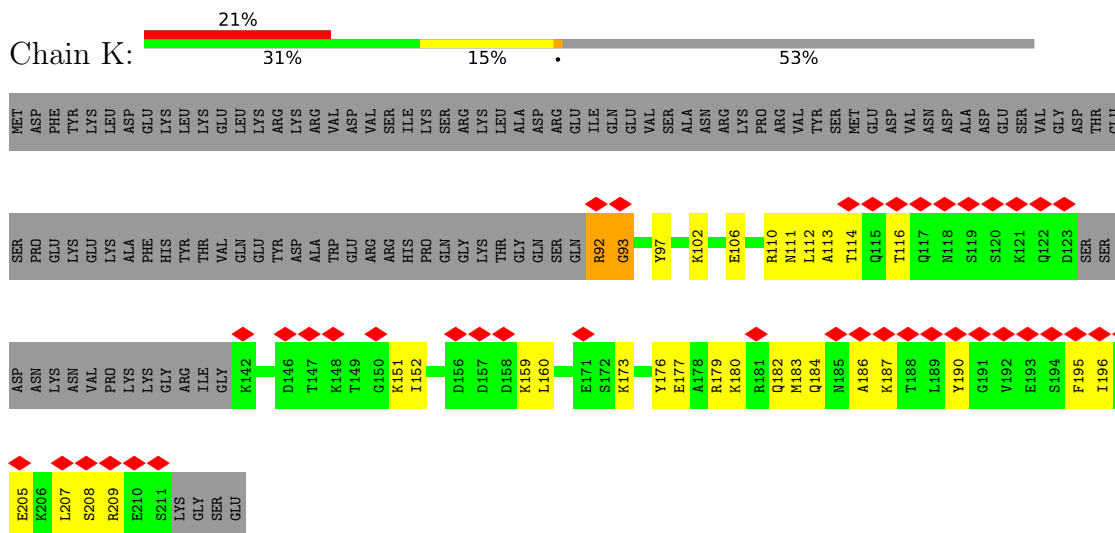


• Molecule 10: Pre-mRNA-splicing factor CEF1

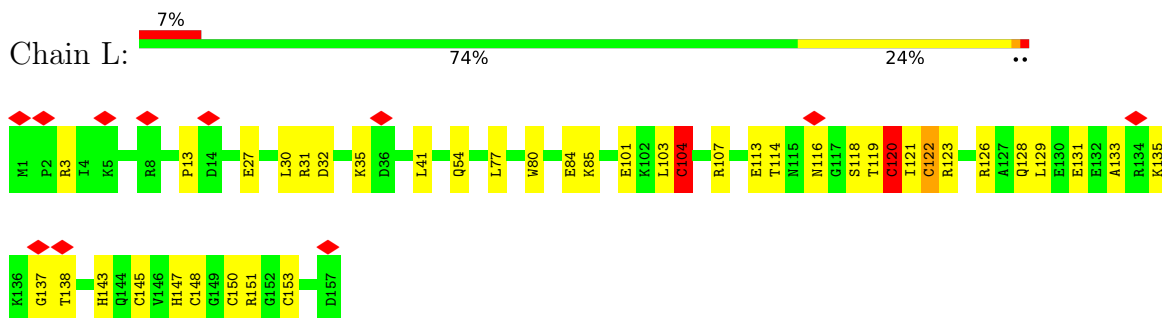




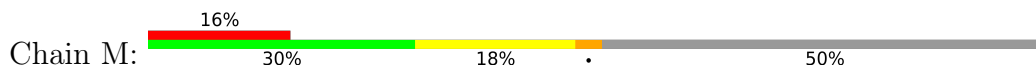
- Molecule 11: Pre-mRNA-splicing factor SYF2

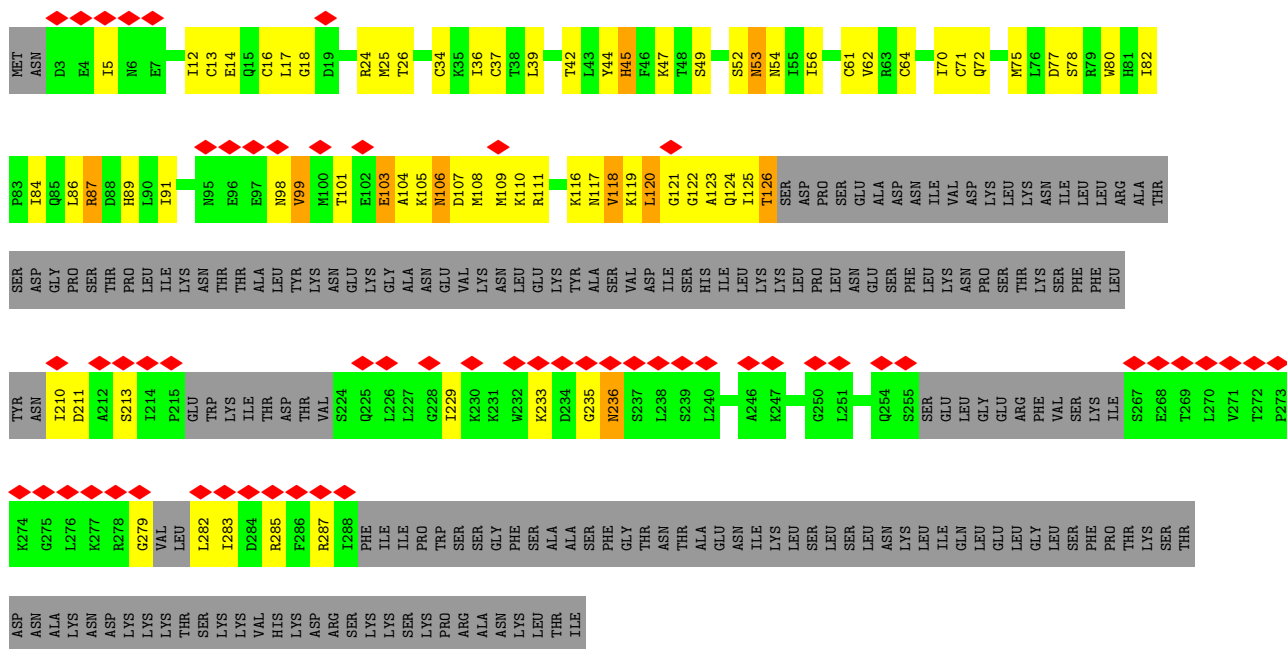


- Molecule 12: Pre-mRNA-splicing factor BUD31

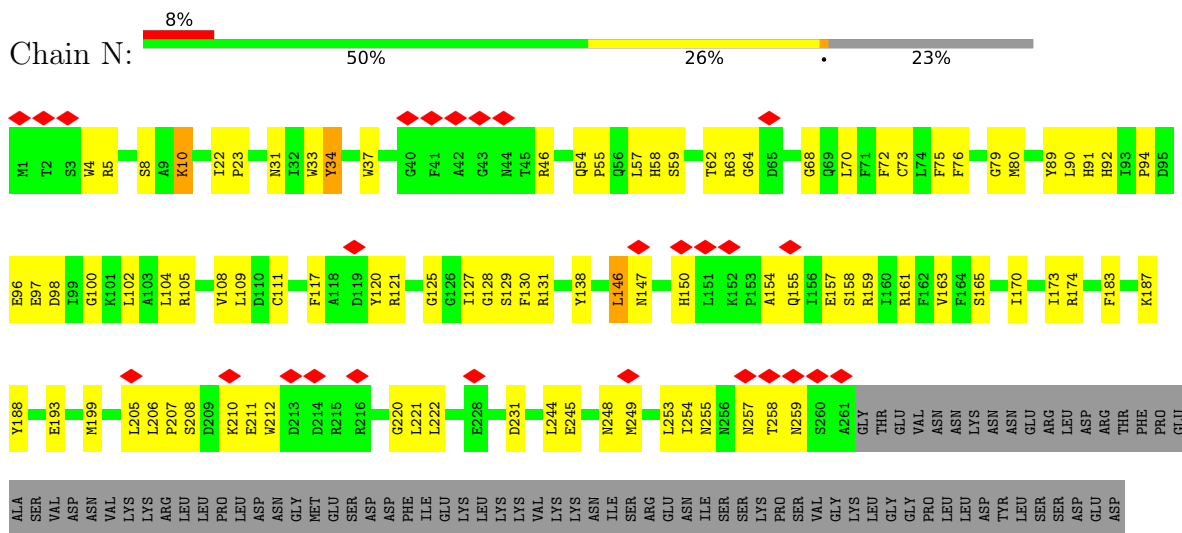


- Molecule 13: Pre-mRNA-splicing factor SLT11

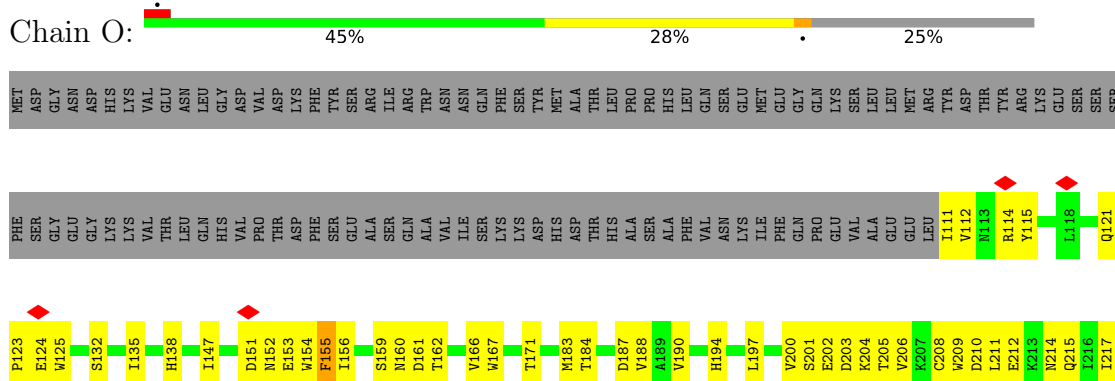


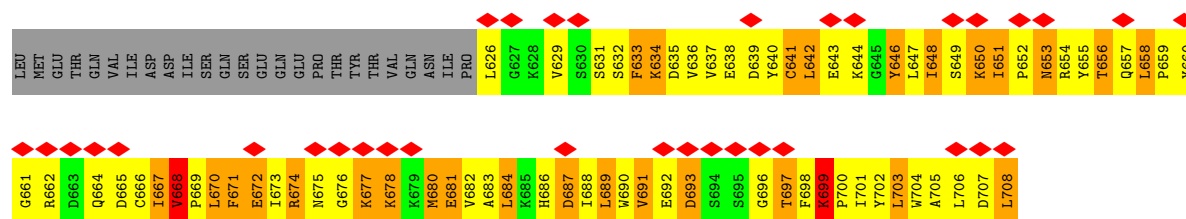


- Molecule 14: Pre-mRNA-splicing factor CWC2

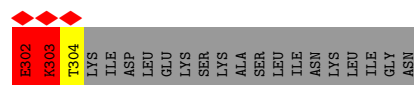
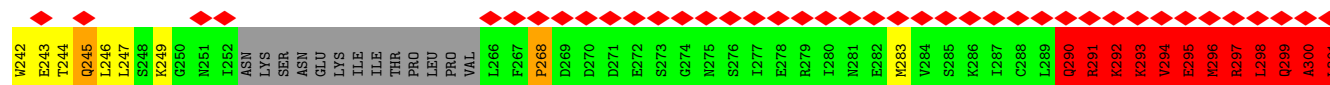
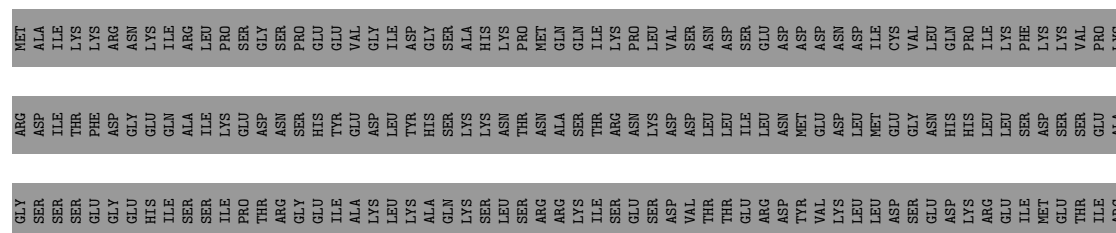


- Molecule 15: Pre-mRNA-splicing factor PRP46

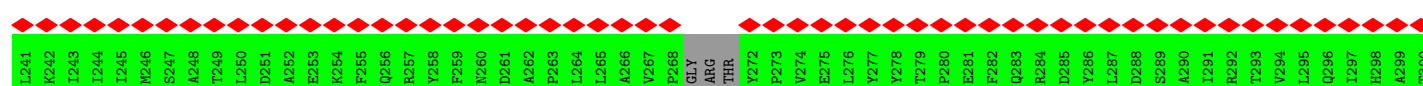
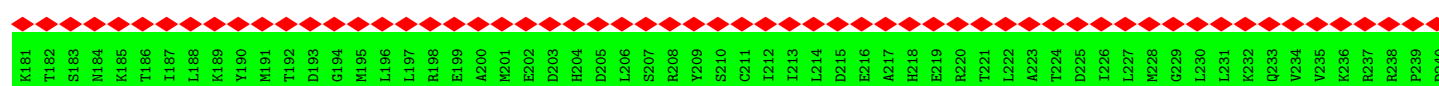
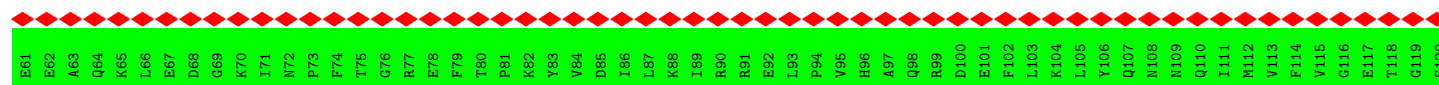
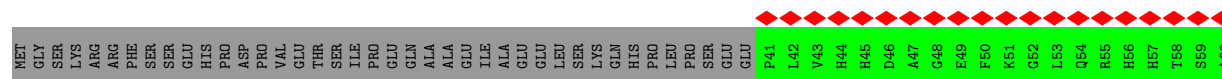
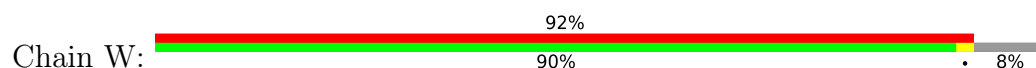




• Molecule 22: Pre-mRNA-splicing factor NTR2



• Molecule 23: Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43



A661	K601	E541	D481	A421	P361	E301
K662	W602	I542	F482	Q422	E362	E302
K663	C603	L543	M483	Q423	S363	A303
R664	R604	T544	D484	R424	H364	G304
S665	D605	I545	P485	A425	N365	D305
G666	H606	V546	P486	G426	G366	I306
A667	Y607	A547	A487	R427	R367	L307
K668	L608	M548	P488	A428	P368	L308
G669	N609	L549	E489	G429	G369	F309
Y670	Y610	S550	T490	R430	R370	L310
I671	R611	V551	M491	T431	K371	T311
T672	S612	P552	M492	R432	V372	G312
V673	L613	N553	R493	P433	V373	E313
K674	S614	V554	A494	G434	I374	D314
D675	A615	F555	L495	K435	S375	E315
N676	A616	I556	E496	C436	T376	I316
Q677	D617	R557	E497	F437	N377	E317
D678	N618	P558	L498	R438	I378	D318
V679	I619	T559	M499	L439	A379	A319
L680	R620	K560	Y500	Y440	E380	V320
I681	S621	D561	L501	T441	T381	R321
H682	Q622	K562	A502	E442	S382	K322
P683	L623	K563	C503	E443	L383	I323
S684	E624	R564	L504	A444	T384	S324
T685	R625	A565	D505	F445	I385	L325
V686	L626	D566	D506	Q446	D386	E326
L687	M627	D567	E507	K447	G327	G327
G688	N628	A568	G508	E448	I388	D328
H689	R629	K569	N509	L449	V389	Q329
D690	Y630	N570	L510	I450	Y390	L330
A691	N631	I571	T511	E451	V391	V331
E692	L632	F572	P512	Q452	G392	R332
W693	E633	A573	L513	S453	D393	E333
V694	L634	H574	G514	Y454	P394	E334
I695	N635	P575	R515	P455	G395	G335
Y696	T636	D576	L516	E456	F396	C336
N697	T637	G577	A517	I457	S397	G337
E698	D638	D578	S518	L458	K398	P338
F699	Y639	H579	Q519	R459	Q399	L339
V700	E640	I580	F520	S460	K400	S340
L701	S641	T581	P521	M461	V401	V341
T702	P642	L582	L522	L462	Y402	Y342
S703	K643	L583	D523	S463	N403	P343
K704	Y644	N584	P524	S464	P404	L344
N705	F645	V585	M525	T465	R405	Y345
Y706	D646	Y586	L526	Y466	I406	G346
I707	N647	H587	A527	L467	R407	S347
R708	I648	A588	V528	E468	V408	L348
T709	R649	F589	M529	L469	E409	P349
V710	K650	K590	L530	K470	S410	P350
T711	A651	S591	I531	K471	L411	H351
S712	L652	D592	G532	L472	L412	Q352
V713	A653	E593	S533	G473	V413	Q353
R714	S654	A594	F534	I474	S414	Q354
F715	G655	Y595	E535	D475	P415	R355
E716	P656	E596	F536	D476	I416	I356
W717	F657	Y597	Q537	L477	S417	F357
L718	M658	G598	C538	V478	K418	E358
I719	Q659	I599	S539	H479	A419	P359
E720	V660	H600	N540	F480	S420	A360

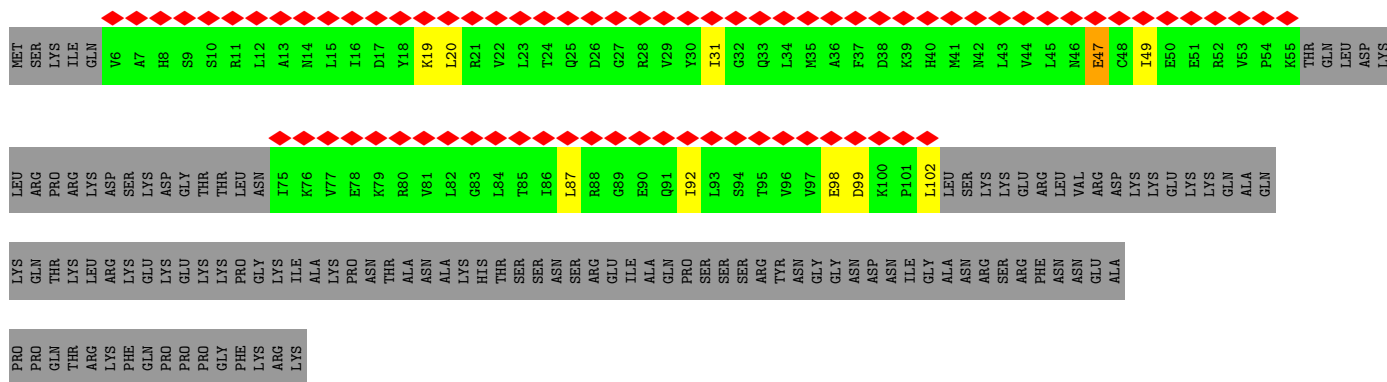
• Molecule 24: Small nuclear ribonucleoprotein-associated protein B

Chain a: 

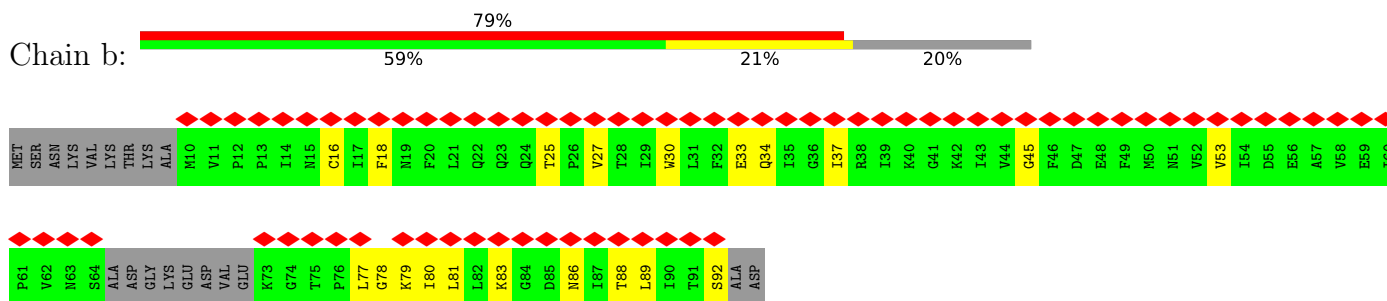
GLN	THR	LEU	ARG	LYS	ARG	GLY	GLN	PRO	PRO	GLY	LYS	PRO	GLY	LYS	LYS	ILE	ALA	LYS	PRO	ASN	THR	ASN	ALA	ALA	LYS	HIS	THR	SER	SER	ASN	SER	ARG	GLU	ILE	GLN	PRO	SER	SER	SER	ARG	TYR	ASN	GLY	GLY	ASN	ASP	ASN	ILE	GLY	ALA	ALA	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN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

• Molecule 24: Small nuclear ribonucleoprotein-associated protein B

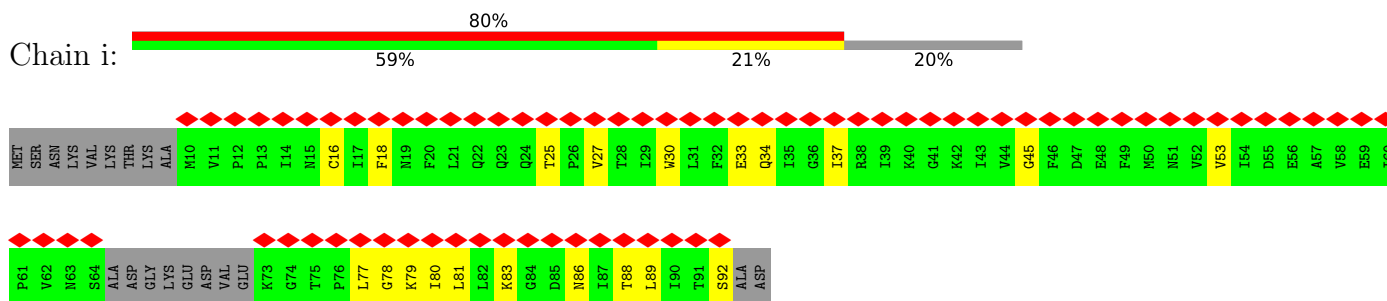
Chain h: 



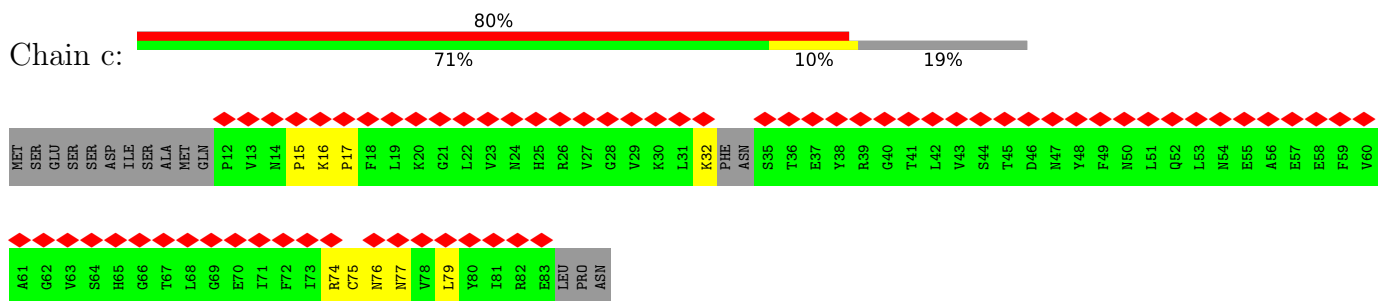
- Molecule 25: Small nuclear ribonucleoprotein E



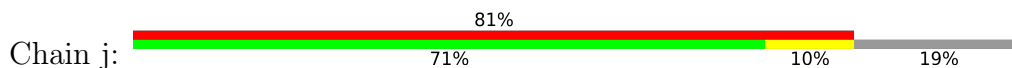
- Molecule 25: Small nuclear ribonucleoprotein E

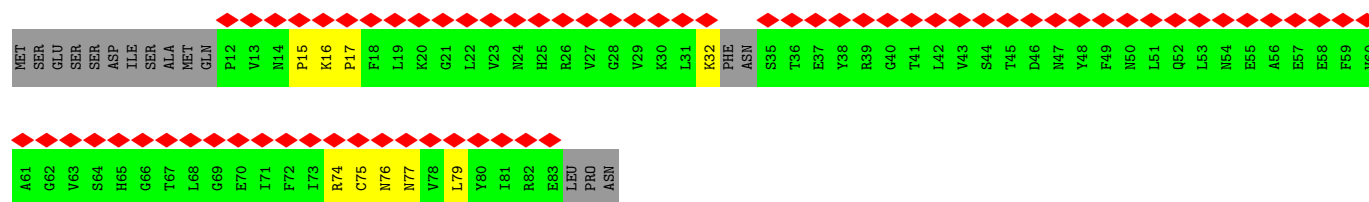


- Molecule 26: Small nuclear ribonucleoprotein F

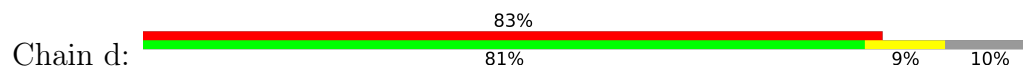


- Molecule 26: Small nuclear ribonucleoprotein F

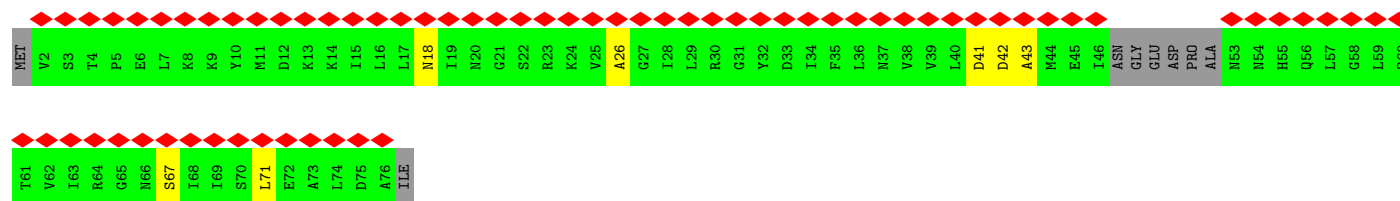
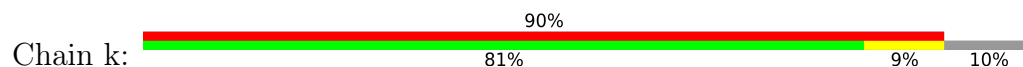




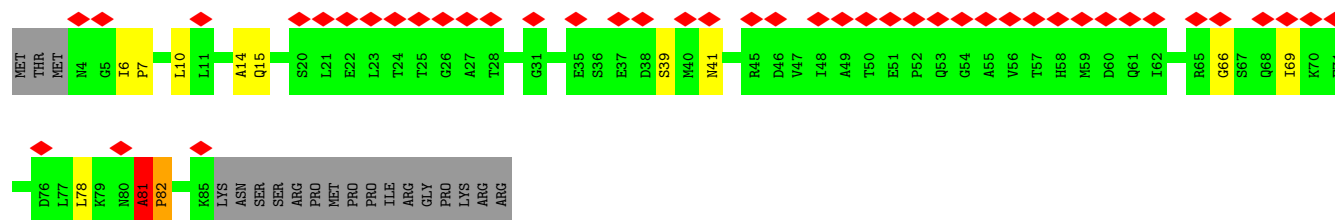
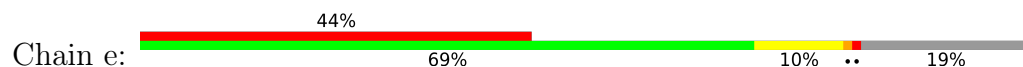
• Molecule 27: Small nuclear ribonucleoprotein G



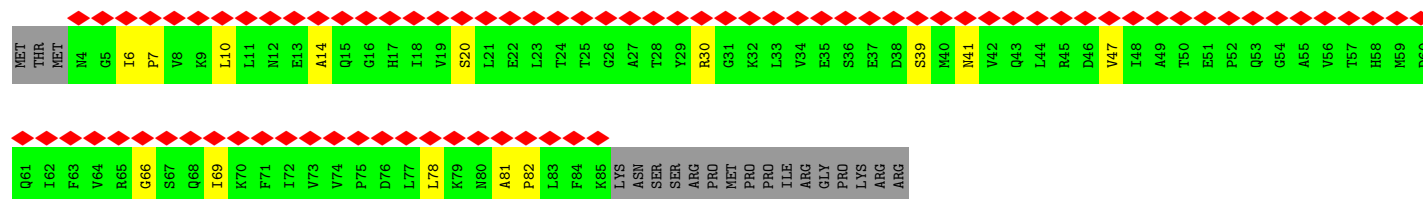
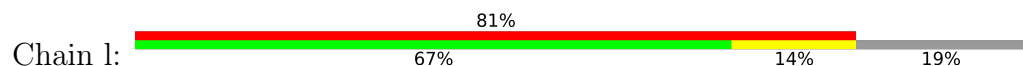
• Molecule 27: Small nuclear ribonucleoprotein G



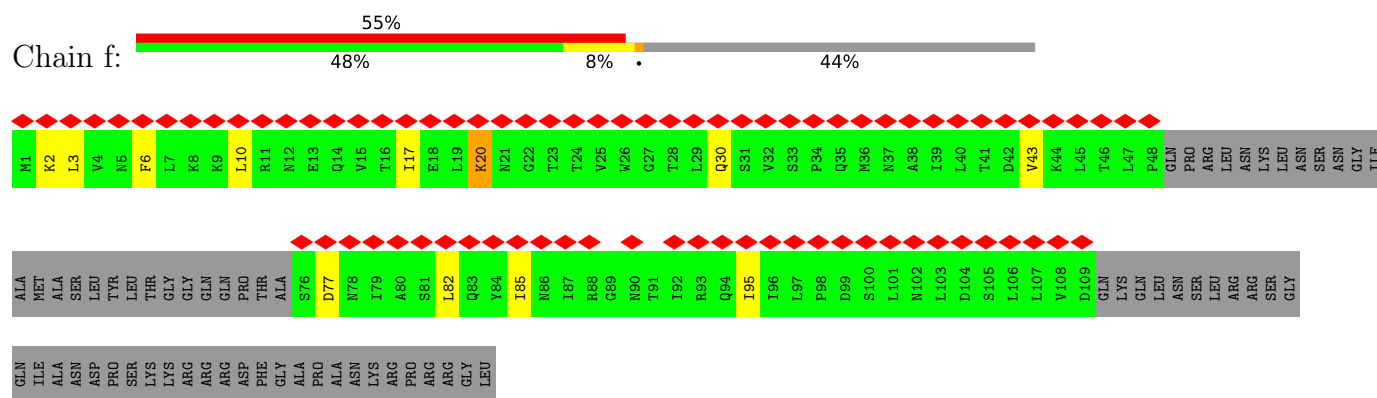
• Molecule 28: Small nuclear ribonucleoprotein Sm D3



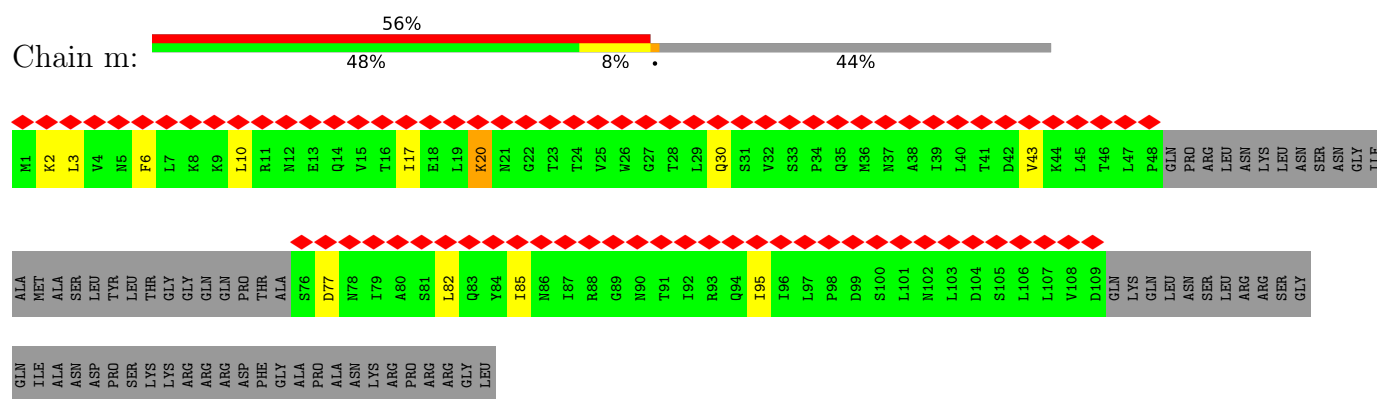
• Molecule 28: Small nuclear ribonucleoprotein Sm D3



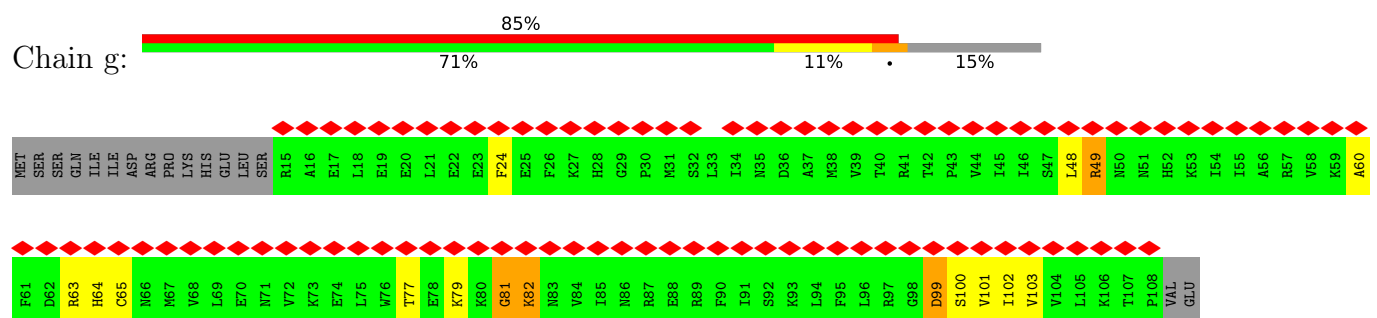
- Molecule 29: Small nuclear ribonucleoprotein Sm D1



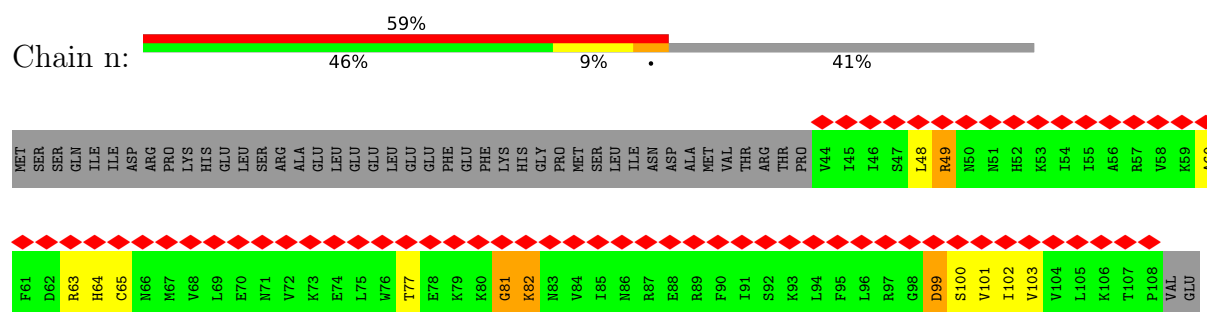
- Molecule 29: Small nuclear ribonucleoprotein Sm D1



- Molecule 30: Small nuclear ribonucleoprotein Sm D2



- Molecule 30: Small nuclear ribonucleoprotein Sm D2



- Molecule 31: U2 small nuclear ribonucleoprotein A'



[illegible]

- Molecule 33: Pre-mRNA-processing factor 19



M1	L2	C3	A4	I5	S6	G7	K8	V9	P10	R11	R12	P13	V14	L15	S16	P17	K18	S19	R20	T21	T22	F23	E24	K25	S26	T27	L28	E29	Q30	Y31	V32	K33	D34	T35	G36	N37	D38	P39	I40	T41	N42	E43	P44	L45	L46	T47	E48	E49	I50	V51	E52	I53	VAL	PRO	S56	A57	Q58	Q59	A60
----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

S61	L62	T63	E64	S65	THR	ASN	ASN	SER	ALA	THR	LEU	LYS	ALA	ALA	ASN	TYR	SER	I77	F78	M79	L80	L81	T82	S83	L84	L84	Q85	M86	E87	M88	D89	A90	I91	M92	L93	E94	N95	F96	K97	L98	R99	S100	T101	L102	D103	S104	L105	T106	K107	L108	L109	S110	T111	V112	M113	Y114	E115	R116	D117	A118	A119	V120
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

L121	V122	A123	A124	Q125	L126	L127	M128	E129	K130	M131	E132	D133	S134	K135	D136	L137	P138	K139	S140	S141	Q142	GLN	ALA	VAL	ALA	ALA	ILE	THR	ARG	ARG	GLU	GLU	PHE	LEU	GLN	GLY	LEU	LEU	LEU	GLN	SER	SER	ARG	ASP	PHE	VAL	ALA	ALA	ARG	GLY	LYS	LEU	LEU	ALA	LYS	ALA	PRO	LYS	TRP	PRO	ILE	LEU	LYS	LYS	ASN	LEU
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

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

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

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

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

CYS GLY ASP GLY GLY ILE ALA ALA ILE LEU LYS THR ASN ASP SER PHE ASN ILE VAL ALA LEU THR PRO

- Molecule 33: Pre-mRNA-processing factor 19



M1	L2	C3	A4	I5	S6	G7	K8	V9	P10	R11	I12	P13	V14	L15	S16	P17	K18	S19	R20	T21	I22	F23	E24	K25	S26	L27	L28	E29	Q30	Y31	V32	K33	D34	T35	C36	N37	D38	P39	I40	T41	N42	E43	P44	L45	S46	I47	E48	E49	I50	V51	E52	I53	V54	P55	S56	A57	Q58	Q59	A60
----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

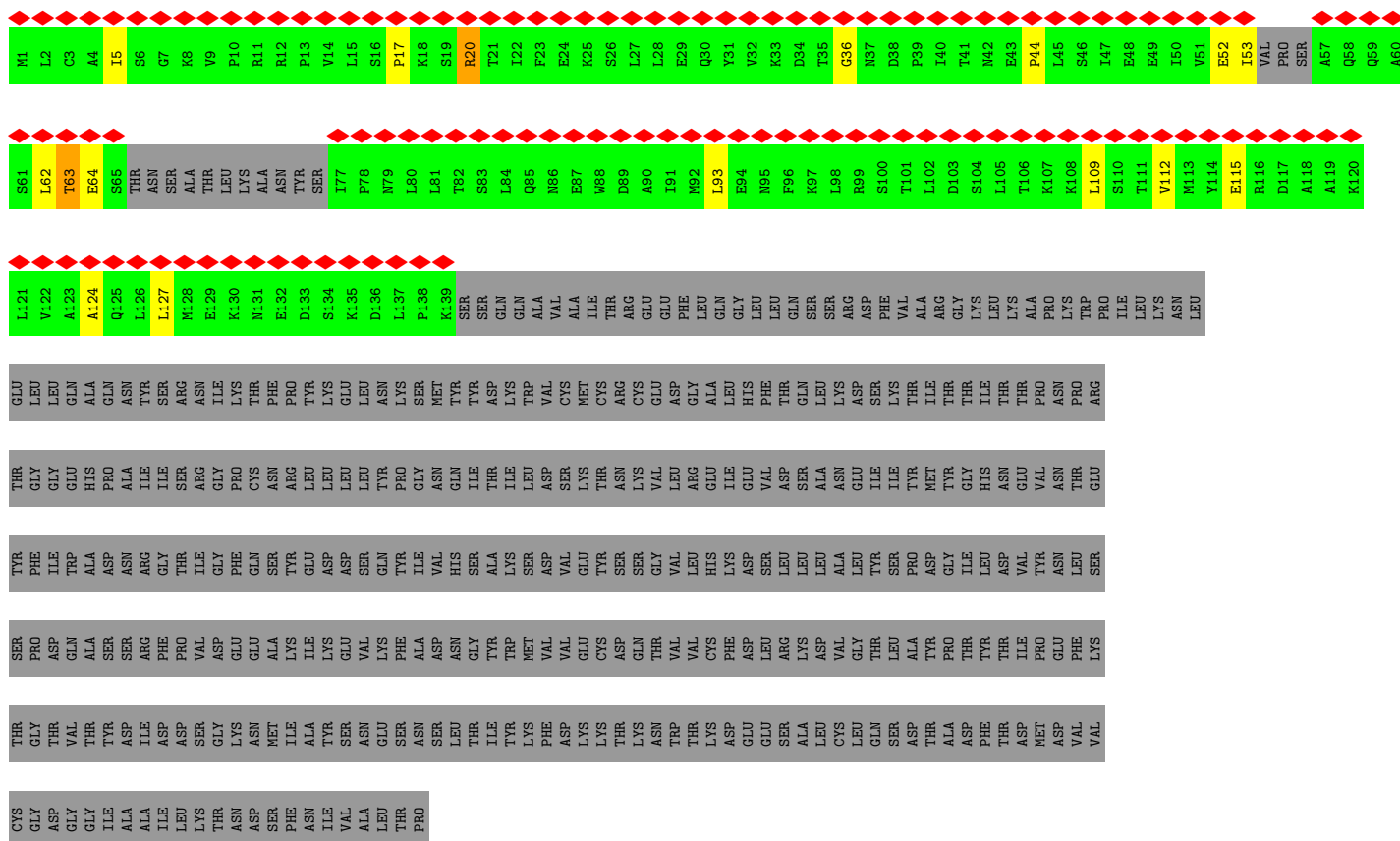
S61	LEU	THR	GLU	SER	ASN	SER	ALA	THR	LEU	LYS	ALA	ASN	TYR	S76	S77	P78	M79	L80	L81	T82	S83	L84	Q85	N86	E87	W88	D89	A90	I91	M92	L93	E94	N95	P96	K97	L98	R99	S100	T101	L102	D103	S104	L105	T106	K107	K108	L109	S110	T111	V112	M113	Y114	E115	R116	D117	A118	A119	V120
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

L121	V122	A123	A124	G125		L126	L127	M128	E129	K130	N131	E132	D133	S134	K135	D136	L137	P138	K139	S140	S141	Q142	Q143	ALA	VAL	ALA	ILE	THR	ARG	GLU	GIU	PHE	LEU	LEU	GLN	GLY	GLY	LEU	LEU	GLN	SER	SER	ASP	ASP	PHE	VAL	ALA	ALA	ARG	GLY	LYS	PRO	TRP	PRO	ILE	LEU	LYS	ASN
------	------	------	------	------	--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

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

- Molecule 33: Pre-mRNA-processing factor 19



- Molecule 34: RNA (intron or U6 snRNA)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	150363	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	37.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.282	Depositor
Minimum map value	-0.140	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	522.4, 522.4, 522.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3060001, 1.3060001, 1.3060001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.80	16/16117 (0.1%)	0.84	33/21848 (0.2%)
2	B	0.48	0/2747	0.66	1/4267 (0.0%)
3	C	0.91	10/7434 (0.1%)	0.92	17/10070 (0.2%)
4	D	0.48	0/2405	0.66	0/3744
5	E	0.39	0/653	0.64	0/1010
6	F	0.73	11/1922 (0.6%)	0.95	13/2984 (0.4%)
7	G	0.58	0/919	1.06	2/1237 (0.2%)
8	H	0.65	9/3180 (0.3%)	0.97	27/4331 (0.6%)
9	I	0.68	0/3574	0.82	7/4863 (0.1%)
10	J	0.56	1/2962 (0.0%)	0.92	11/3987 (0.3%)
11	K	0.60	0/826	0.75	1/1097 (0.1%)
12	L	0.87	0/1314	0.90	1/1759 (0.1%)
13	M	0.85	1/1308 (0.1%)	0.85	1/1758 (0.1%)
14	N	0.77	0/2135	0.77	1/2871 (0.0%)
15	O	1.06	1/2704 (0.0%)	0.93	2/3676 (0.1%)
16	P	0.73	0/568	1.30	8/758 (1.1%)
17	Q	0.68	0/1604	0.83	1/2160 (0.0%)
18	R	0.36	0/378	0.75	0/498
19	S	0.73	0/200	1.15	1/264 (0.4%)
20	T	0.87	5/825 (0.6%)	1.44	17/1100 (1.5%)
21	U	0.92	1/2684 (0.0%)	1.98	70/3680 (1.9%)
22	V	0.69	1/622 (0.2%)	2.02	22/843 (2.6%)
23	W	0.36	1/3502 (0.0%)	0.95	2/4877 (0.0%)
24	a	0.55	0/636	0.76	0/856
24	h	0.55	0/615	0.76	0/829
25	b	0.64	0/585	0.86	0/795
25	i	0.64	0/585	0.86	0/795
26	c	0.61	0/564	0.87	0/761
26	j	0.61	0/564	0.87	0/761
27	d	0.53	0/532	0.82	1/715 (0.1%)
27	k	0.53	0/532	0.82	1/715 (0.1%)
28	e	0.55	0/634	0.96	2/859 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	l	0.54	0/634	0.96	0/859
29	f	0.58	0/649	0.81	0/880
29	m	0.58	0/649	0.81	0/880
30	g	0.65	0/753	0.96	2/1013 (0.2%)
30	n	0.65	0/535	0.86	2/717 (0.3%)
31	o	1.24	6/839 (0.7%)	2.35	43/1127 (3.8%)
32	p	1.00	2/514 (0.4%)	1.86	8/686 (1.2%)
33	q	0.54	0/837	0.84	0/1129
33	r	0.54	0/854	0.91	0/1151
33	s	0.57	0/856	0.92	0/1155
33	t	0.54	0/828	0.86	0/1117
34	x	0.29	0/194	0.54	0/298
All	All	0.74	65/73972 (0.1%)	0.99	297/101780 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
3	C	0	2
11	K	0	1
13	M	0	2
15	O	0	6
16	P	0	2
17	Q	0	1
19	S	0	2
20	T	0	9
21	U	0	47
22	V	0	14
23	W	0	1
27	d	0	1
27	k	0	1
28	e	0	2
28	l	0	2
30	g	0	2
30	n	0	2
All	All	0	104

The worst 5 of 65 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	934	HIS	N-CA	-10.65	1.32	1.46
31	o	69	ASP	CA-CB	-10.65	1.38	1.53
3	C	933	TRP	CA-C	-10.48	1.38	1.52
8	H	712	CYS	CB-SG	-8.52	1.53	1.81
1	A	1497	ARG	CA-C	8.12	1.63	1.52

The worst 5 of 297 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	o	44	PRO	N-CA-CB	15.99	113.94	103.23
16	P	6	ARG	CA-C-N	15.58	139.31	119.84
16	P	6	ARG	C-N-CA	15.58	139.31	119.84
23	W	462	LEU	CA-C-N	-14.27	94.29	121.54
23	W	462	LEU	C-N-CA	-14.27	94.29	121.54

There are no chirality outliers.

5 of 104 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1375	LEU	Peptide
1	A	239	PHE	Mainchain,Peptide
1	A	539	PRO	Peptide
1	A	772	GLU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	15715	0	15685	1134	0
2	B	2465	0	1251	66	0
3	C	7278	0	7450	659	0
4	D	2150	0	1085	120	0
5	E	587	0	295	58	0
6	F	1727	0	877	176	0
7	G	921	0	604	11	0
8	H	3204	0	1664	59	0
9	I	3542	0	2625	129	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	2944	0	2434	194	0
11	K	822	0	845	54	0
12	L	1290	0	1312	36	0
13	M	1298	0	1176	100	0
14	N	2089	0	2053	80	0
15	O	2646	0	2639	115	0
16	P	554	0	540	50	0
17	Q	1583	0	1608	123	0
18	R	379	0	375	60	0
19	S	195	0	198	29	0
20	T	816	0	737	127	0
21	U	2690	0	1500	258	0
22	V	619	0	506	133	0
23	W	3505	0	1553	14	0
24	a	631	0	670	3	0
24	h	610	0	640	17	0
25	b	575	0	597	21	0
25	i	575	0	597	21	0
26	c	554	0	556	18	0
26	j	554	0	556	18	0
27	d	529	0	557	2	0
27	k	529	0	557	2	0
28	e	625	0	647	8	0
28	l	625	0	647	8	0
29	f	644	0	686	14	0
29	m	644	0	686	15	0
30	g	741	0	778	18	0
30	n	528	0	573	17	0
31	o	841	0	614	17	0
32	p	513	0	402	13	0
33	q	831	0	667	11	0
33	r	849	0	677	12	0
33	s	850	0	682	11	0
33	t	823	0	654	7	0
34	x	177	0	91	13	0
35	A	36	0	6	7	0
36	C	32	0	12	4	0
37	C	1	0	0	0	0
37	D	5	0	0	0	0
38	L	3	0	0	0	0
38	M	2	0	0	0	0
38	N	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	72347	0	61564	3431	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 26.

The worst 5 of 3431 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)
1:A:1343:PHE:CD1	1:A:1350:ILE:HD13	1.33	1.60
1:A:1343:PHE:HD1	1:A:1350:ILE:CD1	1.12	1.59
3:C:274:ILE:CD1	3:C:385:PHE:HD2	1.17	1.56
3:C:681:CYS:HB3	3:C:850:LEU:CD1	1.33	1.54
1:A:1394:LEU:CD1	1:A:1556:ILE:HG21	1.37	1.49

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1895/2413 (78%)	1750 (92%)	125 (7%)	20 (1%)	11	42
3	C	907/1008 (90%)	820 (90%)	70 (8%)	17 (2%)	6	33
7	G	149/175 (85%)	134 (90%)	12 (8%)	3 (2%)	6	32
8	H	529/859 (62%)	505 (96%)	18 (3%)	6 (1%)	11	42
9	I	500/687 (73%)	468 (94%)	30 (6%)	2 (0%)	30	62
10	J	413/590 (70%)	384 (93%)	22 (5%)	7 (2%)	7	35
11	K	98/215 (46%)	96 (98%)	2 (2%)	0	100	100
12	L	155/157 (99%)	136 (88%)	17 (11%)	2 (1%)	9	39
13	M	172/364 (47%)	151 (88%)	19 (11%)	2 (1%)	10	41

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	N	259/339 (76%)	241 (93%)	18 (7%)	0	100	100
15	O	335/451 (74%)	295 (88%)	34 (10%)	6 (2%)	6	34
16	P	62/175 (35%)	56 (90%)	4 (6%)	2 (3%)	3	24
17	Q	193/379 (51%)	175 (91%)	13 (7%)	5 (3%)	4	27
18	R	44/278 (16%)	44 (100%)	0	0	100	100
19	S	21/455 (5%)	19 (90%)	1 (5%)	1 (5%)	2	16
20	T	97/283 (34%)	93 (96%)	4 (4%)	0	100	100
21	U	442/708 (62%)	430 (97%)	5 (1%)	7 (2%)	7	36
22	V	87/322 (27%)	82 (94%)	4 (5%)	1 (1%)	11	42
23	W	702/767 (92%)	657 (94%)	39 (6%)	6 (1%)	14	46
24	a	76/196 (39%)	69 (91%)	7 (9%)	0	100	100
24	h	74/196 (38%)	67 (90%)	7 (10%)	0	100	100
25	b	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
25	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
26	c	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	37
26	j	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	37
27	d	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
27	k	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
28	e	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	39
28	l	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	39
29	f	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
29	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
30	g	92/110 (84%)	85 (92%)	6 (6%)	1 (1%)	11	42
30	n	63/110 (57%)	58 (92%)	4 (6%)	1 (2%)	7	36
31	o	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	7	36
32	p	77/111 (69%)	75 (97%)	2 (3%)	0	100	100
33	q	120/503 (24%)	114 (95%)	4 (3%)	2 (2%)	7	35
33	r	123/503 (24%)	117 (95%)	6 (5%)	0	100	100
33	s	125/503 (25%)	115 (92%)	6 (5%)	4 (3%)	3	24
33	t	119/503 (24%)	111 (93%)	5 (4%)	3 (2%)	4	28
All	All	8774/14606 (60%)	8126 (93%)	544 (6%)	104 (1%)	13	41

5 of 104 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1347	ARG
1	A	1359	ILE
1	A	1385	PRO
1	A	1403	SER
3	C	363	PRO

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	1727/2182 (79%)	1648 (95%)	79 (5%)	24	51
3	C	822/910 (90%)	783 (95%)	39 (5%)	23	51
7	G	40/165 (24%)	27 (68%)	13 (32%)	0	2
8	H	59/786 (8%)	48 (81%)	11 (19%)	1	9
9	I	219/633 (35%)	216 (99%)	3 (1%)	59	72
10	J	213/525 (41%)	202 (95%)	11 (5%)	21	49
11	K	92/193 (48%)	92 (100%)	0	100	100
12	L	141/141 (100%)	138 (98%)	3 (2%)	47	66
13	M	121/332 (36%)	115 (95%)	6 (5%)	22	49
14	N	224/296 (76%)	221 (99%)	3 (1%)	61	73
15	O	295/397 (74%)	295 (100%)	0	100	100
16	P	55/151 (36%)	54 (98%)	1 (2%)	51	70
17	Q	173/328 (53%)	161 (93%)	12 (7%)	14	41
18	R	40/256 (16%)	29 (72%)	11 (28%)	0	3
19	S	20/413 (5%)	13 (65%)	7 (35%)	0	1
20	T	75/272 (28%)	56 (75%)	19 (25%)	0	3
21	U	76/663 (12%)	48 (63%)	28 (37%)	0	1
22	V	47/296 (16%)	31 (66%)	16 (34%)	0	2
24	a	70/176 (40%)	69 (99%)	1 (1%)	59	72

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	h	67/176 (38%)	66 (98%)	1 (2%)	57	72
25	b	65/83 (78%)	60 (92%)	5 (8%)	12	38
25	i	65/83 (78%)	60 (92%)	5 (8%)	12	38
26	c	61/77 (79%)	60 (98%)	1 (2%)	55	71
26	j	61/77 (79%)	60 (98%)	1 (2%)	55	71
27	d	58/66 (88%)	56 (97%)	2 (3%)	32	59
27	k	58/66 (88%)	56 (97%)	2 (3%)	32	59
28	e	69/89 (78%)	68 (99%)	1 (1%)	59	72
28	l	69/89 (78%)	68 (99%)	1 (1%)	59	72
29	f	77/129 (60%)	74 (96%)	3 (4%)	28	56
29	m	77/129 (60%)	74 (96%)	3 (4%)	28	56
30	g	79/103 (77%)	73 (92%)	6 (8%)	12	38
30	n	59/103 (57%)	54 (92%)	5 (8%)	10	35
31	o	47/219 (22%)	44 (94%)	3 (6%)	16	43
32	p	25/100 (25%)	25 (100%)	0	100	100
33	q	62/451 (14%)	56 (90%)	6 (10%)	8	31
33	r	62/451 (14%)	54 (87%)	8 (13%)	4	21
33	s	63/451 (14%)	55 (87%)	8 (13%)	4	22
33	t	60/451 (13%)	55 (92%)	5 (8%)	10	35
All	All	5693/12508 (46%)	5364 (94%)	329 (6%)	20	45

5 of 329 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	U	672	GLU
25	i	18	PHE
21	U	687	ASP
22	V	245	GLN
30	n	99	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 108 such sidechains are listed below:

Mol	Chain	Res	Type
13	M	81	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	O	382	HIS
25	i	86	ASN
14	N	58	HIS
14	N	227	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	114/214 (53%)	30 (26%)	3 (2%)
34	x	8/9 (88%)	5 (62%)	0
4	D	100/112 (89%)	35 (35%)	8 (8%)
5	E	27/38 (71%)	15 (55%)	7 (25%)
6	F	79/1175 (6%)	30 (37%)	11 (13%)
All	All	328/1548 (21%)	115 (35%)	29 (8%)

5 of 115 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	29	G
2	B	31	G
2	B	32	G
2	B	33	U
2	B	42	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	E	9	U
6	F	1107	C
5	E	500	A
6	F	40	U
5	E	499	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 12 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	GTP	C	1500	37	33,34,34	1.32	4 (12%)	50,54,54	1.96	11 (22%)
35	IHP	A	3000	-	36,36,36	0.69	0	60,60,60	0.98	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GTP	C	1500	37	-	5/22/38/38	0/3/3/3
35	IHP	A	3000	-	-	10/30/54/54	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	C	1500	GTP	C5-N7	-3.25	1.32	1.39
36	C	1500	GTP	C6-N1	-2.92	1.33	1.38
36	C	1500	GTP	PA-O3A	-2.92	1.56	1.59
36	C	1500	GTP	C4-N9	-2.07	1.32	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	C	1500	GTP	N9-C4-N3	6.22	138.38	125.95
36	C	1500	GTP	C5-C4-N3	-5.98	118.87	128.39
36	C	1500	GTP	C2-N3-C4	4.89	120.72	112.30
36	C	1500	GTP	O6-C6-C5	-3.98	116.02	126.53
36	C	1500	GTP	C8-N9-C4	2.71	111.11	106.03

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

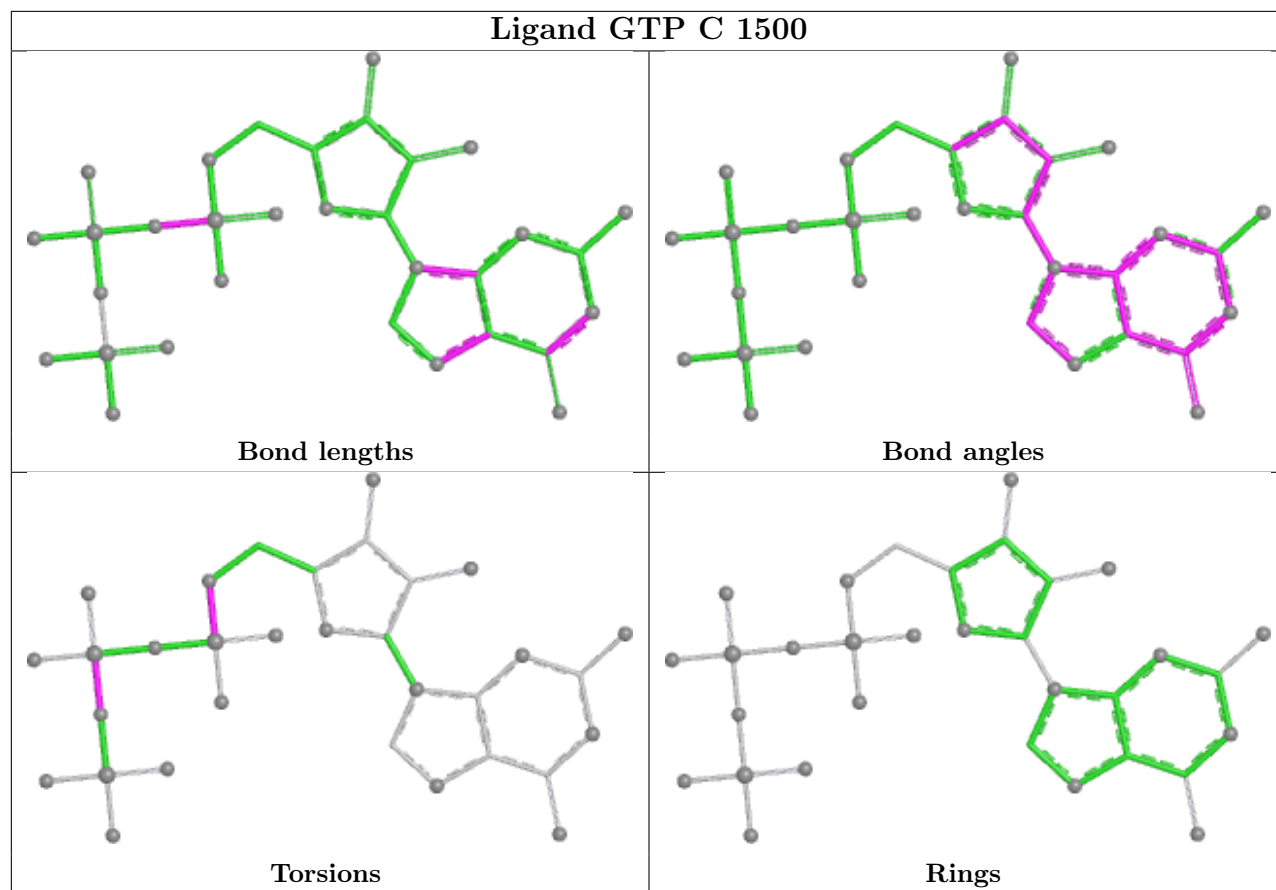
Mol	Chain	Res	Type	Atoms
35	A	3000	IHP	C1-C6-O16-P6
35	A	3000	IHP	C5-C6-O16-P6
36	C	1500	GTP	C5'-O5'-PA-O1A
36	C	1500	GTP	C5'-O5'-PA-O2A
35	A	3000	IHP	C4-O14-P4-O24

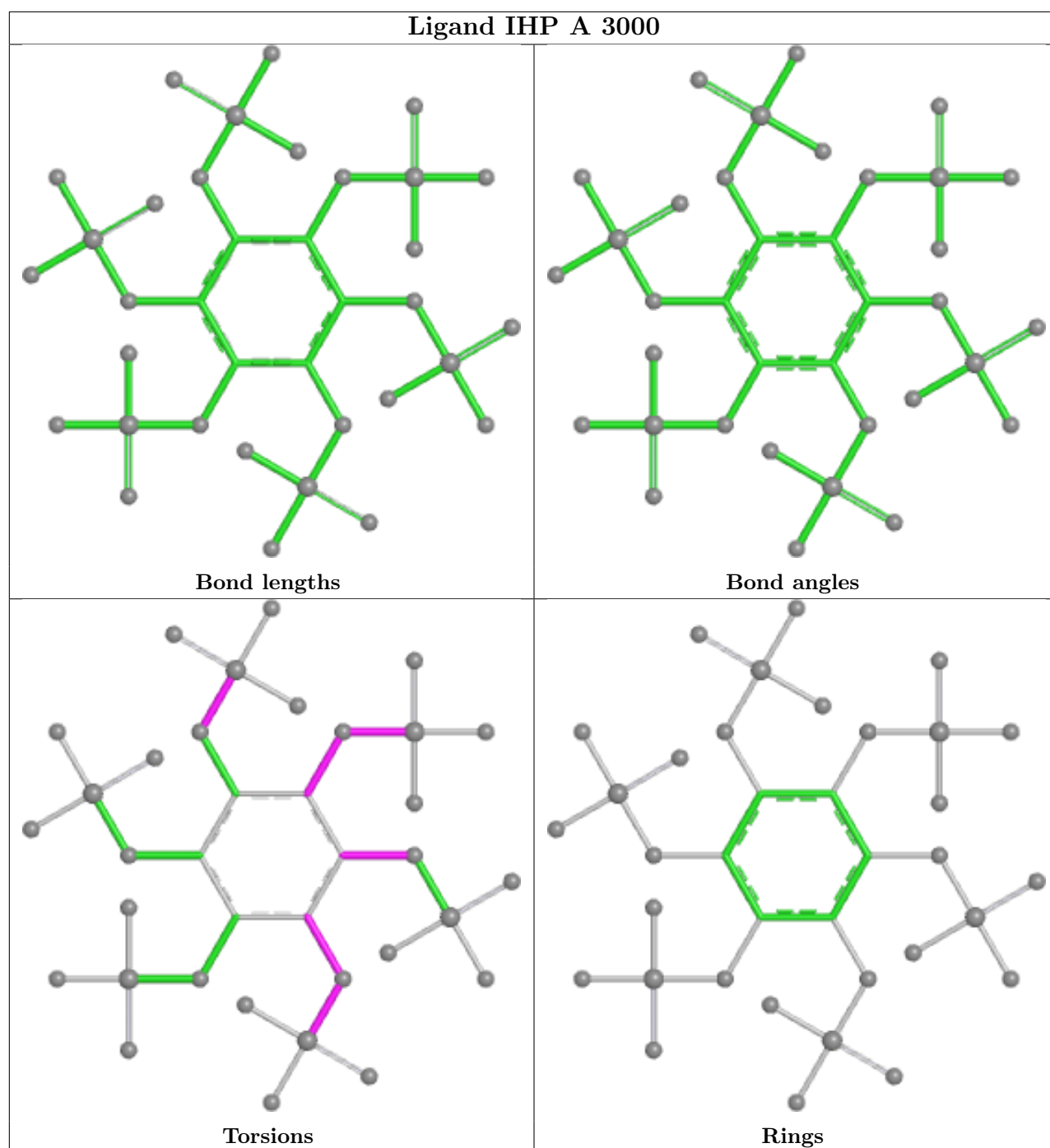
There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	C	1500	GTP	4	0
35	A	3000	IHP	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.

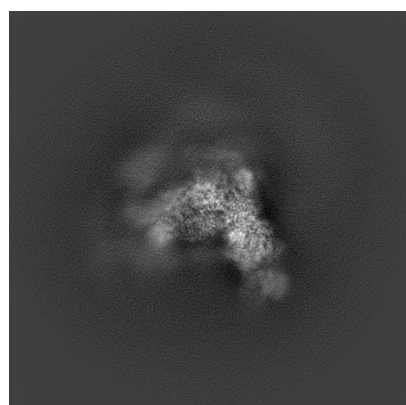
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6817. These allow visual inspection of the internal detail of the map and identification of artifacts.

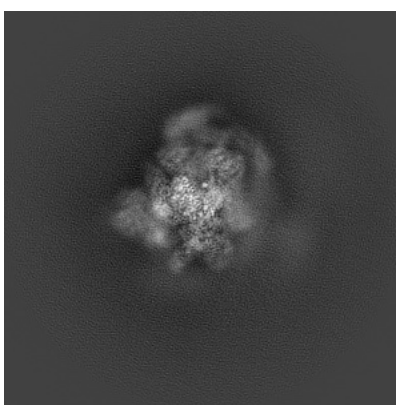
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

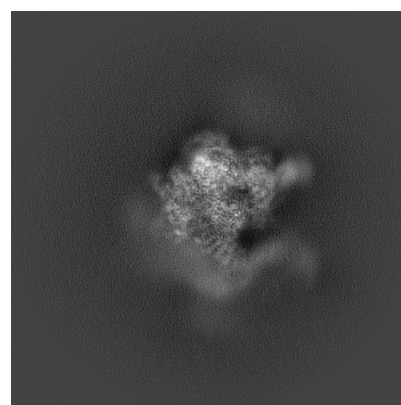
6.1.1 Primary map



X



Y

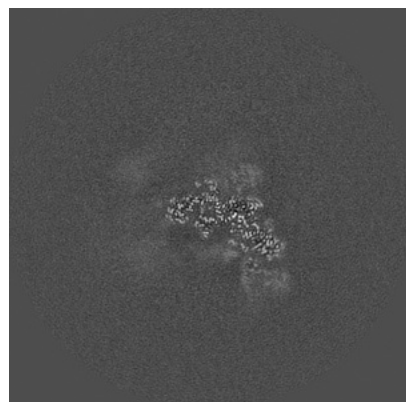


Z

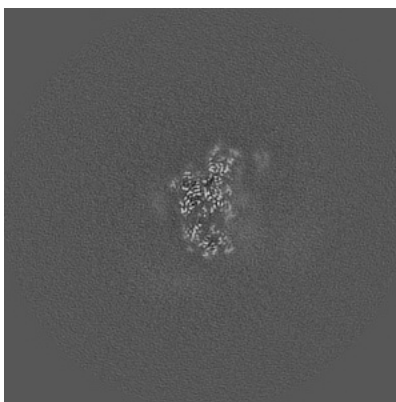
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

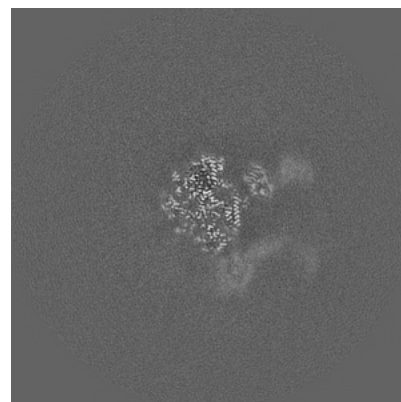
6.2.1 Primary map



X Index: 200



Y Index: 200

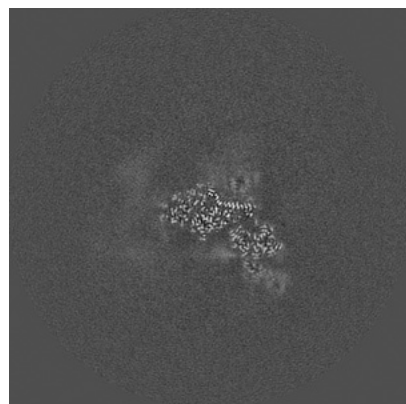


Z Index: 200

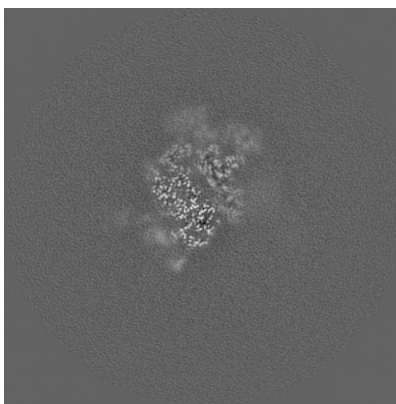
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

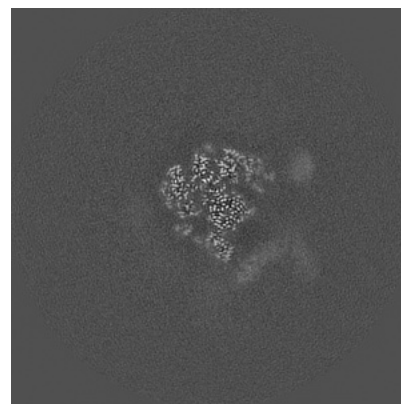
6.3.1 Primary map



X Index: 204



Y Index: 230

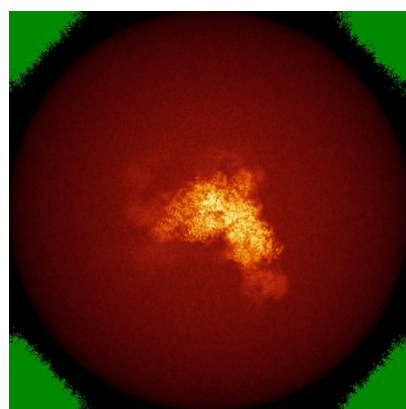


Z Index: 186

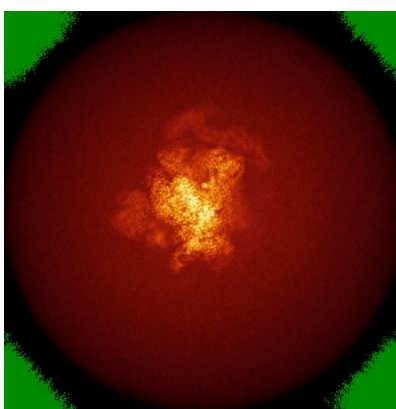
The images above show the largest variance slices of the map in three orthogonal directions.

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

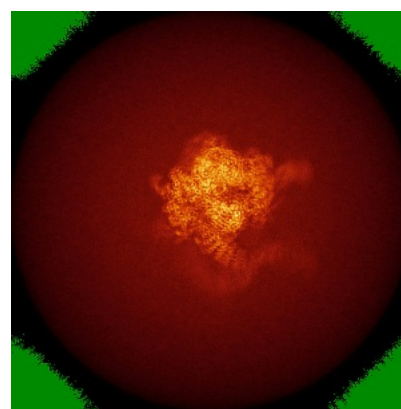
6.4.1 Primary map



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



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

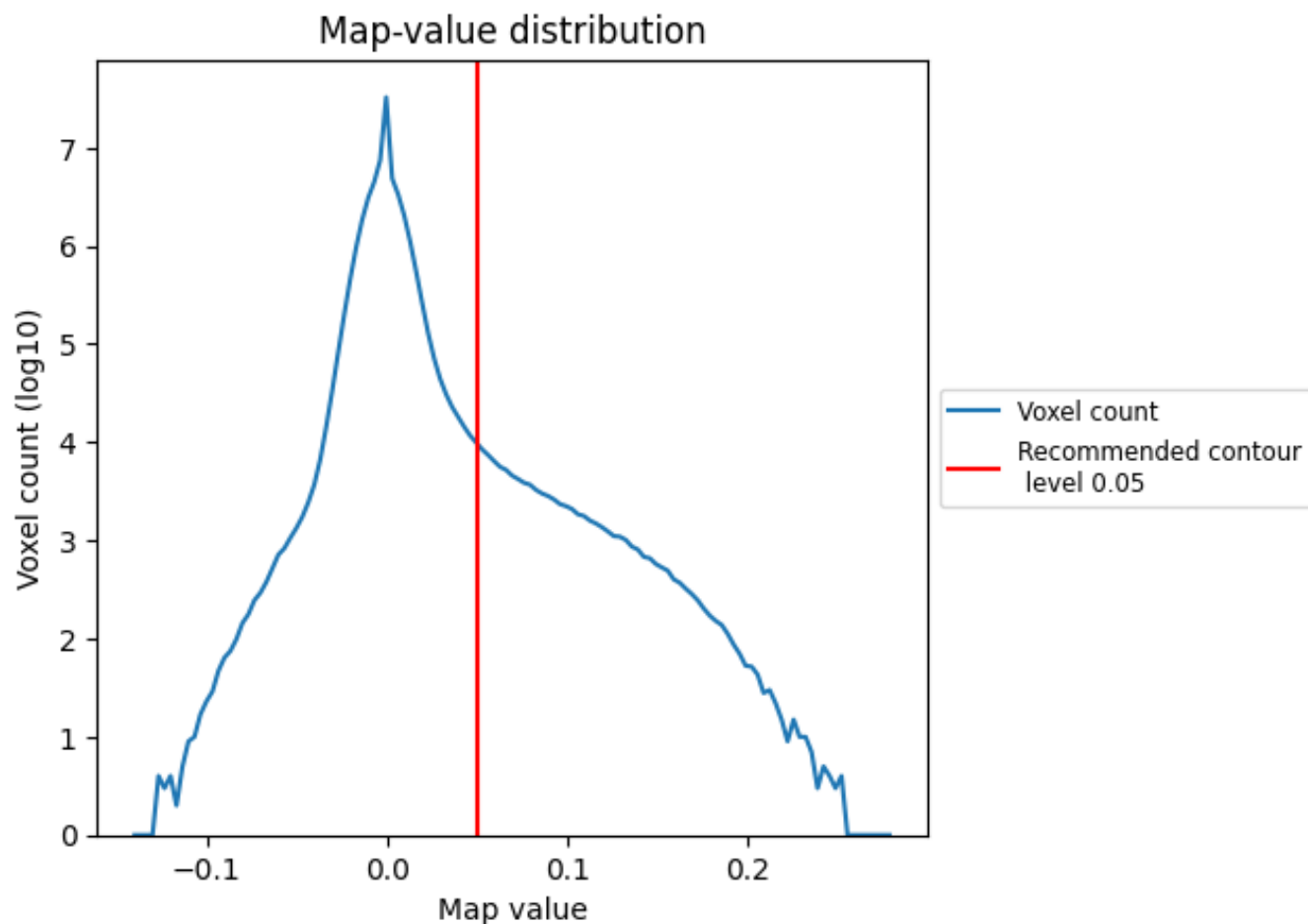
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

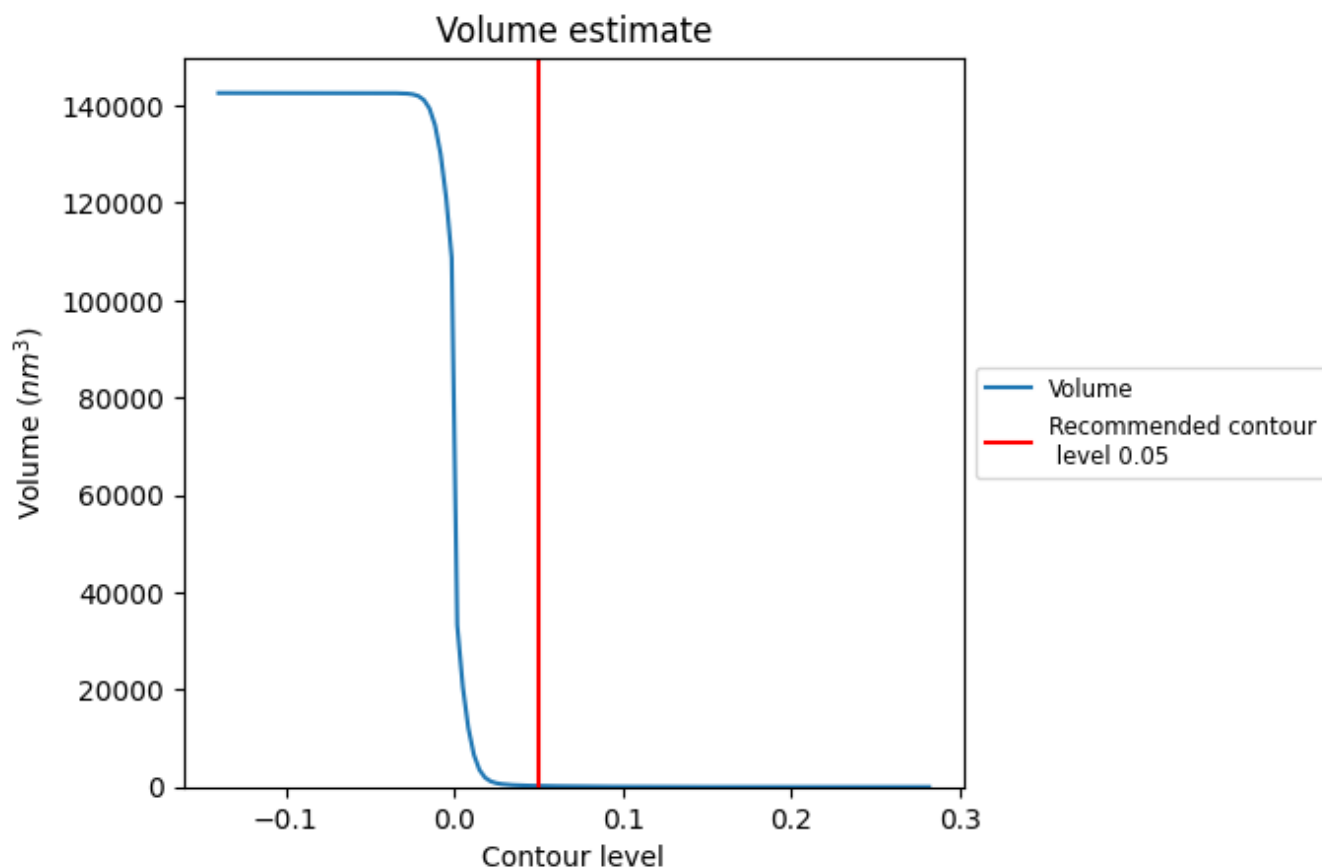
This section contains the results of statistical analysis of the map.

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.

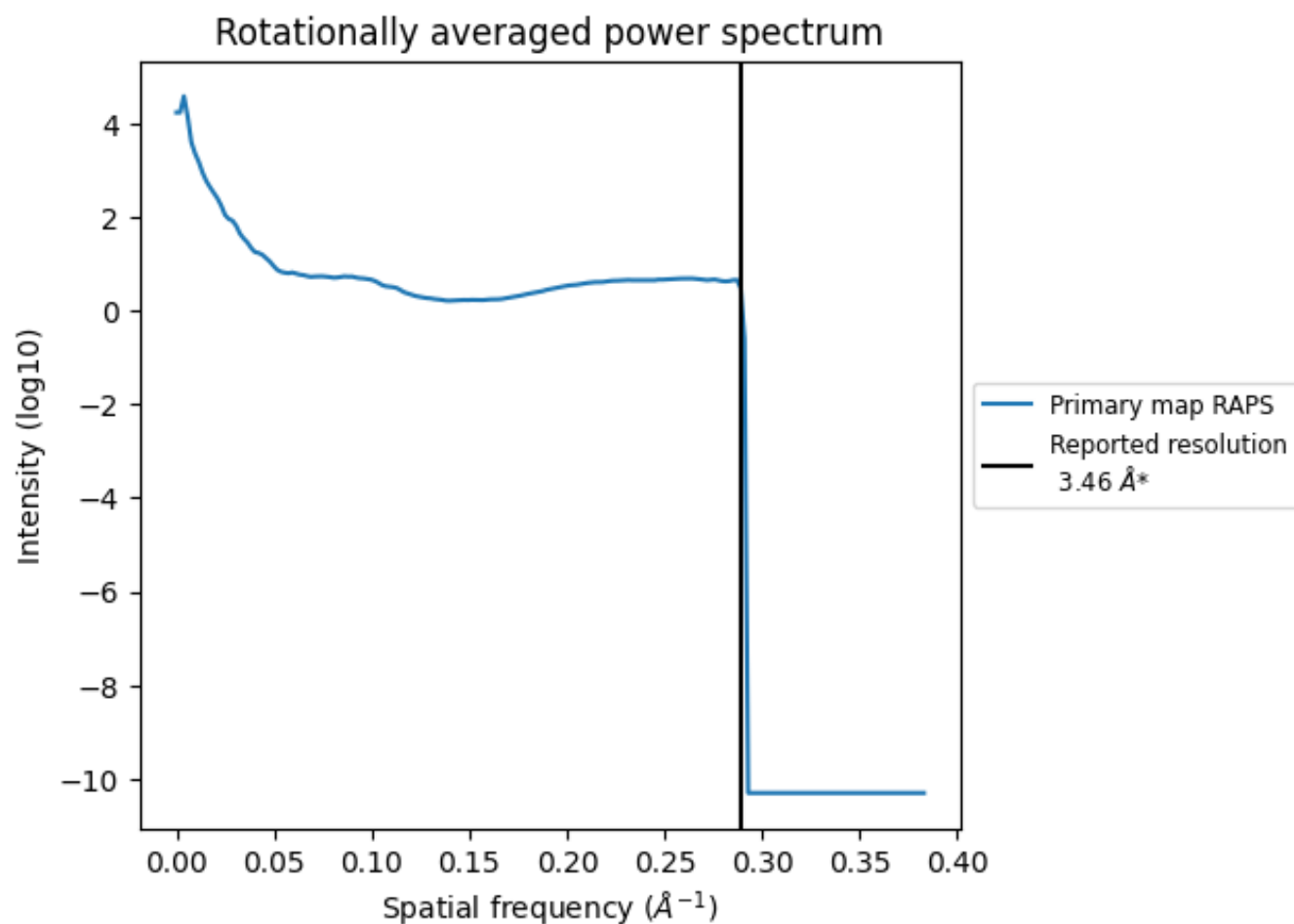
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 214 nm³; this corresponds to an approximate mass of 193 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 0.289 $\text{\AA}^{-1}$

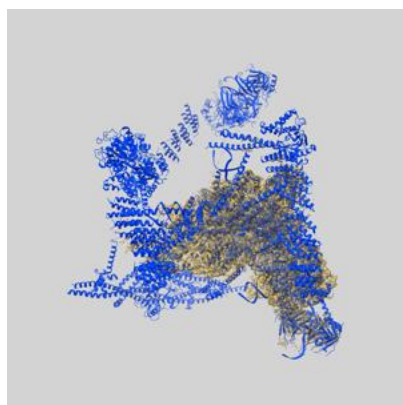
8 Fourier-Shell correlation

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

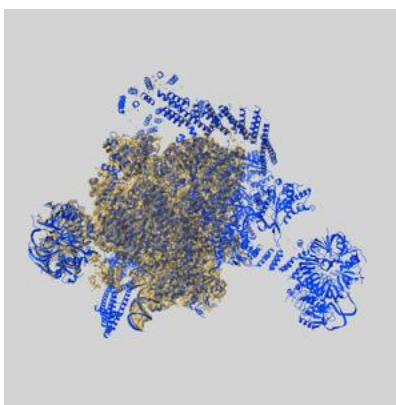
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6817 and PDB model 5Y88. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

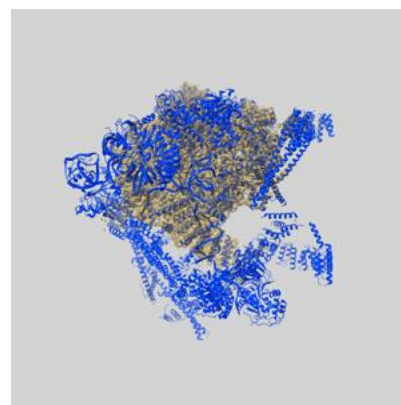
9.1 Map-model overlay [i](#)



X



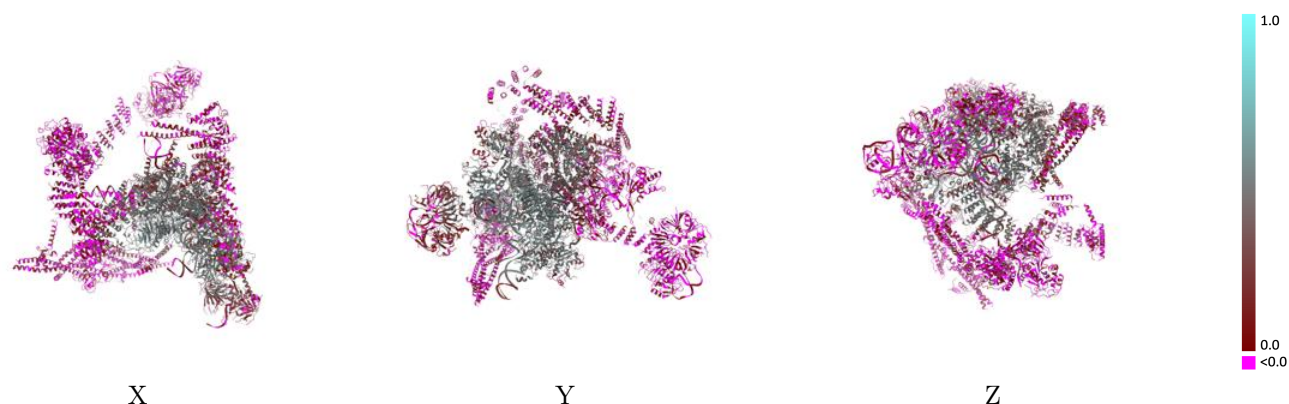
Y



Z

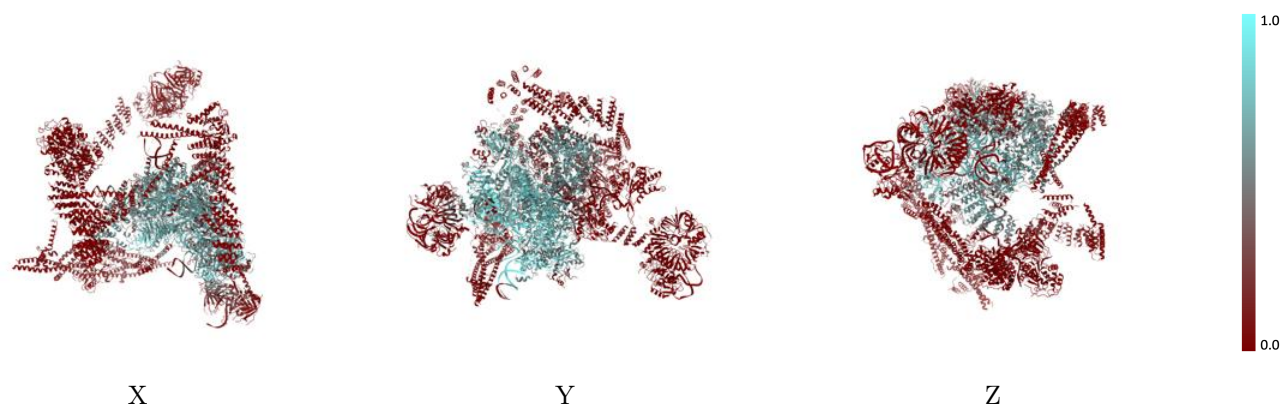
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



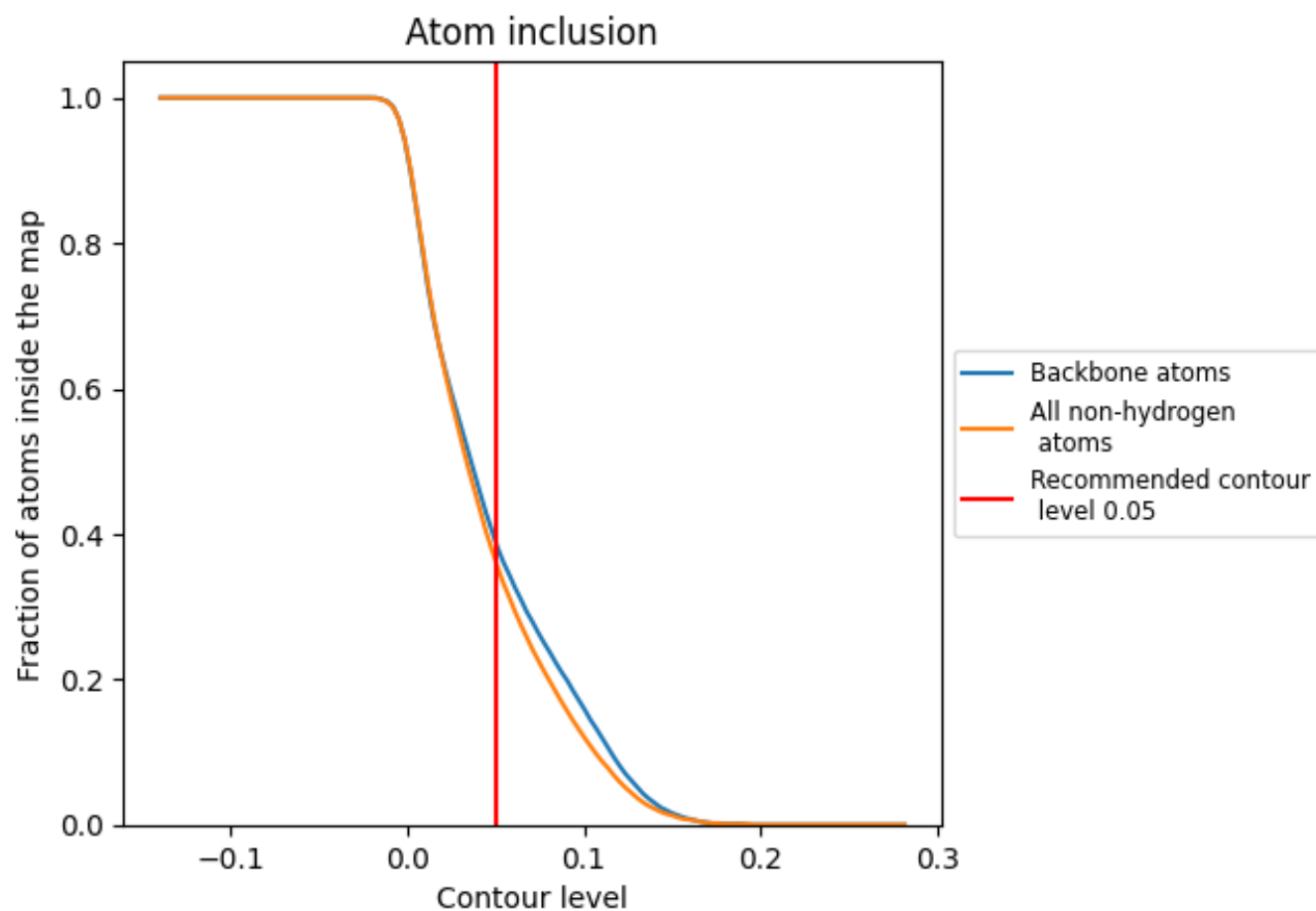
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion ⓘ



At the recommended contour level, 39% of all backbone atoms, 36% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3620	 0.2640
A	 0.4920	 0.3410
B	 0.6360	 0.3930
C	 0.6660	 0.4500
D	 0.7370	 0.4380
E	 0.2590	 0.1780
F	 0.1930	 0.1400
G	 0.0000	 0.0050
H	 0.0110	 0.0250
I	 0.3750	 0.2640
J	 0.2990	 0.2320
K	 0.3900	 0.3570
L	 0.7300	 0.4710
M	 0.5540	 0.4190
N	 0.6640	 0.4310
O	 0.7480	 0.5060
P	 0.4470	 0.4480
Q	 0.4960	 0.4030
R	 0.0920	 0.2520
S	 0.6430	 0.4470
T	 0.1840	 0.1710
U	 0.1330	 0.1710
V	 0.2630	 0.2790
W	 0.0000	 0.0080
a	 0.1670	 0.3050
b	 0.0380	 0.1550
c	 0.0370	 0.0920
d	 0.1570	 0.2530
e	 0.3560	 0.3730
f	 0.0770	 0.1570
g	 0.0500	 0.1510
h	 0.0000	 -0.0100
i	 0.0000	 -0.0110
j	 0.0000	 0.0030
k	 0.0000	 0.0180



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
l	 0.0000	 0.0080
m	 0.0000	 0.0270
n	 0.0000	 0.0050
o	 0.0000	 -0.0210
p	 0.0000	 0.0010
q	 0.0000	 0.0350
r	 0.0000	 -0.0090
s	 0.0000	 0.0000
t	 0.0000	 -0.0040
x	 0.0000	 -0.0440