



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:55 AM UTC

PDB ID : 6G90 / pdb_00006g90
EMDB ID : EMD-4364
Title : Prespliceosome structure provides insight into spliceosome assembly and regulation (map A2)
Authors : Plaschka, C.; Lin, P.-C.; Charenton, C.; Nagai, K.
Deposited on : 2018-04-10
Resolution : 4.00 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:

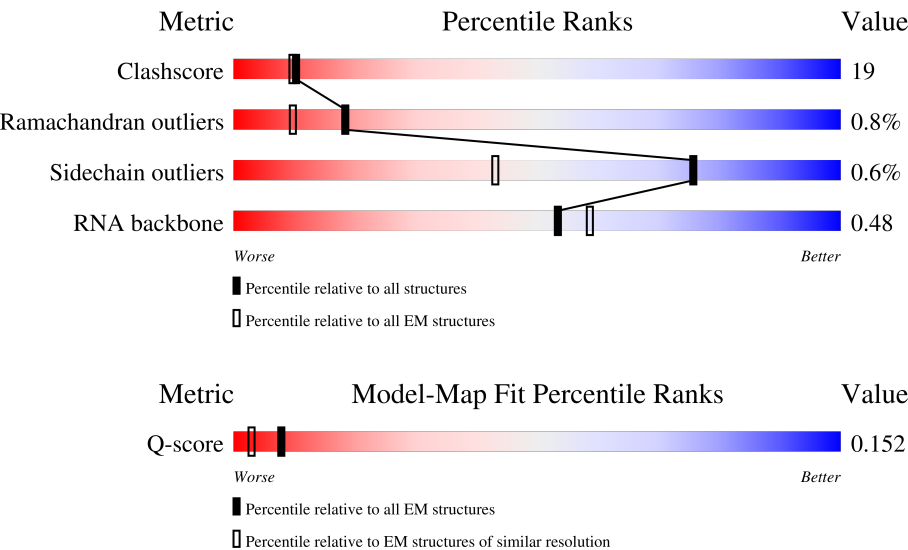
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.00 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	7587 (3.50 - 4.50)

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	1	407	17% 42% 32% 6% 20%
2	2	143	100% 15% 36% 37% 11%
3	A	298	33% 67%

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Mol	Chain	Length	Quality of chain
4	B	300	
5	C	231	
6	D	629	
7	E	544	
8	F	523	
9	G	492	
10	H	261	
11	I	38	
12	J	620	
13	O	971	
14	P	1361	
15	Q	435	
16	R	213	
17	S	107	
18	T	530	
19	U	266	
20	V	280	
21	W	238	
22	X	51	
23	Y	111	
24	Z	85	
25	b	196	
25	s	196	
26	d	101	
26	v	101	

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Mol	Chain	Length	Quality of chain
27	e	94	
27	w	94	
28	f	86	
28	x	86	
29	g	77	
29	y	77	
30	h	146	
30	t	146	
31	i	110	
31	u	110	

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 65050 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 U1 snRNA,U1 snRNA,U1 snRNA,U1 snRNA,U1 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	327	Total	C	N	O	P	0	0
			6625	2951	1072	2275	327		

- Molecule 2 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	143	Total	C	N	O	P	0	0
			3025	1352	513	1017	143		

- Molecule 3 is a protein called U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A,U1 small nuclear ribonucleoprotein A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	A	99	Total	C	N	O	0	0
			492	294	99	99		

- Molecule 4 is a protein called U1 small nuclear ribonucleoprotein 70 kDa homolog,U1 small nuclear ribonucleoprotein 70 kDa homolog,U1 small nuclear ribonucleoprotein 70 kDa homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	193	Total	C	N	O	S	0	0
			1450	929	261	258	2		

- Molecule 5 is a protein called U1 small nuclear ribonucleoprotein C.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	177	Total	C	N	O	S	0	0
			1323	832	246	240	5		

- Molecule 6 is a protein called Pre-mRNA-processing factor 39.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	509	Total	C	N	O	S	0	0
			3462	2188	608	659	7		

- Molecule 7 is a protein called U1 small nuclear ribonucleoprotein component PRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	541	Total	C	N	O	S	0	0
			4574	2996	723	836	19		

- Molecule 8 is a protein called Protein NAM8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	175	Total	C	N	O	S	0	0
			1337	840	232	255	10		

- Molecule 9 is a protein called 56 kDa U1 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	216	Total	C	N	O	S	0	0
			1684	1098	274	301	11		

- Molecule 10 is a protein called Protein LUC7,Protein LUC7,Protein LUC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	158	Total	C	N	O	S	0	0
			1083	675	198	201	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	83	VAL	GLU	conflict	UNP Q07508
H	84	GLU	VAL	conflict	UNP Q07508

- Molecule 11 is a RNA chain called Yeast UBC4 pre-mRNA (mutant).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	38	Total	C	N	O	P	0	0
			789	355	132	264	38		

- Molecule 12 is a protein called U1 small nuclear ribonucleoprotein component SNU71.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	J	42	Total	C	N	O	0	0
			324	210	55	59		

- Molecule 13 is a protein called U2 snRNP component HSH155.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	833	Total	C	N	O	S	0	0
			6612	4258	1121	1192	41		

- Molecule 14 is a protein called Pre-mRNA-splicing factor RSE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	1186	Total	C	N	O	S	0	0
			9437	6034	1589	1763	51		

- Molecule 15 is a protein called Cold sensitive U2 snRNA suppressor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	220	Total	C	N	O	S	0	0
			1786	1157	307	313	9		

- Molecule 16 is a protein called Protein HSH49.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	173	Total	C	N	O	S	0	0
			1429	930	239	258	2		

- Molecule 17 is a protein called Pre-mRNA-splicing factor RDS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	103	Total	C	N	O	S	0	0
			814	503	154	143	14		

- Molecule 18 is a protein called Pre-mRNA-splicing factor PRP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	462	Total	C	N	O	S	0	0
			3915	2487	677	735	16		

- Molecule 19 is a protein called Pre-mRNA-splicing factor PRP11,Pre-mRNA-splicing factor PRP11,Pre-mRNA-splicing factor PRP11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	196	Total	C	N	O	S	0	0
			1489	934	258	291	6		

- Molecule 20 is a protein called Pre-mRNA-splicing factor PRP21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	127	Total	C	N	O	S	0	0
			1084	689	193	196	6		

- Molecule 21 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	170	Total	C	N	O	S	0	0
			1383	866	253	257	7		

- Molecule 22 is a protein called Unknown.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	X	51	Total	C	N	O	0	0
			255	153	51	51		

- Molecule 23 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	84	Total	C	N	O	S	0	0
			683	439	119	122	3		

- Molecule 24 is a protein called RDS3 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	83	Total	C	N	O	S	0	0
			685	424	129	131	1		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	121	Total	C	N	O	S	0	0
			972	613	183	173	3		
25	s	65	Total	C	N	O	S	0	0
			518	331	91	93	3		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	93	Total	C	N	O	S	0	0
			714	453	125	133	3		
26	v	82	Total	C	N	O	S	0	0
			632	402	109	119	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	e	77	Total	C	N	O	S	0	0
			600	395	96	106	3		
27	w	77	Total	C	N	O	S	0	0
			602	396	95	108	3		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	f	73	Total	C	N	O	S	0	0
			585	376	102	106	1		
28	x	73	Total	C	N	O	S	0	0
			585	376	102	106	1		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	g	72	Total	C	N	O	S	0	0
			556	352	97	105	2		
29	y	75	Total	C	N	O	S	0	0
			577	363	100	112	2		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	h	107	Total	C	N	O	S	0	0
			834	525	149	157	3		
30	t	72	Total	C	N	O	S	0	0
			569	364	99	104	2		

- Molecule 31 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	i	99	Total	C	N	O	S	0	0
			805	514	148	139	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
31	u	92	Total	C	N	O	S	0	0
			752	481	136	131	4		

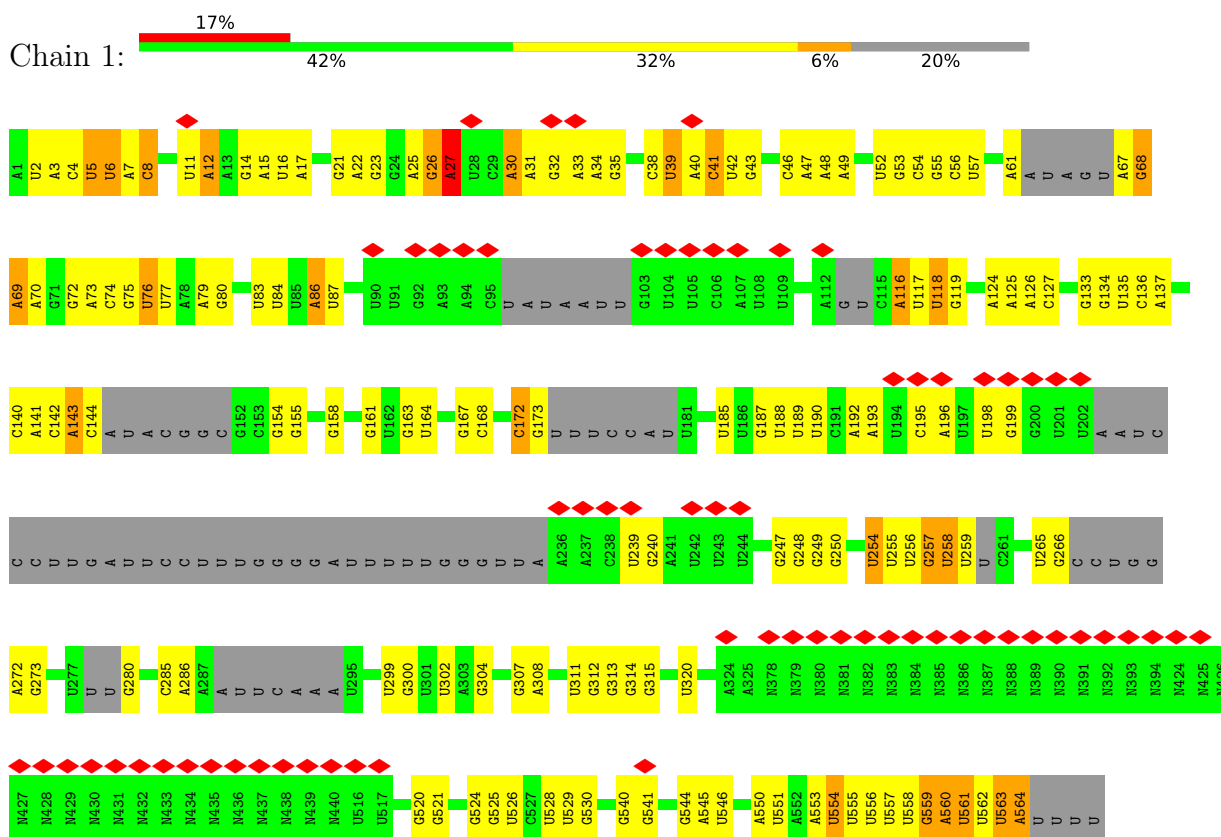
- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	C	1	Total	Zn	0
			1	1	
32	H	2	Total	Zn	0
			2	2	
32	S	3	Total	Zn	0
			3	3	
32	T	2	Total	Zn	0
			2	2	
32	U	1	Total	Zn	0
			1	1	

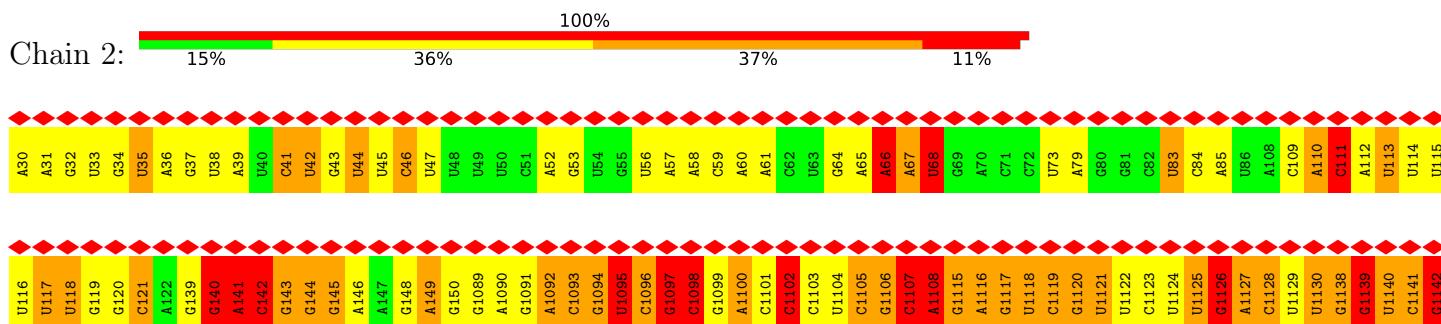
3 Residue-property plots

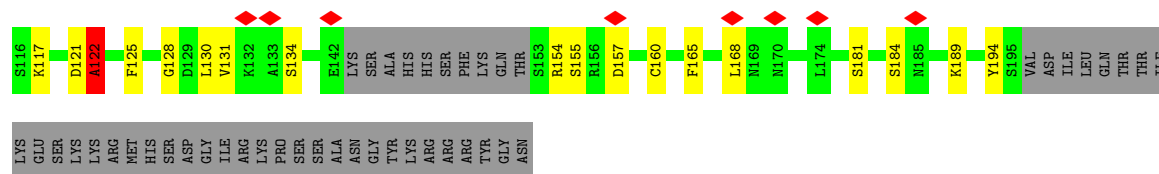
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: U1 snRNA,U1 snRNA,U1 snRNA,U1 snRNA,U1 snRNA

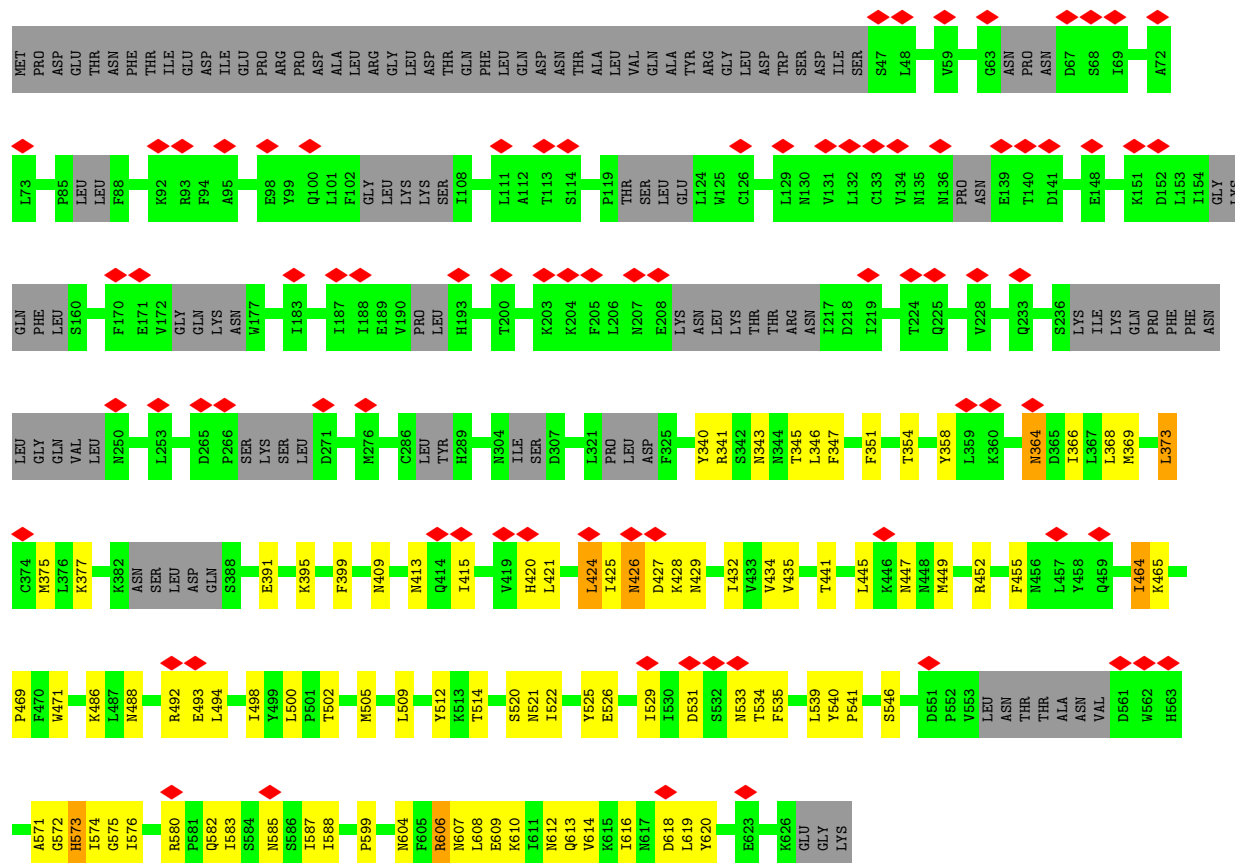


- Molecule 2: U2 snRNA

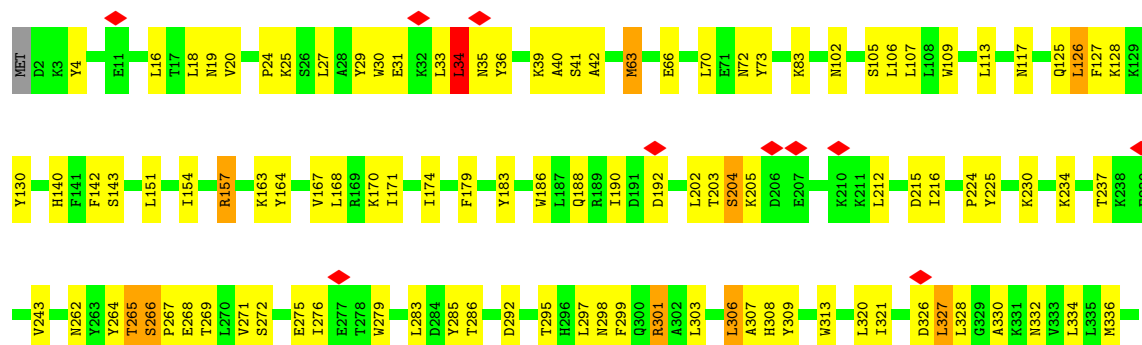


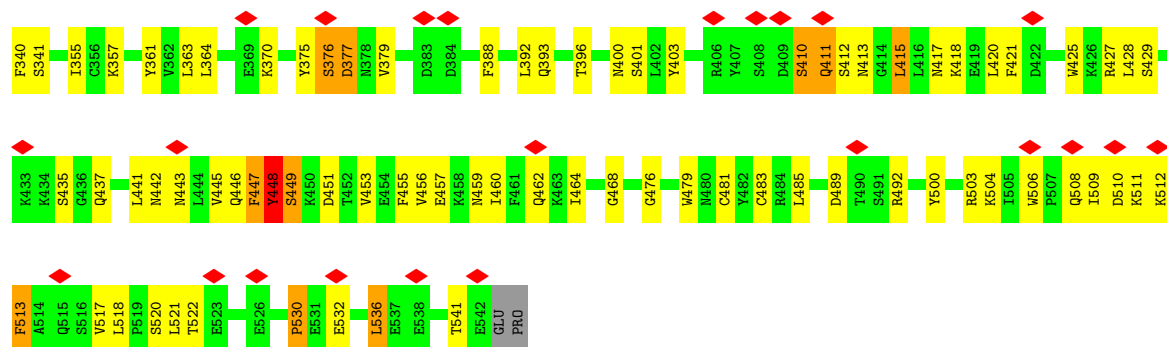


• Molecule 6: Pre-mRNA-processing factor 39



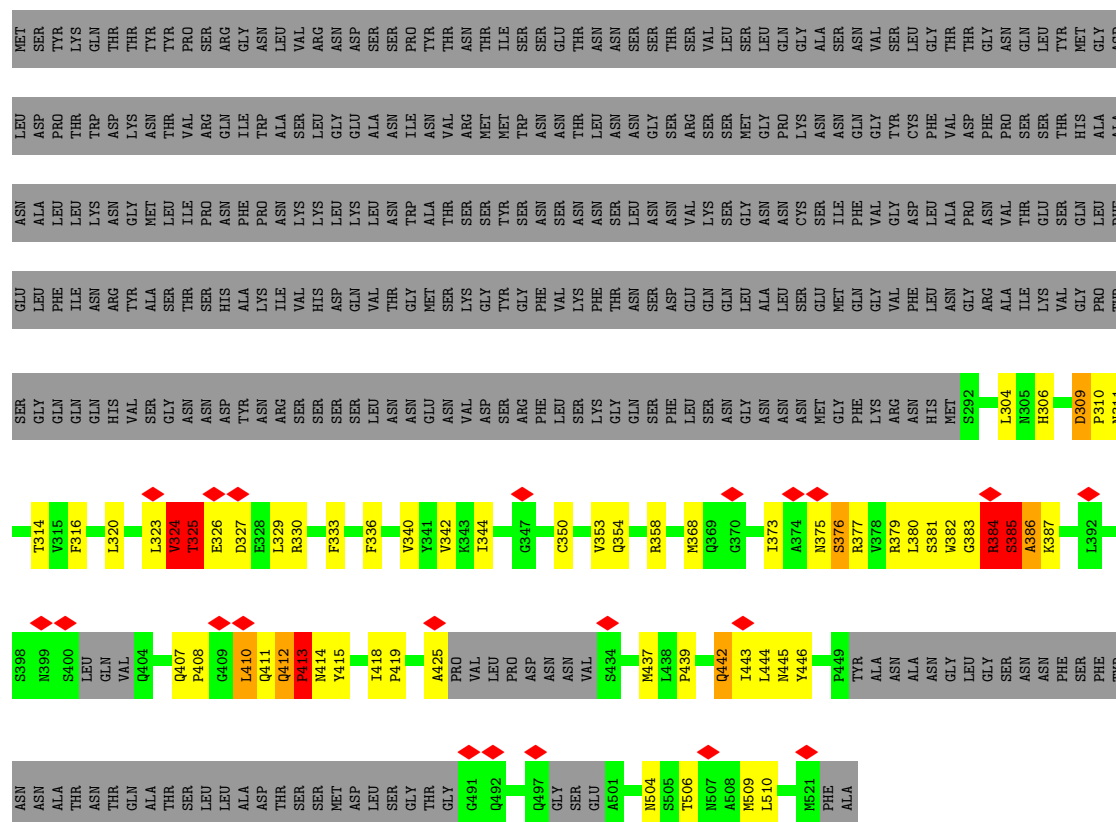
• Molecule 7: U1 small nuclear ribonucleoprotein component PRP42





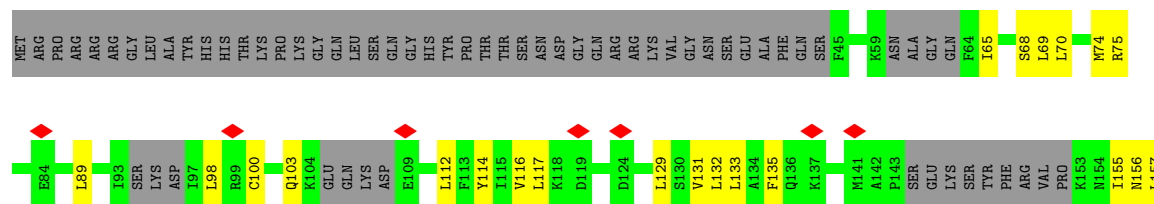
• Molecule 8: Protein NAM8

Chain F: 22% 9% 67%

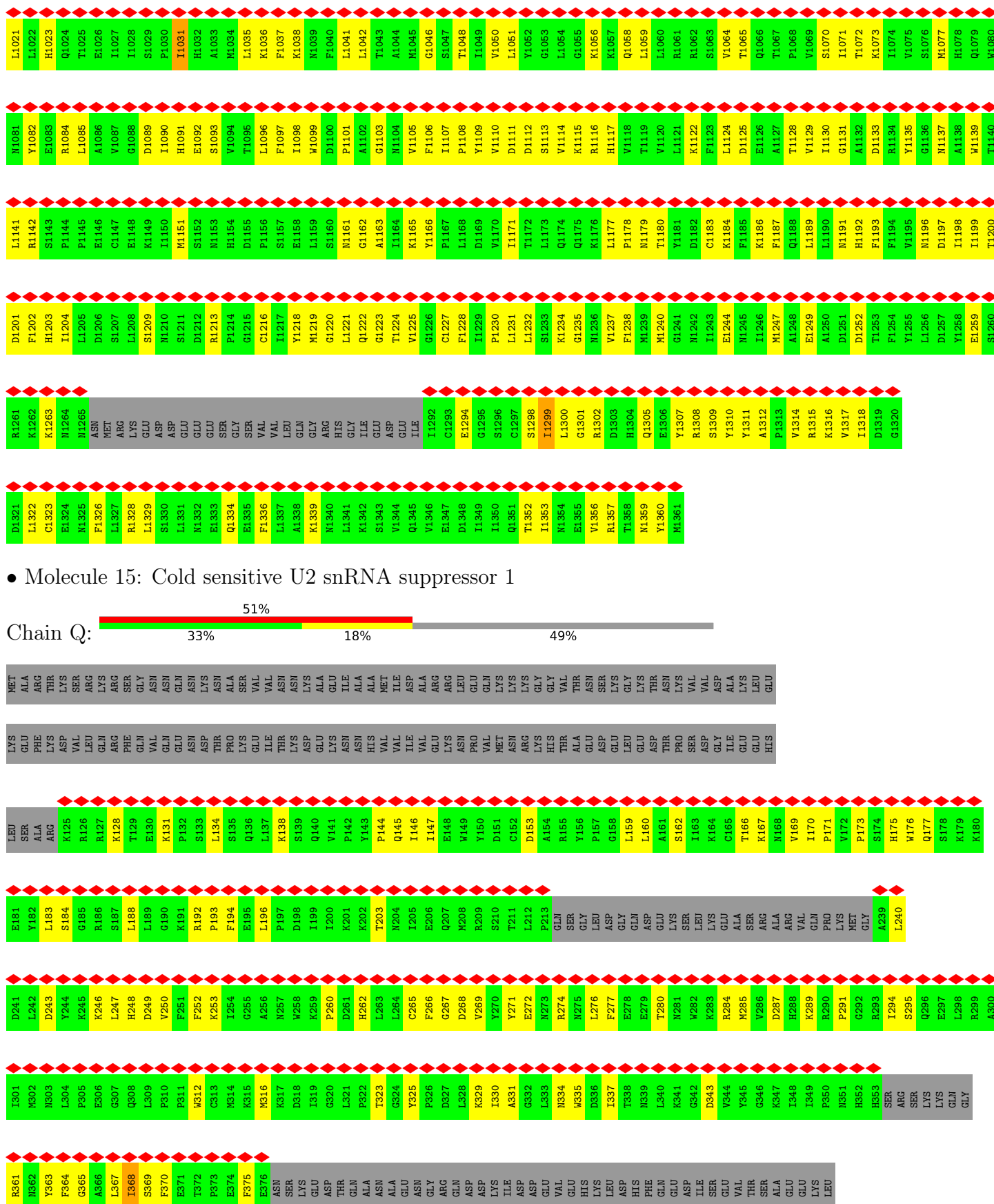


• Molecule 9: 56 kDa U1 small nuclear ribonucleoprotein component

Chain G: 33% 11% 56%

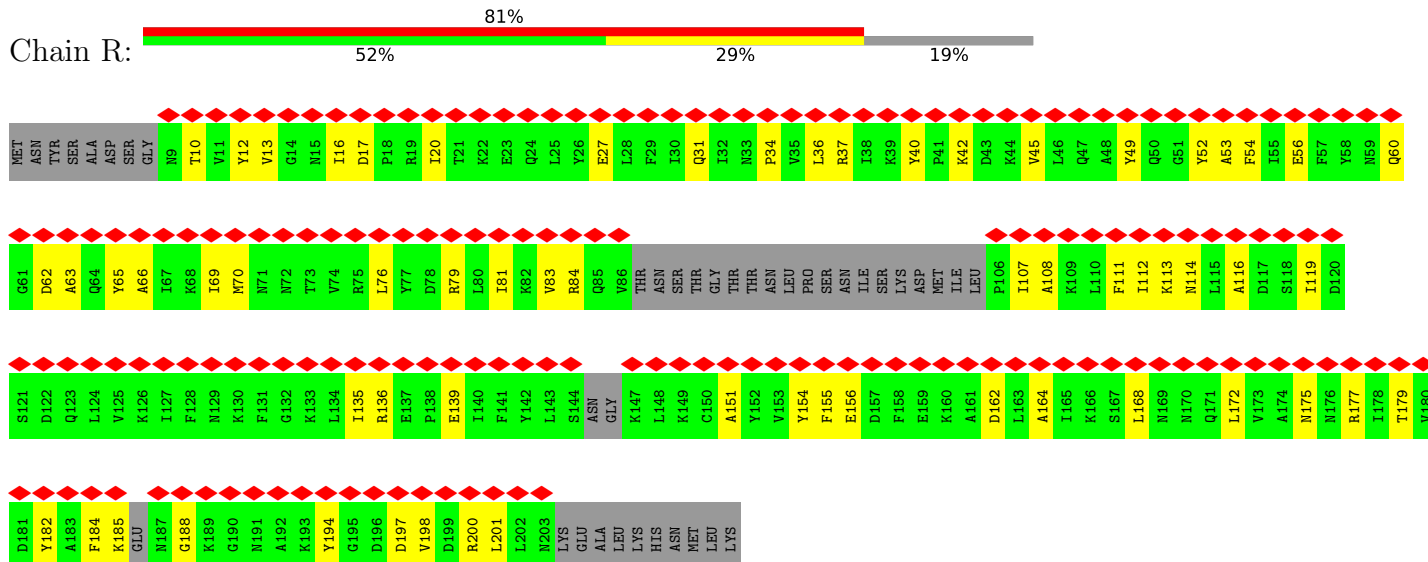


C961	L962	K963	F964	G965	S966	S967	D968	H969	L970	Y971	K972	L973	D974	D975	D976	I977	D978	C979	V980	S981	A982	A983	I984	I985	D986	F987	T988	R989	Q990	A991	D992	H993	L994	I995	I996	C997	A998	G999	D1000	K1001	R1002	L1003	L1004	T1005	I1006	K1007	I1008	L1009	V1010	N1011	D1012	D1013	K1014	L1015	S1016	F1017	D1018	I1019	E1020			
GLY	ASP	GLU	SER	ASN	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ASP	ASP	ASP	GLU	LYS	GLU	GLU	GLU	ILE	SER	SER	GLY	ALA	K814	W815	R816	S817	C818	V819	V820	C821	H822	S823	S824	S825	T826	W827	V828	S829	L882	L1003	G947	K948	K949	Q950	C951	R952	I953	S954	SER	SER	VAL	ASN	LYS	GLN	GLU	ASN	GLY	GLY
L841	K842	D843	Q844	N845	M846	L847	S848	C849	S850	L851	F852	W853	N854	A855	D856	W857	A858	I859	N860	G861	R862	C863	S864	I865	S866	S867	S868	G869	R870	L871	H872	I873	G874	R875	V876	S877	H878	F879	P880	T881	L882	S829	L1003	G947	K948	K949	Q950	C951	R952	I953	S954	SER	SER	VAL	ASN	LYS	GLN	GLU	ASN	GLY	GLY	
R781	E782	I783	S784	VAL	SER	LEU	ASN	ASN	GLU	GLU	GLU	GLU	GLU	GLU	ASP	ASP	ASP	LYS	GLU	GLU	GLU	ILE	SER	SER	GLY	ALA	K814	W815	R816	S817	C818	V819	V820	C821	H822	S823	S824	S825	T826	W827	V828	S829	L882	L1003	G947	K948	K949	Q950	C951	R952	I953	S954	SER	SER	VAL	ASN	LYS	GLN	GLU	ASN	GLY	GLY
V721	S722	E723	K724	I725	S726	D727	M728	I729	M730	V731	R732	D733	S734	S735	I736	G737	Q738	L739	N740	L741	H742	V743	G744	L745	E746	N747	G748	V749	Y750	M751	K752	F753	H754	I755	G756	D757	V758	D759	G760	S761	F762	T763	D764	I765	K766	R767	R768	F769	L770	G771	L772	K773	P774	V775	S776	L777	S778	Y779	L780			
D661	S662	L663	I664	E665	L666	T667	T668	H669	P670	E671	L672	D673	T674	M675	P676	S677	K678	V679	A680	GLU	L681	V682	Q683	D684	T685	Q686	H687	A688	D689	L690	S817	L691	A692	L693	A694	D695	N696	E697	G698	M699	I700	K701	I702	M703	S704	L705	LYS	ASP	GLN	GLU	GLU	D711	F712	L651	V652	T714	V715	I716	S717	L718	Q719	L720
Q601	V602	C603	T604	A605	E606	L607	R608	H609	I610	V611	P612	T613	G614	K615	S616	R617	V618	S619	N620	K621	L622	T623	V624	V625	P626	P627	A628	G629	R630	L631	L632	V633	C634	A635	T636	S637	S638	K639	T640	Q641	L642	L643	I644	S645	L646	S647	N648	Y649	E650	L651	V652	V653	F654	K655	L656	D657	V658	S659	S660			
A541	T542	T543	G544	D545	N546	N547	T548	L549	L550	F551	I552	T553	F554	P555	K556	K557	T558	M559	I560	L561	Q562	T563	D564	N565	E566	S567	M568	E569	E570	L571	THR	PRO	ASP	GLU	ALA	THR	THR	ARG	SER	ALA	F581	K582	L583	S584	Q585	D586	T587	T588	L589	H590	T591	C592	L593	M594	G595	S596	H597	S598	L599	I600		
Q481	L482	M483	L484	M485	P486	S487	L488	K489	S490	Q491	I492	V493	S494	D495	S496	P497	L498	S499	I500	A501	T502	K503	H504	F505	T506	N507	N508	K509	I510	I511	T512	L513	T514	N515	A516	V517	N518	Y519	S520	N521	L522	I523	T524	T525	S526	L527	P528	P529	N530	A531	T532	K533	L534	W535	L536	I537	P538	D539	P540			
I421	F422	K423	M424	G425	Y426	L427	F428	A429	L430	S431	E432	M433	M434	M435	M436	F437	L438	F439	Q440	F441	E442	K443	L444	G445	V446	E447	K448	M449	D450	F451	S452	M453	V454	L455	T456	S457	K458	D459	P460	M461	K462	S463	L464	V465	F466	E467	P468	S469	I470	K471	L472	Q473	M474	L475	S476	I477	L478	S479	D480			
K361	N362	V363	T364	I365	I366	S367	G368	I369	V370	Q371	K372	L373	K374	N375	D376	F377	F378	V379	L380	L381	Q382	S383	N384	H385	G386	D387	L388	F389	K390	L391	T392	V393	S394	P395	D396	T397	N398	D399	R400	N401	R402	P403	L404	V405	Q406	L407	P408	Y409	F410	D411	T412	I413	Q414	N415	S416	H417	Q418	L419	H420			
L301	S302	R303	Y304	N305	ILE	THR	THR	SER	LEU	ASP	ASN	ASN	ASP	THR	THR	ASP	THR	THR	F323	N324	P325	F326	V327	V328	I329	G330	F331	E332	N333	H334	I335	L336	V337	K338	D339	M340	N341	G342	F343	F344	N345	L346	K347	V348	D349	E349	I350	P351	K352	R353	S354	S291	I355	T356	N357	Q414	S358	R359	H360			
A241	V242	D244	V245	N246	F247	N248	N249	P250	C251	F252	V253	T254	E255	E256	I257	D258	N259	A260	A261	T262	Q263	L264	S265	V266	H267	L268	I269	F270	Y271	Y272	L273	E274	L275	G276	G277	L278	H279	I280	V281	K282	K283	A284	D285	Y286	L287	V288	N289	P290	S291	A292	N293	F294	V295	L296	S297	L298	P299	D300				

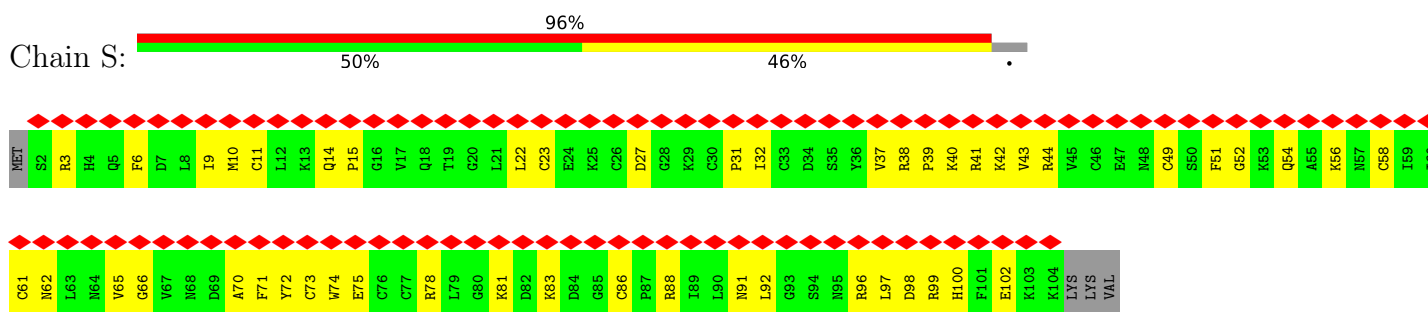


GLU
ARG
ASN
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GLU
ASP
SER
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TYR
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VAL
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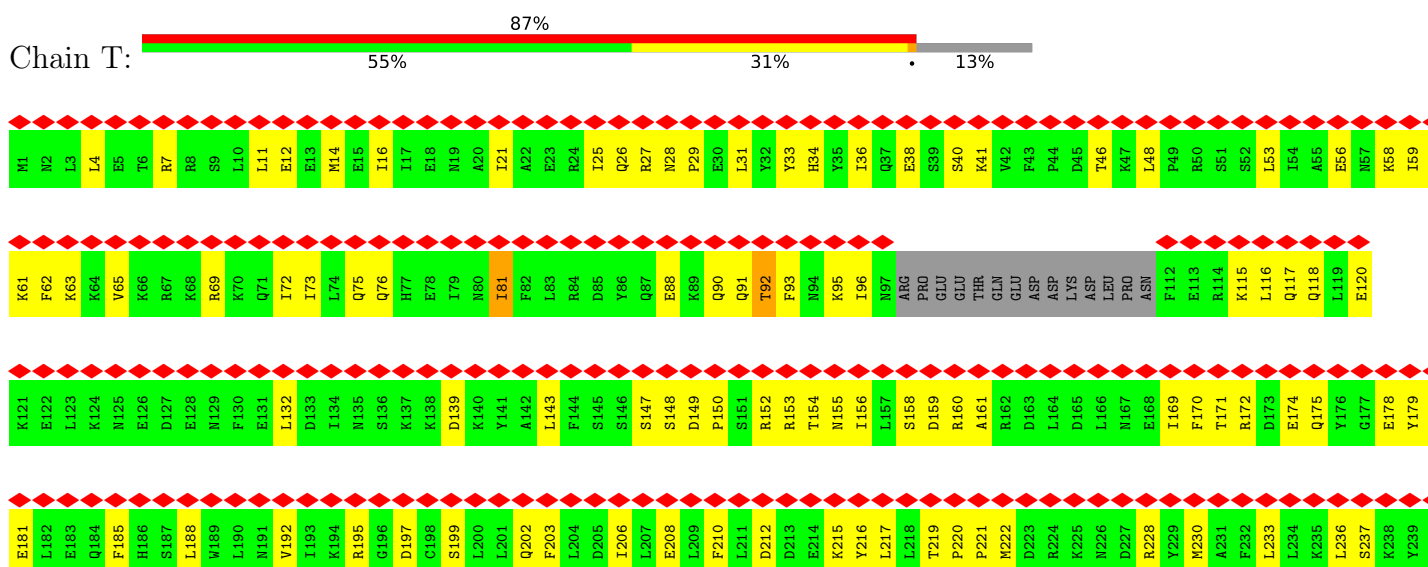
• Molecule 16: Protein HSH49

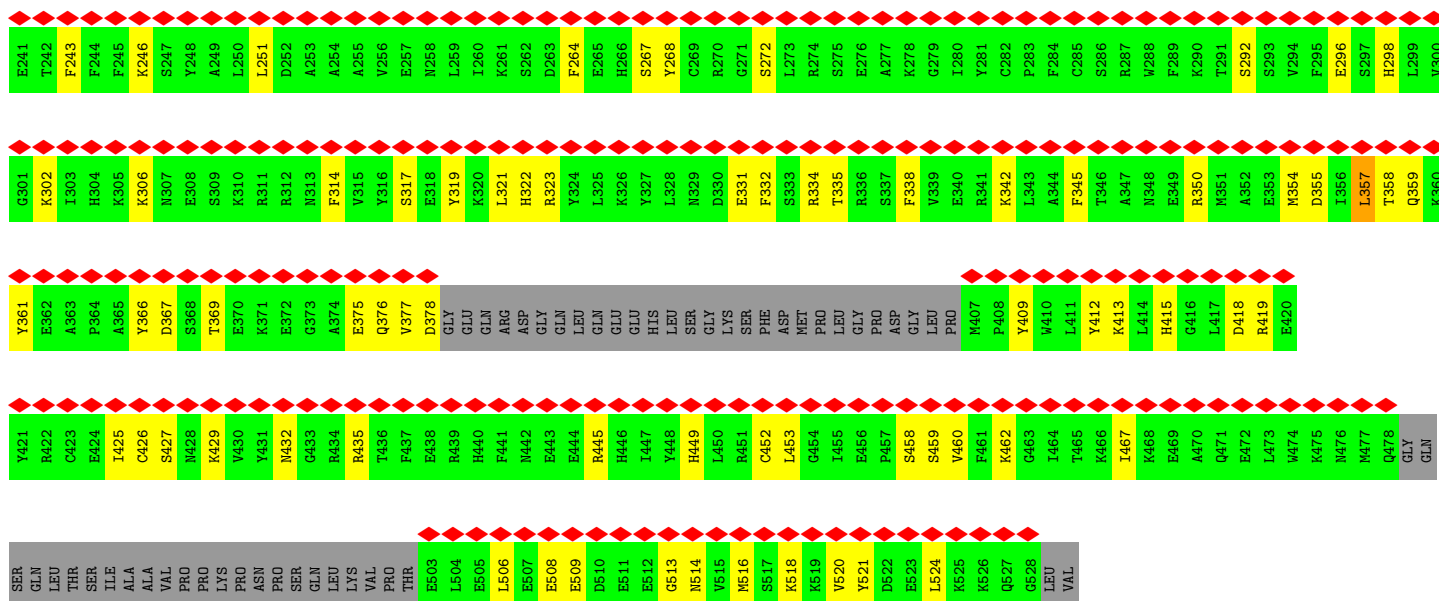


• Molecule 17: Pre-mRNA-splicing factor RDS3

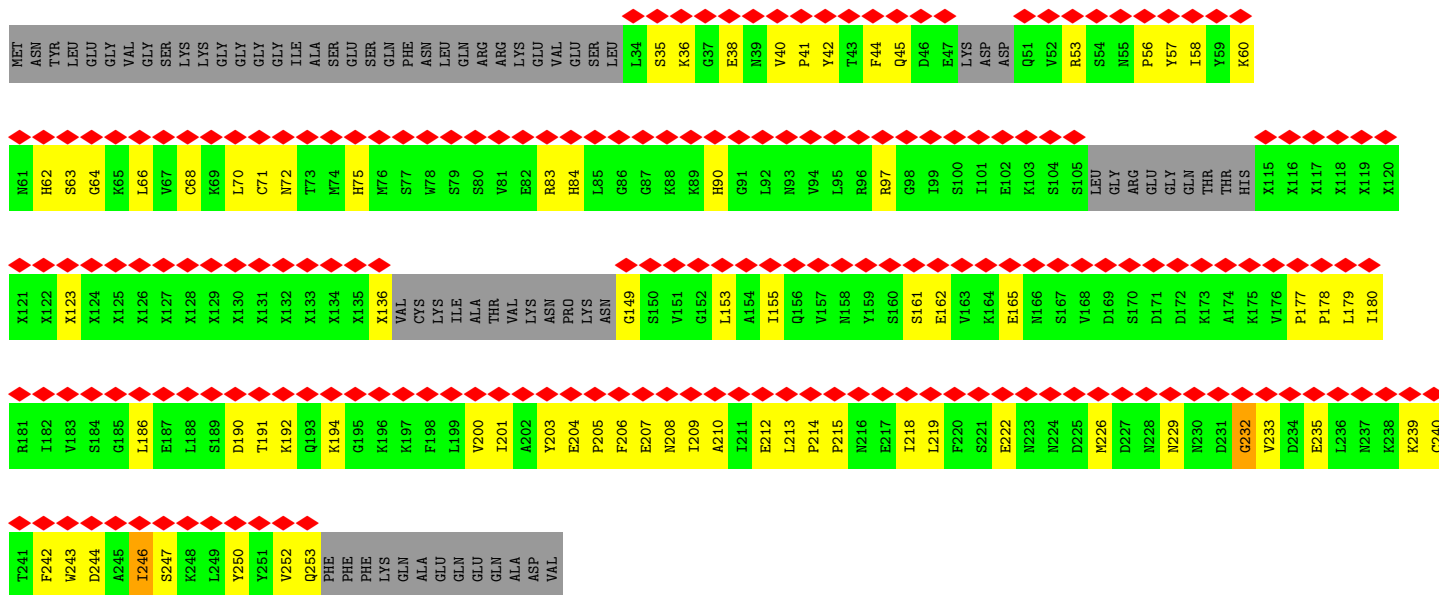
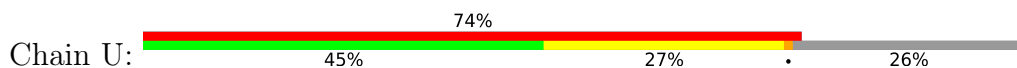


• Molecule 18: Pre-mRNA-splicing factor PRP9

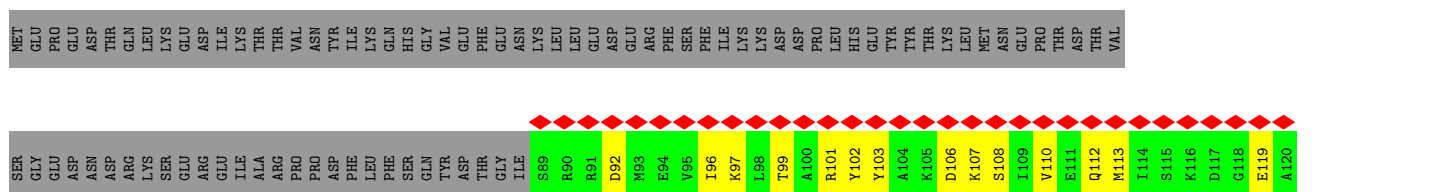
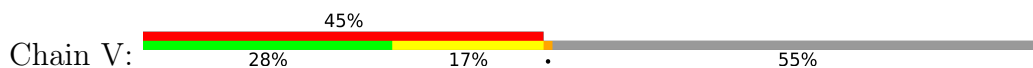


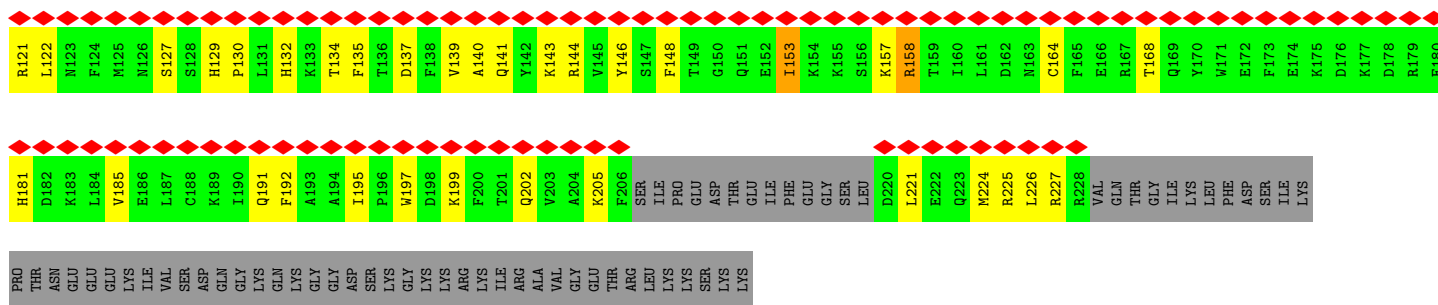


- Molecule 19: Pre-mRNA-splicing factor PRP11,Pre-mRNA-splicing factor PRP11,Pre-mRNA-splicing factor PRP11

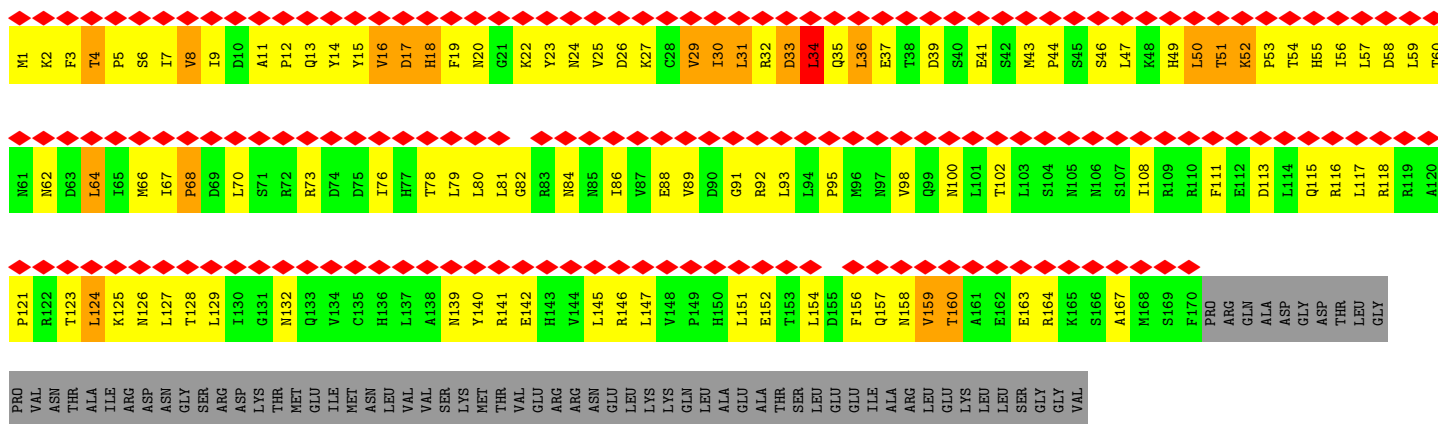
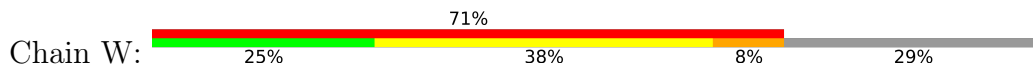


- Molecule 20: Pre-mRNA-splicing factor PRP21

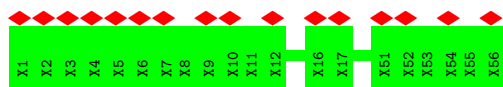




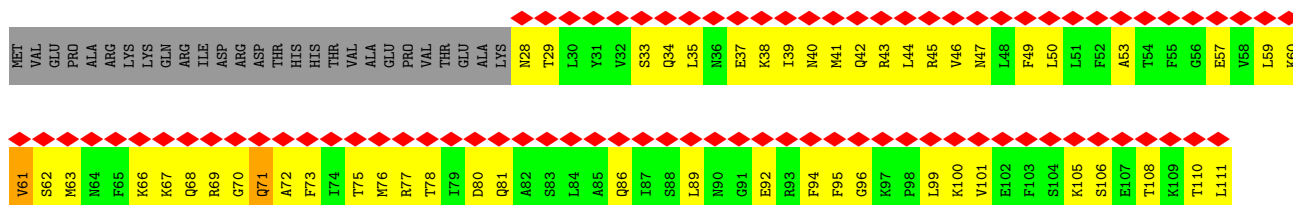
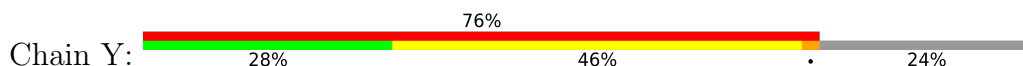
- Molecule 21: U2 small nuclear ribonucleoprotein A'



- Molecule 22: Unknown

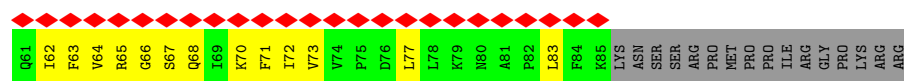


- Molecule 23: U2 small nuclear ribonucleoprotein B''

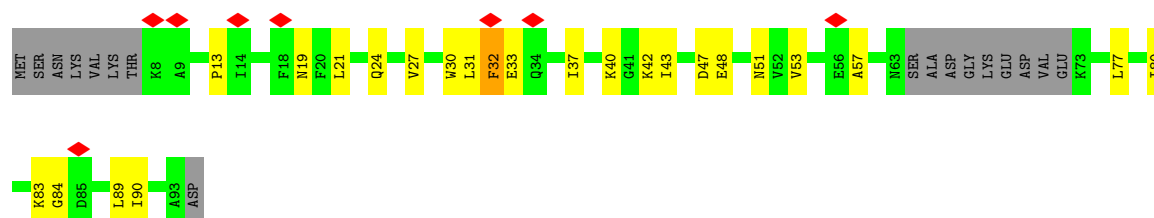


- Molecule 24: RDS3 complex subunit 10

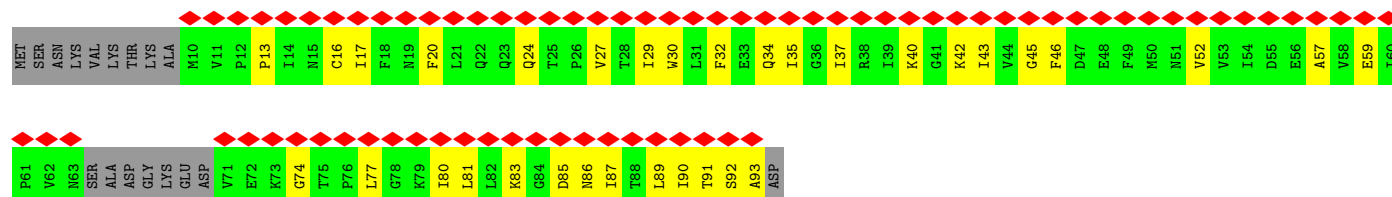
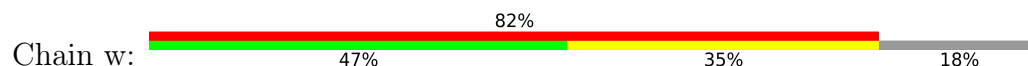




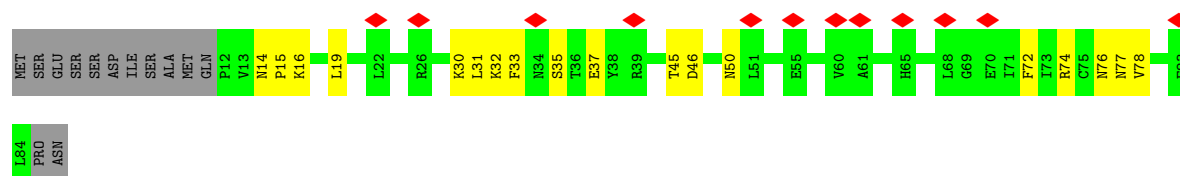
• Molecule 27: Small nuclear ribonucleoprotein E



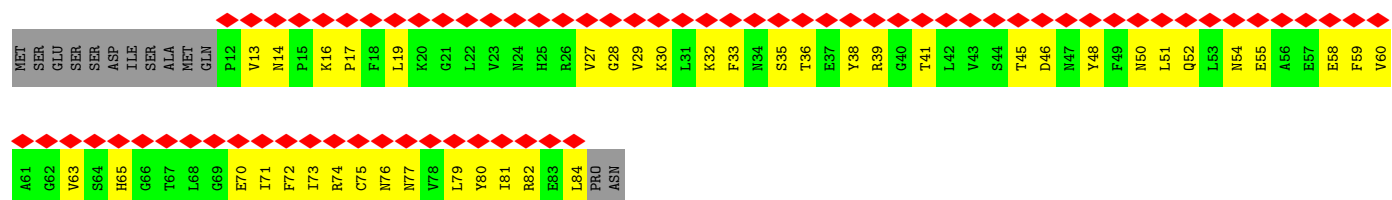
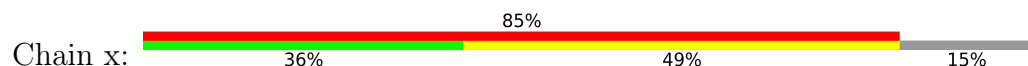
• Molecule 27: Small nuclear ribonucleoprotein E



• Molecule 28: Small nuclear ribonucleoprotein F



• Molecule 28: Small nuclear ribonucleoprotein F

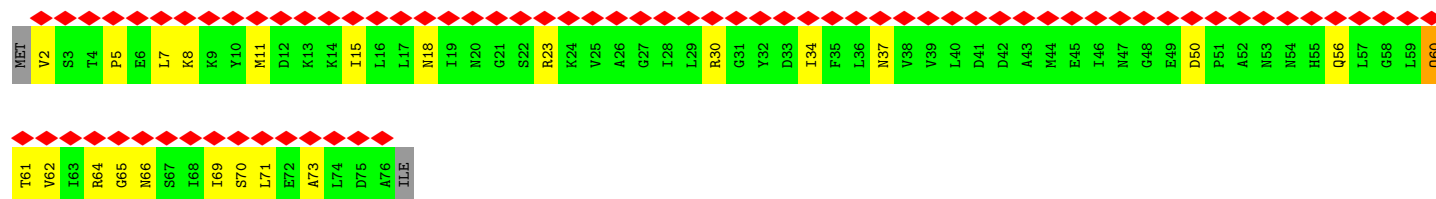


• Molecule 29: Small nuclear ribonucleoprotein G

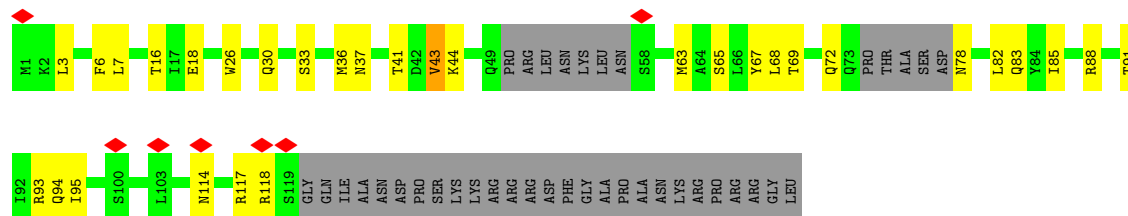




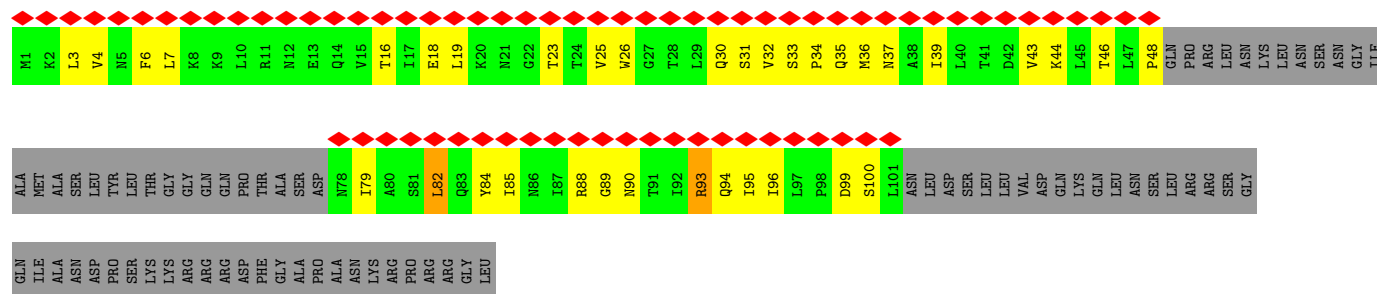
- Molecule 29: Small nuclear ribonucleoprotein G



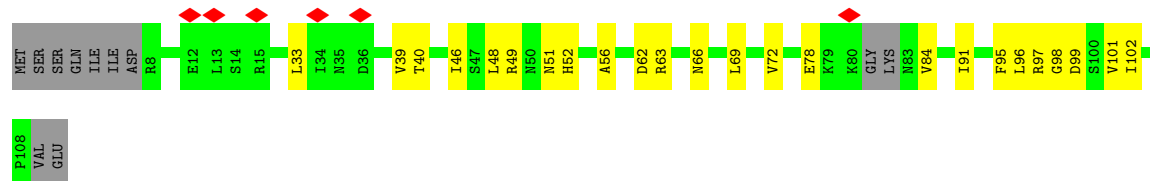
- Molecule 30: Small nuclear ribonucleoprotein Sm D1



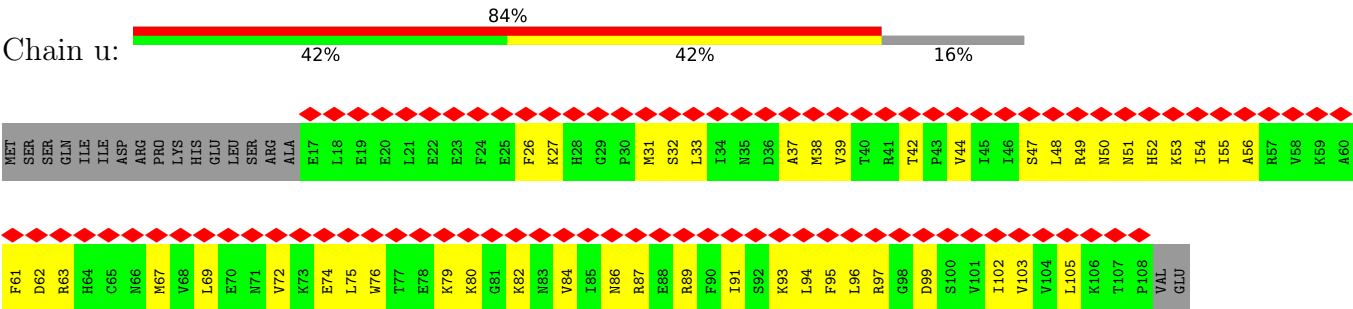
- Molecule 30: Small nuclear ribonucleoprotein Sm D1



- Molecule 31: Small nuclear ribonucleoprotein Sm D2



- Molecule 31: Small nuclear ribonucleoprotein Sm D2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	153556	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 ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.152	Depositor
Minimum map value	-0.083	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0369	Depositor
Map size (Å)	632.8, 632.8, 632.8	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.13, 1.13, 1.13	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	1	0.38	0/6890	0.52	4/10700 (0.0%)
2	2	1.22	46/3302 (1.4%)	1.79	138/5123 (2.7%)
3	A	0.28	0/388	0.90	1/535 (0.2%)
4	B	0.45	0/1325	0.93	2/1784 (0.1%)
5	C	0.52	0/1348	0.91	5/1825 (0.3%)
6	D	0.47	0/3499	0.84	6/4772 (0.1%)
7	E	0.68	2/4688 (0.0%)	1.00	16/6331 (0.3%)
8	F	0.61	0/1361	1.02	13/1843 (0.7%)
9	G	0.54	0/1716	0.86	0/2314
10	H	0.41	0/816	0.72	0/1094
11	I	0.24	0/878	0.31	0/1357
12	J	0.48	0/331	0.96	0/448
13	O	0.20	0/6745	0.47	1/9157 (0.0%)
14	P	0.22	0/9623	0.53	1/13041 (0.0%)
15	Q	0.17	0/1835	0.53	0/2480
16	R	0.14	0/1453	0.40	0/1954
17	S	0.21	0/827	0.55	0/1105
18	T	0.28	0/3992	0.66	2/5346 (0.0%)
19	U	0.24	0/1403	0.62	1/1889 (0.1%)
20	V	0.27	0/1105	0.63	0/1475
21	W	0.35	0/1406	0.71	0/1905
23	Y	0.20	0/692	0.47	0/923
24	Z	0.22	0/694	0.46	0/929
25	b	0.64	0/978	0.99	0/1306
25	s	0.32	0/521	0.59	0/701
26	d	0.69	0/726	0.91	0/984
26	v	0.36	0/641	0.58	0/868
27	e	0.58	0/610	0.91	2/826 (0.2%)
27	w	0.39	0/612	0.65	0/830
28	f	0.58	0/597	1.01	0/807
28	x	0.33	0/597	0.63	0/807
29	g	0.62	0/559	0.91	2/751 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
29	y	0.16	0/582	0.41	0/785
30	h	0.55	0/839	0.85	0/1132
30	t	0.38	0/574	0.64	1/777 (0.1%)
31	i	0.54	0/818	0.84	0/1099
31	u	0.33	0/764	0.57	0/1026
All	All	0.47	48/65735 (0.1%)	0.79	195/91029 (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	2	0	1
4	B	0	3
5	C	0	3
6	D	0	5
7	E	0	12
8	F	0	8
9	G	0	1
10	H	0	1
14	P	0	2
18	T	0	1
21	W	0	1
27	e	0	1
29	g	0	1
30	h	0	1
All	All	0	41

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1149	G	O3'-P	19.50	1.90	1.61
2	2	143	G	O3'-P	15.07	1.83	1.61
2	2	143	G	C3'-O3'	14.28	1.63	1.42
2	2	1161	U	O3'-P	-12.47	1.42	1.61
2	2	1092	A	O3'-P	-11.84	1.43	1.61

The worst 5 of 195 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	144	G	C4'-C3'-O3'	-25.53	74.71	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1151	U	C4'-C3'-O3'	-20.00	83.00	113.00
2	2	143	G	C4'-C3'-O3'	18.16	140.24	113.00
2	2	1092	A	C2'-C3'-O3'	17.91	140.56	113.70
2	2	1097	G	C3'-C2'-O2'	16.46	135.40	110.70

There are no chirality outliers.

5 of 41 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	2	141	A	Sidechain
4	B	166	LYS	Peptide
4	B	170	VAL	Peptide
4	B	43	GLY	Peptide
5	C	103	ASP	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	1	6625	0	3415	98	0
2	2	3025	0	1535	246	0
3	A	492	0	190	1	0
4	B	1450	0	1340	36	0
5	C	1323	0	1217	28	0
6	D	3462	0	2785	64	0
7	E	4574	0	4581	128	0
8	F	1337	0	1304	39	0
9	G	1684	0	1618	40	0
10	H	1083	0	830	19	0
11	I	789	0	403	31	0
12	J	324	0	310	3	0
13	O	6612	0	6823	315	0
14	P	9437	0	9532	493	0
15	Q	1786	0	1778	68	0
16	R	1429	0	1458	44	0
17	S	814	0	809	39	0
18	T	3915	0	3853	147	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	U	1489	0	1392	74	0
20	V	1084	0	1081	52	0
21	W	1383	0	1407	225	0
22	X	255	0	55	0	0
23	Y	683	0	715	91	0
24	Z	685	0	693	28	0
25	b	972	0	1048	33	0
25	s	518	0	548	42	0
26	d	714	0	738	18	0
26	v	632	0	653	52	0
27	e	600	0	634	16	0
27	w	602	0	631	46	0
28	f	585	0	587	15	0
28	x	585	0	587	41	0
29	g	556	0	583	22	0
29	y	577	0	595	29	0
30	h	834	0	883	26	0
30	t	569	0	616	54	0
31	i	805	0	834	20	0
31	u	752	0	786	65	0
32	C	1	0	0	0	0
32	H	2	0	0	0	0
32	S	3	0	0	0	0
32	T	2	0	0	0	0
32	U	1	0	0	0	0
All	All	65050	0	58847	2366	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 19.

The worst 5 of 2366 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)
2:2:143:G:C3'	2:2:143:G:O3'	1.63	1.45
2:2:1098:C:O3'	21:W:158:ASN:ND2	1.69	1.23
2:2:1099:G:O2'	2:2:1100:A:H5'	1.42	1.16
2:2:118:U:C5	31:u:99:ASP:HB3	1.83	1.12
2:2:1099:G:OP1	21:W:158:ASN:CG	1.91	1.12

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	
3	A	72/298 (24%)	59 (82%)	12 (17%)	1 (1%)	9	39
4	B	158/300 (53%)	135 (85%)	22 (14%)	1 (1%)	21	57
5	C	171/231 (74%)	152 (89%)	18 (10%)	1 (1%)	21	57
6	D	475/629 (76%)	435 (92%)	37 (8%)	3 (1%)	21	57
7	E	539/544 (99%)	482 (89%)	44 (8%)	13 (2%)	4	30
8	F	165/523 (32%)	142 (86%)	17 (10%)	6 (4%)	2	23
9	G	204/492 (42%)	186 (91%)	18 (9%)	0	100	100
10	H	94/261 (36%)	89 (95%)	5 (5%)	0	100	100
12	J	40/620 (6%)	34 (85%)	6 (15%)	0	100	100
13	O	829/971 (85%)	788 (95%)	41 (5%)	0	100	100
14	P	1170/1361 (86%)	1059 (90%)	104 (9%)	7 (1%)	21	57
15	Q	214/435 (49%)	202 (94%)	11 (5%)	1 (0%)	24	60
16	R	165/213 (78%)	162 (98%)	3 (2%)	0	100	100
17	S	101/107 (94%)	88 (87%)	13 (13%)	0	100	100
18	T	454/530 (86%)	416 (92%)	38 (8%)	0	100	100
19	U	168/266 (63%)	143 (85%)	24 (14%)	1 (1%)	21	57
20	V	123/280 (44%)	112 (91%)	11 (9%)	0	100	100
21	W	168/238 (71%)	129 (77%)	28 (17%)	11 (6%)	1	15
23	Y	82/111 (74%)	76 (93%)	5 (6%)	1 (1%)	10	42
24	Z	81/85 (95%)	76 (94%)	4 (5%)	1 (1%)	10	42
25	b	117/196 (60%)	108 (92%)	9 (8%)	0	100	100
25	s	61/196 (31%)	58 (95%)	3 (5%)	0	100	100
26	d	91/101 (90%)	87 (96%)	4 (4%)	0	100	100
26	v	80/101 (79%)	77 (96%)	3 (4%)	0	100	100
27	e	73/94 (78%)	68 (93%)	4 (6%)	1 (1%)	9	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	w	73/94 (78%)	72 (99%)	1 (1%)	0	100	100
28	f	71/86 (83%)	66 (93%)	5 (7%)	0	100	100
28	x	71/86 (83%)	69 (97%)	2 (3%)	0	100	100
29	g	68/77 (88%)	61 (90%)	6 (9%)	1 (2%)	8	38
29	y	73/77 (95%)	64 (88%)	6 (8%)	3 (4%)	2	21
30	h	101/146 (69%)	97 (96%)	4 (4%)	0	100	100
30	t	68/146 (47%)	67 (98%)	1 (2%)	0	100	100
31	i	95/110 (86%)	90 (95%)	5 (5%)	0	100	100
31	u	90/110 (82%)	89 (99%)	1 (1%)	0	100	100
All	All	6605/10115 (65%)	6038 (91%)	515 (8%)	52 (1%)	18	52

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	D	426	ASN
6	D	608	LEU
7	E	448	TYR
8	F	325	THR
8	F	385	SER

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	
4	B	136/236 (58%)	135 (99%)	1 (1%)	76	79
5	C	127/214 (59%)	127 (100%)	0	100	100
6	D	266/603 (44%)	265 (100%)	1 (0%)	84	84
7	E	515/519 (99%)	511 (99%)	4 (1%)	73	77
8	F	148/451 (33%)	146 (99%)	2 (1%)	59	71
9	G	175/448 (39%)	175 (100%)	0	100	100
10	H	84/183 (46%)	83 (99%)	1 (1%)	63	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	J	34/568 (6%)	34 (100%)	0	100	100
13	O	739/867 (85%)	739 (100%)	0	100	100
14	P	1093/1244 (88%)	1093 (100%)	0	100	100
15	Q	192/391 (49%)	192 (100%)	0	100	100
16	R	154/189 (82%)	154 (100%)	0	100	100
17	S	93/97 (96%)	93 (100%)	0	100	100
18	T	429/492 (87%)	420 (98%)	9 (2%)	47	65
19	U	158/216 (73%)	157 (99%)	1 (1%)	78	81
20	V	118/259 (46%)	116 (98%)	2 (2%)	53	68
21	W	161/219 (74%)	151 (94%)	10 (6%)	16	41
23	Y	76/100 (76%)	75 (99%)	1 (1%)	61	72
24	Z	75/77 (97%)	75 (100%)	0	100	100
25	b	108/176 (61%)	108 (100%)	0	100	100
25	s	58/176 (33%)	58 (100%)	0	100	100
26	d	81/89 (91%)	81 (100%)	0	100	100
26	v	71/89 (80%)	71 (100%)	0	100	100
27	e	68/83 (82%)	68 (100%)	0	100	100
27	w	69/83 (83%)	69 (100%)	0	100	100
28	f	65/77 (84%)	65 (100%)	0	100	100
28	x	65/77 (84%)	65 (100%)	0	100	100
29	g	62/66 (94%)	62 (100%)	0	100	100
29	y	64/66 (97%)	64 (100%)	0	100	100
30	h	96/129 (74%)	96 (100%)	0	100	100
30	t	67/129 (52%)	66 (98%)	1 (2%)	57	70
31	i	90/103 (87%)	90 (100%)	0	100	100
31	u	85/103 (82%)	85 (100%)	0	100	100
All	All	5822/8819 (66%)	5789 (99%)	33 (1%)	76	81

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	W	50	LEU
21	W	64	LEU

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Mol	Chain	Res	Type
30	t	82	LEU
18	T	92	THR
18	T	81	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 137 such sidechains are listed below:

Mol	Chain	Res	Type
25	b	5	GLN
28	f	14	ASN
30	t	94	GLN
13	O	894	HIS
13	O	887	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	281/407 (69%)	67 (23%)	12 (4%)
11	I	35/38 (92%)	8 (22%)	2 (5%)
2	2	136/143 (95%)	46 (33%)	25 (18%)
All	All	452/588 (76%)	121 (26%)	39 (8%)

5 of 121 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	8	C
1	1	11	U
1	1	12	A
1	1	17	A
1	1	21	G

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	1122	U
2	2	1144	U
2	2	1123	C
2	2	1138	G
11	I	77	C

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

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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$
2	PSU	2	42	2,11	18,21,22	1.13	1 (5%)	21,30,33	1.85	4 (19%)
1	PSU	1	6	11,1	18,21,22	1.40	2 (11%)	21,30,33	1.31	2 (9%)
1	PSU	1	5	1	18,21,22	1.51	2 (11%)	21,30,33	1.37	2 (9%)
2	PSU	2	44	2,11	18,21,22	1.07	1 (5%)	21,30,33	1.80	4 (19%)
2	PSU	2	35	2,11	18,21,22	1.10	1 (5%)	21,30,33	1.86	5 (23%)

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
2	PSU	2	42	2,11	-	0/7/25/26	0/2/2/2
1	PSU	1	6	11,1	-	0/7/25/26	0/2/2/2
1	PSU	1	5	1	-	0/7/25/26	0/2/2/2
2	PSU	2	44	2,11	-	0/7/25/26	0/2/2/2
2	PSU	2	35	2,11	-	0/7/25/26	0/2/2/2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	5	PSU	C2-N1	4.54	1.42	1.36
1	1	6	PSU	C2-N1	4.11	1.42	1.36
2	2	42	PSU	C6-C5	3.71	1.39	1.35
2	2	35	PSU	C6-C5	3.53	1.39	1.35
2	2	44	PSU	C6-C5	3.44	1.39	1.35

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	42	PSU	C4-N3-C2	-4.82	119.74	126.37
2	2	35	PSU	C4-N3-C2	-4.70	119.90	126.37
2	2	42	PSU	N1-C2-N3	4.67	120.09	115.17
2	2	35	PSU	N1-C2-N3	4.65	120.07	115.17
2	2	44	PSU	N1-C2-N3	4.60	120.02	115.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	42	PSU	2	0
1	1	6	PSU	3	0
1	1	5	PSU	4	0
2	2	44	PSU	5	0
2	2	35	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
2	2	10
1	1	4
11	I	2
10	H	2
22	X	1

The worst 5 of 19 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	10:A	O3'	51:C	P	64.91
1	1	440:N	O3'	516:U	P	49.12
1	1	325:A	O3'	378:N	P	48.87
1	2	122:A	O3'	139:G	P	46.36
1	1	532:U	O3'	538:C	P	25.27

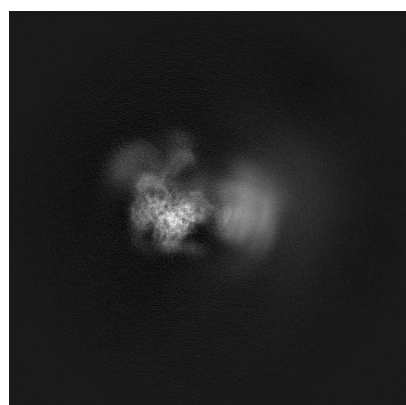
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4364. These allow visual inspection of the internal detail of the map and identification of artifacts.

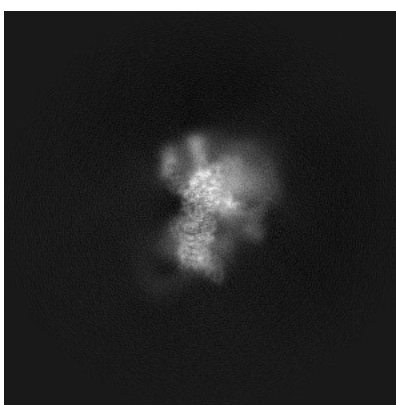
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

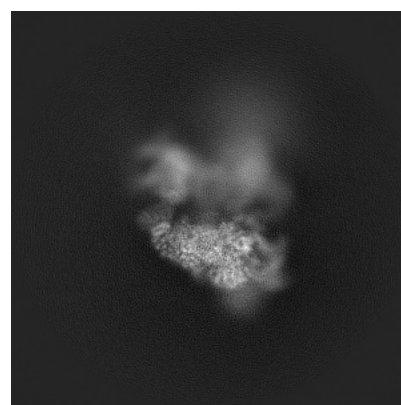
6.1.1 Primary map



X



Y

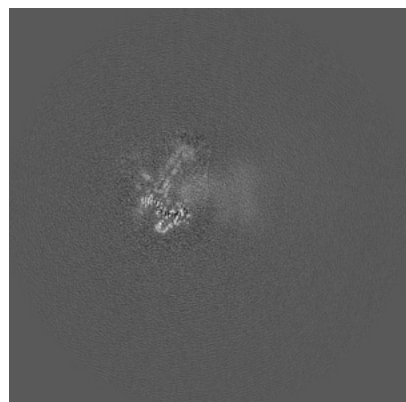


Z

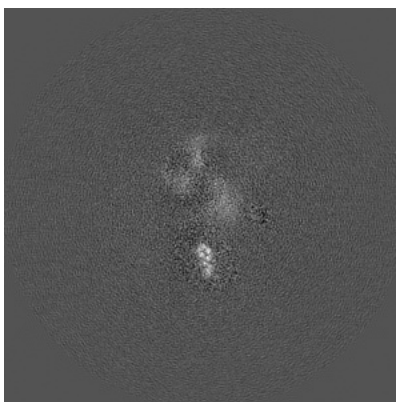
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

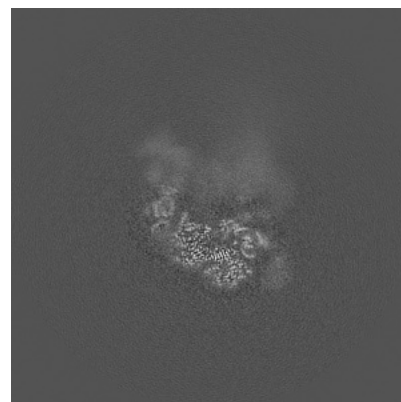
6.2.1 Primary map



X Index: 280



Y Index: 280

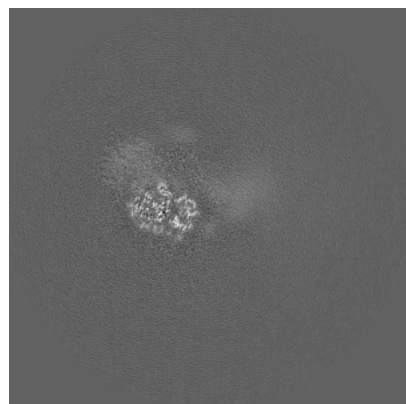


Z Index: 280

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

6.3 Largest variance slices [i](#)

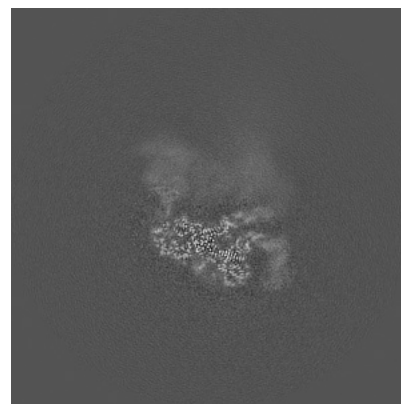
6.3.1 Primary map



X Index: 303



Y Index: 225

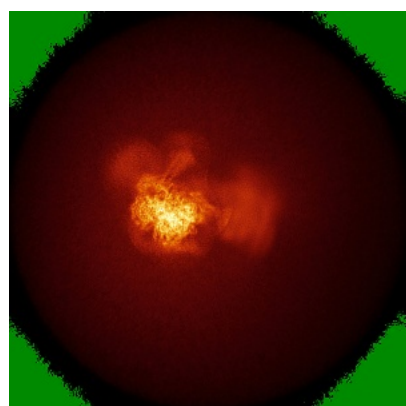


Z Index: 271

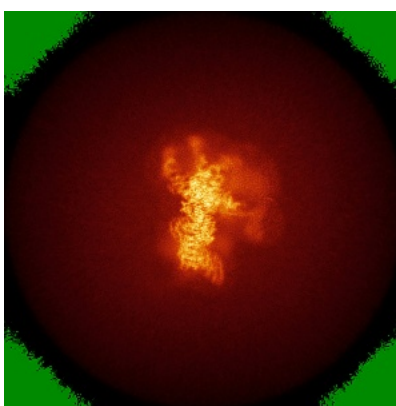
The images above show the largest variance slices of the map in three orthogonal directions.

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

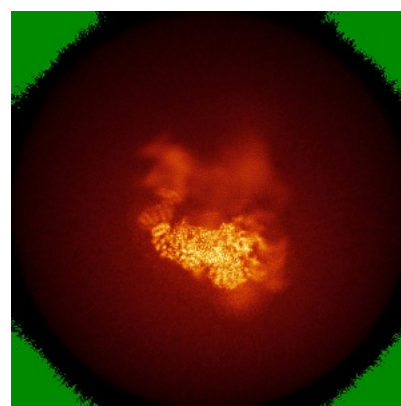
6.4.1 Primary map



X



Y

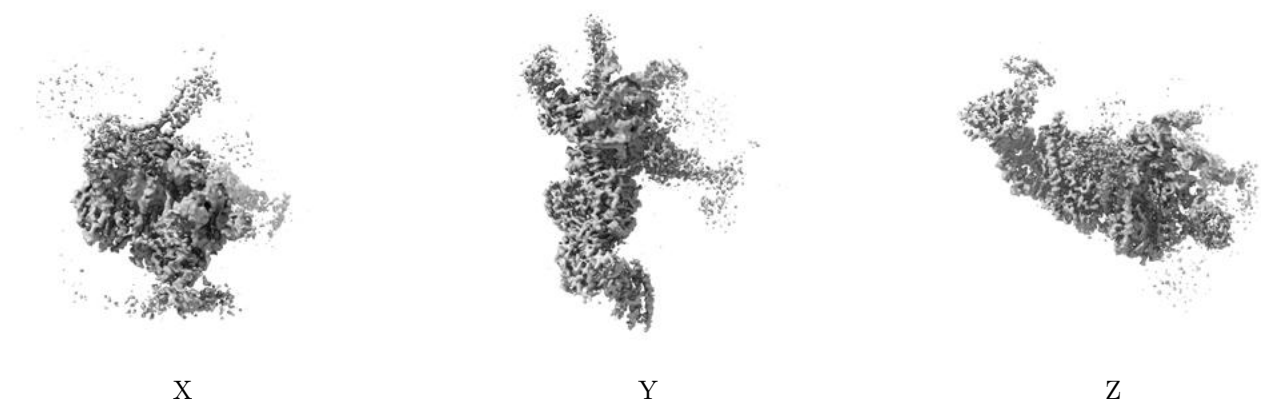


Z

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 0.0369. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

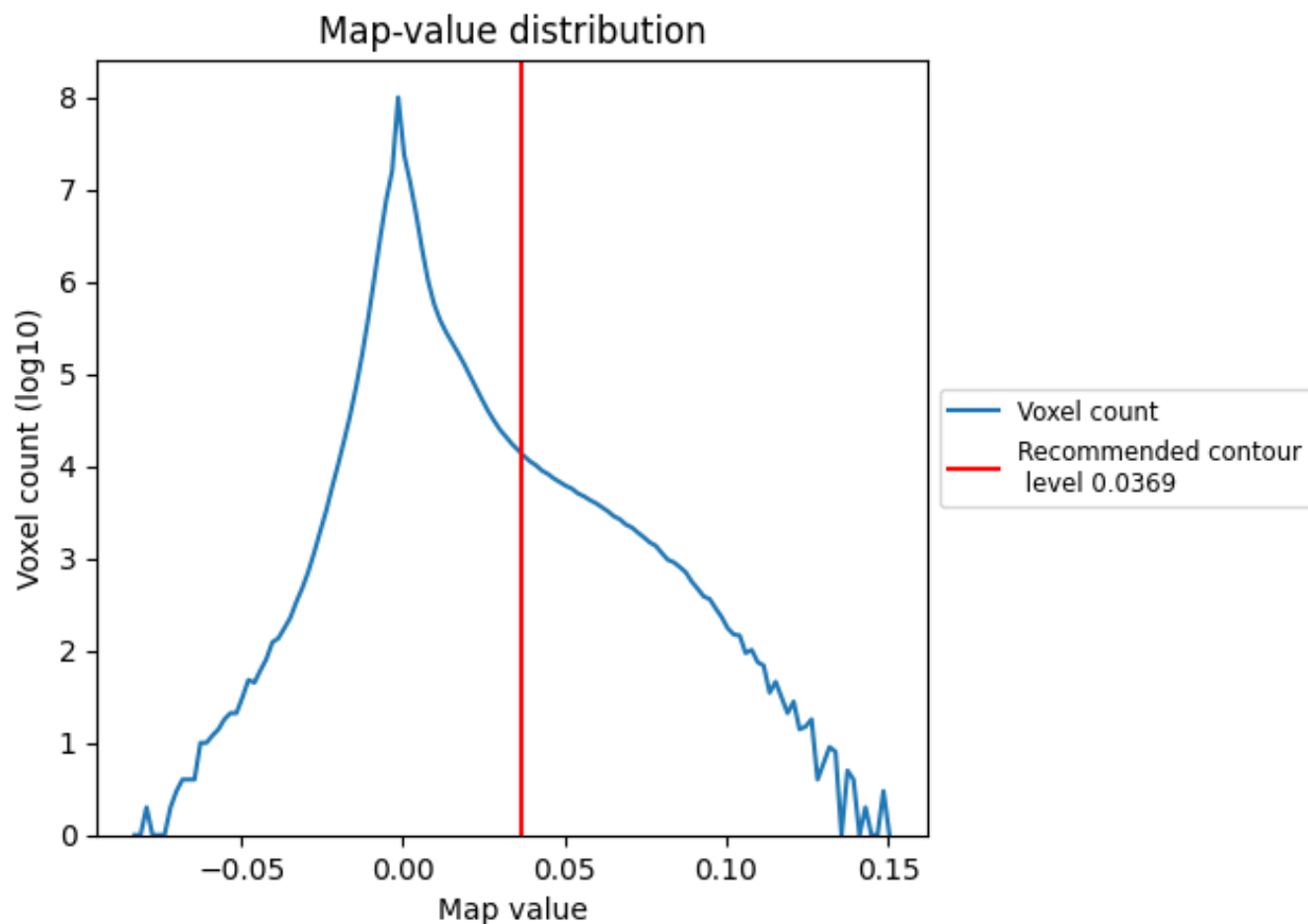
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

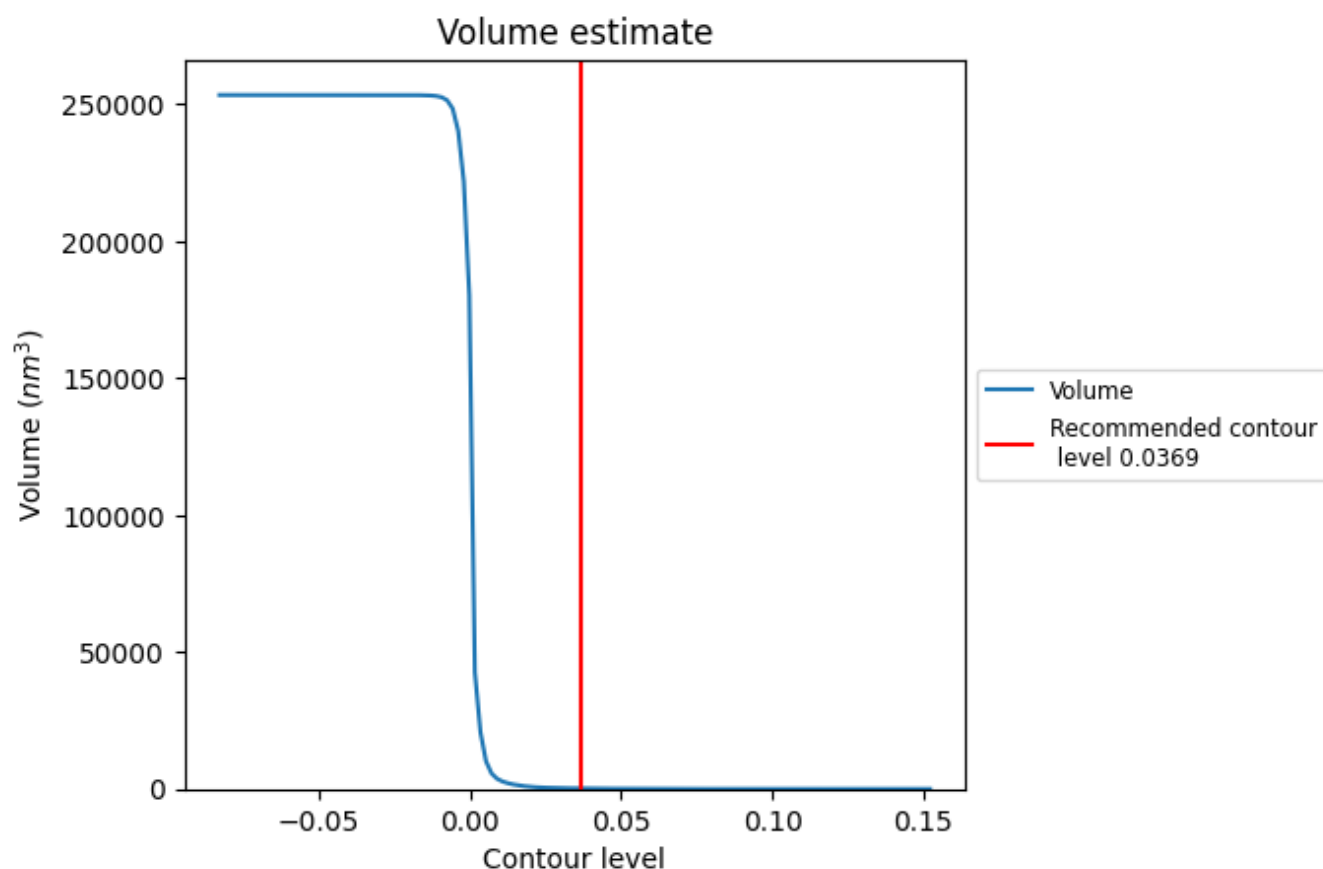
This section contains the results of statistical analysis of the map.

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.

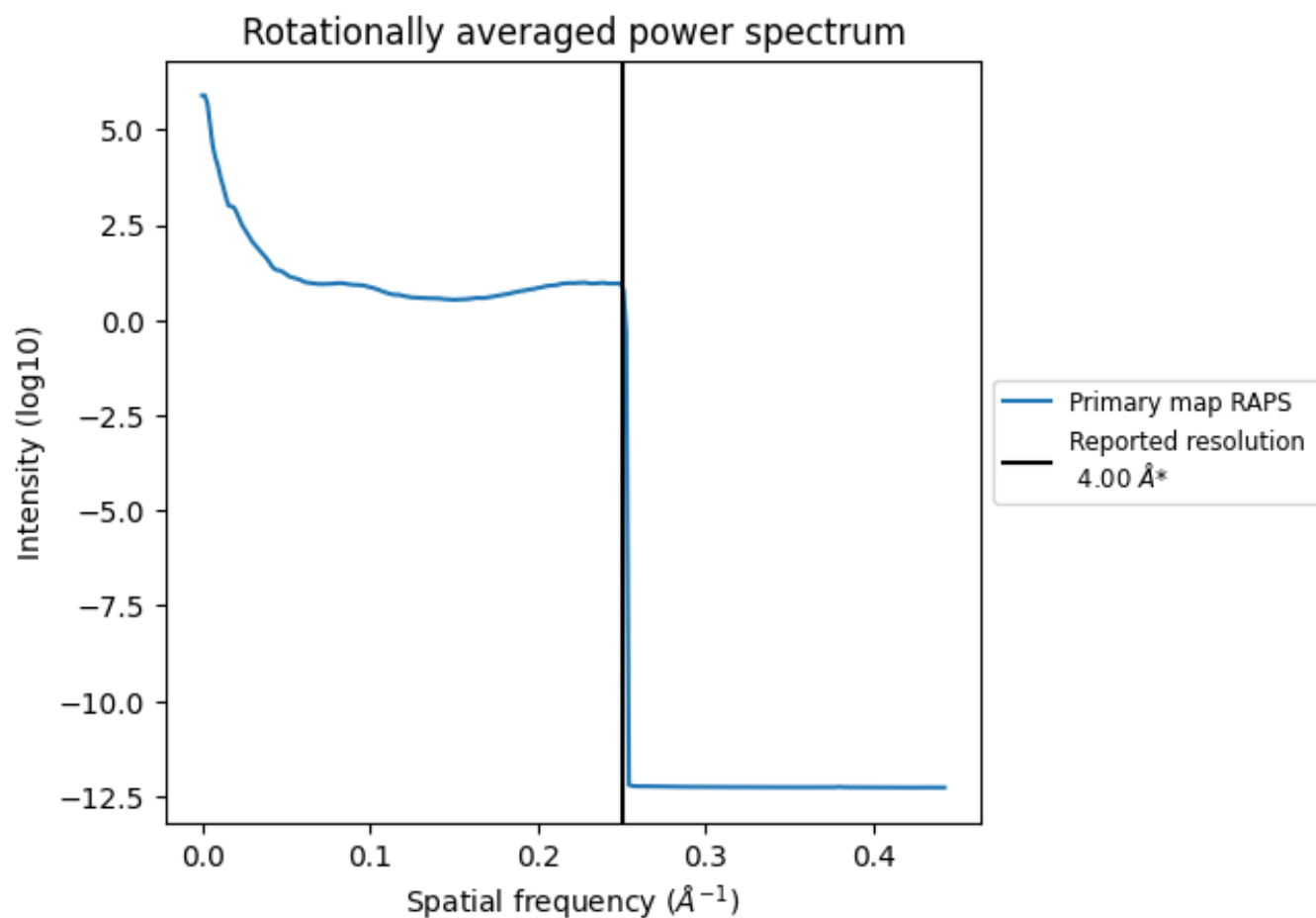
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 189 nm³; this corresponds to an approximate mass of 171 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 0.250 Å⁻¹

8 Fourier-Shell correlation

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

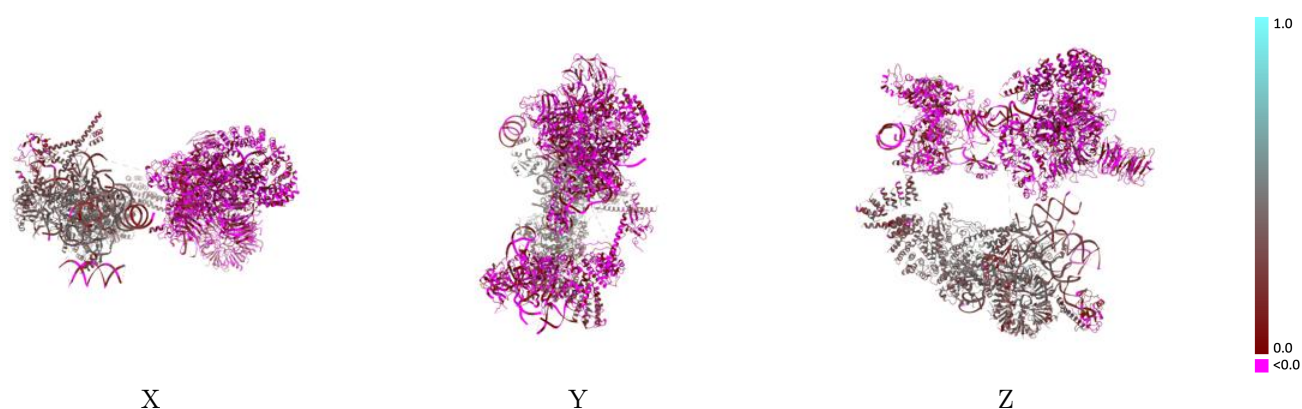
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4364 and PDB model 6G90. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

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

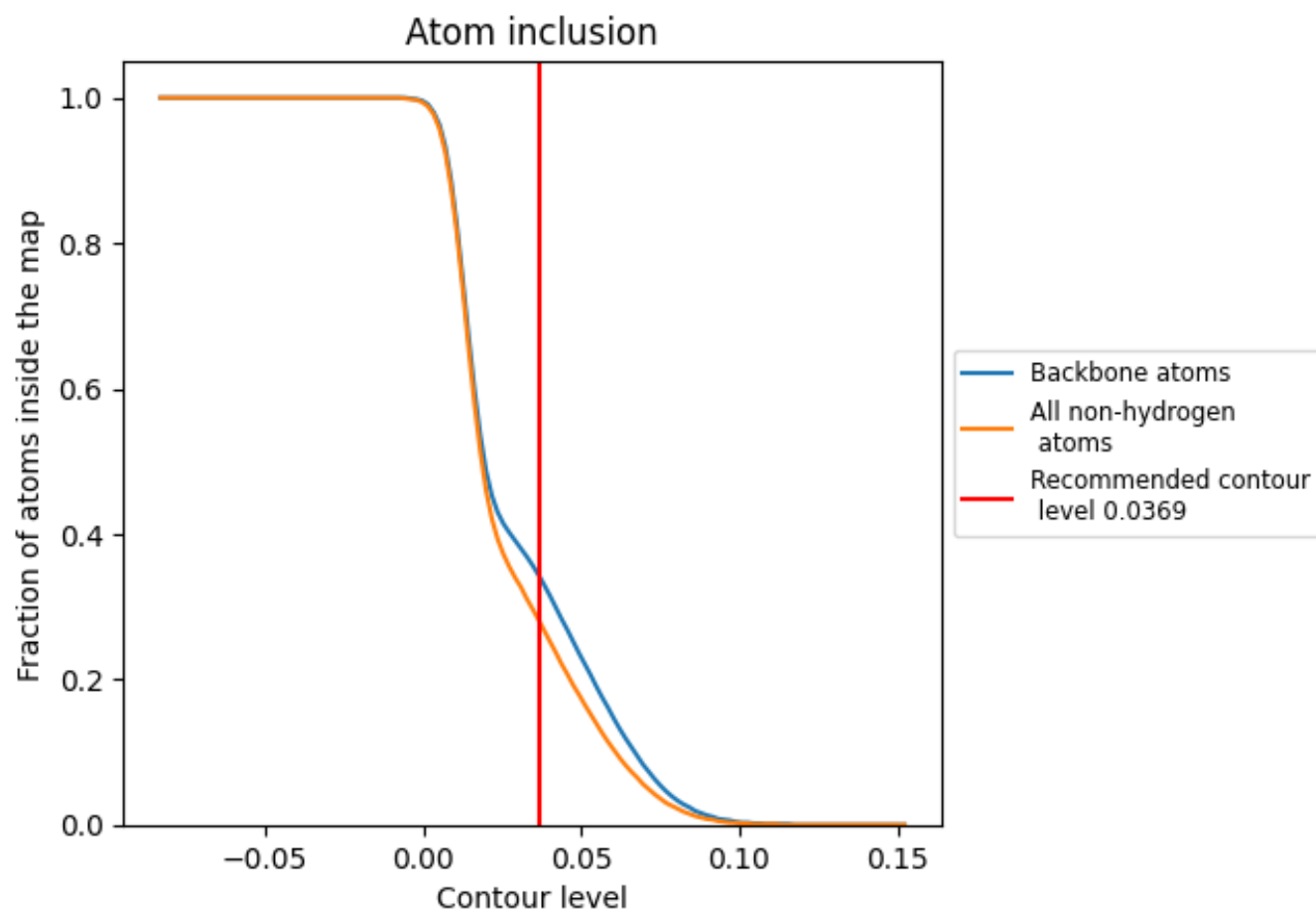


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 34% of all backbone atoms, 28% 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 (0.0369) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2790	 0.1520
1	 0.6780	 0.2970
2	 0.0000	 0.0010
A	 0.7990	 0.3950
B	 0.3390	 0.1890
C	 0.6650	 0.4050
D	 0.6580	 0.3440
E	 0.6800	 0.3970
F	 0.6370	 0.3920
G	 0.6570	 0.3800
H	 0.5710	 0.3040
I	 0.2190	 0.0990
J	 0.7040	 0.4150
O	 0.0000	 -0.0020
P	 0.0000	 0.0010
Q	 0.0000	 -0.0020
R	 0.0000	 0.0120
S	 0.0000	 0.0090
T	 0.0000	 0.0070
U	 0.0000	 0.0040
V	 0.0000	 -0.0060
W	 0.0310	 0.0250
X	 0.6120	 0.3000
Y	 0.0210	 0.0230
Z	 0.0000	 0.0080
b	 0.6260	 0.4070
d	 0.6770	 0.4380
e	 0.6250	 0.3770
f	 0.6290	 0.3320
g	 0.6440	 0.4250
h	 0.6390	 0.3970
i	 0.6240	 0.3460
s	 0.0000	 -0.0080
t	 0.0000	 -0.0400
u	 0.0000	 0.0300



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Chain	Atom inclusion	Q-score
v	 0.0000	 0.0160
w	 0.0000	 -0.0150
x	 0.0000	 0.0370
y	 0.0000	 0.0090