



wwPDB EM Validation Summary Report ⓘ

Sep 23, 2026 – 05:09 pm BST

PDB ID : 9IF7 / pdb_00009if7
EMDB ID : EMD-52843
Title : Cryo-EM structure of the kinetoplastid trans-spliceosome activated for catalytic step II (C* complex)
Authors : Nadenoen, T.; Vanden Broeck, A.
Deposited on : 2025-02-17
Resolution : 2.70 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:

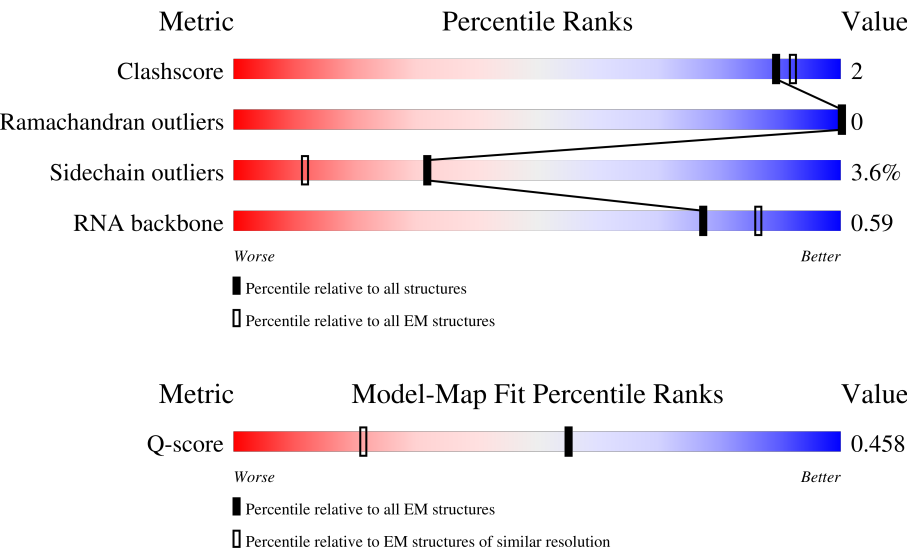
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 2.70 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	10327 (2.20 - 3.20)

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	L7	389	88%11%.
2	L8	153	5% 78%.18%
3	L9	162	6% 88%6%6%

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Mol	Chain	Length	Quality of chain
4	LA	2427	
5	LB	2367	
6	LC	1016	
7	LD	166	
8	LF	706	
9	LG	82	
10	LH	159	
11	LJ	509	
12	LL	326	
13	LN	322	
14	LP	207	
15	LQ	804	
16	LR	197	
17	LS	824	
18	LT	794	
19	LV	1087	
20	LW	307	
21	LY	114	
22	LZ	403	
23	SA	564	
24	SC	417	
25	SD	546	
26	SF	258	
27	SJ	414	
28	SK	175	

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Mol	Chain	Length	Quality of chain
29	SL	544	
30	SN	192	
31	SO	621	
32	SP	269	
33	SQ	150	
34	SS	284	
35	ST	513	
35	SU	513	
35	SV	513	
35	SW	513	
36	TN	1181	
37	UX	21	
38	62	190	
39	63	134	
40	64	116	
41	65	151	
42	66	80	
43	67	91	
44	68	131	
45	RN	68	
46	24	102	
46	51	102	
46	U1	102	
47	25	103	
47	52	103	

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Mol	Chain	Length	Quality of chain
47	U2	103	
48	2C	128	
49	2D	141	
50	2H	86	
50	5E	86	
50	UE	86	
51	2I	76	
51	5F	76	
51	UF	76	
52	2J	81	
52	5G	81	
52	UG	81	
53	53	113	
53	U3	113	
54	5B	111	
54	UB	111	
55	LE	39	
56	LO	57	
57	N2	142	
58	N5	71	
59	N6	100	

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 135855 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 Probable eukaryotic initiation factor 4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L7	382	Total	C	N	O	S	0	0
			3021	1906	536	558	21		

- Molecule 2 is a protein called RRM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L8	125	Total	C	N	O	S	0	0
			999	634	165	198	2		

- Molecule 3 is a protein called Mago nashi-like protein,putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L9	152	Total	C	N	O	S	0	0
			1243	795	211	233	4		

- Molecule 4 is a protein called Prp8 protein homologue, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LA	2347	Total	C	N	O	S	2	0
			18216	11549	3257	3315	95		

- Molecule 5 is a protein called ATP-dependent RNA helicase, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	LB	2128	Total	C	N	O	0	0
			10536	6280	2128	2128		

- Molecule 6 is a protein called Small nuclear ribonucleoprotein component-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	911	Total	C	N	O	S	0	0
			7002	4420	1231	1323	28		

- Molecule 7 is a protein called PRKR-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	125	Total	C	N	O	S	0	0
			1006	603	215	187	1		

- Molecule 8 is a protein called Splicing factor Cactin C-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LF	408	Total	C	N	O	S	0	0
			3311	2102	598	594	17		

- Molecule 9 is a protein called RNA-binding motif protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LG	80	Total	C	N	O	S	0	0
			592	372	101	115	4		

- Molecule 10 is a protein called Splicing regulator SDE2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LH	42	Total	C	N	O	S	0	0
			331	208	68	54	1		

- Molecule 11 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LJ	413	Total	C	N	O	S	0	0
			3196	2015	575	590	16		

- Molecule 12 is a protein called G10 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	185	Total	C	N	O	S	1	0
			1455	910	275	254	16		

- Molecule 13 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LN	316	Total	C	N	O	S	0	0
			2314	1430	418	448	18		

- Molecule 14 is a protein called Spliceosome-associated CWC15-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LP	72	Total	C	N	O	S	1	0
			598	378	114	104	2		

- Molecule 15 is a protein called Cell division control protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LQ	551	Total	C	N	O	S	0	0
			4277	2620	824	817	16		

- Molecule 16 is a protein called CWF21 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LR	161	Total	C	N	O	S	0	0
			1230	746	243	236	5		

- Molecule 17 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LS	772	Total	C	N	O	S	0	0
			6209	3867	1170	1149	23		

- Molecule 18 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LT	794	Total	C	N	O	S	0	0
			6284	3978	1133	1142	31		

- Molecule 19 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LV	973	Total	C	N	O	S	0	0
			7589	4749	1326	1465	49		

- Molecule 20 is a protein called U2 small nuclear ribonucleoprotein 40K, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LW	188	Total	C	N	O	S	0	0
			1545	979	280	280	6		

- Molecule 21 is a protein called RRM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LY	107	Total	C	N	O	S	0	0
			876	558	163	151	4		

- Molecule 22 is a protein called NF-kappa-B-activating protein C-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LZ	89	Total	C	N	O	S	0	0
			619	376	123	118	2		

- Molecule 23 is a protein called MI domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SA	511	Total	C	N	O	S	0	0
			4239	2656	764	793	26		

- Molecule 24 is a protein called Pre-mRNA-splicing factor SLU7.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SC	261	Total	C	N	O	S	0	0
			2108	1298	389	414	7		

- Molecule 25 is a protein called Pre-mRNA-splicing factor 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SD	322	Total	C	N	O	S	0	0
			2577	1630	464	468	15		

- Molecule 26 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	SF	48	Total	C	N	O	0	0
			237	141	48	48		

- Molecule 27 is a protein called PRP19-related complex protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SJ	273	Total	C	N	O	S	0	0
			2197	1359	412	417	9		

- Molecule 28 is a protein called Unspecified product.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SK	87	Total	C	N	O	S	0	0
			699	452	118	125	4		

- Molecule 29 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SL	239	Total	C	N	O	P S	0	0
			1770	1074	324	362	1 9		

- Molecule 30 is a protein called peptidylprolyl isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SN	185	Total	C	N	O	S	0	0
			1396	885	239	264	8		

- Molecule 31 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SO	424	Total	C	N	O	S	0	0
			3334	2111	598	611	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	SP	83	Total	C	N	O	S	0	0
			683	423	127	132	1		

- Molecule 33 is a protein called Zinc knuckle.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SQ	106	Total	C	N	O	S	0	0
			838	523	154	156	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SQ	0	ACE	-	acetylation	UNP A0A640KSY0

- Molecule 34 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	SS	186	Total	C	N	O	S	0	0
			1504	936	279	282	7		

- Molecule 35 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	ST	488	Total	C	N	O	S	0	0
			3606	2238	650	700	18		
35	SU	133	Total	C	N	O	S	0	0
			1022	637	184	195	6		
35	SV	133	Total	C	N	O	S	0	0
			1022	637	184	195	6		
35	SW	121	Total	C	N	O	S	0	0
			949	593	172	178	6		

- Molecule 36 is a protein called Probable RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	TN	44	Total	C	N	O	S	0	0
			351	227	59	63	2		

- Molecule 37 is a protein called Unidentified protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	UX	21	Total	C	N	O	0	0
			105	63	21	21		

- Molecule 38 is a protein called LSM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	62	124	Total	C	N	O	S	0	0
			937	578	177	175	7		

- Molecule 39 is a protein called Sm domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	63	79	Total	C	N	O	S	0	0
			602	377	102	119	4		

- Molecule 40 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	64	83	Total	C	N	O	S	0	0
			640	390	123	121	6		

- Molecule 41 is a protein called LSM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	65	114	Total	C	N	O	S	0	0
			876	547	151	172	6		

- Molecule 42 is a protein called Sm domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	66	71	Total	C	N	O	S	0	0
			541	338	94	106	3		

- Molecule 43 is a protein called Lsm7p protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	67	91	Total	C	N	O	S	0	0
			701	444	129	126	2		

- Molecule 44 is a protein called Sm domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	68	102	Total	C	N	O	S	0	0
			774	486	136	147	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
68	0	ACE	-	acetylation	UNP A0A640KIZ1

- Molecule 45 is a RNA chain called Y-branched pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	RN	21	Total	C	N	O	P	0	0
			283	120	15	127	21		

- Molecule 46 is a protein called Small nuclear ribonucleoprotein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	24	102	Total	C	N	O	S	0	0
			783	489	132	157	5		
46	51	98	Total	C	N	O	S	0	0
			758	475	127	151	5		
46	U1	98	Total	C	N	O		0	0
			484	288	98	98			

- Molecule 47 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	25	82	Total	C	N	O	S	0	0
			654	418	116	118	2		
47	52	89	Total	C	N	O	S	0	0
			715	457	128	128	2		
47	U2	83	Total	C	N	O		0	0
			411	245	83	83			

- Molecule 48 is a protein called Lsm5p, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	2C	114	Total	C	N	O	S	0	0
			881	535	174	168	4		

- Molecule 49 is a protein called Small nuclear ribonucleoprotein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2D	99	Total	C	N	O	S	0	0
			792	502	140	148	2		

- Molecule 50 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2H	81	Total	C	N	O	S	0	0
			657	409	124	120	4		
50	5E	78	Total	C	N	O	S	0	0
			629	393	117	116	3		
50	UE	79	Total	C	N	O		0	0
			388	230	79	79			

- Molecule 51 is a protein called Sm protein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2I	76	Total	C	N	O	S	0	0
			598	377	104	113	4		
51	5F	76	Total	C	N	O	S	0	0
			598	377	104	113	4		
51	UF	76	Total	C	N	O		0	0
			375	223	76	76			

- Molecule 52 is a protein called Sm protein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2J	77	Total	C	N	O	S	0	0
			583	361	107	112	3		
52	5G	77	Total	C	N	O	S	0	0
			583	361	107	112	3		
52	UG	77	Total	C	N	O		0	0
			379	225	77	77			

- Molecule 53 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	53	104	Total	C	N	O	S	0	0
			801	502	147	150	2		
53	U3	81	Total	C	N	O		0	0
			400	238	81	81			

- Molecule 54 is a protein called Sm protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	5B	99	Total	C	N	O	S	0	0
			738	458	133	141	6		
54	UB	81	Total	C	N	O		0	0
			398	236	81	81			

- Molecule 55 is a RNA chain called SL RNA exon.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LE	25	Total	C	N	O	P	1	0
			547	245	88	188	26		

- Molecule 56 is a RNA chain called SL RNA outtron.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LO	47	Total	C	N	O	P	0	0
			1006	449	183	327	47		

- Molecule 57 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	N2	76	Total	C	N	O	P	0	0
			1604	718	270	540	76		

- Molecule 58 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	N5	63	Total	C	N	O	P	0	0
			1328	595	230	440	63		

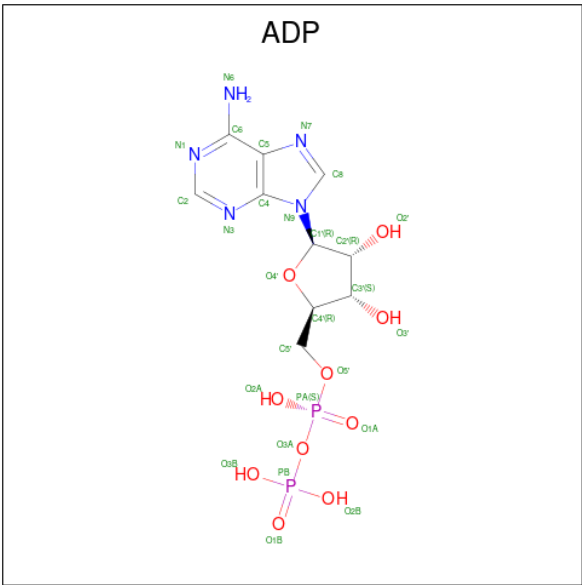
- Molecule 59 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	N6	100	Total	C	N	O	P	0	0
			2127	952	381	694	100		

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	L7	1	Total	Mg	0
			1	1	
60	LA	1	Total	Mg	0
			1	1	
60	LC	1	Total	Mg	0
			1	1	
60	N5	1	Total	Mg	0
			1	1	
60	N6	8	Total	Mg	0
			8	8	

- Molecule 61 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

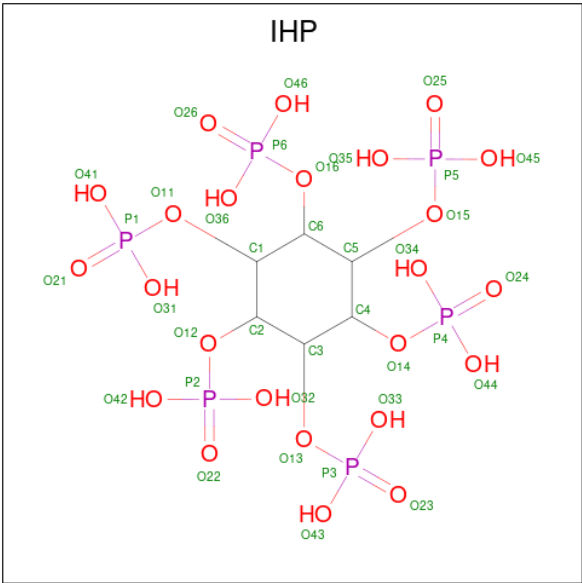


Mol	Chain	Residues	Atoms					AltConf
61	L7	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 62 is POTASSIUM ION (CCD ID: K) (formula: K).

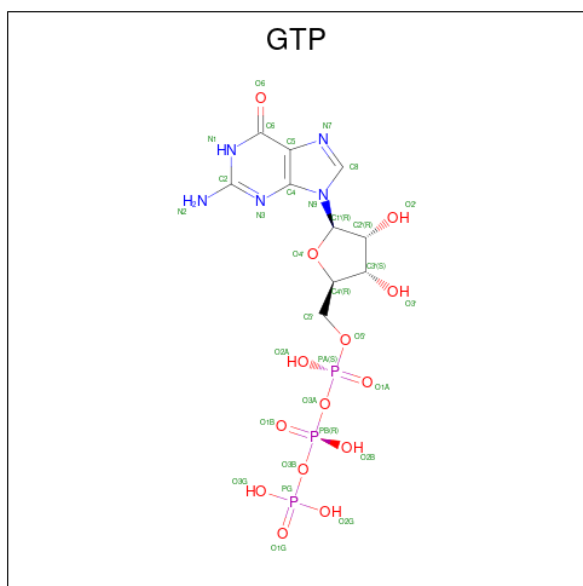
Mol	Chain	Residues	Atoms		AltConf
62	L7	1	Total	K	0
			1	1	

- Molecule 63 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆).



Mol	Chain	Residues	Atoms				AltConf
63	LA	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 64 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

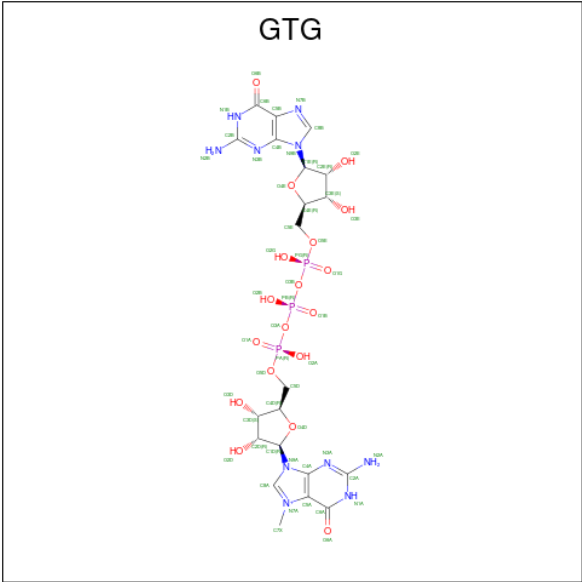


Mol	Chain	Residues	Atoms					AltConf
64	LC	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

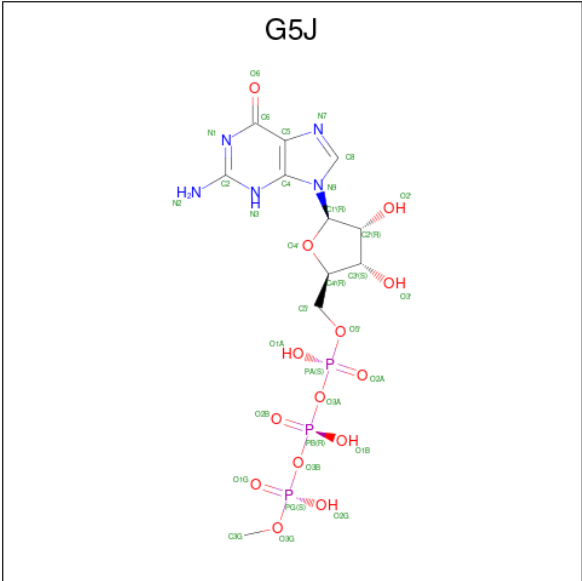
Mol	Chain	Residues	Atoms		AltConf
65	LL	3	Total	Zn	0
			3	3	
65	SC	1	Total	Zn	0
			1	1	
65	SQ	1	Total	Zn	0
			1	1	

- Molecule 66 is 7-METHYL-GUANOSINE-5'-TRIPHOSPHATE-5'-GUANOSINE (CCD ID: GTG) (formula: $C_{21}H_{30}N_{10}O_{18}P_3$).



Mol	Chain	Residues	Atoms					AltConf
66	N5	1	Total	C	N	O	P	0
			52	21	10	18	3	

- Molecule 67 is 5'-O-[(S)-hydroxy{[(R)-hydroxy{[(S)-hydroxy(methoxy)phosphoryl]oxy}phosphoryl]oxy}phosphoryl]guanosine (CCD ID: G5J) (formula: C₁₁H₁₈N₅O₁₄P₃).

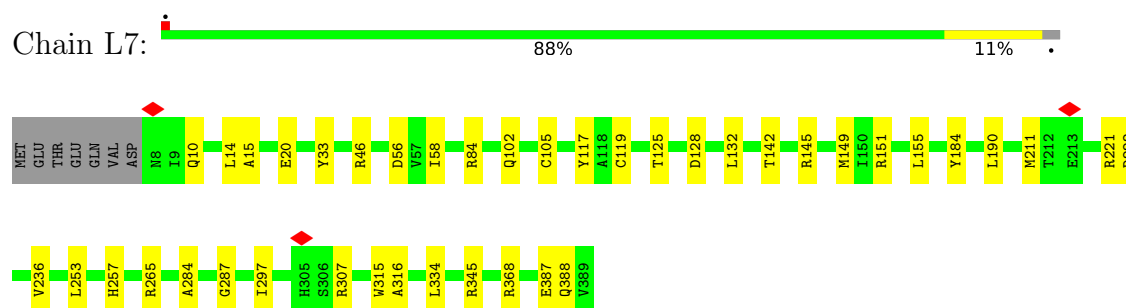


Mol	Chain	Residues	Atoms					AltConf
67	N6	1	Total	C	N	O	P	0
			33	11	5	14	3	

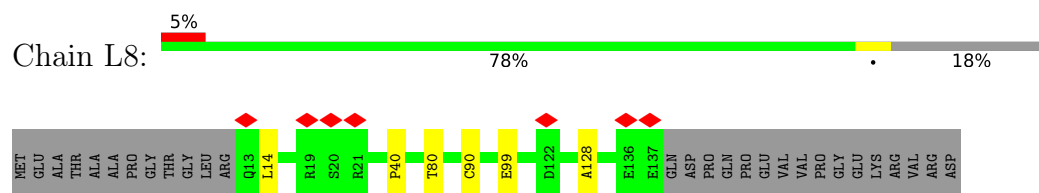
3 Residue-property plots [i](#)

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

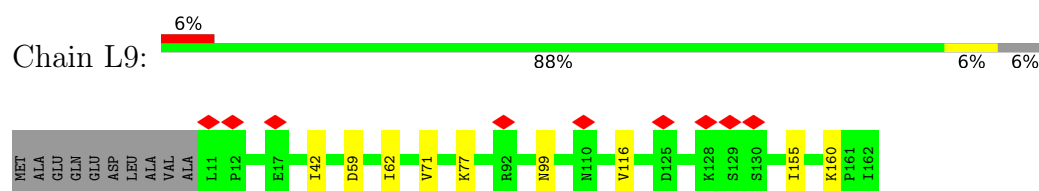
- Molecule 1: Probable eukaryotic initiation factor 4A



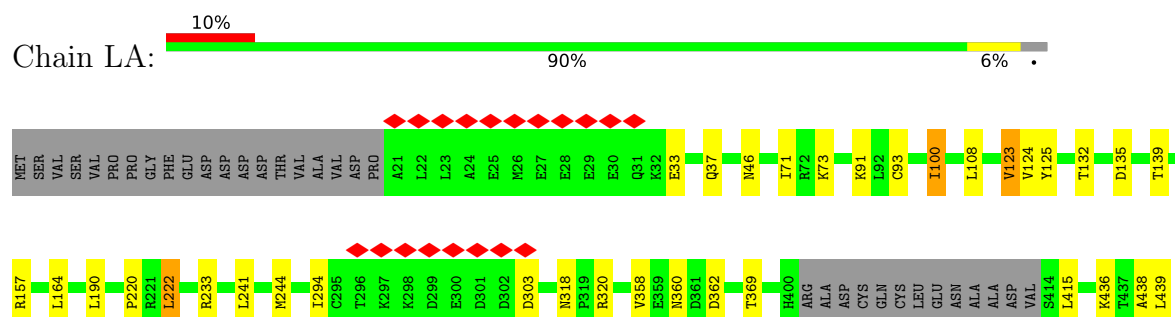
- Molecule 2: RRM domain-containing protein

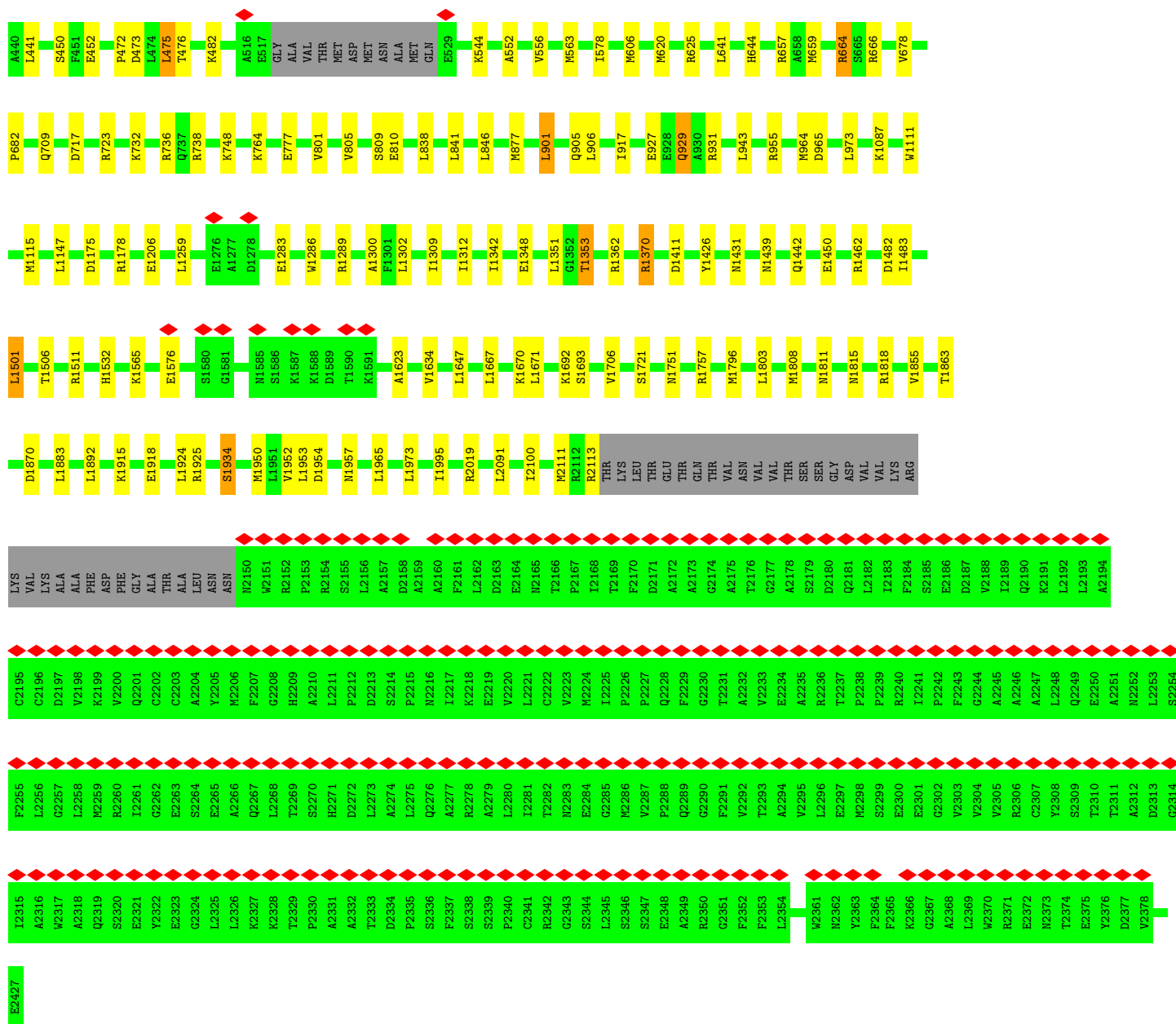


- Molecule 3: Mago nashi-like protein, putative

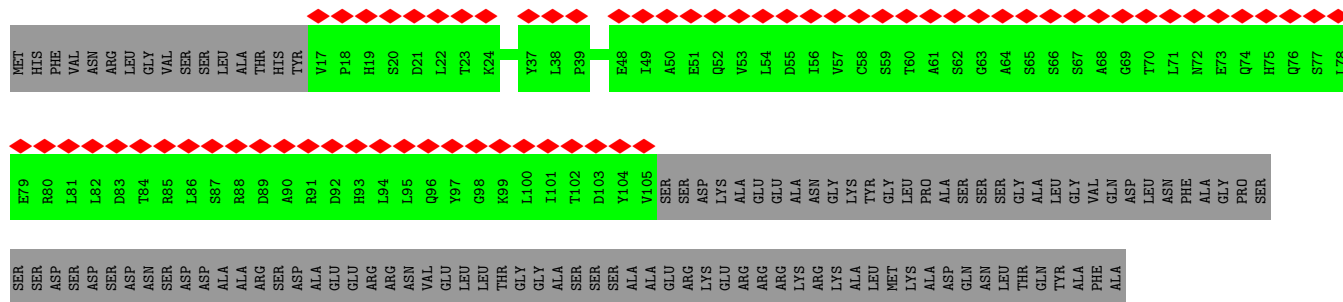
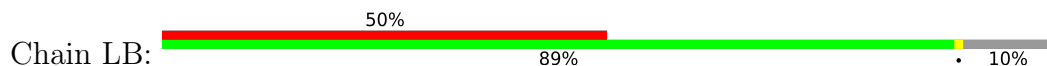


- Molecule 4: Prp8 protein homologue, putative

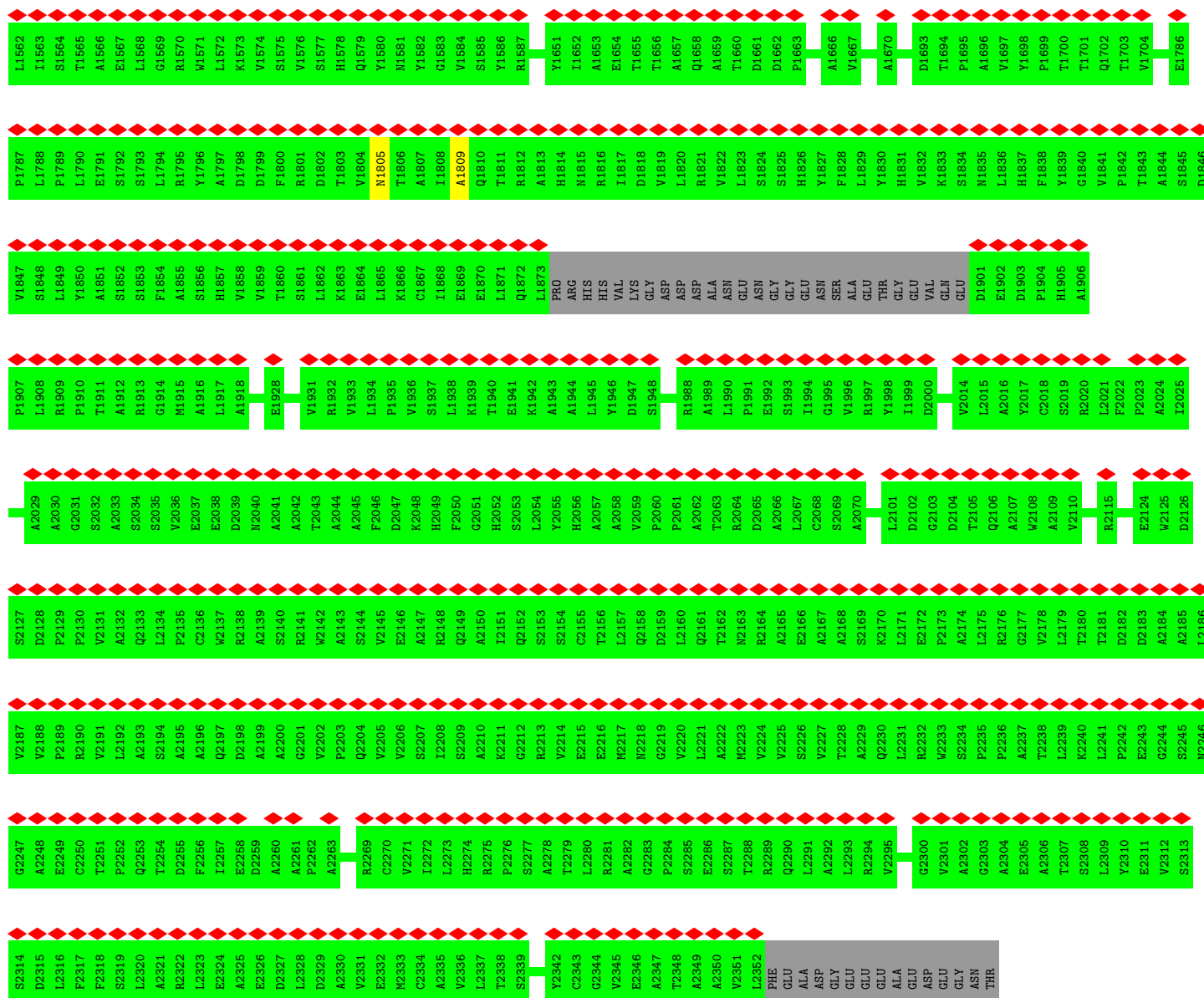




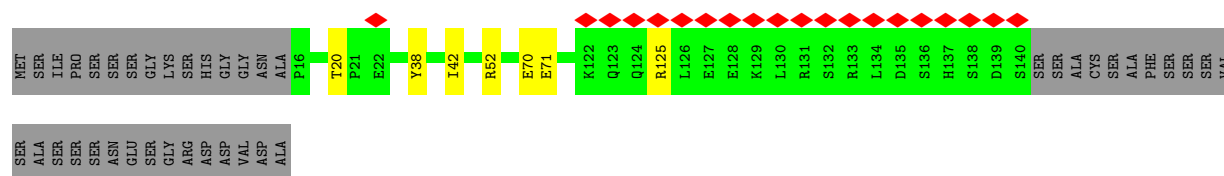
• Molecule 5: ATP-dependent RNA helicase, putative



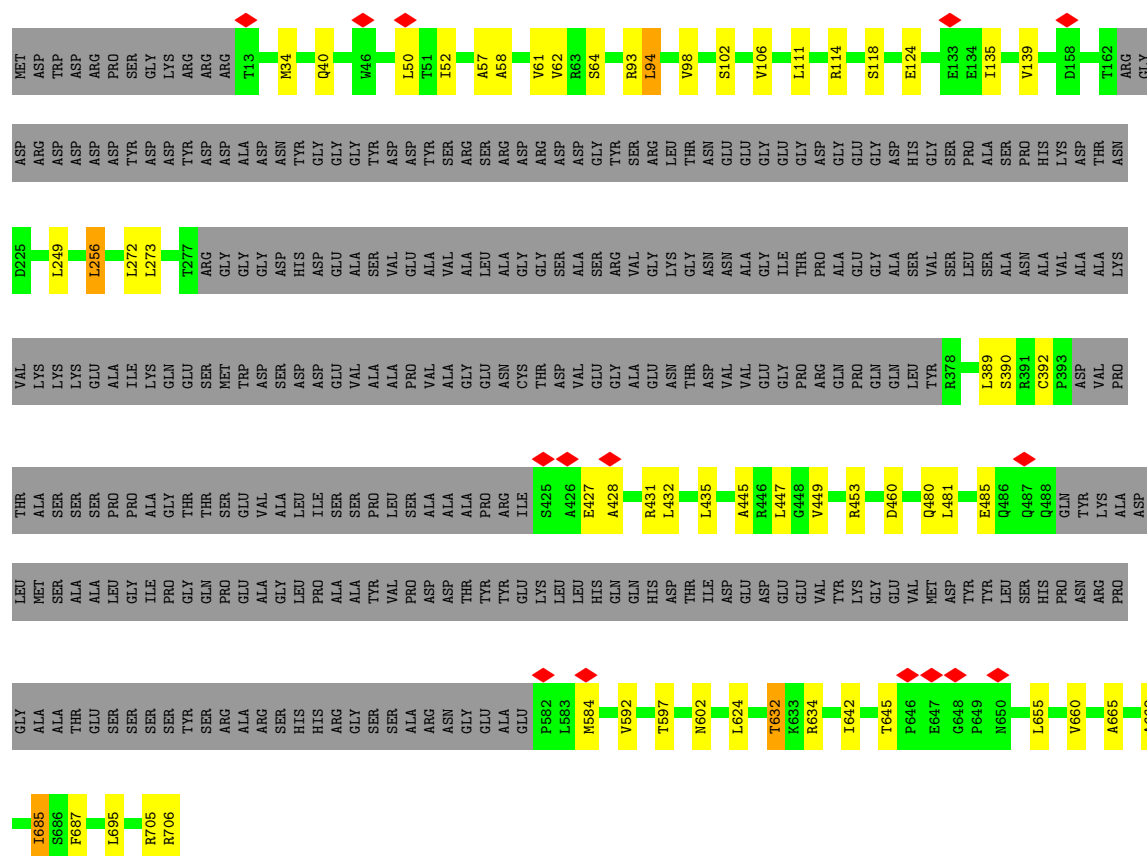
GLU	GLU	GLY	GLY	ILE	ALA	ASP	THR	VAL	GLU	GLU	GLN	ALA	TRP	ARG	ASP	ALA	PRO	PRO	GLY	THR	ALA	GLY	THR	GLU	GLY	GLY	ASP	LEU	THR	ARG	GLY	VAL	ASP	THR	PRO	R249	I250	P251	F252	E253	E254	V255	S256	C257	N258														
A259	Q260	F261	L262	K263	D264	T265	V266	R267	R268	L269	F270	A271	P272	H273	D274	A275	D276	T277	C278	H279	H280	L281	A282	Q283	R284	V285	L286	N287	F288	L289	S290	E291	K292	E293	E294	D295	D296	F297	T298	L299	E300	T301	Q302	L303	T304	T305	C306	L307	G308	G309	Y310	E311	D312	E313	A314	V315	M316	D317	W318
I319	G320	D321	V322	Q323	Q324	S325	R326	S327	S328	V329	V330	Y331	G332	L333	R334	Y335	A336	Q337	C338	A339	T340	Q341	K342	E343	R344	H345	A346	V347	M348	D349	S350	M351	Q352	H353	H354	Y365	Q366	S367	L368	T369	G370	LYS	GLU	VAL	ASP	PRO	LEU	ASN	THR	GLN	SER	GLN	GLN	ARG	ARG	GLU	ALA		
ALA	ALA	ALA	GLY	GLY	ASP	GLU	GLU	ALA	ALA	SER	LYS	PHE	ALA	SER	ARG	GLN	PRO	L409	R431	A432	T433	V434	P435	Q436	G437	T438	Q439	R440	L441	T442	Y443	E444	T445	H446	D447	E448	V449	L450	L451	P452	P453	T454	S455	S456	Y457	M458	T459	S460	M461	P462	F463	T464	Q465	V466	G467				
T468	S469	F470	P471	D472	H473	A474	H475	P476	L477	F478	A479	G480	V481	E482	E483	L484	N485	A486	N487	Q488	S489	K490	V491	Y492	D493	C494	A495	F496	H497	S498	D499	E500	L503	V504	S505	P507	T508	G509	G511	K512	T513	N514	V515	A516	N517	M518	L521	R522	T523	I524	A525	A526	S527	R528	N529				
P530	K531	T532	G533	V534	I535	K561	R562	L563	E564	S565	L566	E606	A610	E620	L656	T659	L660	P661	N662	H663	A664	N673	R674	Q675	R676	G677	L678	F679	V680	F681	D682	S684	N683	Y685	R686	P687	L688	P689	L690	E691	Q692	T693	Y694	C695	A696	T697	K698	K699	I700	K701	G702	M703							
A704	Q705	S706	A707	V708	M709	N710	L711	V712	A713	Y714	D715	K716	V717	L718	Q719	T720	V721	Q722	A723	E724	E725	Q726	V727	M728	I729	T737	E738	H739	T740	A741	R742	Y743	L744	Q745	K746	R747	A748	A749	E750	E751	R752	R753	G754	Y755	Y756	F757	V758	R759	P760	D761	S762	S764	H765	A767	L768	L769			
E770	A771	S772	S773	G774	A775	G776	G777	A778	V779	L780	R781	R782	S783	L784	Q785	Q786	L787	L788	P789	D790	G791	F792	R804	N805	T806	V807	E808	Q809	L810	F811	A812	D813	G814	H815	L816	R817	V818	L819	E820	P832	A833	N834	R835	V836	I837	A866	G867	R868	A869	G870	Y871	G872	A873	A874	V875	G876			
R877	A878	T879	P884	D885	H888	N895	Q896	Q897	Q942	R950	P951	S952	A953	S954	D955	P956	L957	K1148	H1149	W1170	S1171	E1173	D1174	L1175	A1176	E1177	K1178	L1179	S1180	D1181	D1182	R1183	R1184	A1185	Q1186	S1187	A1188	Y1189	V1204	R1205	P1206	L1207	T1208	R1209	G1210	M1211	L1212	Y1213	N1244										
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L1493	G1496	V1503	R1504	R1505	G1506	D1507	P1508	A1509	L1510	A1511	G1512	V1513	T1514	H1515	I1516	V1517	V1518	D1519	H1520	L1521	H1522	L1523	L1524	R1525	Q1530	E1531	V1532	E1533	E1534	C1535	M1536	A1537	R1538	L1539	N1540	S1541	E1542	P1543	F1544	L1545	V1546	R1547	R1548	G1549	G1550	R1552	A1553	R1554	V1555	L1556	G1557	L1558	T1559	Y1560	P1561				



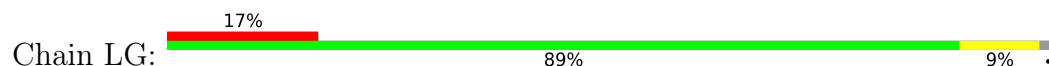
- Molecule 7: PRKR-interacting protein 1

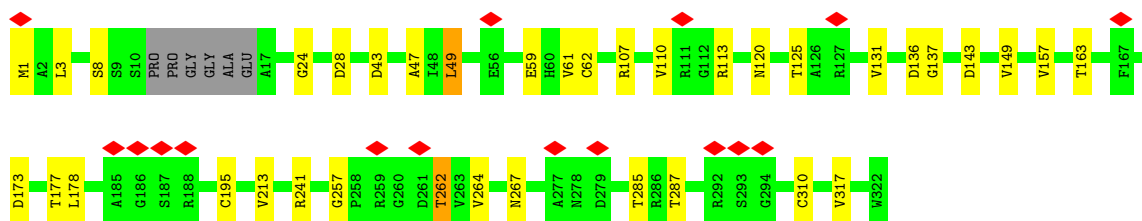
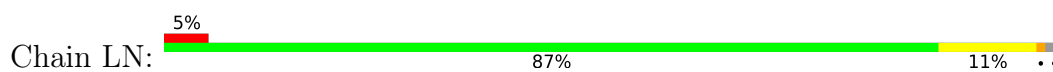


- Molecule 8: Splicing factor Cactin C-terminal domain-containing protein

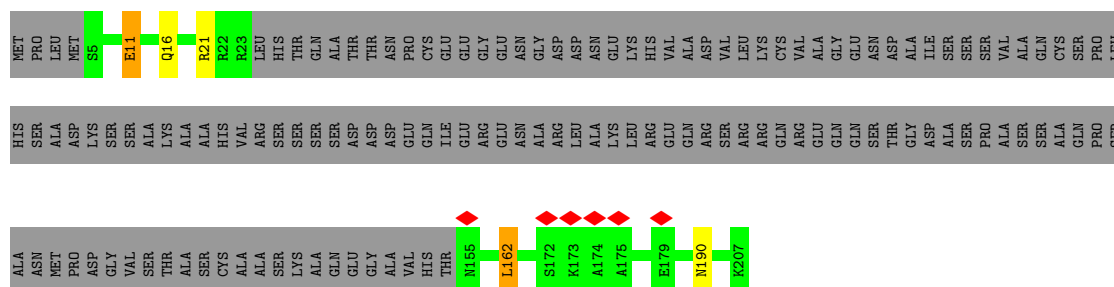


- Molecule 9: RNA-binding motif protein

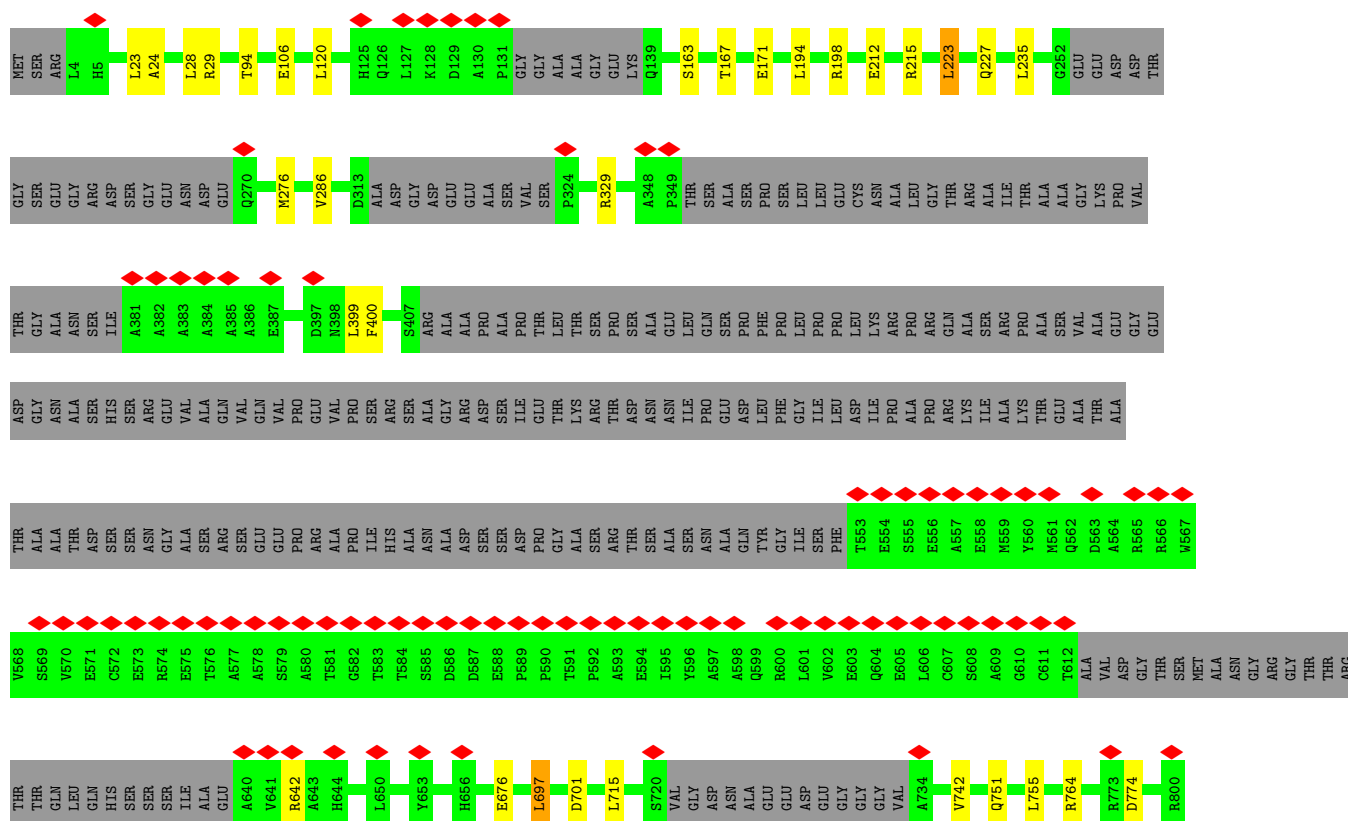


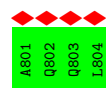


• Molecule 14: Spliceosome-associated CWC15-like protein

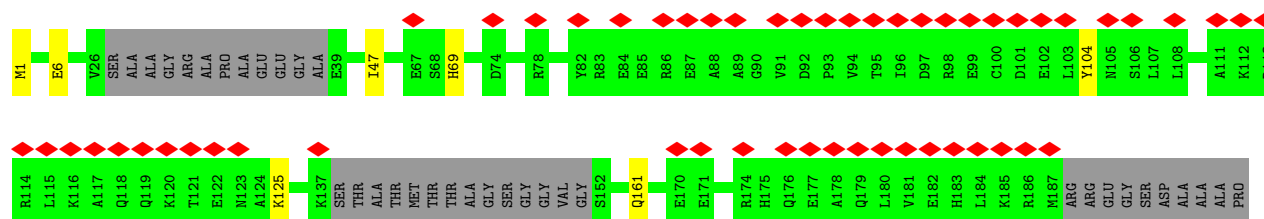
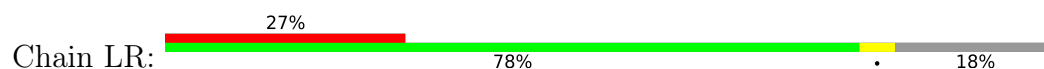


• Molecule 15: Cell division control protein

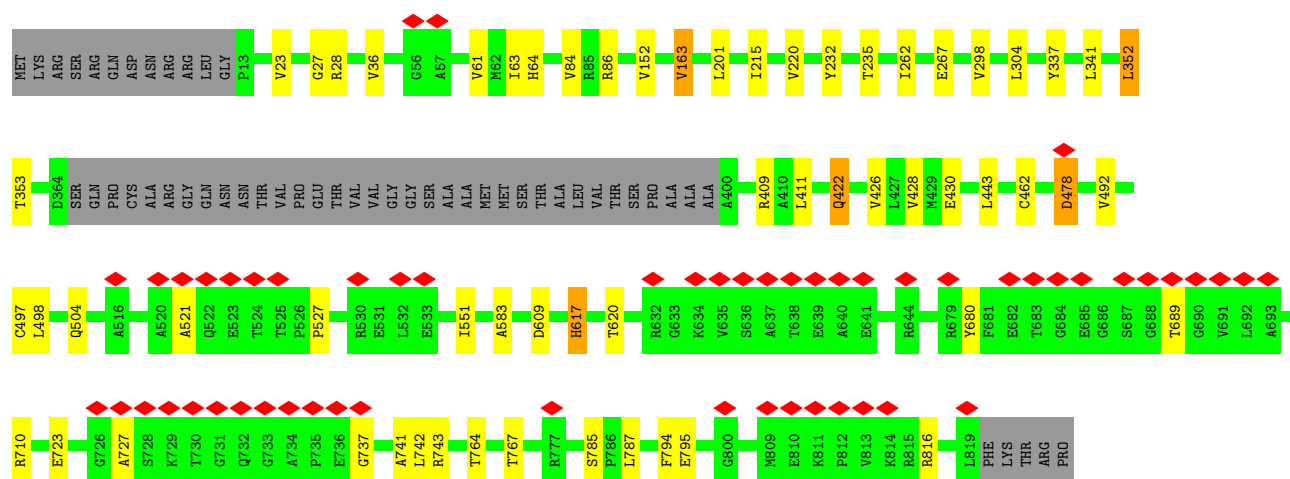
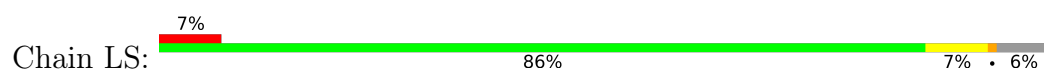




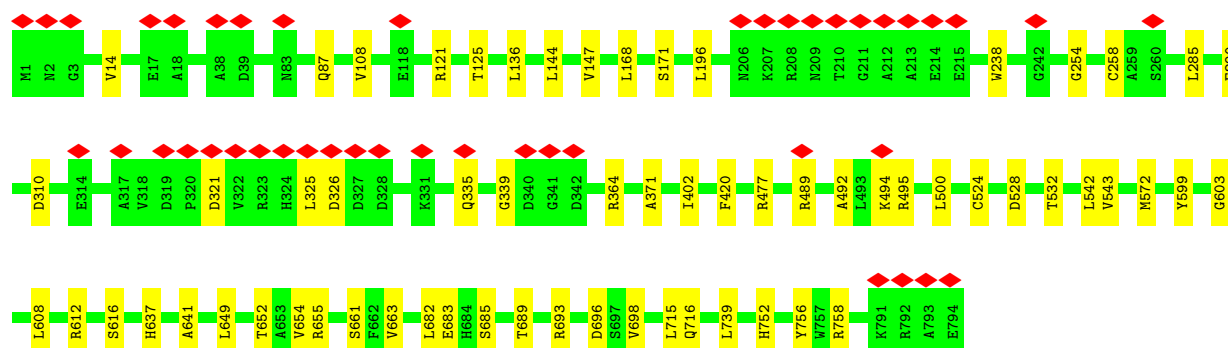
- Molecule 16: CWF21 domain-containing protein



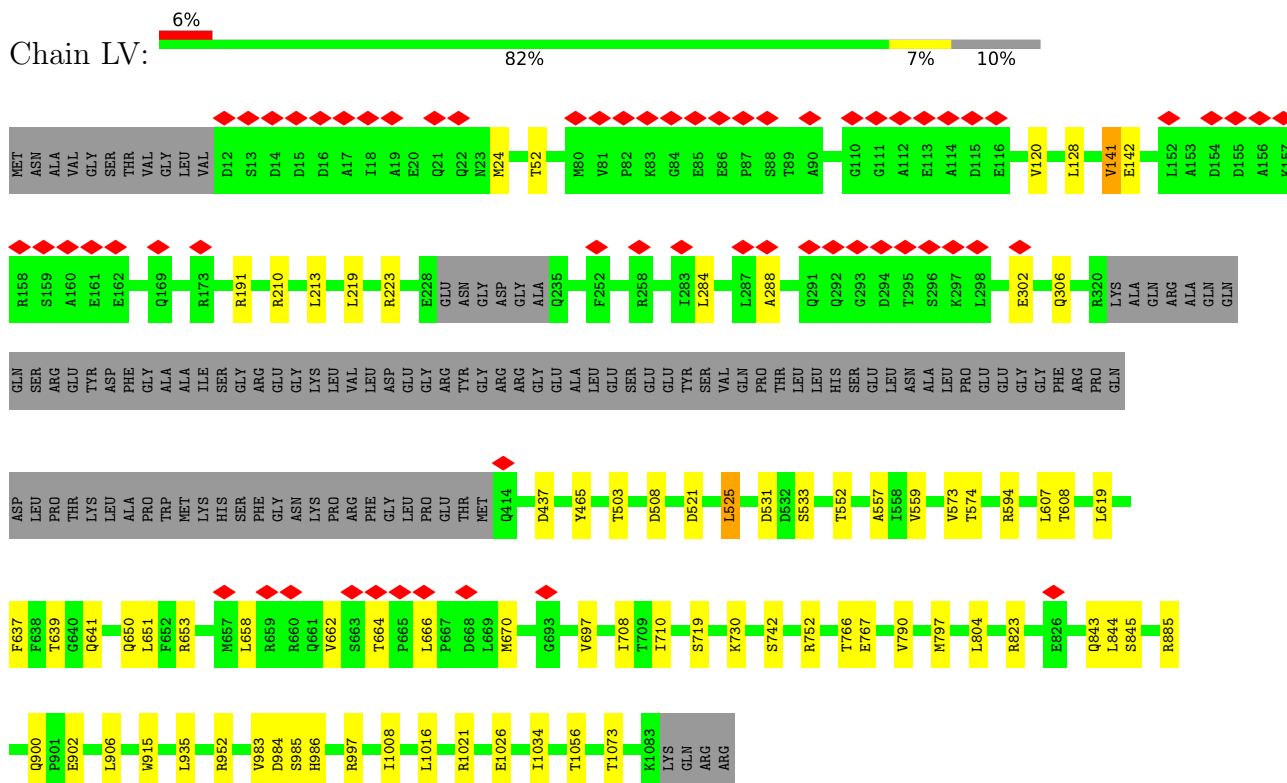
- Molecule 17: Crooked neck-like protein 1



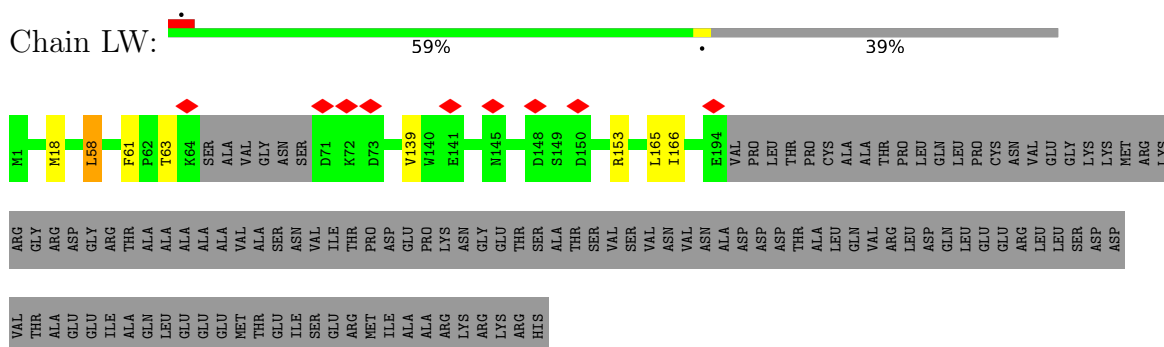
- Molecule 18: Pre-mRNA-splicing factor SYF1



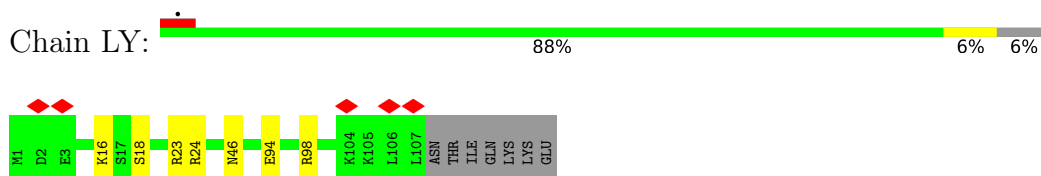
- Molecule 19: RNA helicase



- Molecule 20: U2 small nuclear ribonucleoprotein 40K, putative



- Molecule 21: RRM domain-containing protein

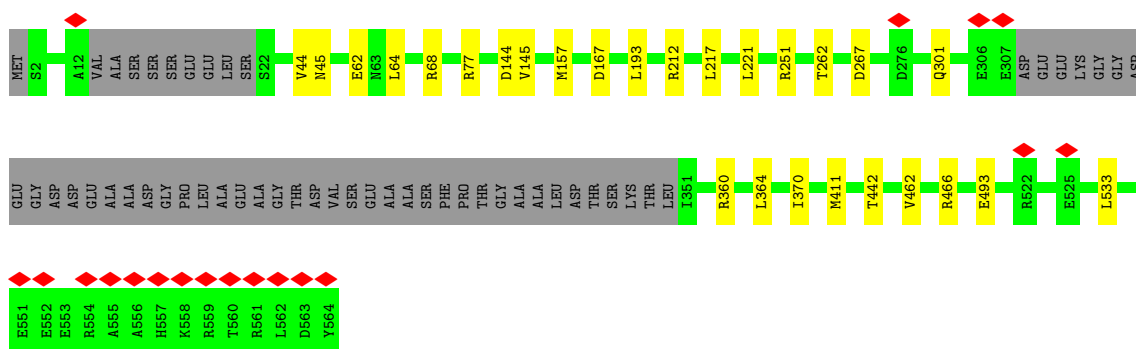


- Molecule 22: NF-kappa-B-activating protein C-terminal domain-containing protein

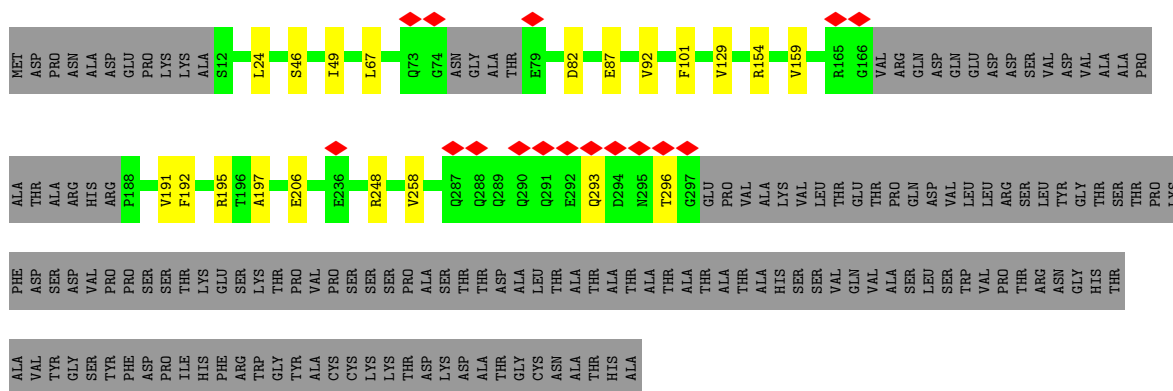




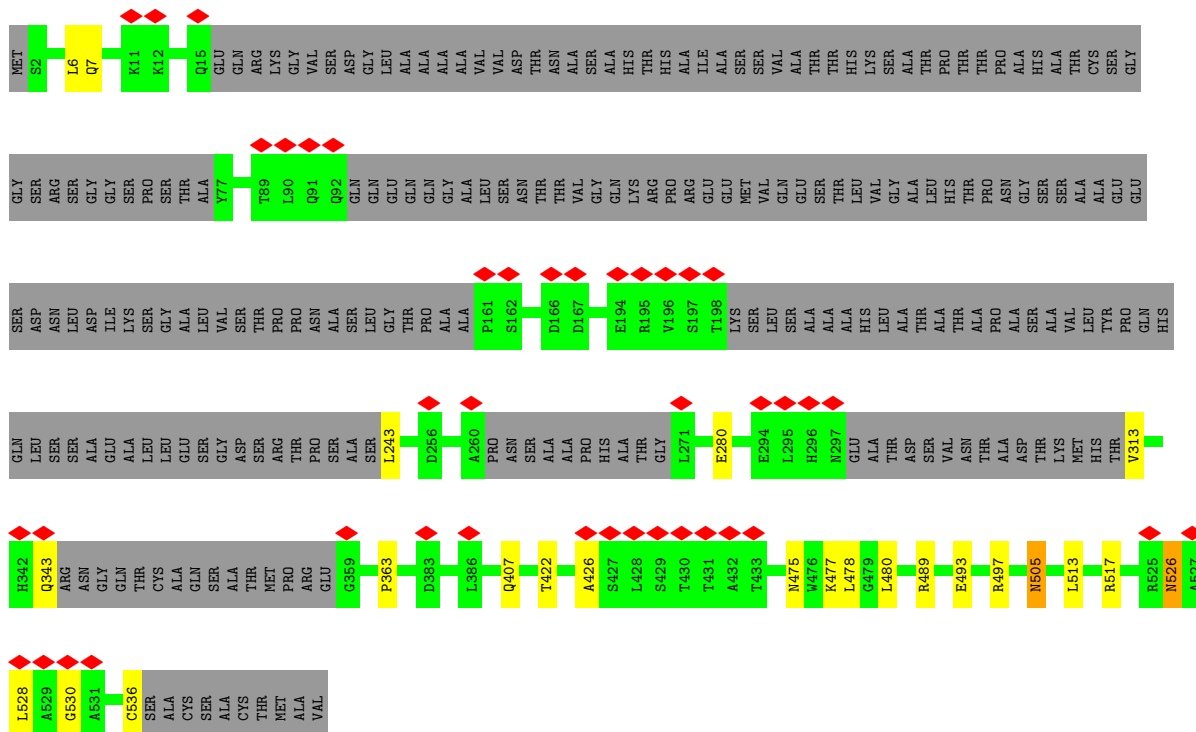
Chain SA: 86% 5% 9%



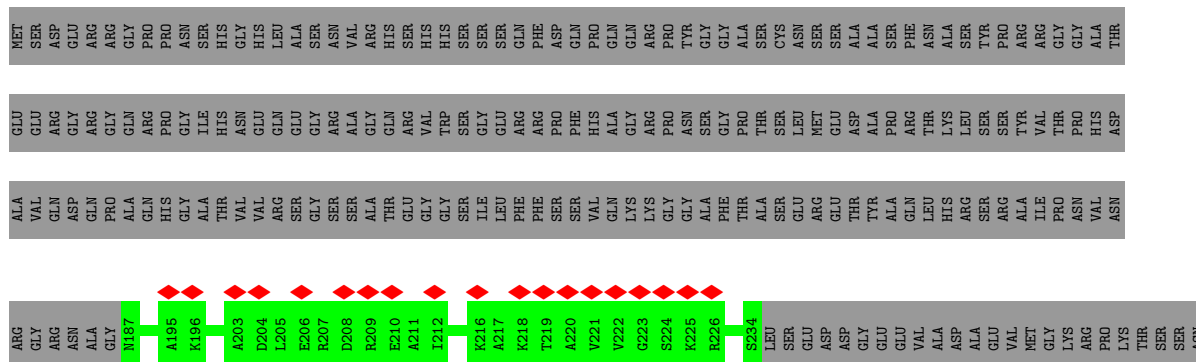
Chain SC:



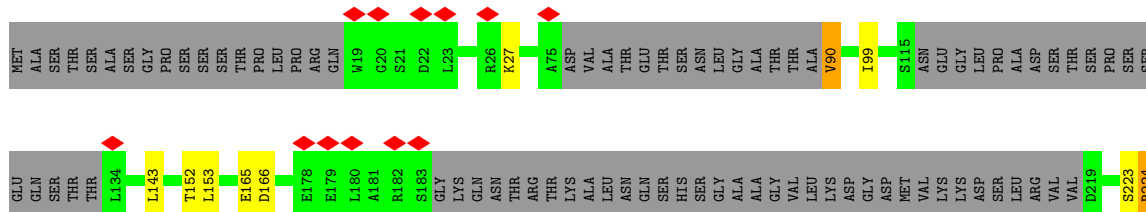
Chain SD:

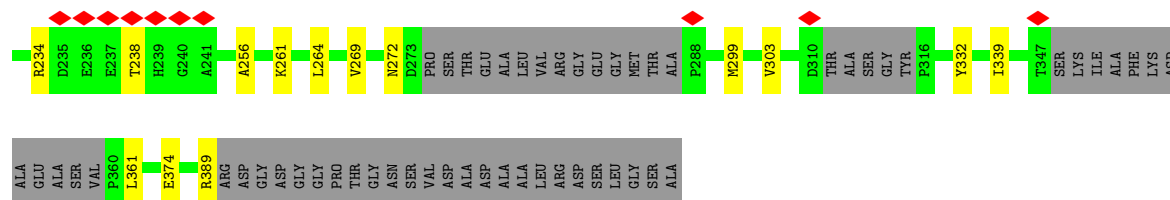


- Molecule 26: Uncharacterized protein

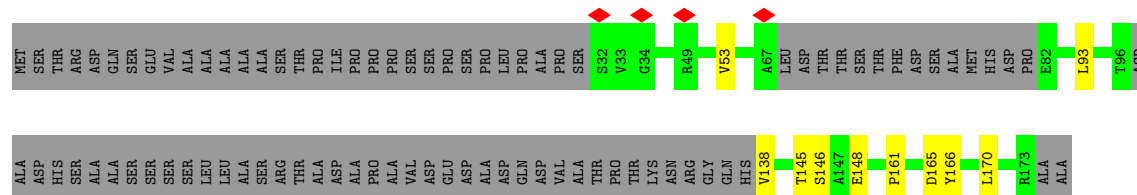


- Molecule 27: PRP19-related complex protein 3

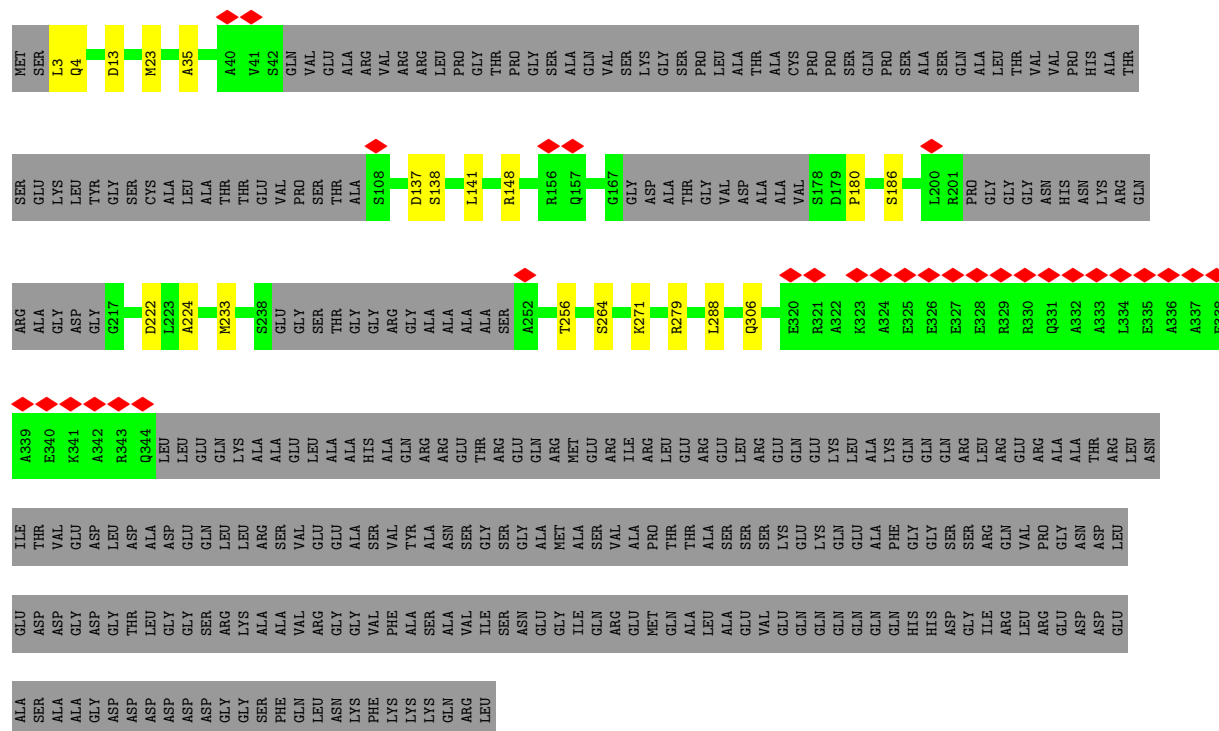
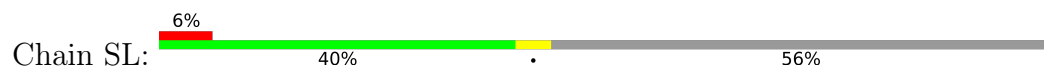




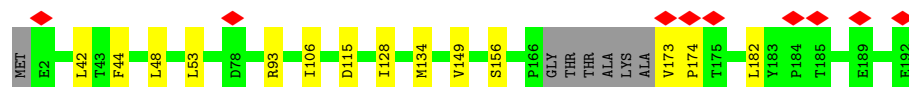
• Molecule 28: Unspecified product



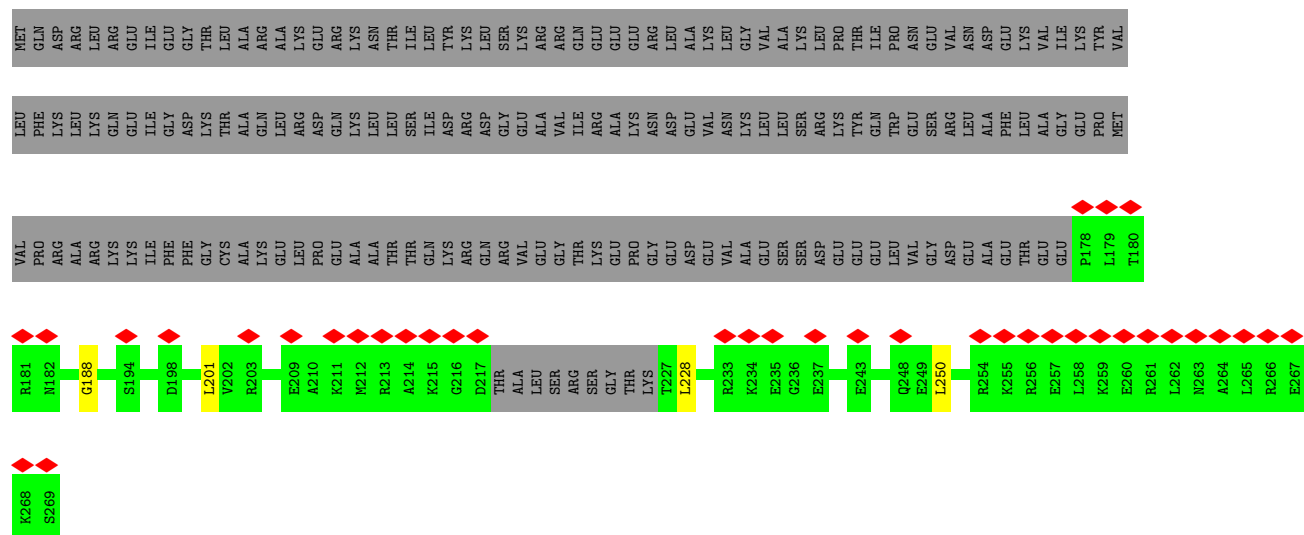
• Molecule 29: SNW domain-containing protein 1



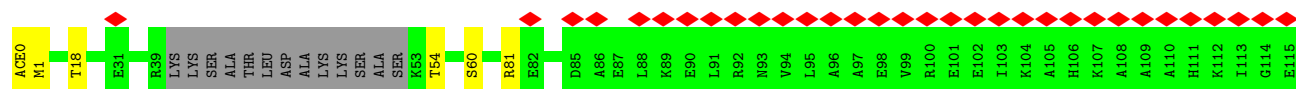
• Molecule 30: peptidylprolyl isomerase



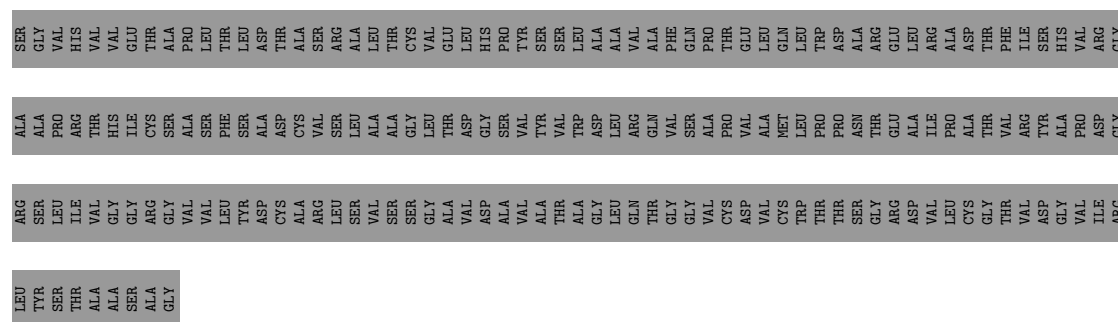
Chain SO:



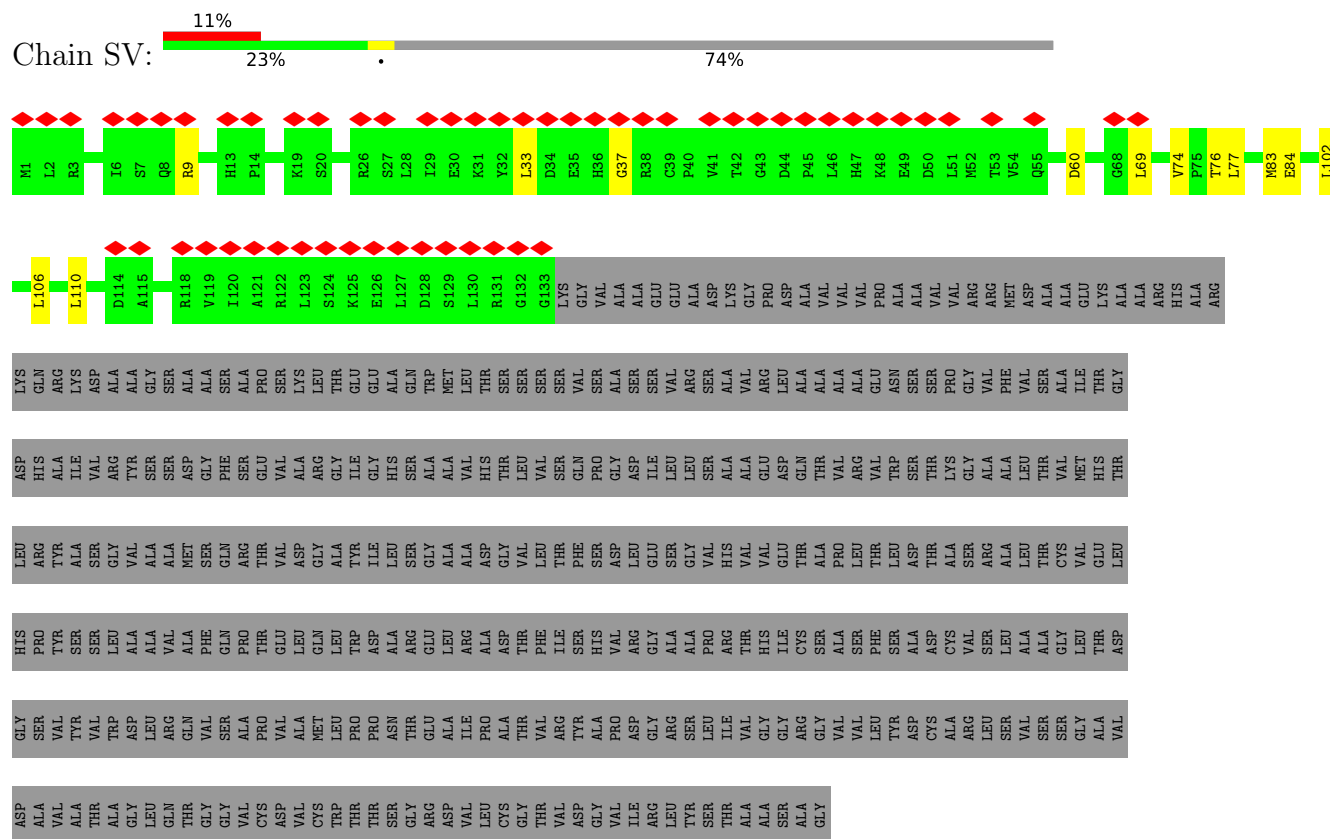
Chain SQ:



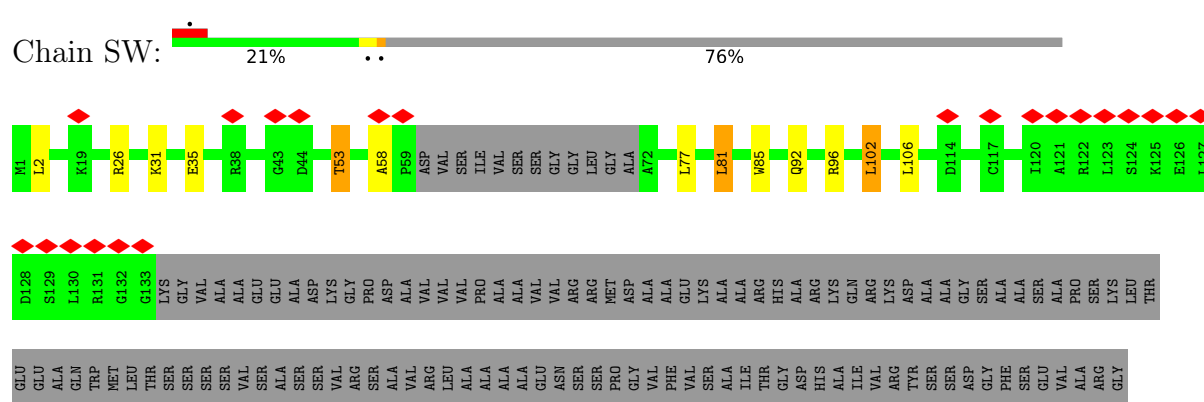




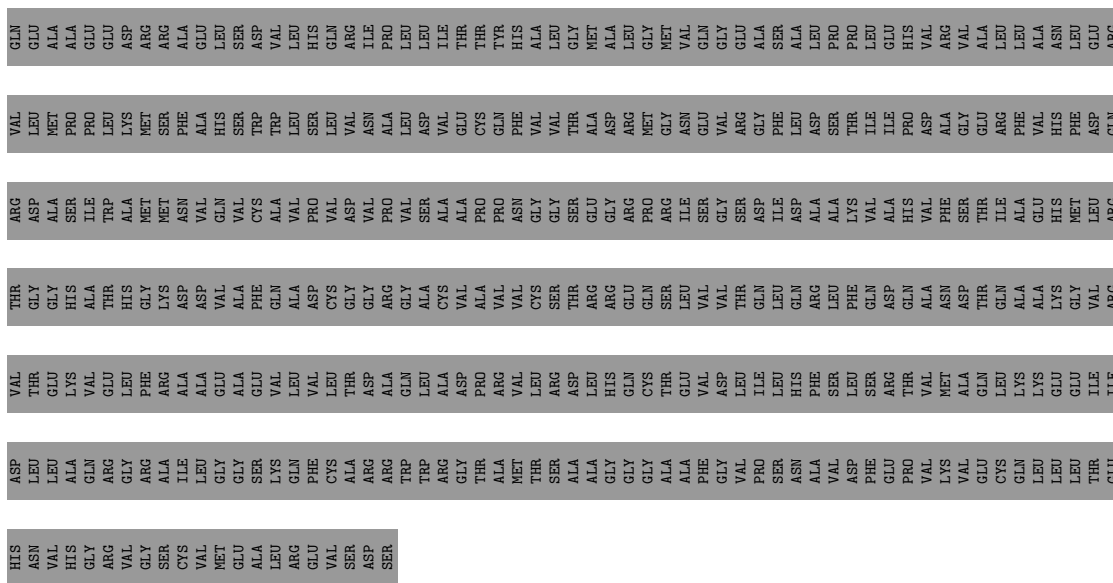
- Molecule 35: Pre-mRNA-processing factor 19



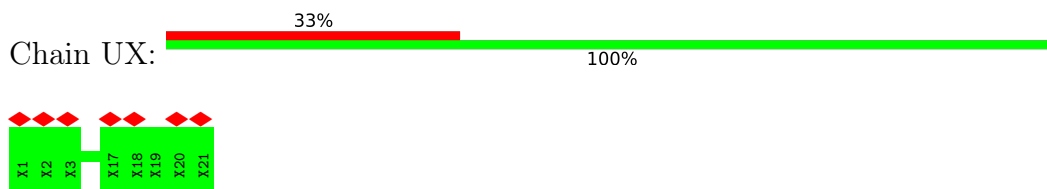
- Molecule 35: Pre-mRNA-processing factor 19



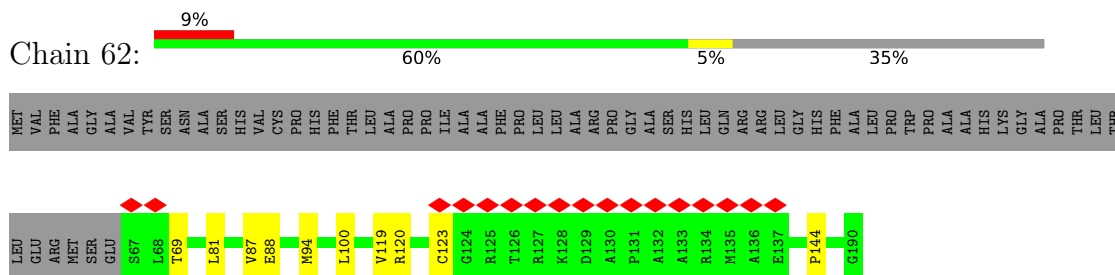




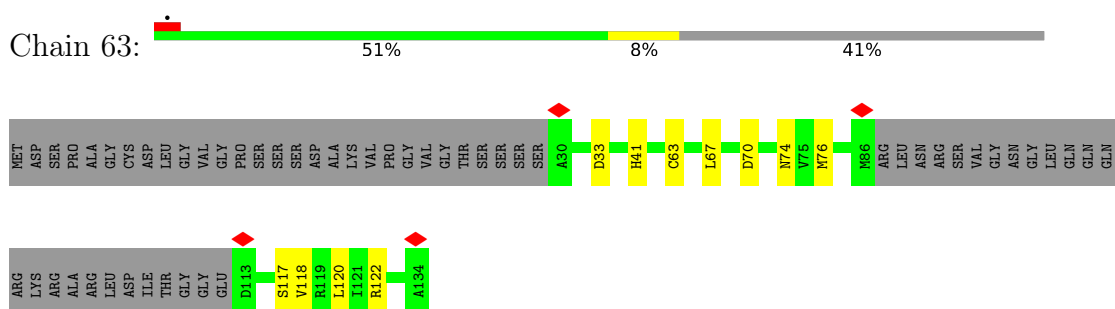
- Molecule 37: Unidentified protein



- Molecule 38: LSM domain-containing protein



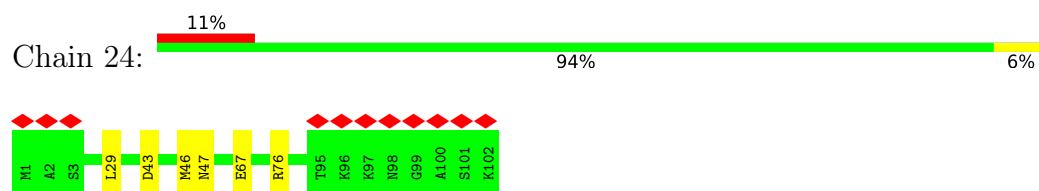
- Molecule 39: Sm domain-containing protein



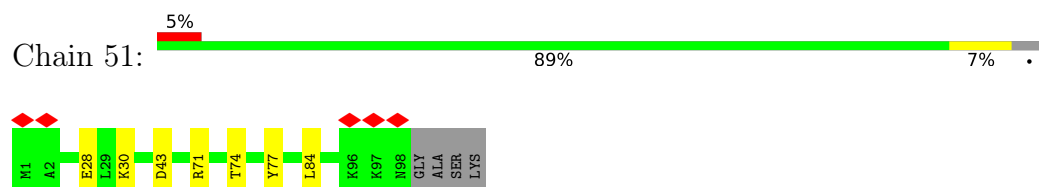
- Molecule 40: U6 snRNA-associated Sm-like protein LSm4



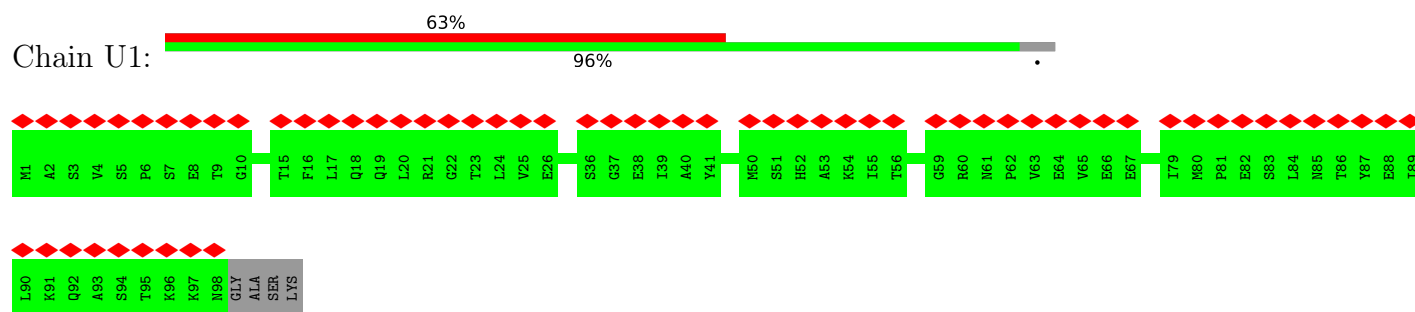
- Molecule 46: Small nuclear ribonucleoprotein, putative



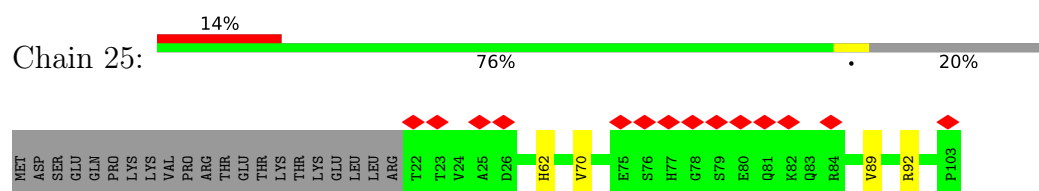
- Molecule 46: Small nuclear ribonucleoprotein, putative



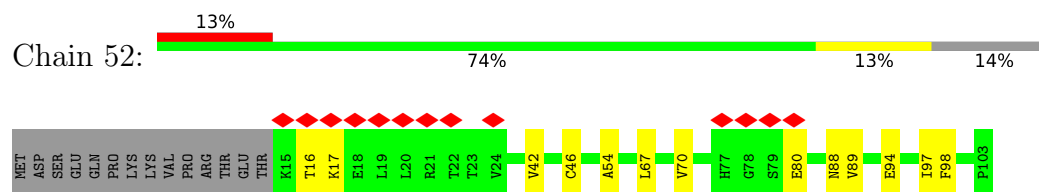
- Molecule 46: Small nuclear ribonucleoprotein, putative



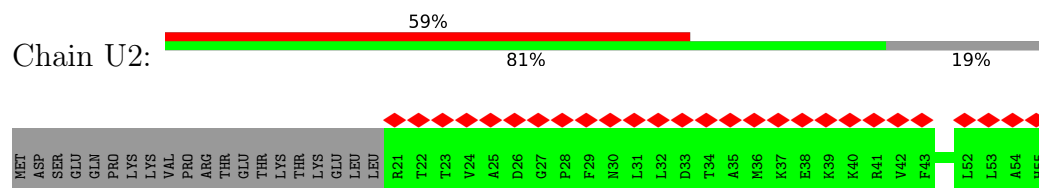
- Molecule 47: Small nuclear ribonucleoprotein Sm D2

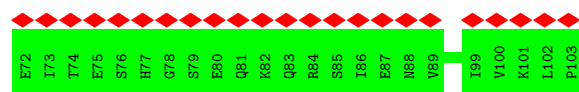


- Molecule 47: Small nuclear ribonucleoprotein Sm D2

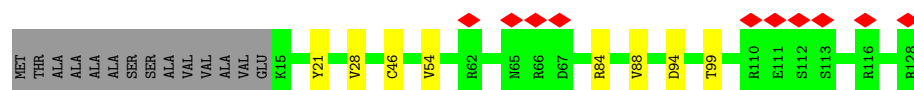
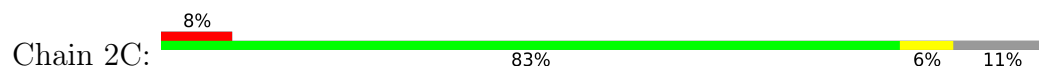


- Molecule 47: Small nuclear ribonucleoprotein Sm D2

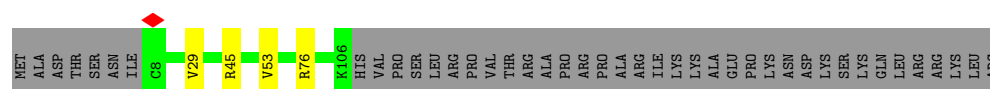




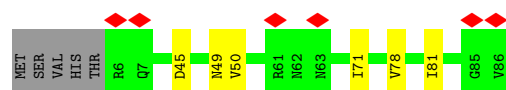
- Molecule 48: Lsm5p, putative



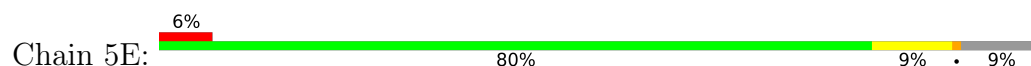
- Molecule 49: Small nuclear ribonucleoprotein, putative



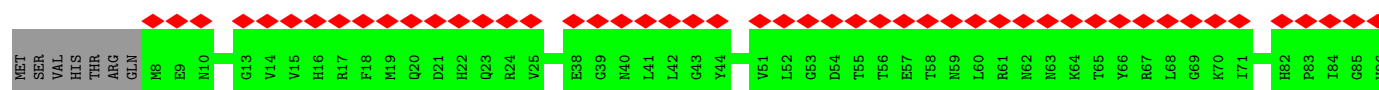
- Molecule 50: Small nuclear ribonucleoprotein E



- Molecule 50: Small nuclear ribonucleoprotein E



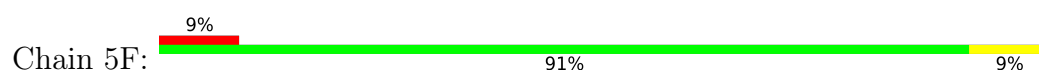
- Molecule 50: Small nuclear ribonucleoprotein E



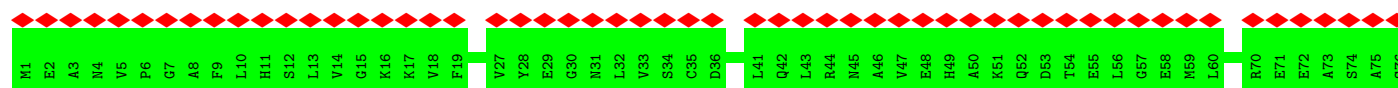
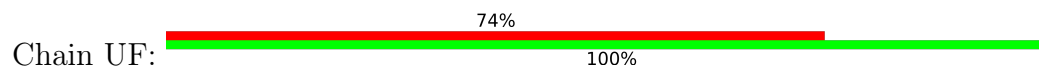
- Molecule 51: Sm protein F



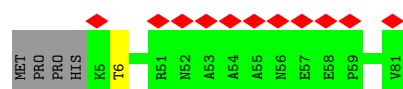
- Molecule 51: Sm protein F



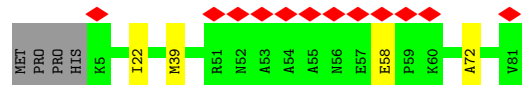
- Molecule 51: Sm protein F



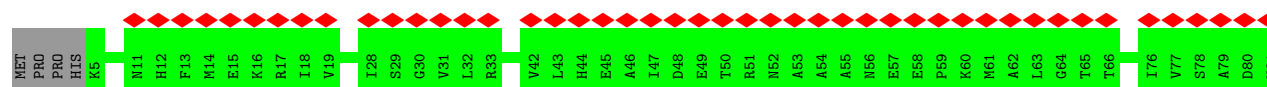
- Molecule 52: Sm protein G



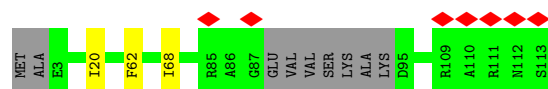
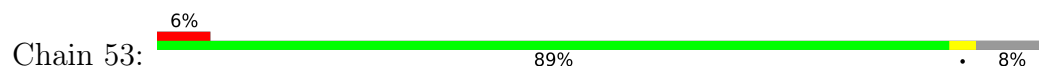
- Molecule 52: Sm protein G



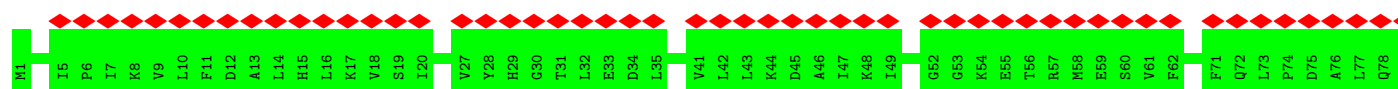
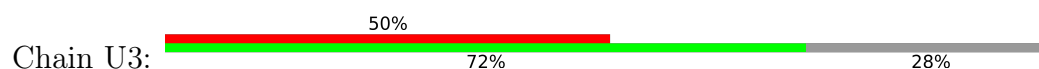
- Molecule 52: Sm protein G



- Molecule 53: Small nuclear ribonucleoprotein Sm D3



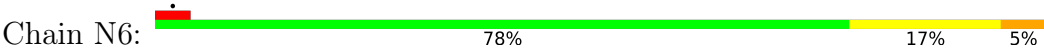
- Molecule 53: Small nuclear ribonucleoprotein Sm D3







● Molecule 59: U6 snRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	325589	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	9.611	Depositor
Minimum map value	0.000	Depositor
Average map value	0.120	Depositor
Map value standard deviation	0.210	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	426.00003, 426.00003, 426.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: G5J, ACE, SEP, GTG, K, ZN, MG, IHP, GTP, ADP, PSU

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	L7	0.18	0/3070	0.37	0/4139
2	L8	0.16	0/1023	0.34	0/1392
3	L9	0.18	0/1271	0.35	0/1715
4	LA	0.20	0/18638	0.37	0/25264
5	LB	0.13	0/10532	0.31	0/14676
6	LC	0.18	0/7137	0.35	0/9693
7	LD	0.15	0/1015	0.30	0/1351
8	LF	0.15	0/3385	0.30	0/4582
9	LG	0.11	0/600	0.24	0/810
10	LH	0.10	0/333	0.22	0/435
11	LJ	0.20	0/3268	0.36	0/4432
12	LL	0.17	0/1488	0.32	0/2008
13	LN	0.17	0/2358	0.32	0/3205
14	LP	0.20	0/617	0.36	0/826
15	LQ	0.15	0/4328	0.30	0/5818
16	LR	0.14	0/1241	0.26	0/1663
17	LS	0.16	0/6335	0.30	0/8567
18	LT	0.15	0/6427	0.29	0/8731
19	LV	0.15	0/7721	0.32	0/10452
20	LW	0.15	0/1569	0.32	0/2119
21	LY	0.17	0/895	0.29	0/1201
22	LZ	0.13	0/625	0.28	0/843
23	SA	0.16	0/4310	0.29	0/5802
24	SC	0.17	0/2147	0.31	0/2887
25	SD	0.13	0/2621	0.27	0/3538
26	SF	0.11	0/236	0.23	0/327
27	SJ	0.14	0/2240	0.29	0/3029
28	SK	0.17	0/721	0.33	0/982
29	SL	0.16	0/1774	0.30	0/2392
30	SN	0.18	0/1424	0.33	0/1940
31	SO	0.21	0/3423	0.37	0/4651
32	SP	0.12	0/690	0.26	0/918

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	SQ	0.27	1/853 (0.1%)	0.35	0/1144
34	SS	0.12	0/1526	0.27	0/2057
35	ST	0.14	0/3666	0.30	0/4992
35	SU	0.15	0/1037	0.33	0/1403
35	SV	0.15	0/1037	0.30	0/1403
35	SW	0.15	0/963	0.30	0/1301
36	TN	0.17	0/359	0.34	0/486
38	62	0.15	0/947	0.31	0/1282
39	63	0.16	0/611	0.30	0/831
40	64	0.17	0/646	0.33	0/869
41	65	0.17	0/888	0.33	0/1198
42	66	0.16	0/551	0.34	0/745
43	67	0.19	0/712	0.36	0/962
44	68	0.29	1/781 (0.1%)	0.36	0/1063
45	RN	0.17	0/74	0.34	0/111
46	24	0.14	0/792	0.27	0/1066
46	51	0.18	0/767	0.33	0/1035
46	U1	0.13	0/483	0.28	0/671
47	25	0.16	0/664	0.32	0/890
47	52	0.18	0/725	0.33	0/970
47	U2	0.10	0/410	0.29	0/570
48	2C	0.15	0/887	0.30	0/1192
49	2D	0.14	0/806	0.30	0/1086
50	2H	0.13	0/669	0.31	0/905
50	5E	0.15	0/641	0.36	0/869
50	UE	0.11	0/387	0.30	0/536
51	2I	0.16	0/608	0.34	0/818
51	5F	0.18	0/608	0.38	0/818
51	UF	0.16	0/374	0.33	0/519
52	2J	0.15	0/588	0.31	0/791
52	5G	0.14	0/588	0.29	0/791
52	UG	0.11	0/378	0.30	0/524
53	53	0.18	0/810	0.34	0/1085
53	U3	0.14	0/399	0.32	0/554
54	5B	0.18	0/745	0.37	0/997
54	UB	0.13	0/397	0.26	0/550
55	LE	0.21	0/586	0.29	0/907
56	LO	0.15	0/1124	0.25	0/1748
57	N2	0.22	0/1787	0.34	0/2774
58	N5	0.23	0/1480	0.29	0/2298
59	N6	0.22	0/2378	0.30	0/3702
All	All	0.17	2/138194 (0.0%)	0.32	0/188901

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	68	0	ACE	C-N	6.39	1.46	1.33
33	SQ	0	ACE	C-N	6.21	1.45	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	L7	3021	0	3080	22	0
2	L8	999	0	956	5	0
3	L9	1243	0	1230	5	0
4	LA	18216	0	17438	88	0
5	LB	10536	0	4965	6	0
6	LC	7002	0	6999	26	0
7	LD	1006	0	1048	4	0
8	LF	3311	0	3287	23	0
9	LG	592	0	578	3	0
10	LH	331	0	354	1	0
11	LJ	3196	0	3166	31	0
12	LL	1455	0	1471	3	0
13	LN	2314	0	2243	9	0
14	LP	598	0	587	6	0
15	LQ	4277	0	4111	15	0
16	LR	1230	0	1184	8	0
17	LS	6209	0	6075	30	0
18	LT	6284	0	6228	35	0
19	LV	7589	0	7426	33	0
20	LW	1545	0	1586	3	0
21	LY	876	0	888	3	0
22	LZ	619	0	531	2	0
23	SA	4239	0	4212	14	0
24	SC	2108	0	2017	13	0
25	SD	2577	0	2581	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	SF	237	0	122	0	0
27	SJ	2197	0	2133	12	0
28	SK	699	0	675	10	0
29	SL	1770	0	1756	13	0
30	SN	1396	0	1400	11	0
31	SO	3334	0	3286	20	0
32	SP	683	0	691	1	0
33	SQ	838	0	832	3	0
34	SS	1504	0	1485	8	0
35	ST	3606	0	3602	15	0
35	SU	1022	0	1039	10	0
35	SV	1022	0	1039	7	0
35	SW	949	0	965	12	0
36	TN	351	0	361	2	0
37	UX	105	0	23	0	0
38	62	937	0	973	3	0
39	63	602	0	598	5	0
40	64	640	0	656	5	0
41	65	876	0	864	5	0
42	66	541	0	522	2	0
43	67	701	0	730	7	0
44	68	774	0	795	7	0
45	RN	283	0	178	2	0
46	24	783	0	803	4	0
46	51	758	0	777	5	0
46	U1	484	0	219	0	0
47	25	654	0	678	4	0
47	52	715	0	752	11	0
47	U2	411	0	182	0	0
48	2C	881	0	911	6	0
49	2D	792	0	807	2	0
50	2H	657	0	651	4	0
50	5E	629	0	621	11	0
50	UE	388	0	161	0	0
51	2I	598	0	597	4	0
51	5F	598	0	597	7	0
51	UF	375	0	175	0	0
52	2J	583	0	603	1	0
52	5G	583	0	603	3	0
52	UG	379	0	178	0	0
53	53	801	0	822	3	0
53	U3	400	0	181	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	5B	738	0	765	3	0
54	UB	398	0	176	0	0
55	LE	547	0	276	6	0
56	LO	1006	0	509	4	0
57	N2	1604	0	813	10	0
58	N5	1328	0	680	7	0
59	N6	2127	0	1078	14	0
60	L7	1	0	0	0	0
60	LA	1	0	0	0	0
60	LC	1	0	0	0	0
60	N5	1	0	0	0	0
60	N6	8	0	0	0	0
61	L7	27	0	12	0	0
62	L7	1	0	0	0	0
63	LA	36	0	6	2	0
64	LC	32	0	12	0	0
65	LL	3	0	0	0	0
65	SC	1	0	0	0	0
65	SQ	1	0	0	0	0
66	N5	52	0	25	0	0
67	N6	33	0	0	3	0
All	All	135855	0	123636	472	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 472 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)
47:52:17:LYS:HE3	50:5E:47:PHE:HZ	1.11	1.09
47:52:17:LYS:HE3	50:5E:47:PHE:CZ	1.90	1.05
4:LA:415:LEU:HD22	6:LC:357:ALA:HB1	1.51	0.89
47:52:17:LYS:CE	50:5E:47:PHE:HZ	1.85	0.88
31:SO:335:PRO:HD3	31:SO:340:HIS:CE1	2.16	0.80

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L7	380/389 (98%)	375 (99%)	5 (1%)	0	100	100
2	L8	123/153 (80%)	122 (99%)	1 (1%)	0	100	100
3	L9	150/162 (93%)	149 (99%)	1 (1%)	0	100	100
4	LA	2341/2427 (96%)	2306 (98%)	35 (2%)	0	100	100
5	LB	2120/2367 (90%)	2095 (99%)	25 (1%)	0	100	100
6	LC	901/1016 (89%)	890 (99%)	11 (1%)	0	100	100
7	LD	123/166 (74%)	123 (100%)	0	0	100	100
8	LF	398/706 (56%)	396 (100%)	2 (0%)	0	100	100
9	LG	78/82 (95%)	78 (100%)	0	0	100	100
10	LH	38/159 (24%)	38 (100%)	0	0	100	100
11	LJ	405/509 (80%)	401 (99%)	4 (1%)	0	100	100
12	LL	182/326 (56%)	179 (98%)	3 (2%)	0	100	100
13	LN	312/322 (97%)	303 (97%)	9 (3%)	0	100	100
14	LP	69/207 (33%)	68 (99%)	1 (1%)	0	100	100
15	LQ	535/804 (66%)	532 (99%)	3 (1%)	0	100	100
16	LR	155/197 (79%)	153 (99%)	2 (1%)	0	100	100
17	LS	768/824 (93%)	760 (99%)	8 (1%)	0	100	100
18	LT	792/794 (100%)	790 (100%)	2 (0%)	0	100	100
19	LV	967/1087 (89%)	953 (99%)	14 (1%)	0	100	100
20	LW	184/307 (60%)	182 (99%)	2 (1%)	0	100	100
21	LY	105/114 (92%)	105 (100%)	0	0	100	100
22	LZ	87/403 (22%)	86 (99%)	1 (1%)	0	100	100
23	SA	505/564 (90%)	500 (99%)	5 (1%)	0	100	100
24	SC	255/417 (61%)	251 (98%)	4 (2%)	0	100	100
25	SD	308/546 (56%)	303 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	SF	46/258 (18%)	46 (100%)	0	0	100	100
27	SJ	259/414 (63%)	258 (100%)	1 (0%)	0	100	100
28	SK	81/175 (46%)	80 (99%)	1 (1%)	0	100	100
29	SL	228/544 (42%)	224 (98%)	4 (2%)	0	100	100
30	SN	181/192 (94%)	178 (98%)	3 (2%)	0	100	100
31	SO	416/621 (67%)	405 (97%)	11 (3%)	0	100	100
32	SP	79/269 (29%)	79 (100%)	0	0	100	100
33	SQ	102/150 (68%)	101 (99%)	1 (1%)	0	100	100
34	SS	178/284 (63%)	176 (99%)	2 (1%)	0	100	100
35	ST	482/513 (94%)	473 (98%)	9 (2%)	0	100	100
35	SU	131/513 (26%)	129 (98%)	2 (2%)	0	100	100
35	SV	131/513 (26%)	130 (99%)	1 (1%)	0	100	100
35	SW	117/513 (23%)	115 (98%)	2 (2%)	0	100	100
36	TN	42/1181 (4%)	40 (95%)	2 (5%)	0	100	100
38	62	122/190 (64%)	122 (100%)	0	0	100	100
39	63	75/134 (56%)	75 (100%)	0	0	100	100
40	64	81/116 (70%)	81 (100%)	0	0	100	100
41	65	108/151 (72%)	105 (97%)	3 (3%)	0	100	100
42	66	69/80 (86%)	69 (100%)	0	0	100	100
43	67	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
44	68	98/131 (75%)	98 (100%)	0	0	100	100
46	24	100/102 (98%)	100 (100%)	0	0	100	100
46	51	96/102 (94%)	96 (100%)	0	0	100	100
46	U1	96/102 (94%)	96 (100%)	0	0	100	100
47	25	80/103 (78%)	78 (98%)	2 (2%)	0	100	100
47	52	87/103 (84%)	86 (99%)	1 (1%)	0	100	100
47	U2	81/103 (79%)	81 (100%)	0	0	100	100
48	2C	112/128 (88%)	111 (99%)	1 (1%)	0	100	100
49	2D	97/141 (69%)	97 (100%)	0	0	100	100
50	2H	79/86 (92%)	77 (98%)	2 (2%)	0	100	100
50	5E	76/86 (88%)	73 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	UE	77/86 (90%)	76 (99%)	1 (1%)	0	100	100
51	2I	74/76 (97%)	72 (97%)	2 (3%)	0	100	100
51	5F	74/76 (97%)	73 (99%)	1 (1%)	0	100	100
51	UF	74/76 (97%)	72 (97%)	2 (3%)	0	100	100
52	2J	75/81 (93%)	75 (100%)	0	0	100	100
52	5G	75/81 (93%)	75 (100%)	0	0	100	100
52	UG	75/81 (93%)	75 (100%)	0	0	100	100
53	53	100/113 (88%)	98 (98%)	2 (2%)	0	100	100
53	U3	79/113 (70%)	78 (99%)	1 (1%)	0	100	100
54	5B	97/111 (87%)	94 (97%)	3 (3%)	0	100	100
54	UB	79/111 (71%)	77 (98%)	2 (2%)	0	100	100
All	All	17179/24142 (71%)	16968 (99%)	211 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L7	329/336 (98%)	319 (97%)	10 (3%)	36	66
2	L8	108/130 (83%)	108 (100%)	0	100	100
3	L9	139/146 (95%)	134 (96%)	5 (4%)	31	60
4	LA	1824/2116 (86%)	1771 (97%)	53 (3%)	37	67
6	LC	751/831 (90%)	719 (96%)	32 (4%)	26	54
7	LD	104/136 (76%)	102 (98%)	2 (2%)	50	77
8	LF	353/584 (60%)	330 (94%)	23 (6%)	15	37
9	LG	59/61 (97%)	58 (98%)	1 (2%)	53	79
10	LH	33/133 (25%)	32 (97%)	1 (3%)	36	66
11	LJ	336/414 (81%)	316 (94%)	20 (6%)	17	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	LL	154/268 (58%)	151 (98%)	3 (2%)	50	77
13	LN	240/243 (99%)	215 (90%)	25 (10%)	7	17
14	LP	63/171 (37%)	60 (95%)	3 (5%)	23	50
15	LQ	416/657 (63%)	400 (96%)	16 (4%)	29	58
16	LR	118/149 (79%)	117 (99%)	1 (1%)	73	88
17	LS	624/665 (94%)	598 (96%)	26 (4%)	26	55
18	LT	661/661 (100%)	645 (98%)	16 (2%)	43	72
19	LV	808/940 (86%)	782 (97%)	26 (3%)	34	64
20	LW	175/273 (64%)	171 (98%)	4 (2%)	44	73
21	LY	90/97 (93%)	86 (96%)	4 (4%)	25	53
22	LZ	47/321 (15%)	47 (100%)	0	100	100
23	SA	458/496 (92%)	447 (98%)	11 (2%)	43	72
24	SC	228/356 (64%)	222 (97%)	6 (3%)	40	70
25	SD	272/439 (62%)	258 (95%)	14 (5%)	21	48
27	SJ	234/341 (69%)	224 (96%)	10 (4%)	26	54
28	SK	76/145 (52%)	74 (97%)	2 (3%)	40	70
29	SL	182/413 (44%)	176 (97%)	6 (3%)	33	63
30	SN	156/160 (98%)	152 (97%)	4 (3%)	40	70
31	SO	360/511 (70%)	351 (98%)	9 (2%)	42	71
32	SP	73/233 (31%)	70 (96%)	3 (4%)	27	56
33	SQ	89/126 (71%)	87 (98%)	2 (2%)	45	74
34	SS	158/238 (66%)	146 (92%)	12 (8%)	12	30
35	ST	383/398 (96%)	364 (95%)	19 (5%)	22	48
35	SU	113/398 (28%)	110 (97%)	3 (3%)	39	69
35	SV	113/398 (28%)	108 (96%)	5 (4%)	25	53
35	SW	105/398 (26%)	101 (96%)	4 (4%)	29	58
36	TN	40/953 (4%)	40 (100%)	0	100	100
38	62	101/151 (67%)	96 (95%)	5 (5%)	22	48
39	63	70/113 (62%)	66 (94%)	4 (6%)	18	43
40	64	72/98 (74%)	69 (96%)	3 (4%)	26	55
41	65	98/122 (80%)	90 (92%)	8 (8%)	10	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	66	59/64 (92%)	53 (90%)	6 (10%)	7	18
43	67	77/77 (100%)	73 (95%)	4 (5%)	21	47
44	68	86/109 (79%)	79 (92%)	7 (8%)	11	27
46	24	88/88 (100%)	88 (100%)	0	100	100
46	51	86/88 (98%)	85 (99%)	1 (1%)	63	84
47	25	73/94 (78%)	73 (100%)	0	100	100
47	52	80/94 (85%)	76 (95%)	4 (5%)	22	48
48	2C	100/108 (93%)	97 (97%)	3 (3%)	36	66
49	2D	88/126 (70%)	87 (99%)	1 (1%)	65	85
50	2H	74/79 (94%)	73 (99%)	1 (1%)	59	82
50	5E	71/79 (90%)	68 (96%)	3 (4%)	26	55
51	2I	65/65 (100%)	63 (97%)	2 (3%)	35	65
51	5F	65/65 (100%)	64 (98%)	1 (2%)	57	81
52	2J	64/68 (94%)	64 (100%)	0	100	100
52	5G	64/68 (94%)	62 (97%)	2 (3%)	35	65
53	53	86/93 (92%)	86 (100%)	0	100	100
54	5B	82/90 (91%)	79 (96%)	3 (4%)	30	59
All	All	12121/17274 (70%)	11682 (96%)	439 (4%)	32	60

5 of 439 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	LT	608	LEU
24	SC	195	ARG
52	5G	58	GLU
41	65	130	CYS
19	LV	128	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
30	SN	118	HIS
39	63	43	HIS
30	SN	138	GLN
35	ST	255	HIS

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Mol	Chain	Res	Type
42	66	11	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	RN	1/68 (1%)	1 (100%)	0
55	LE	23/39 (58%)	3 (13%)	0
56	LO	45/57 (78%)	5 (11%)	1 (2%)
57	N2	73/142 (51%)	10 (13%)	0
58	N5	61/71 (85%)	8 (13%)	0
59	N6	99/100 (99%)	10 (10%)	1 (1%)
All	All	302/477 (63%)	37 (12%)	2 (0%)

5 of 37 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	RN	44	G
55	LE	16	A
55	LE	22	A
55	LE	23	G
56	LO	73	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
56	LO	81	G
59	N6	9	U

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

2 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
29	SEP	SL	186	29	8,9,10	1.47	1 (12%)	8,12,14	1.16	1 (12%)
55	PSU	LE	28	55	18,21,22	1.06	1 (5%)	22,30,33	1.81	4 (18%)

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
29	SEP	SL	186	29	-	0/5/8/10	-
55	PSU	LE	28	55	-	1/7/25/26	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	LE	28	PSU	C6-C5	3.32	1.39	1.35
29	SL	186	SEP	P-O1P	3.20	1.60	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	LE	28	PSU	C4-N3-C2	-4.66	119.63	126.34
55	LE	28	PSU	N1-C2-N3	4.58	120.32	115.13
55	LE	28	PSU	O2-C2-N1	-2.84	119.67	122.79
55	LE	28	PSU	C6-N1-C2	-2.29	120.34	122.68
29	SL	186	SEP	P-OG-CB	-2.28	112.02	118.30

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	LE	28	PSU	O4'-C1'-C5-C4

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 23 ligands modelled in this entry, 18 are monoatomic - leaving 5 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$
61	ADP	L7	702	62,60	27,29,29	1.30	4 (14%)	42,45,45	1.97	10 (23%)
66	GTG	N5	101	58	53,57,57	3.45	20 (37%)	79,90,90	2.91	33 (41%)
67	G5J	N6	201	59	31,35,35	0.74	1 (3%)	38,55,55	0.92	2 (5%)
63	IHP	LA	2501	-	36,36,36	1.44	6 (16%)	54,60,60	0.98	3 (5%)
64	GTP	LC	1500	60	30,34,34	2.98	14 (46%)	46,54,54	1.93	15 (32%)

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
61	ADP	L7	702	62,60	-	4/16/32/32	0/3/3/3
66	GTG	N5	101	58	-	8/32/64/64	0/6/6/6
67	G5J	N6	201	59	-	5/25/41/41	0/3/3/3
63	IHP	LA	2501	-	-	2/30/54/54	0/1/1/1
64	GTP	LC	1500	60	-	3/22/38/38	0/3/3/3

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	N5	101	GTG	O3D-C3D	-10.17	1.19	1.43
66	N5	101	GTG	O6B-C6B	8.59	1.39	1.23
66	N5	101	GTG	O6A-C6A	8.56	1.39	1.23
64	LC	1500	GTP	O6-C6	8.55	1.39	1.23
66	N5	101	GTG	C5A-N7A	8.10	1.48	1.39

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
66	N5	101	GTG	C8A-N7A-C5A	8.78	118.76	107.78
66	N5	101	GTG	C6A-C5A-N7A	8.60	142.65	132.25
66	N5	101	GTG	C8B-N9B-C4B	7.57	120.46	106.05
66	N5	101	GTG	N9A-C4A-N3A	7.14	140.27	125.94
64	LC	1500	GTP	C8-N9-C4	6.85	119.09	106.05

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

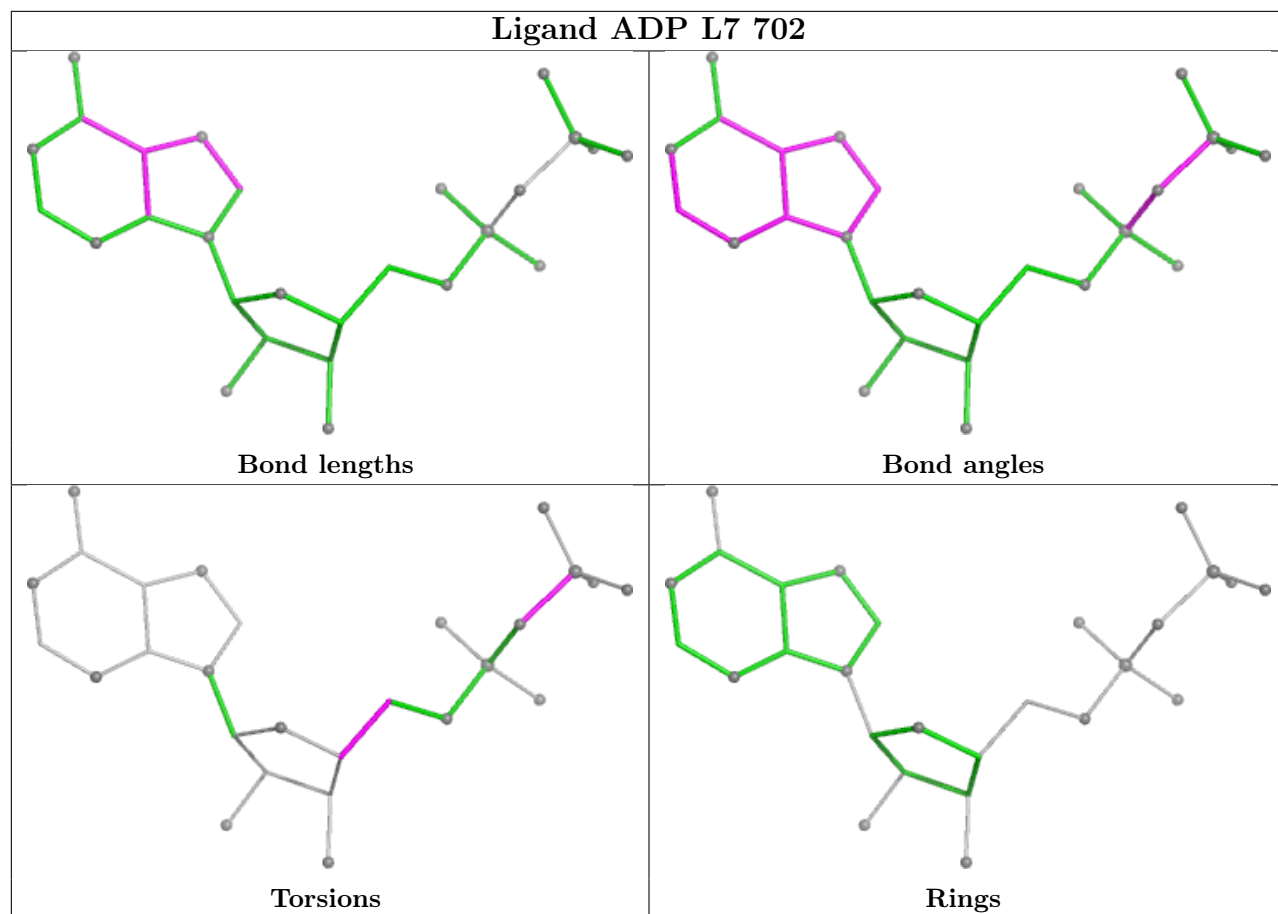
Mol	Chain	Res	Type	Atoms
61	L7	702	ADP	PA-O3A-PB-O2B
64	LC	1500	GTP	PB-O3B-PG-O2G
64	LC	1500	GTP	PB-O3B-PG-O3G
66	N5	101	GTG	C5D-O5D-PA-O3A
66	N5	101	GTG	PB-O3B-PG-O5E

There are no ring outliers.

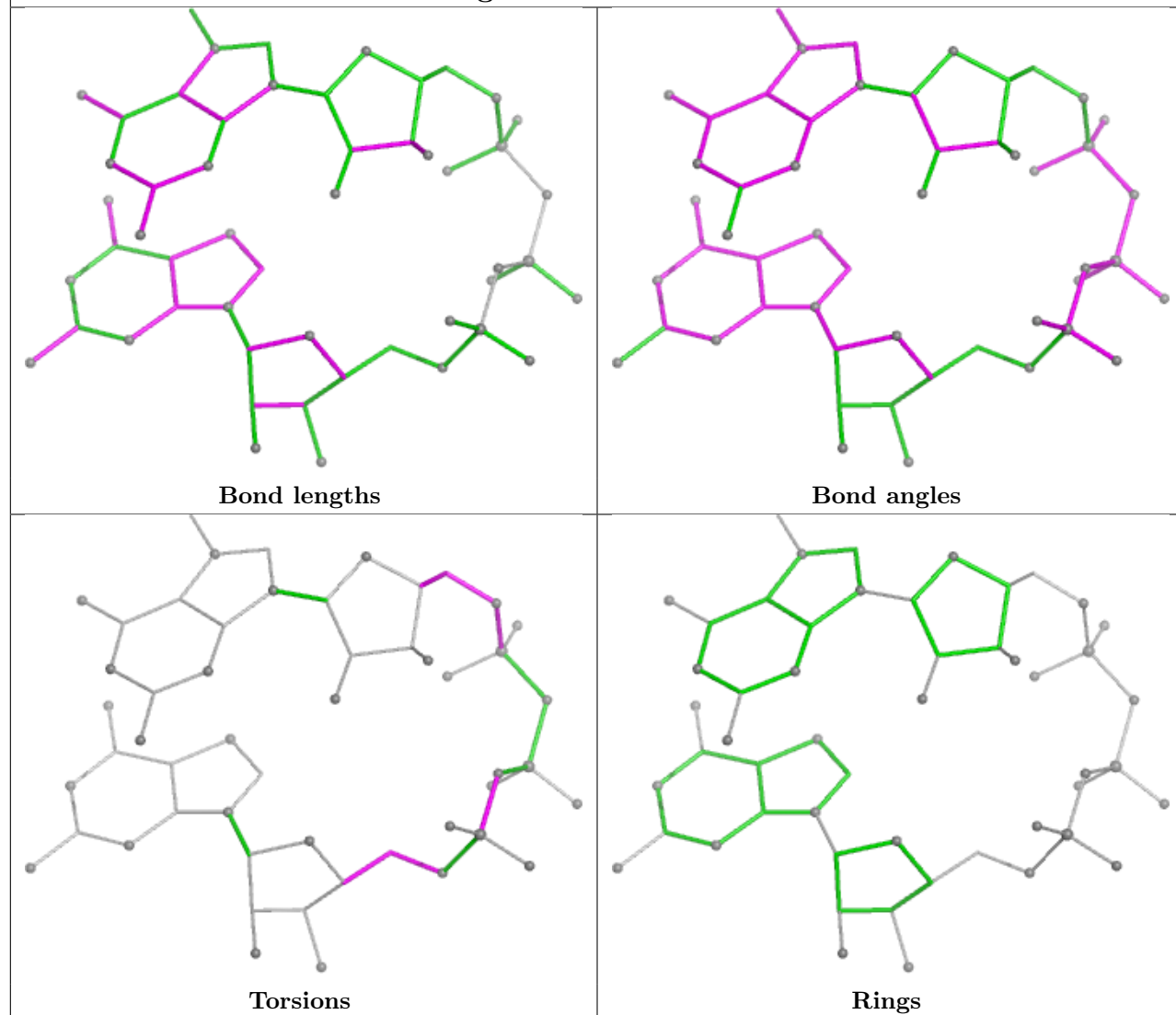
2 monomers are involved in 5 short contacts:

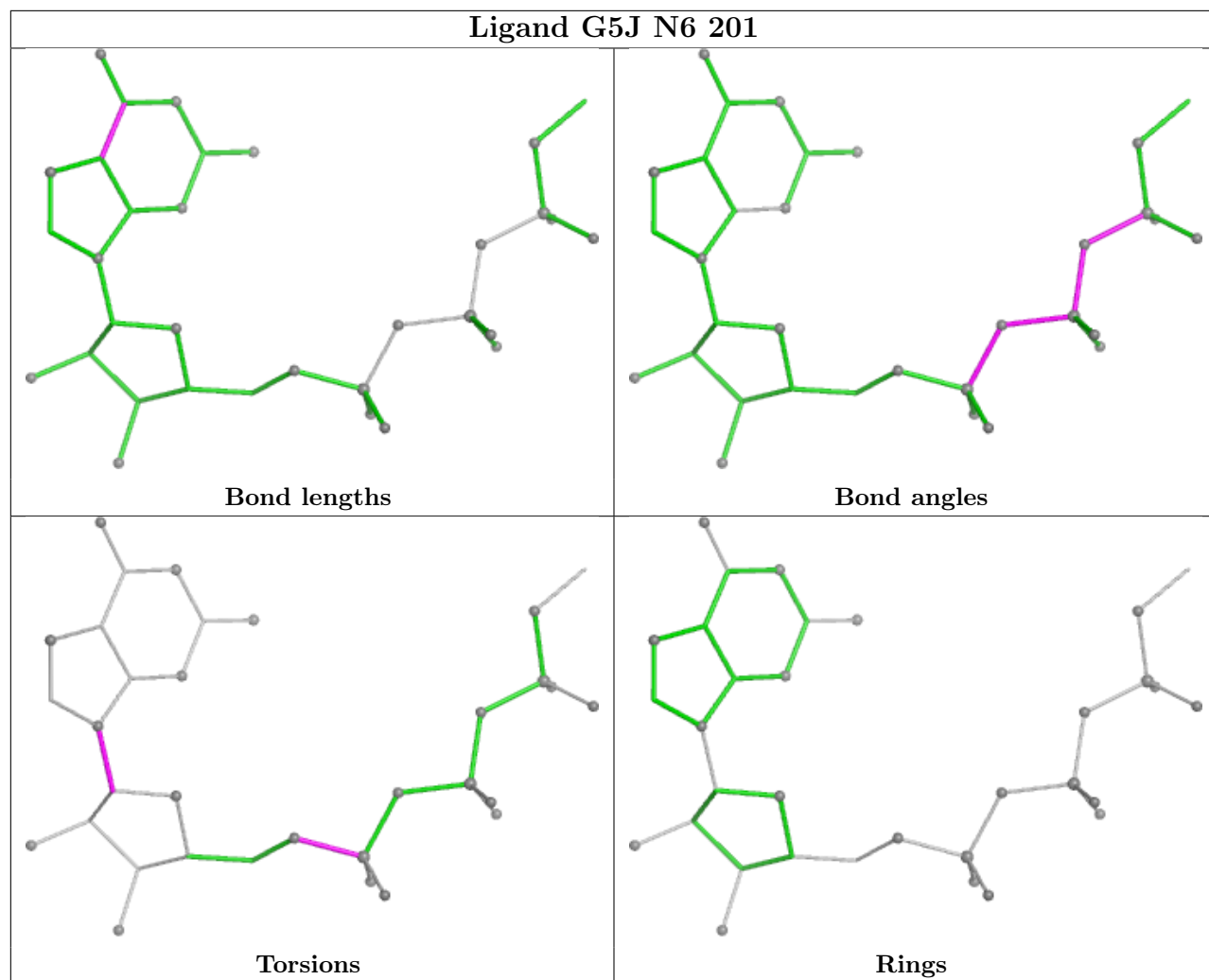
Mol	Chain	Res	Type	Clashes	Symm-Clashes
67	N6	201	G5J	3	0
63	LA	2501	IHP	2	0

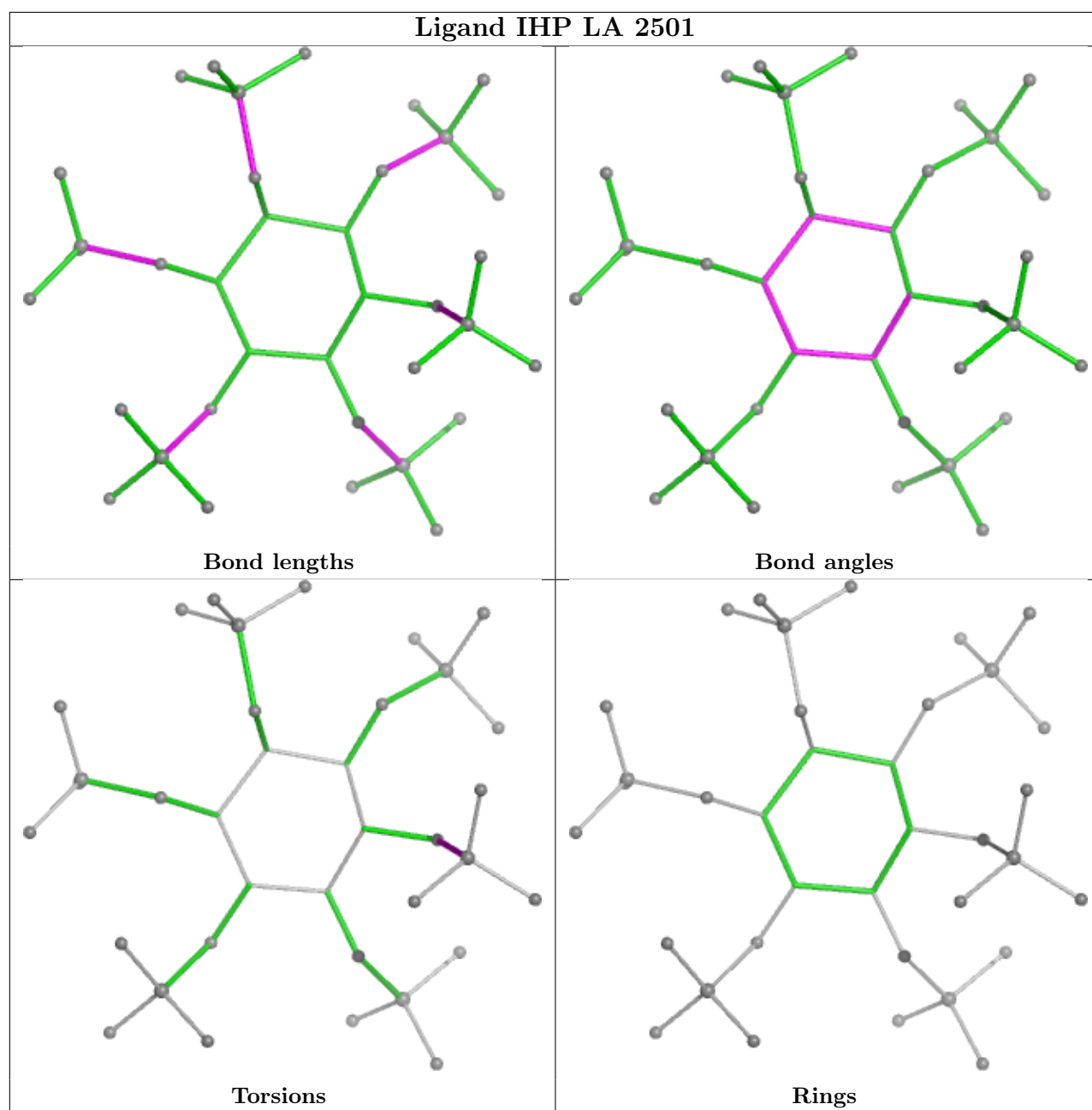
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

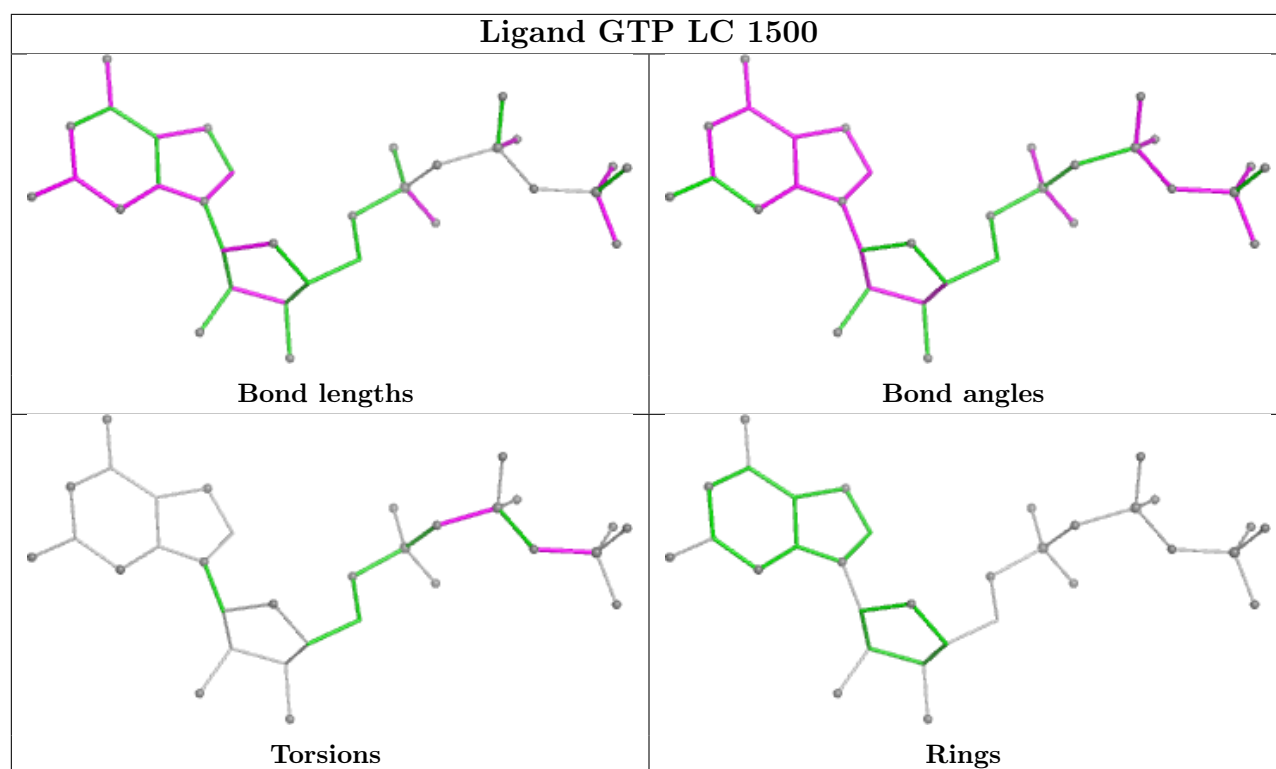


Ligand GTG N5 101









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.

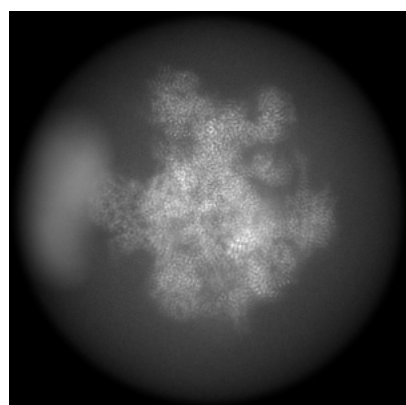
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52843. These allow visual inspection of the internal detail of the map and identification of artifacts.

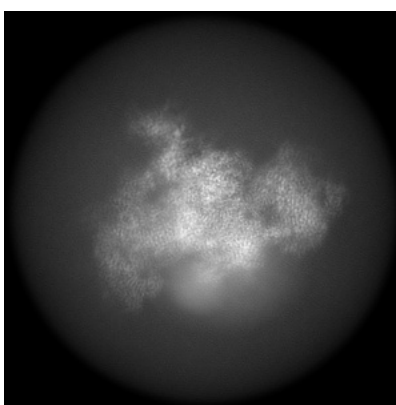
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

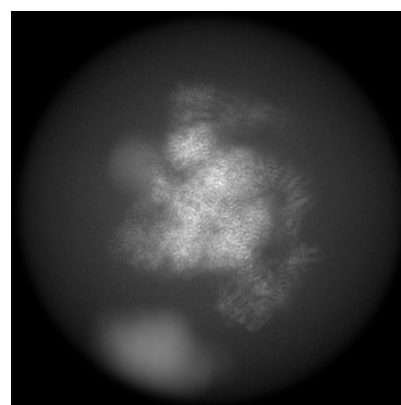
6.1.1 Primary map



X



Y

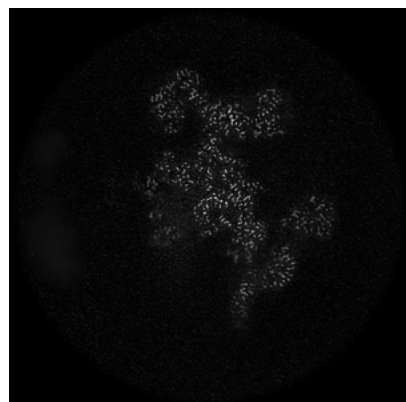


Z

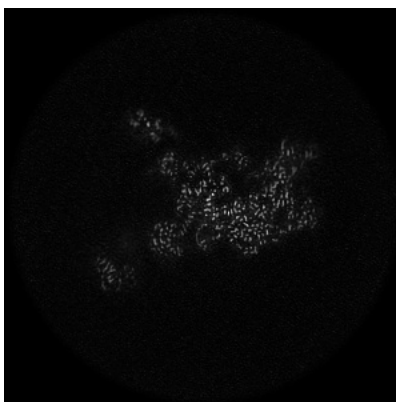
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

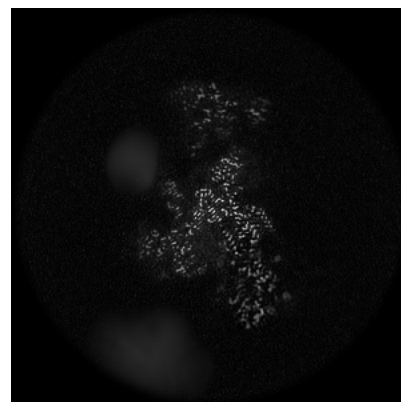
6.2.1 Primary map



X Index: 200



Y Index: 200

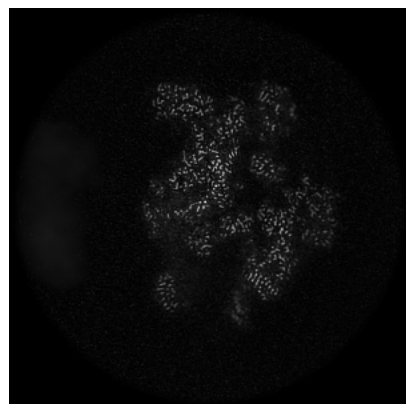


Z Index: 200

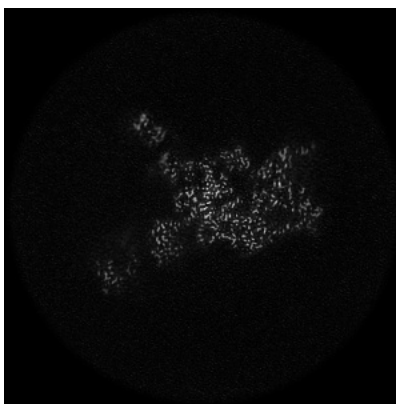
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

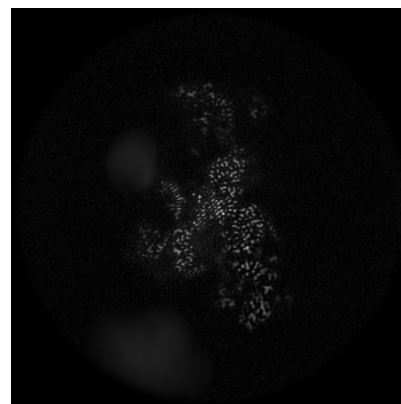
6.3.1 Primary map



X Index: 184



Y Index: 197

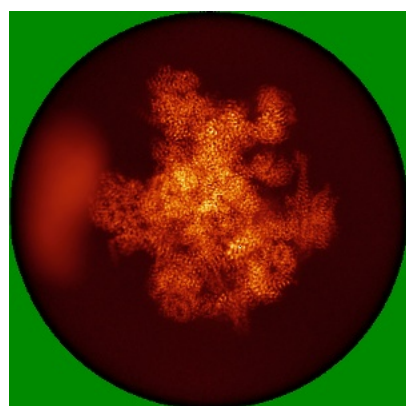


Z Index: 203

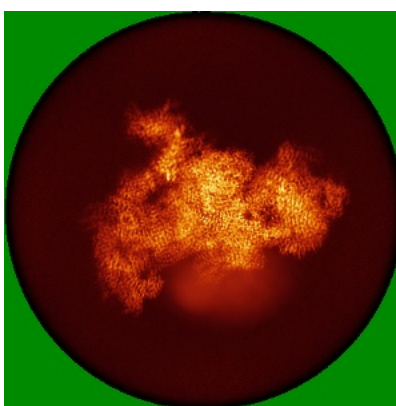
The images above show the largest variance slices of the map in three orthogonal directions.

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

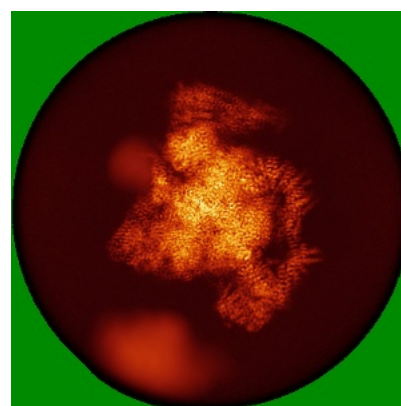
6.4.1 Primary map



X



Y

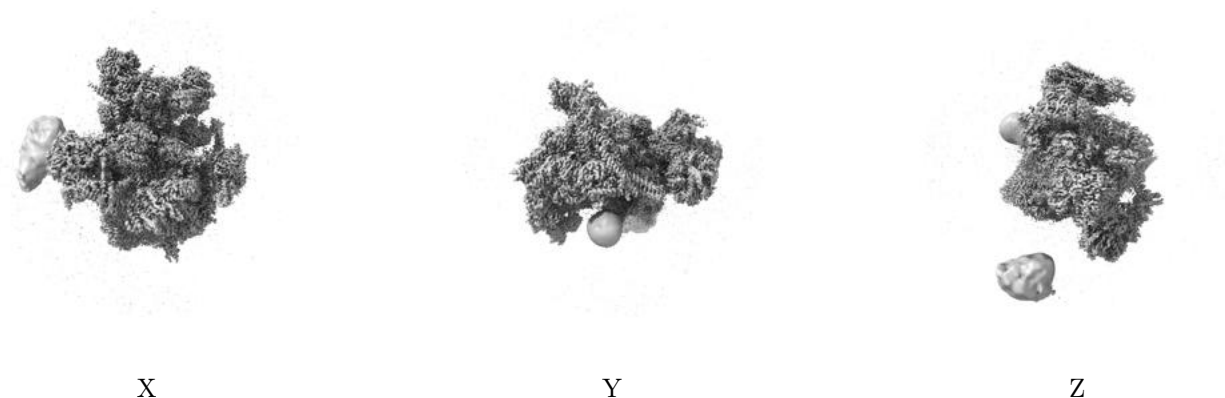


Z

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

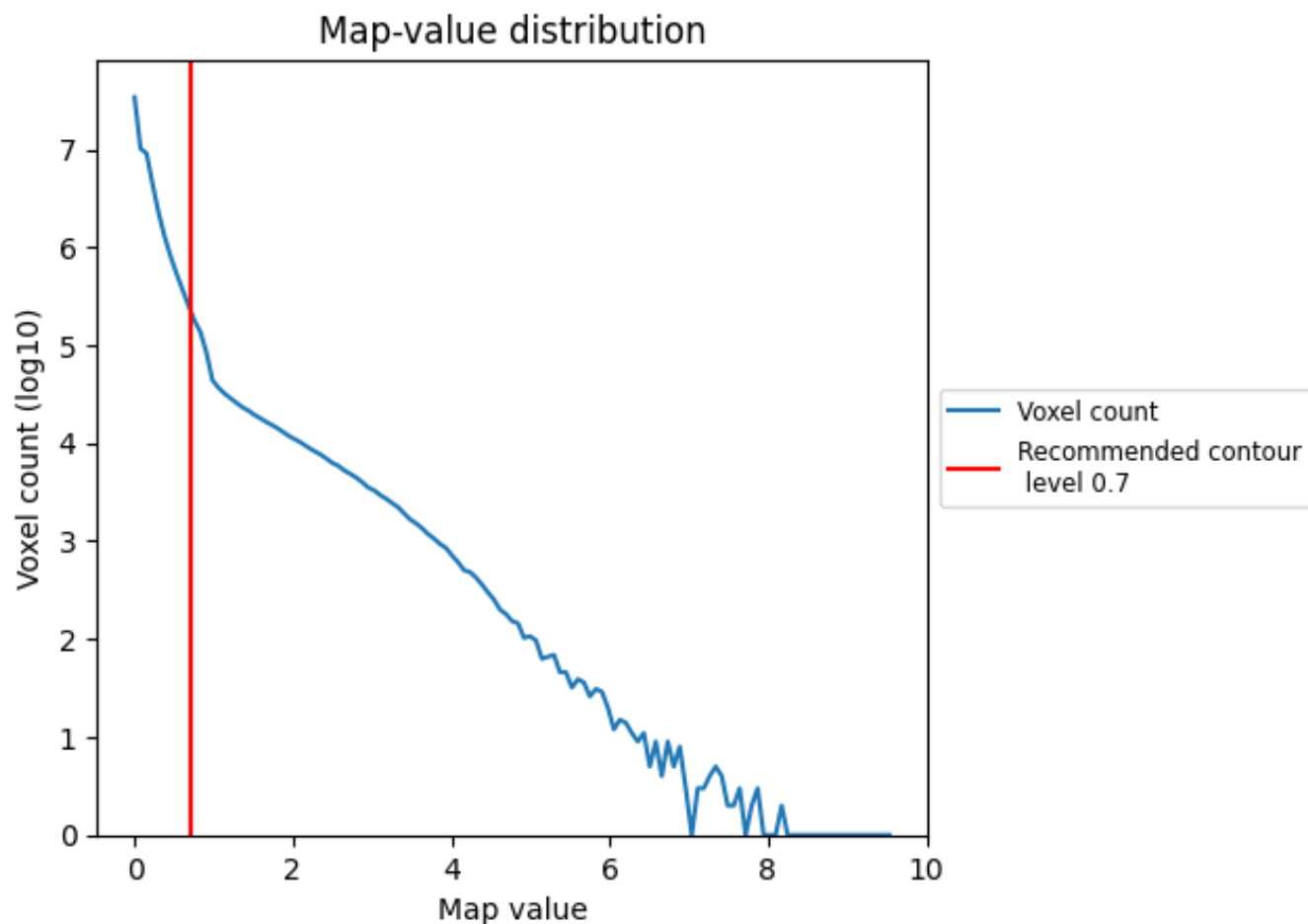
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

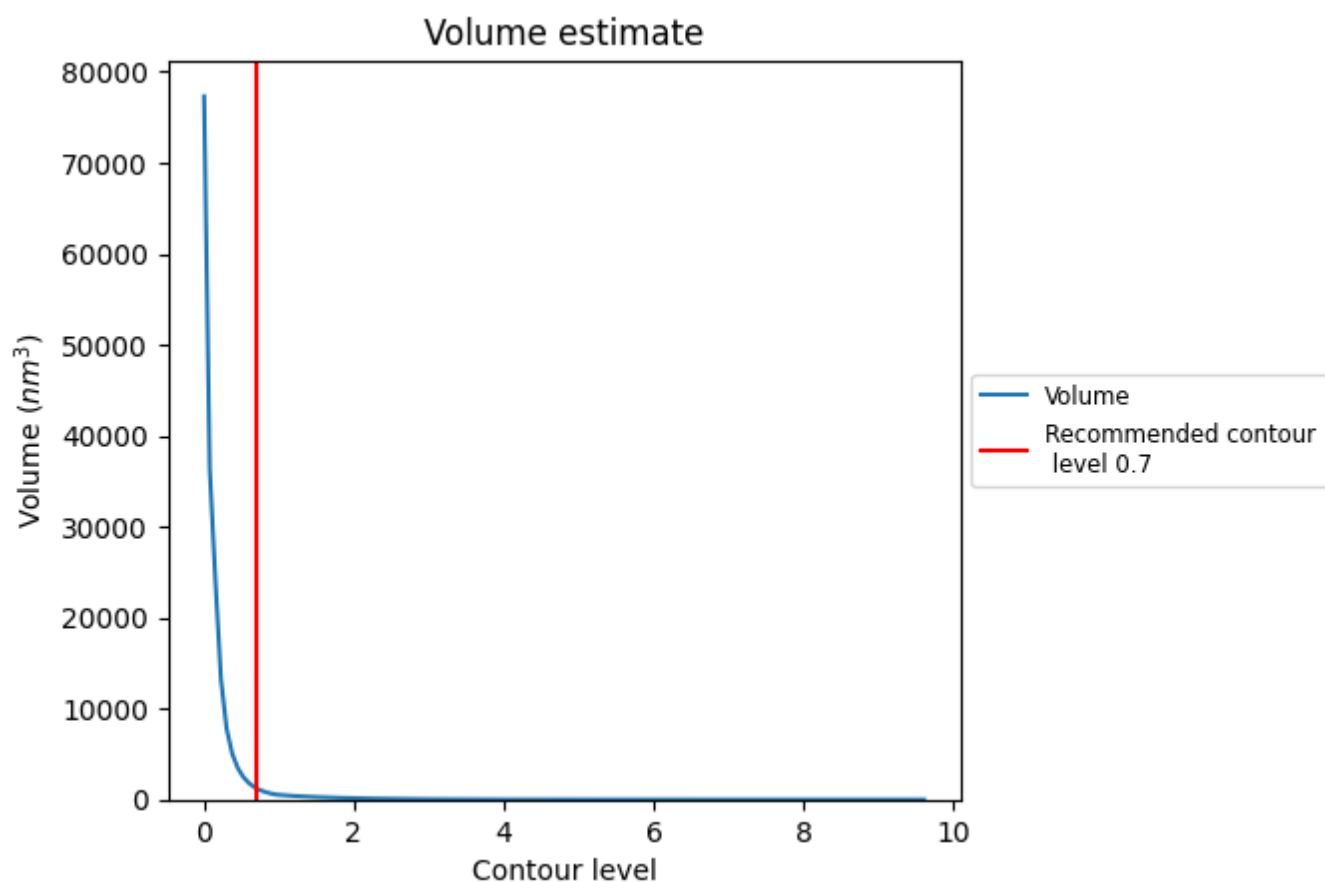
This section contains the results of statistical analysis of the map.

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.

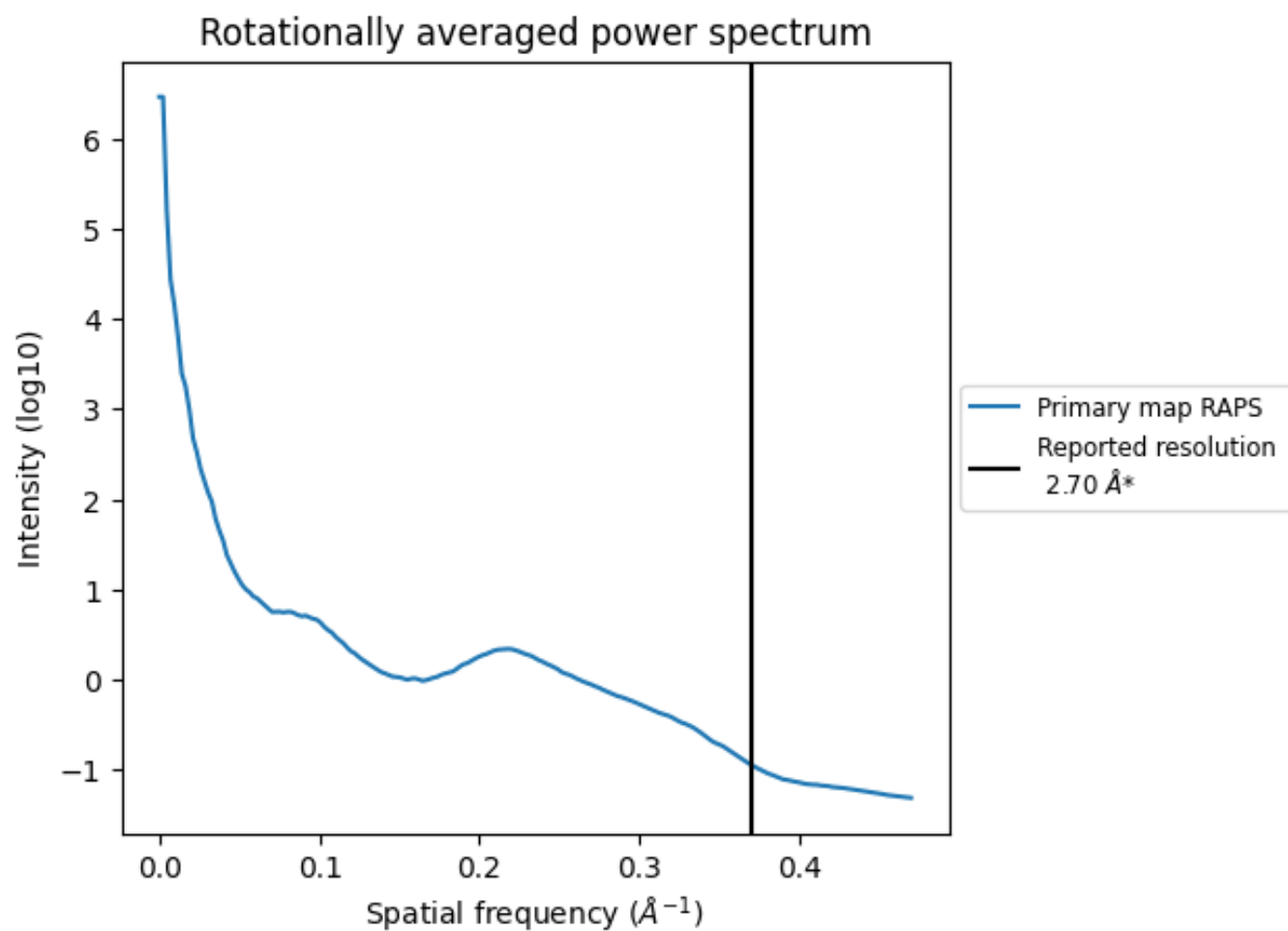
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1240 nm³; this corresponds to an approximate mass of 1120 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 0.370 Å⁻¹

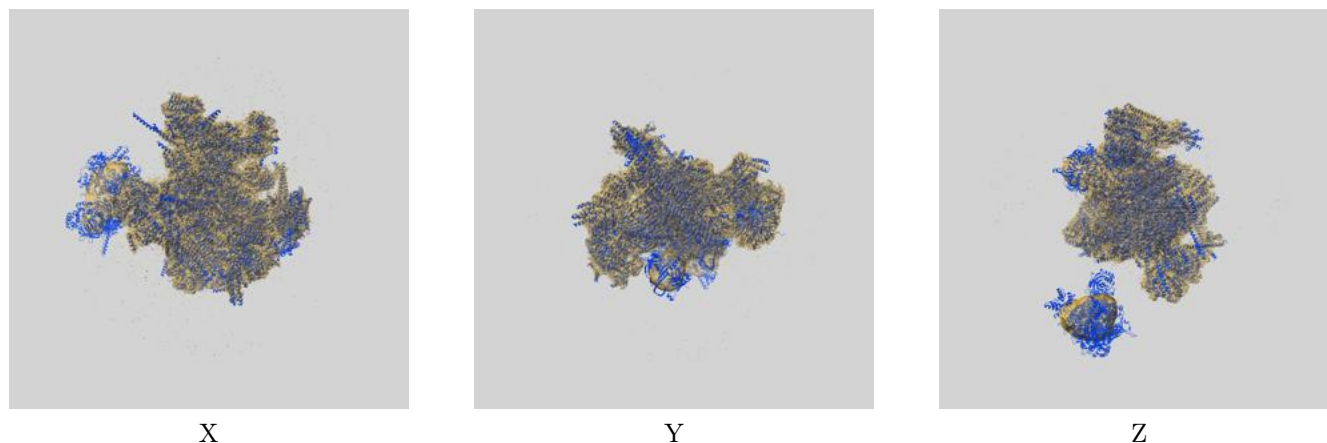
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

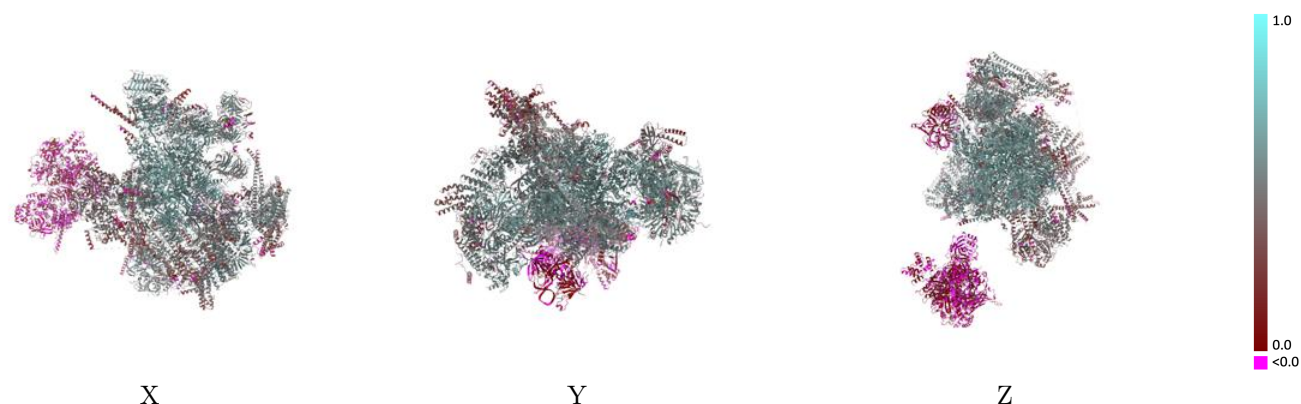
This section contains information regarding the fit between EMDB map EMD-52843 and PDB model 9IF7. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



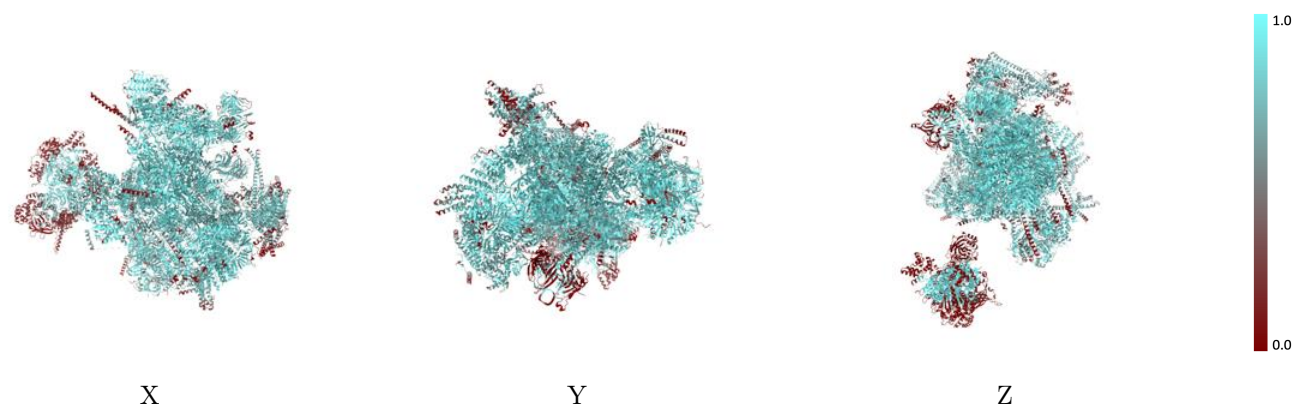
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



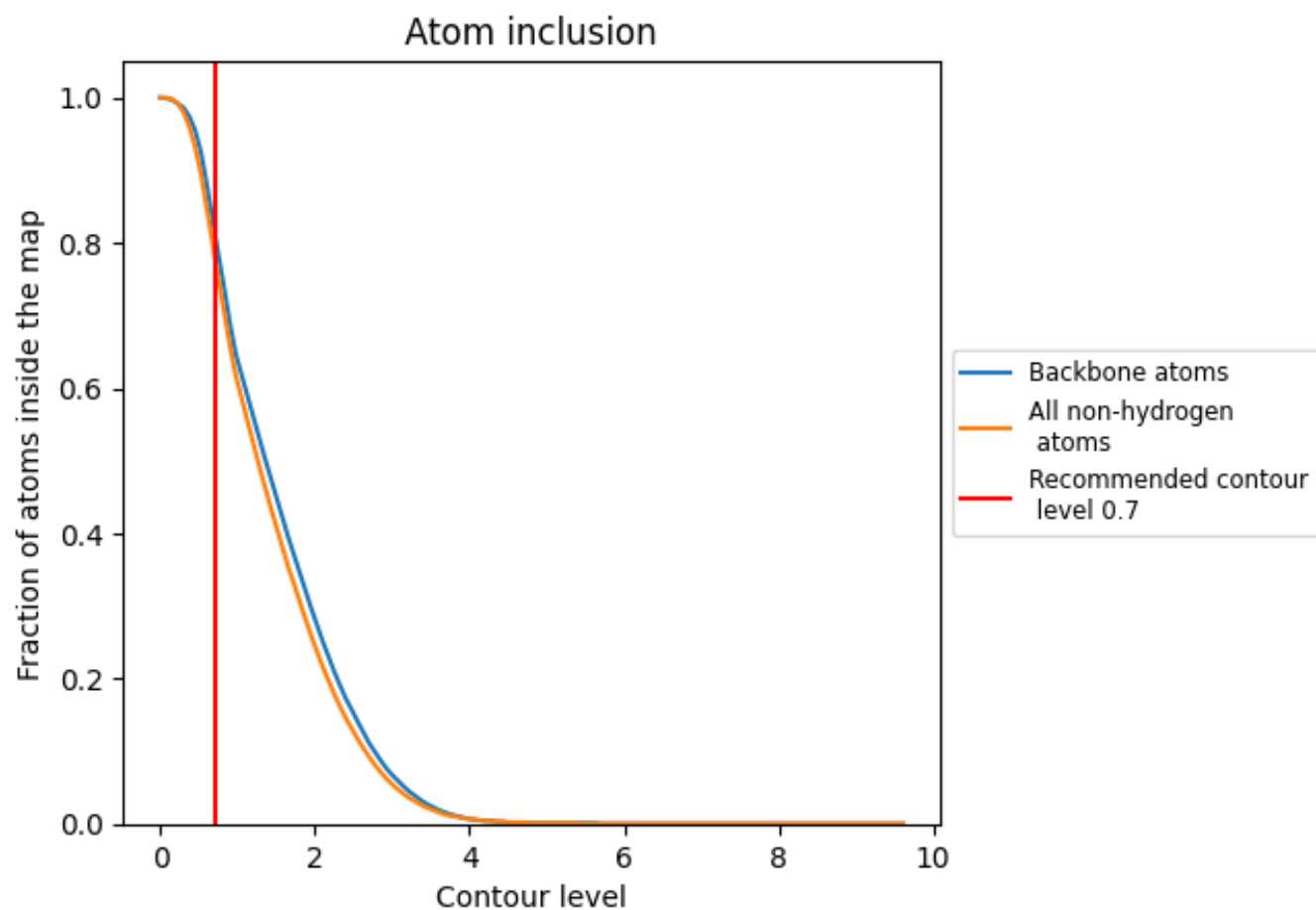
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 78% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7830	 0.4580
24	 0.7540	 0.4860
25	 0.7150	 0.4820
2C	 0.8230	 0.5380
2D	 0.9010	 0.5510
2H	 0.8170	 0.5070
2I	 0.7890	 0.5050
2J	 0.7640	 0.4970
51	 0.8350	 0.4900
52	 0.7560	 0.4640
53	 0.8270	 0.5050
5B	 0.7130	 0.4380
5E	 0.8060	 0.4840
5F	 0.8000	 0.5090
5G	 0.7520	 0.4760
62	 0.8120	 0.5130
63	 0.8690	 0.5350
64	 0.9000	 0.5580
65	 0.8960	 0.5410
66	 0.9100	 0.5590
67	 0.9090	 0.5600
68	 0.8900	 0.5570
L7	 0.9150	 0.5690
L8	 0.8100	 0.5250
L9	 0.8090	 0.5210
LA	 0.8820	 0.5640
LB	 0.4450	 0.0290
LC	 0.8750	 0.5250
LD	 0.6730	 0.4260
LE	 0.9310	 0.5860
LF	 0.8100	 0.4040
LG	 0.6350	 0.4710
LH	 0.6420	 0.4320
LJ	 0.9120	 0.6100
LL	 0.9310	 0.5760



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Chain	Atom inclusion	Q-score
LN	 0.8240	 0.4830
LO	 0.8490	 0.3110
LP	 0.8590	 0.5760
LQ	 0.7790	 0.5170
LR	 0.5800	 0.3850
LS	 0.8230	 0.4430
LT	 0.8490	 0.4830
LV	 0.7650	 0.3940
LW	 0.8250	 0.5450
LY	 0.8530	 0.5620
LZ	 0.7570	 0.4410
N2	 0.9080	 0.5460
N5	 0.9080	 0.5560
N6	 0.9420	 0.5700
RN	 0.8660	 0.4450
SA	 0.8800	 0.5560
SC	 0.8530	 0.5450
SD	 0.7760	 0.4920
SF	 0.5270	 0.4070
SJ	 0.8190	 0.4790
SK	 0.8380	 0.4460
SL	 0.7910	 0.5220
SN	 0.8670	 0.5530
SO	 0.8790	 0.5560
SP	 0.4290	 0.3090
SQ	 0.5990	 0.4310
SS	 0.7040	 0.4660
ST	 0.7120	 0.4850
SU	 0.6930	 0.4660
SV	 0.4610	 0.3280
SW	 0.6360	 0.4320
TN	 0.4650	 0.2660
U1	 0.3640	 0.0390
U2	 0.2700	 0.0130
U3	 0.3100	 0.0410
UB	 0.3670	 0.0520
UE	 0.3890	 0.0280
UF	 0.2720	 -0.0010
UG	 0.3980	 0.0220
UX	 0.6570	 0.3410