



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:30 AM UTC

PDB ID : 7W5A / pdb_00007w5a
EMDB ID : EMD-32319
Title : The cryo-EM structure of human pre-C*-II complex
Authors : Zhan, X.; Lu, Y.; Shi, Y.
Deposited on : 2021-11-29
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

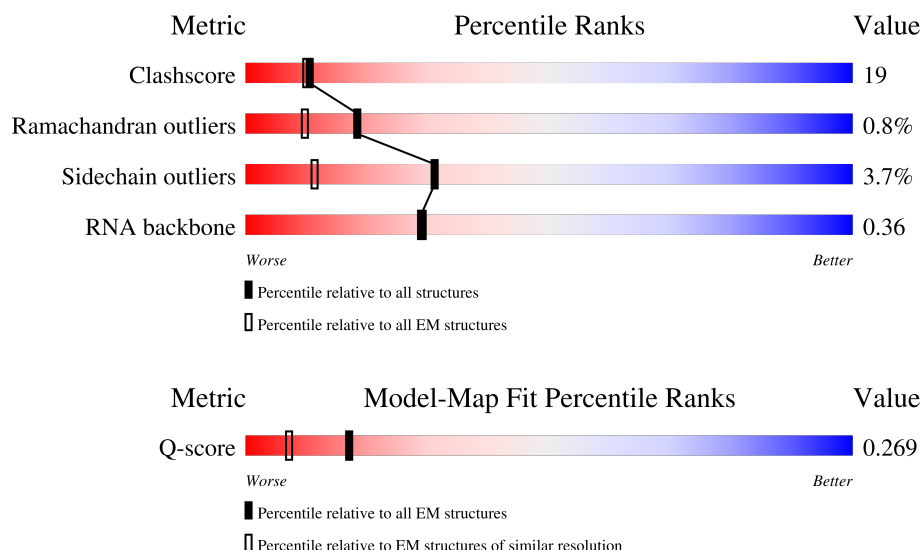
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	A	2335	
2	B	117	
3	C	972	

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Mol	Chain	Length	Quality of chain
4	E	357	
5	F	107	
6	4	46	
7	G	174	
8	H	188	
9	I	855	
10	J	848	
11	K	225	
12	L	802	
13	M	243	
14	N	144	
15	O	420	
16	P	229	
17	Q	1485	
18	R	536	
19	S	166	
20	T	514	
21	U	2752	
22	V	908	
23	W	579	
24	X	254	
25	Y	1220	
26	Z	758	
27	2	184	
28	z	112	

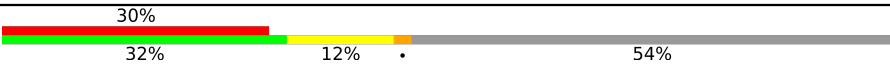
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Mol	Chain	Length	Quality of chain
29	b	240	
29	i	240	
30	y	301	
31	a	126	
31	h	126	
32	c	119	
32	j	119	
33	d	118	
33	k	118	
34	f	86	
34	m	86	
35	e	92	
35	l	92	
36	g	76	
36	n	76	
37	v	146	
38	w	174	
39	u	411	
40	x	703	
41	q	504	
41	r	504	
41	s	504	
41	t	504	
42	o	255	
43	p	225	

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Mol	Chain	Length	Quality of chain
44	1	586	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
45	IHP	A	3000	-	-	X	-

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 96822 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1984	Total	C	N	O	S	0	0
			16449	10601	2879	2899	70		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	84	Total	C	N	O	P	0	0
			1768	792	295	597	84		

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	862	Total	C	N	O	S	0	0
			6791	4341	1138	1280	32		

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	299	Total	C	N	O	S	0	0
			2338	1470	410	445	13		

- Molecule 5 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	97	Total	C	N	O	P	0	0
			2075	928	381	669	97		

- Molecule 6 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	4	13	Total	C	N	O	P	0	0
			276	123	50	90	13		

- Molecule 7 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	82	Total	C	N	O	P	0	0
			1510	666	210	552	82		

- Molecule 8 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	140	Total	C	N	O	P	0	0
			2966	1326	510	990	140		

- Molecule 9 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	618	Total	C	N	O	S	0	0
			3857	2389	722	735	11		

- Molecule 10 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	567	Total	C	N	O	S	0	0
			3809	2373	716	714	6		

- Molecule 11 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	155	Total	C	N	O	0	0
			772	462	155	155		

- Molecule 12 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	437	Total	C	N	O	S	0	0
			3015	1859	584	565	7		

- Molecule 13 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	130	Total	C	N	O	S	0	0
			1098	684	204	208	2		

- Molecule 14 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	143	Total	C	N	O	S	0	0
			1184	746	217	209	12		

- Molecule 15 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	285	Total	C	N	O	S	0	0
			2296	1442	408	426	20		

- Molecule 16 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	113	Total	C	N	O	S	0	0
			953	583	189	179	2		

- Molecule 17 is a protein called RNA helicase aquarius.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	1322	Total	C	N	O	S	4	0
			6562	3918	1322	1322			

- Molecule 18 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	261	Total	C	N	O	P S	0	0
			2073	1300	373	386	2 12		

- Molecule 19 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	159	Total	C	N	O	S	0	0
			1236	787	215	227	7		

- Molecule 20 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	312	Total	C	N	O	S	0	0
			2454	1550	446	450	8		

- Molecule 21 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	72	Total	C	N	O	S	0	0
			422	257	82	82	1		

- Molecule 22 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	452	Total	C	N	O	S	0	0
			2632	1639	492	495	6		

- Molecule 23 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	509	Total	C	N	O	S	0	0
			4129	2628	715	762	24		

- Molecule 24 is a protein called PSME3-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	87	Total	C	N	O	S	0	0
			702	431	128	142	1		

- Molecule 25 is a protein called ATP-dependent RNA helicase DHX8.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	667	Total	C	N	O	S	4	0
			3431	2057	680	693	1		

- Molecule 26 is a protein called Cactin.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	101	Total	C	N	O	S	0	0
			902	592	167	141	2		

- Molecule 27 is a protein called PRKR-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	123	Total	C	N	O	S	0	0
			1013	635	193	180	5		

- Molecule 28 is a protein called Protein FAM32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	z	60	Total	C	N	O	S	0	0
			504	314	96	92	2		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	102	Total	C	N	O	S	0	0
			786	492	148	139	7		
29	i	86	Total	C	N	O	S	0	0
			690	434	126	123	7		

- Molecule 30 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	y	79	Total	C	N	O	0	0
			390	232	79	79		

- Molecule 31 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	77	Total	C	N	O	S	0	0
			609	381	108	115	5		
31	h	81	Total	C	N	O	S	0	0
			633	397	112	118	6		

- Molecule 32 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	82	Total	C	N	O	S	0	0
			649	413	113	119	4		
32	j	82	Total	C	N	O	S	0	0
			649	413	113	119	4		

- Molecule 33 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	97	Total	C	N	O	S	0	0
			776	488	143	140	5		
33	k	85	Total	C	N	O	S	0	0
			688	432	125	126	5		

- Molecule 34 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	74	Total	C	N	O	S	0	0
			576	373	95	103	5		
34	m	74	Total	C	N	O	S	0	0
			572	370	94	103	5		

- Molecule 35 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	79	Total	C	N	O	S	0	0
			652	412	116	119	5		
35	l	79	Total	C	N	O	S	0	0
			652	412	116	119	5		

- Molecule 36 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	74	Total	C	N	O	S	0	0
			577	364	104	103	6		
36	n	69	Total	C	N	O	S	0	0
			542	345	97	94	6		

- Molecule 37 is a protein called Protein mago nashi homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	v	144	Total	C	N	O	0	0
			711	423	144	144		

- Molecule 38 is a protein called RNA-binding protein 8A.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	w	91	Total	C	N	O	0	0
			445	263	91	91		

- Molecule 39 is a protein called Eukaryotic initiation factor 4A-III.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	u	386	Total	C	N	O	0	0
			1907	1135	386	386		

- Molecule 40 is a protein called Protein CASC3.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	x	25	Total	C	N	O	0	0
			124	74	25	25		

- Molecule 41 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	q	132	Total	C	N	O	0	0
			659	395	132	132		
41	r	131	Total	C	N	O	0	0
			654	392	131	131		
41	s	132	Total	C	N	O	0	0
			659	395	132	132		
41	t	131	Total	C	N	O	0	0
			654	392	131	131		

- Molecule 42 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	162	Total	C	N	O	S	0	0
			1282	820	219	240	3		

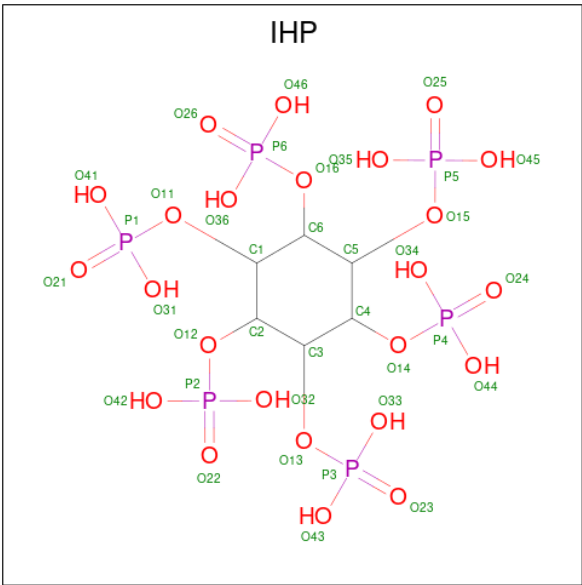
- Molecule 43 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	94	Total	C	N	O	S	0	0
			760	488	135	132	5		

- Molecule 44 is a protein called Pre-mRNA-splicing factor SLU7.

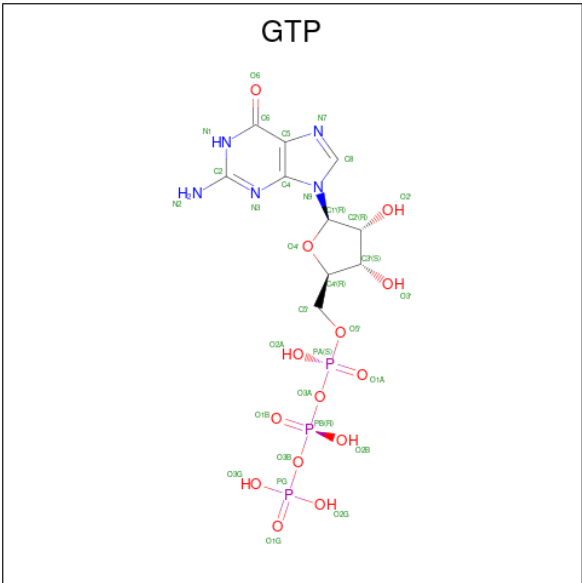
Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	267	Total	C	N	O	S	0	0
			2194	1378	392	416	8		

- Molecule 45 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 46 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



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

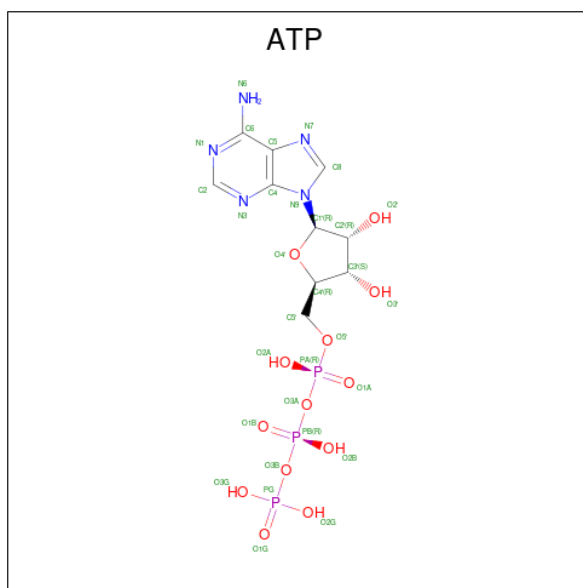
- Molecule 47 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
47	C	1	Total	Mg	0
			1	1	
47	F	6	Total	Mg	0
			6	6	
47	Q	2	Total	Mg	0
			2	2	

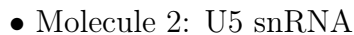
- Molecule 48 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

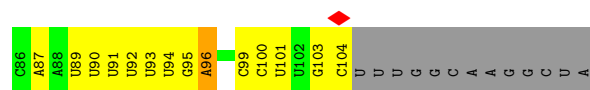
Mol	Chain	Residues	Atoms		AltConf
48	N	3	Total	Zn	0
			3	3	
48	O	3	Total	Zn	0
			3	3	
48	1	1	Total	Zn	0
			1	1	

- Molecule 49 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



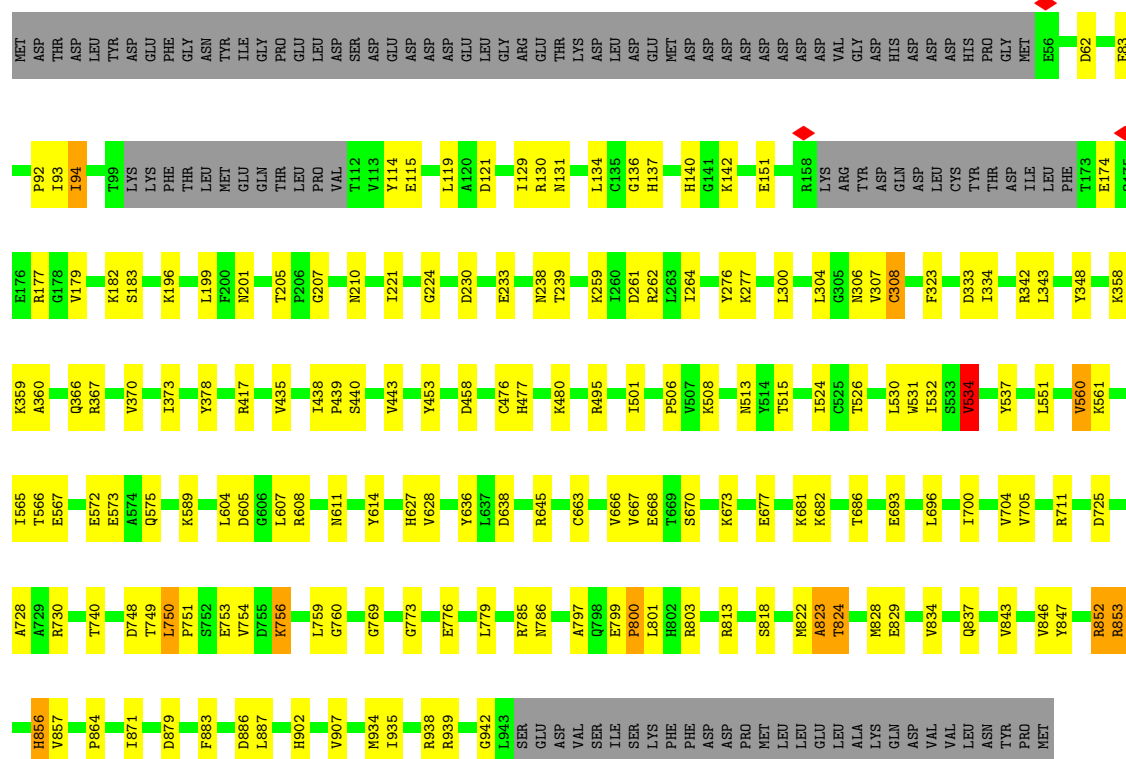
Mol	Chain	Residues	Atoms					AltConf
49	Q	1	Total	C	N	O	P	0
			31	10	5	13	3	





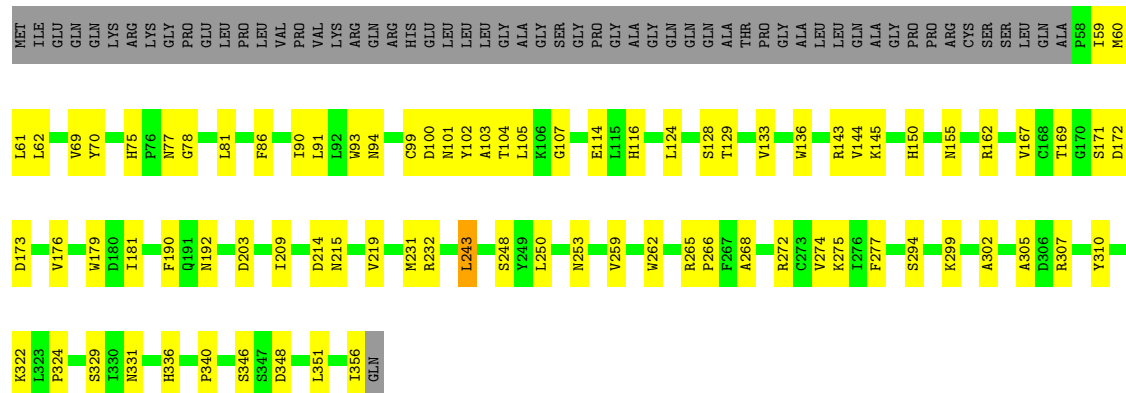
- Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component

Chain C: 71% 17% 11%



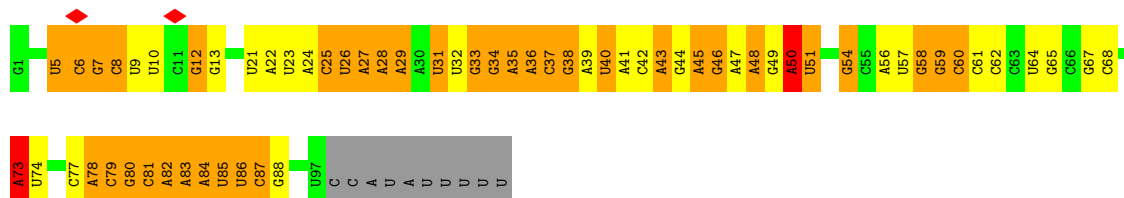
- Molecule 4: U5 small nuclear ribonucleoprotein 40 kDa protein

Chain E: 61% 23% 16%



- Molecule 5: U6 snRNA

Chain F: 31% 23% 35% 9%



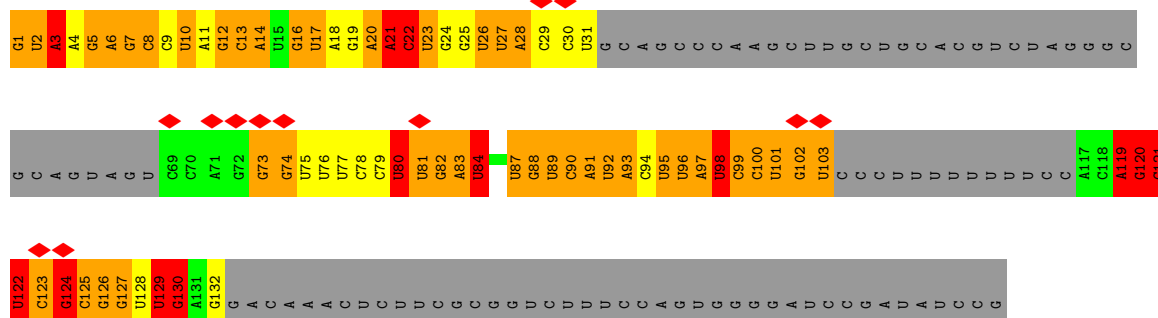
• Molecule 6: Pre-mRNA

Chain 4: 7% 13% . 72%



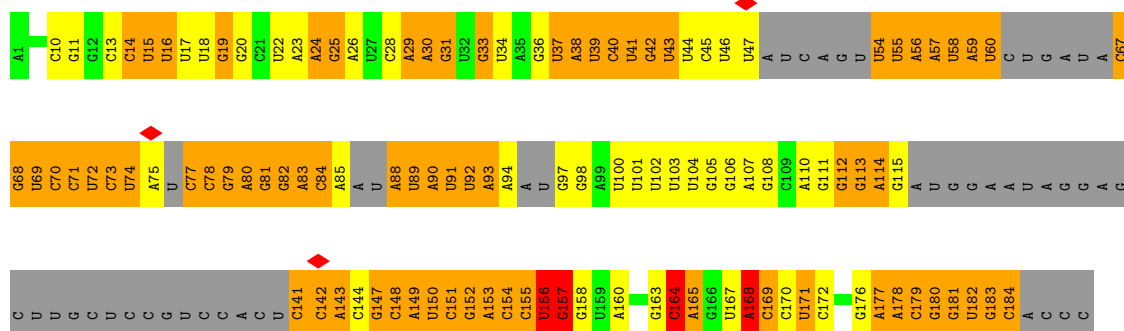
• Molecule 7: Pre-mRNA

Chain G: 7% 6% 10% 24% 7% 53%



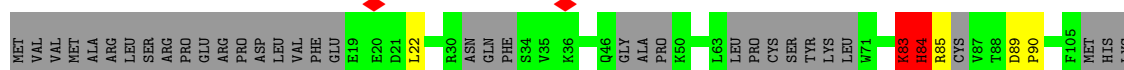
• Molecule 8: U2 snRNA

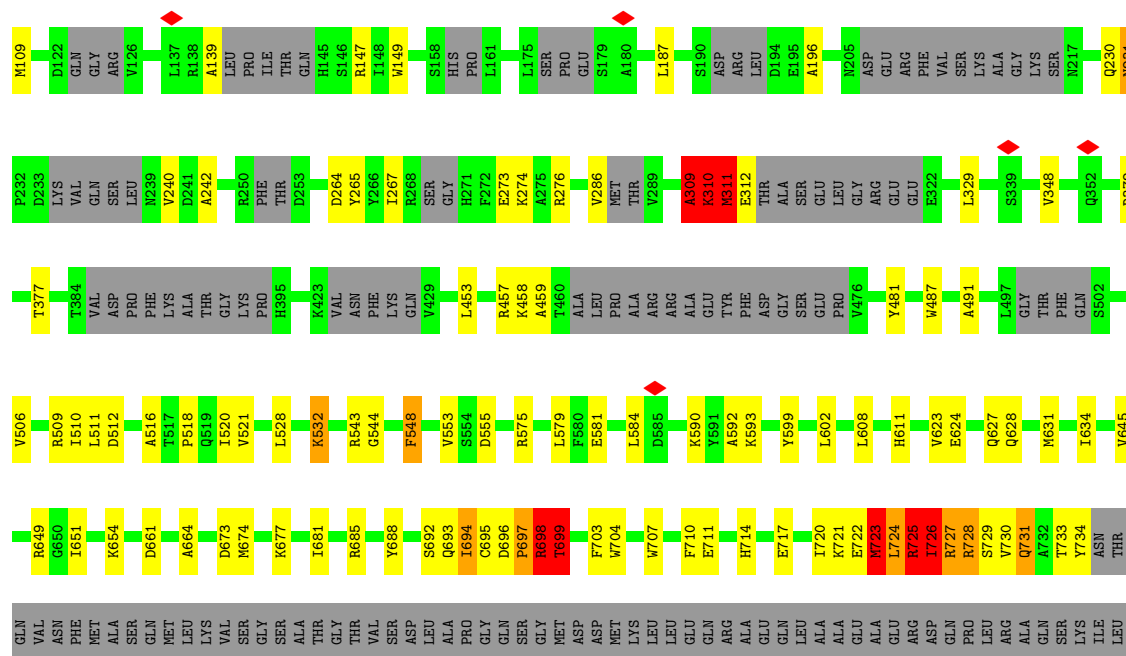
Chain H: 12% 22% 38% . 26%



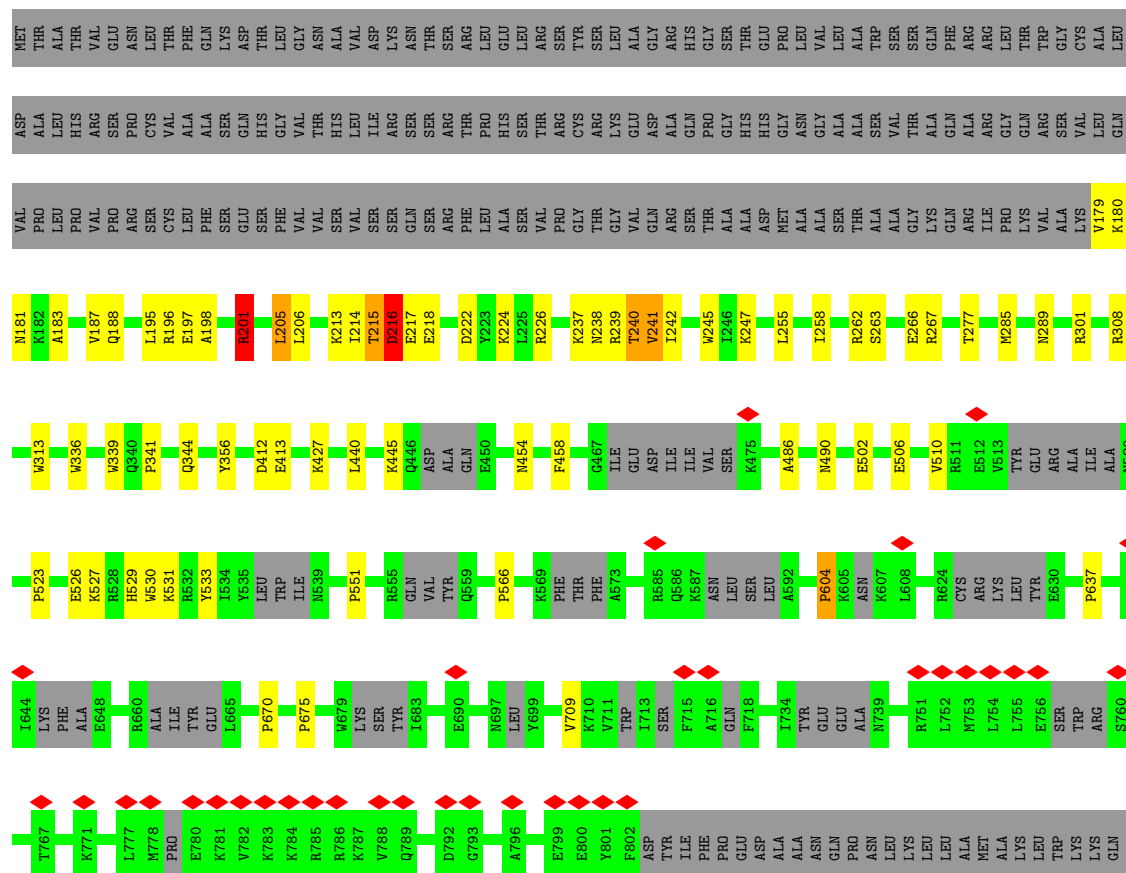
• Molecule 9: Pre-mRNA-splicing factor SYF1

Chain I: 59% 11% . 28%



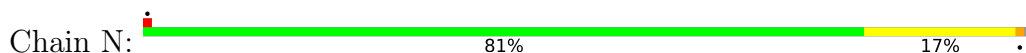


• Molecule 10: Crooked neck-like protein 1

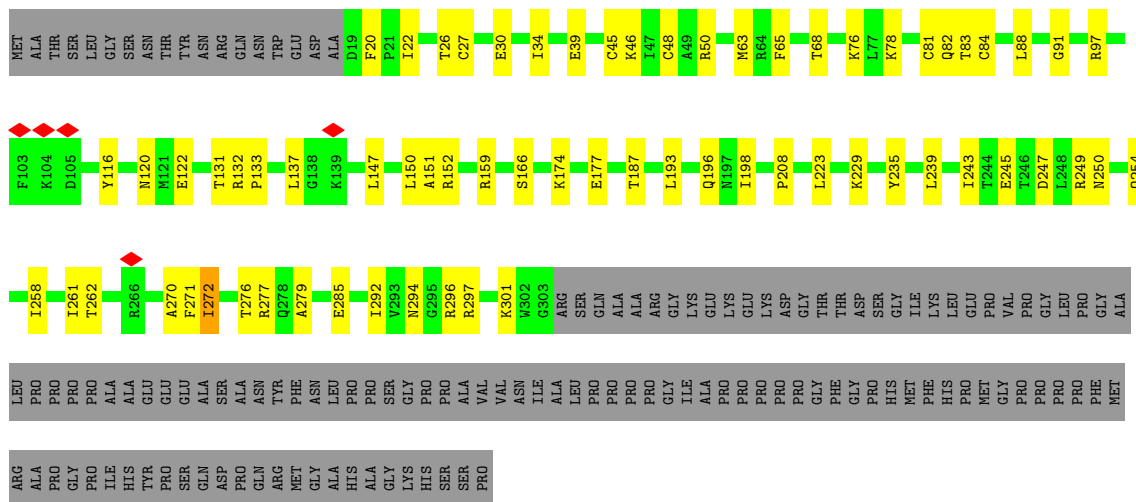




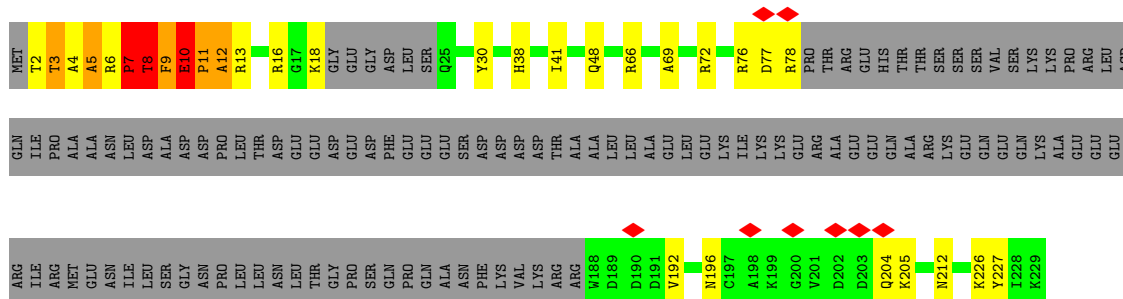
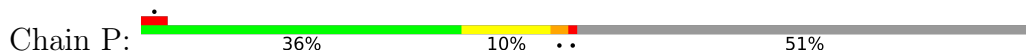
- Molecule 14: Protein BUD31 homolog



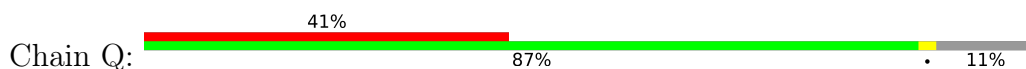
- Molecule 15: Pre-mRNA-splicing factor RBM22



- Molecule 16: Spliceosome-associated protein CWC15 homolog

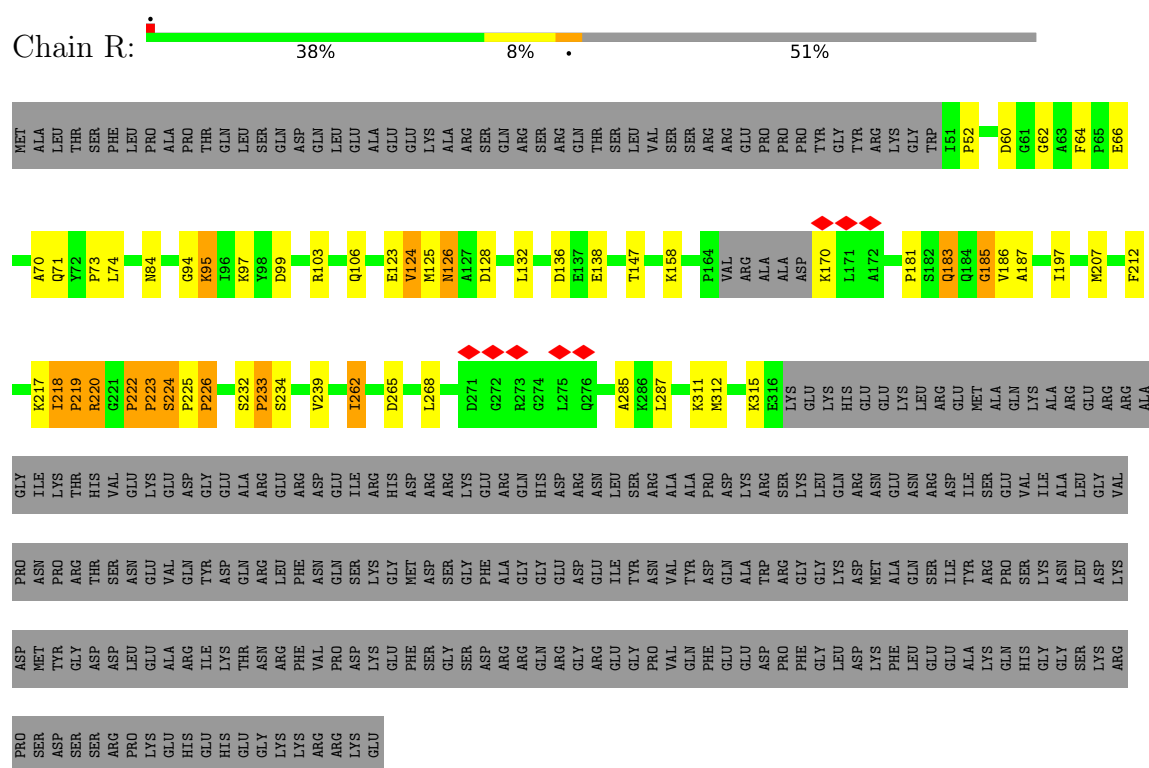


- Molecule 17: RNA helicase aquarius

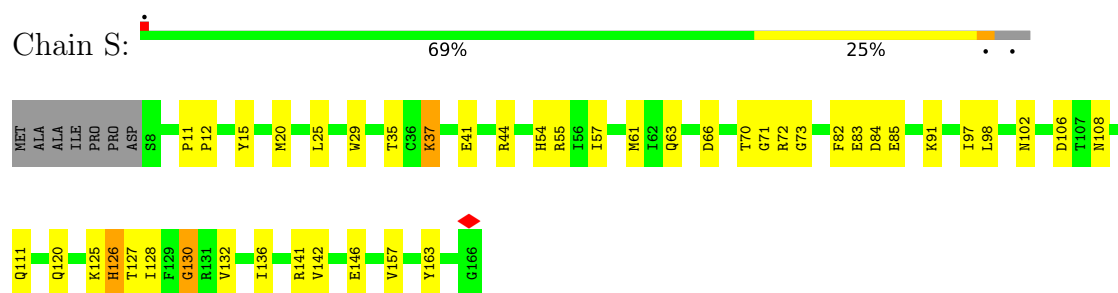




- Molecule 18: SNW domain-containing protein 1



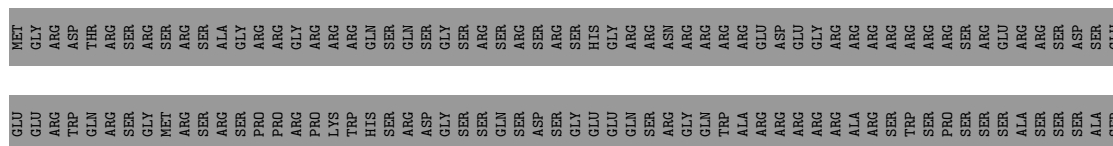
- Molecule 19: Peptidyl-prolyl cis-trans isomerase-like 1



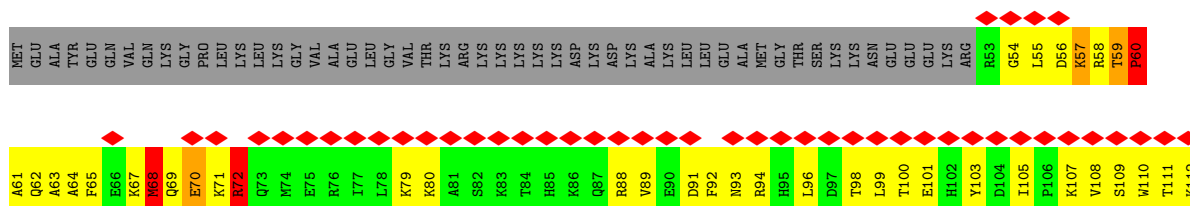
- Molecule 20: Pleiotropic regulator 1

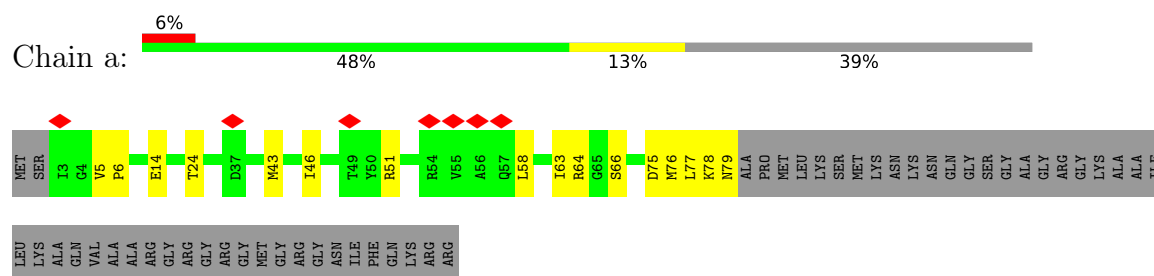


- Molecule 26: Cactin

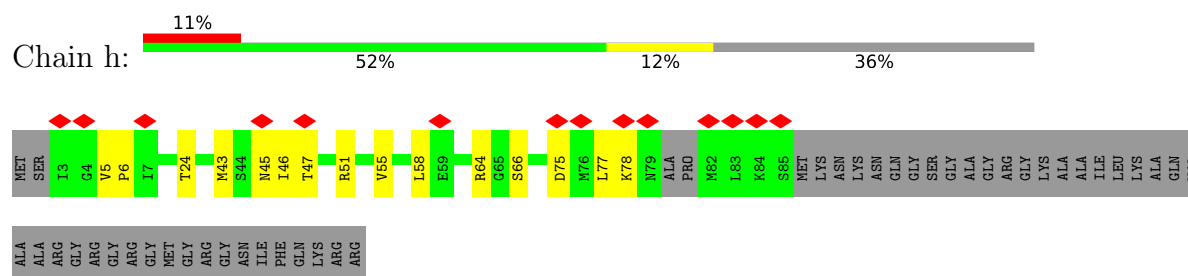


PRO	PRO	LYS	ILE	V673	V682	L685	D687	K688	R689	Y694	A698	C699	A700	D701	N702	K703	D704	F705	A706	R709	F710	F714	P715	D718	L719	N725	R726	E727	R733	C738	Q739	F740	A741	N742	G743	L744	F745	Q746	L747	F751	K752	R753	Y754	R755	Y756	R757	R759
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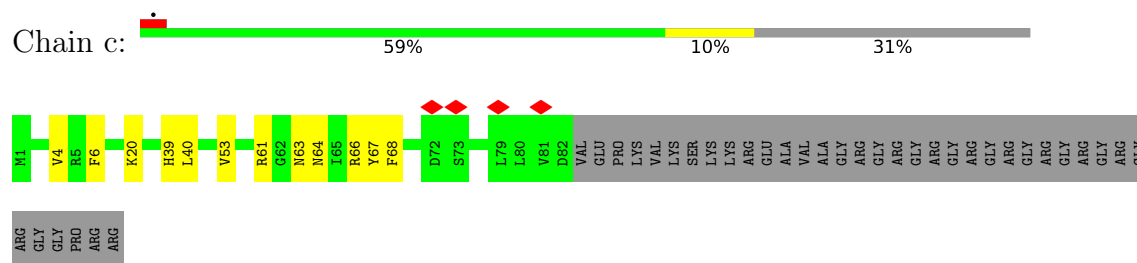




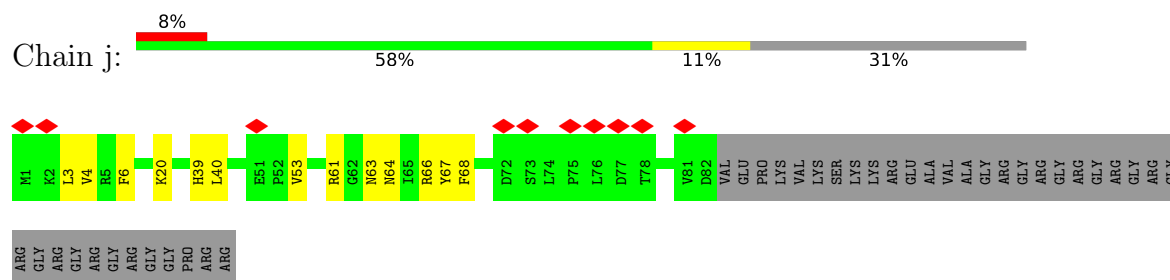
- Molecule 31: Small nuclear ribonucleoprotein Sm D3



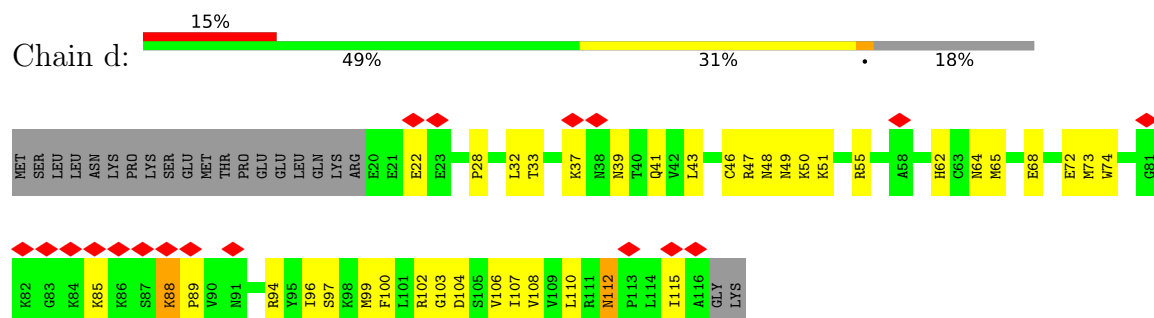
- Molecule 32: Small nuclear ribonucleoprotein Sm D1



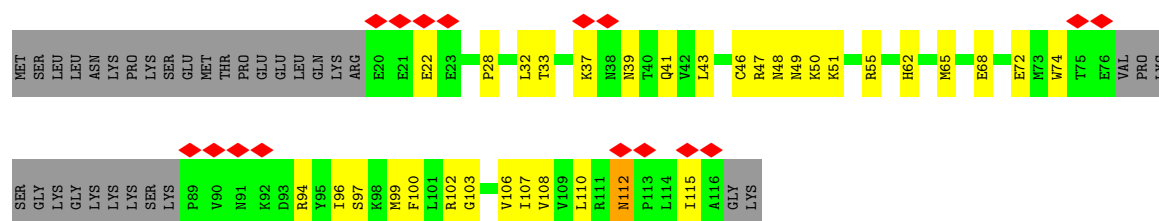
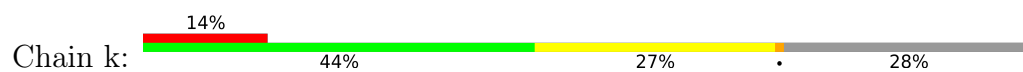
- Molecule 32: Small nuclear ribonucleoprotein Sm D1



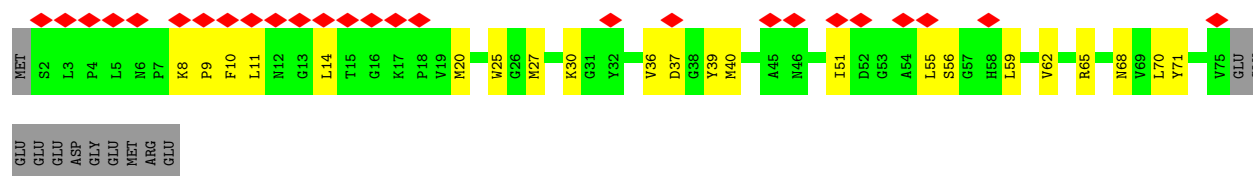
- Molecule 33: Small nuclear ribonucleoprotein Sm D2



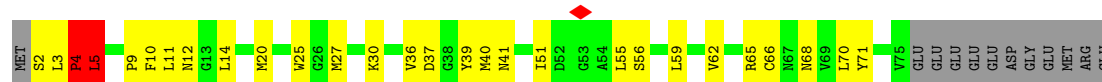
- Molecule 33: Small nuclear ribonucleoprotein Sm D2



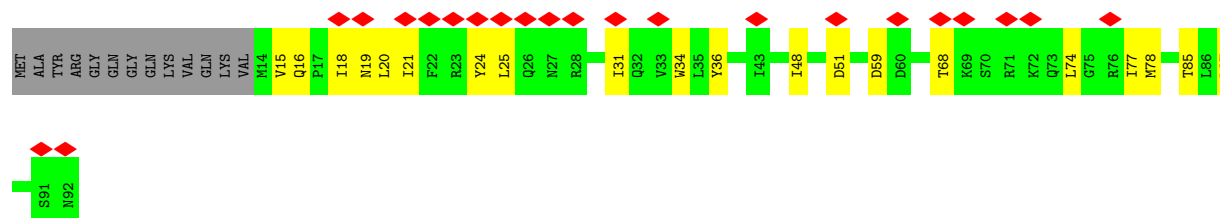
- Molecule 34: Small nuclear ribonucleoprotein F



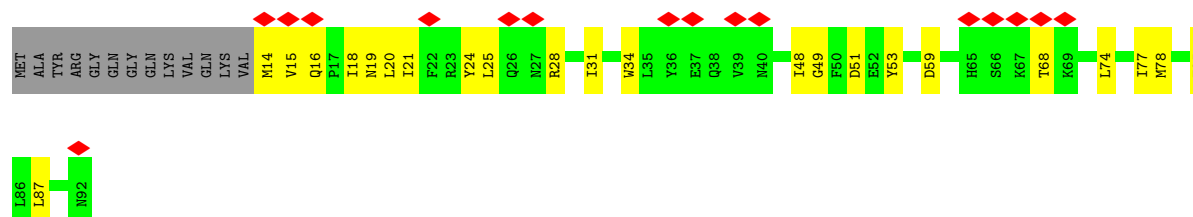
- Molecule 34: Small nuclear ribonucleoprotein F



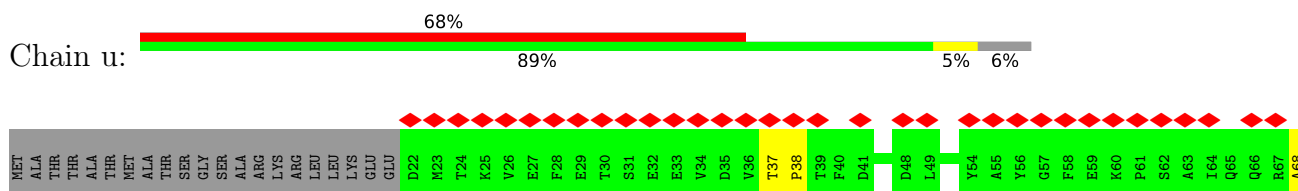
- Molecule 35: Small nuclear ribonucleoprotein E



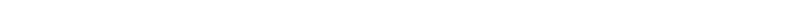
- Molecule 35: Small nuclear ribonucleoprotein E

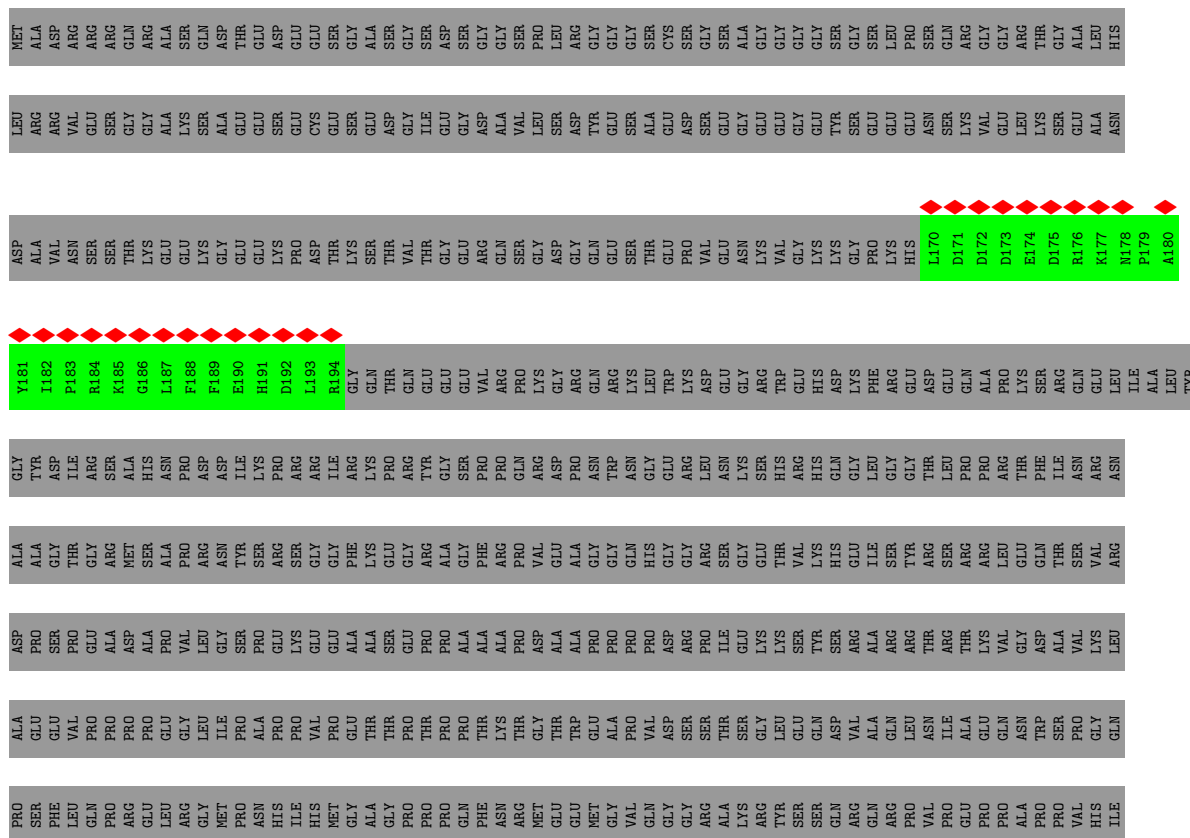


- Molecule 36: Small nuclear ribonucleoprotein G



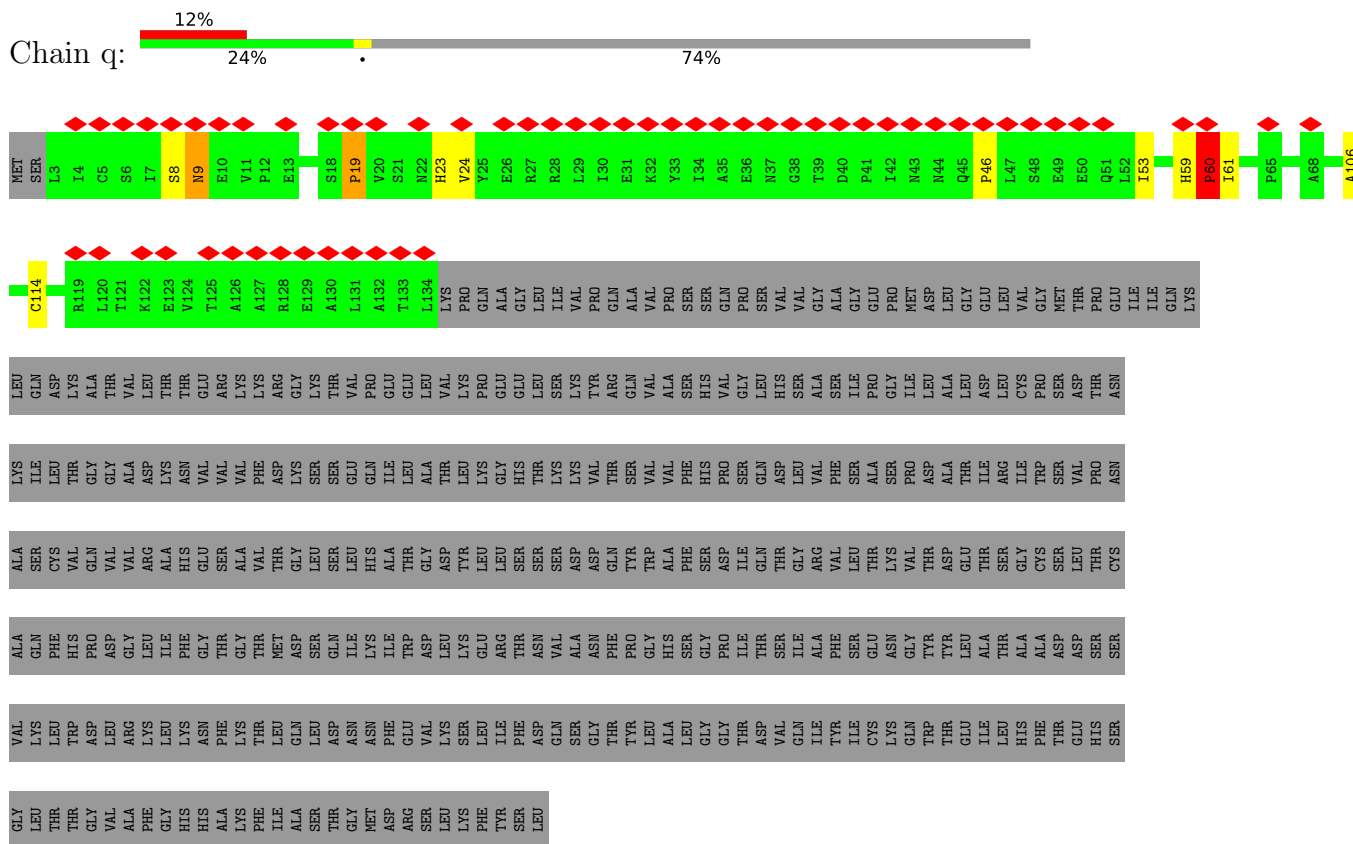
- Molecule 40: Protein CASC3

Chain x:  96%

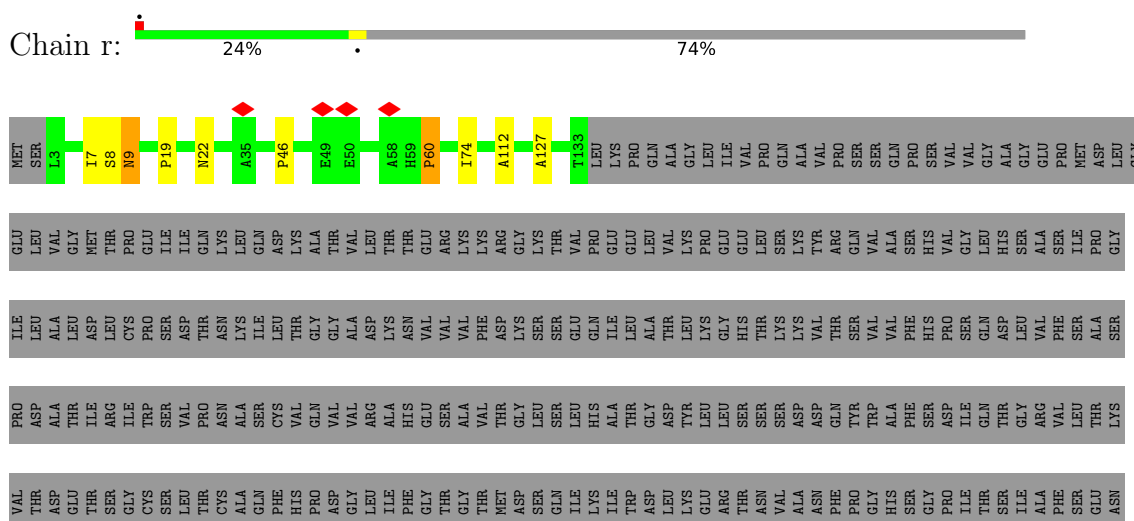


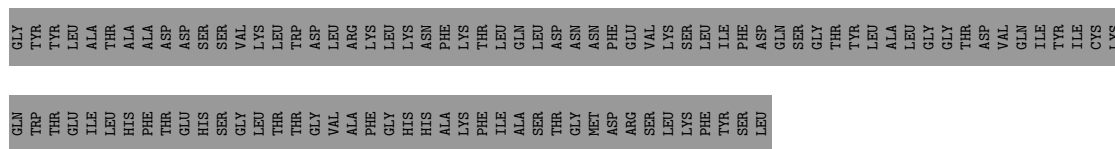
																																TYR	GLY	GLY	VAL	THR	TYR	TYR	ASN	PRO	ALA	GLN	GLN	GLN	VAL	GLN	PRO	LYS	PRO	SER	SER	THR	THR	PRO	GLN	GLN	VAL	VAL	THR	ARG	ARG	ARG	THR	PRO	THR	ALA	PRO	PRO	GLY	GLY	GLY	VAL	VAL	THR	TYR	TYR	ASN	PRO	GLY	GLY	GLY	VAL	VAL	THR	TYR	TYR	ASP	PRO	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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● Molecule 41: Pre-mRNA-processing factor 19

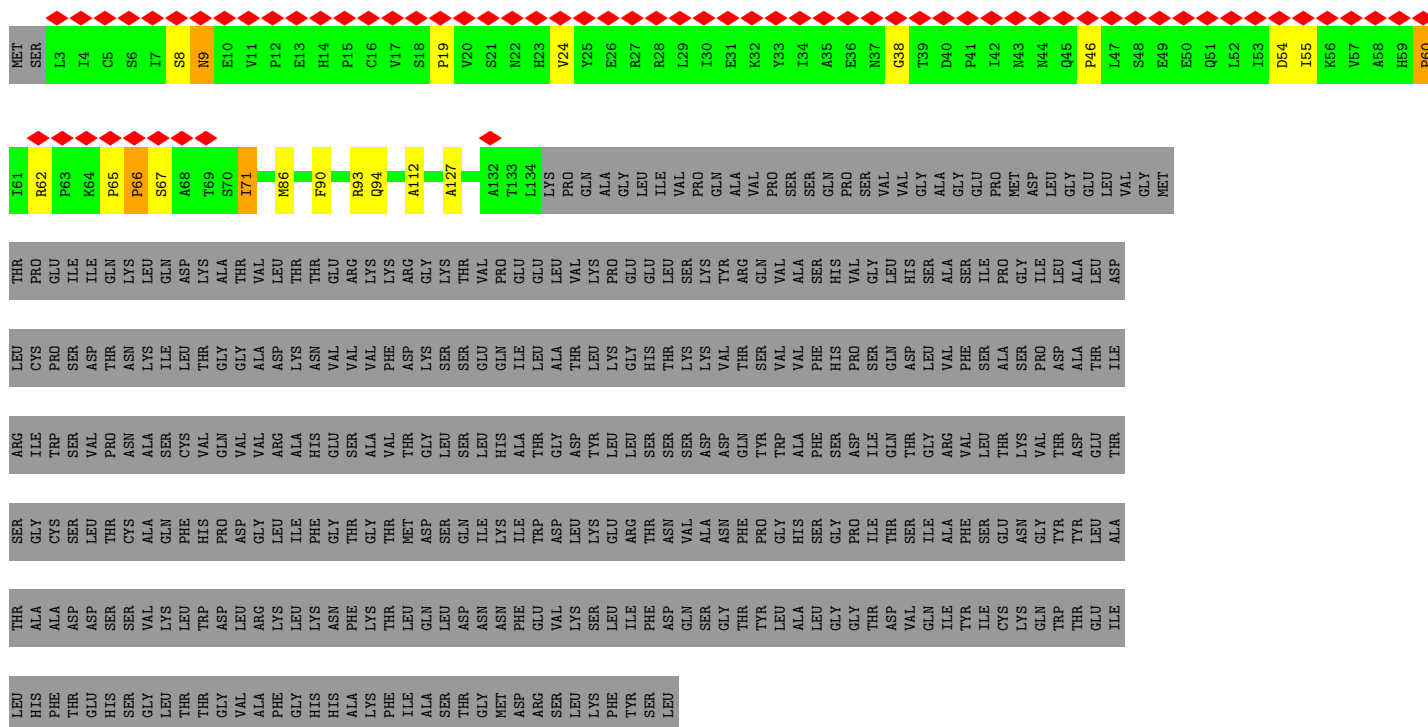


- Molecule 41: Pre-mRNA-processing factor 19

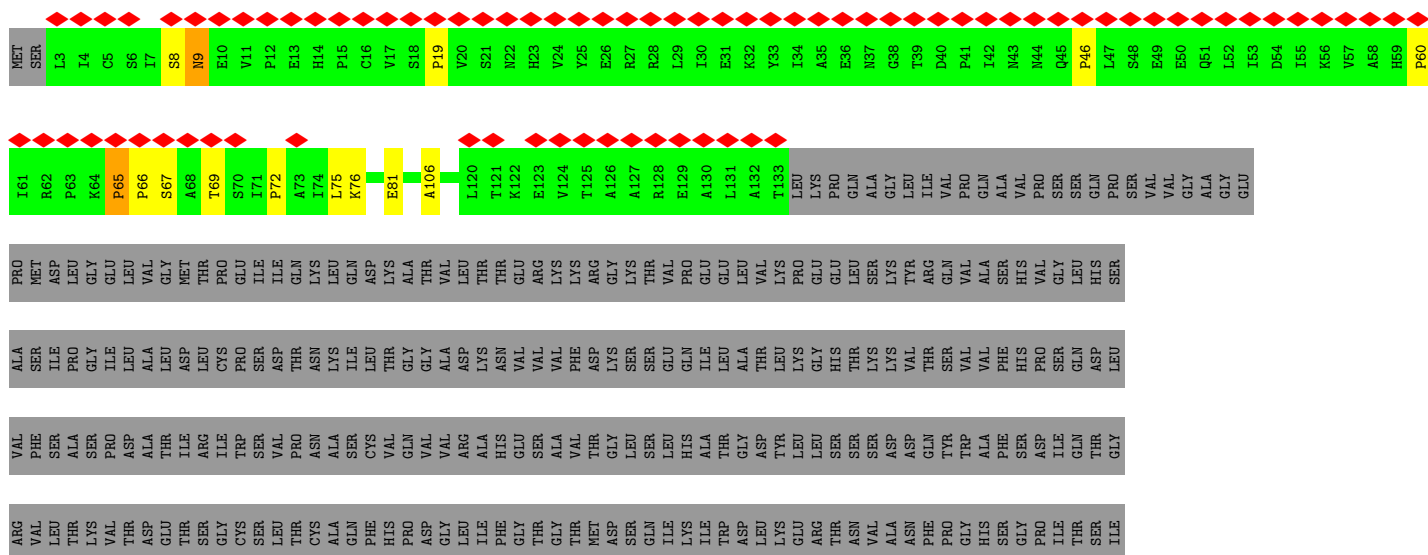




- Molecule 41: Pre-mRNA-processing factor 19

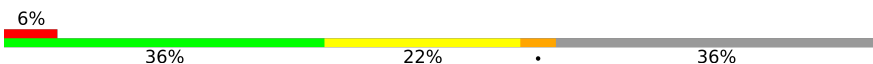


- Molecule 41: Pre-mRNA-processing factor 19



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

• Molecule 42: U2 small nuclear ribonucleoprotein A'

Chain o: 

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• Molecule 43: U2 small nuclear ribonucleoprotein B''

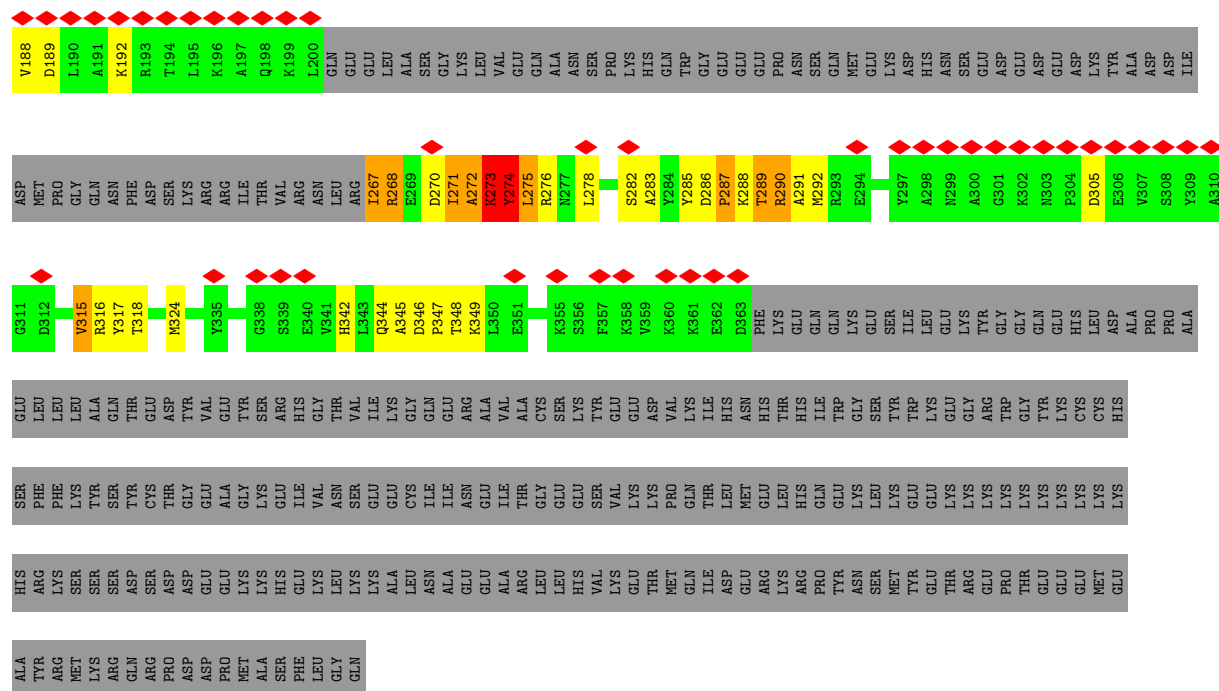
Chain p: 

PRO	GLN	THR	ALA	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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• Molecule 44: Pre-mRNA-splicing factor SLU7

Chain 1: 

MET	SER	ALA	THR	VAL	ASP	ALA	VAL	ASN	ALA	PRO	LEU	SER	GLY	SER	LYS	GLU	MET	GLY	LEU	GLU	PRO	LYS	LYS	MET	THR	ARG	E31	D32	W33	R34	K35	K36	K37	E38	L39	E40	E41	Q42	R43	K44	L45	G46	M47	A48	P49	A50	E51	V52	D53	E54	E55	G56	K57	D58	I59	N60	
P61	H62	I63	P64	Q65	Y66	I67	S68	S69	W72	Y73	K78	R79	P80	T81	L82	K83	H84	Q85	R86	P87	Q88	P89	E90	K91	Q92	K93	Q94	F95	S96	S97	S98	G99	E100	W101	Y102	K103	R104	G105	V106	K107	E108	M109	S110	I111	I112	T113	K114	Y115	R116	K117	G118	A119	C120	E121	N122	C123	G124
A125	M126	T127	H128	K129	K130	K131	D132	C133	F134	E135	R136	P137	R138	R139	V140	G141	A142	K143	F144	T145	G146	T147	N148	I149	A150	P151	D152	E153	H154	V155	Q156	P157	Q158	L159	M160	F161	D162	Y163	D164	D168	R169	W170	Y173	M174	P175	E176	E177	H178	M179	K180	I181	V182	E183	E184	Y185	A186	K187



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	212224	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.505	Depositor
Minimum map value	-1.600	Depositor
Average map value	0.013	Depositor
Map value standard deviation	0.093	Depositor
Recommended contour level	0.39	Depositor
Map size ($\text{\AA}$)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.338, 1.338, 1.338	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.94	79/16897 (0.5%)	1.20	176/22917 (0.8%)
2	B	0.60	2/1970 (0.1%)	0.82	6/3060 (0.2%)
3	C	0.56	0/6942	0.85	11/9432 (0.1%)
4	E	0.53	0/2392	0.73	0/3242
5	F	0.48	0/2323	0.82	3/3619 (0.1%)
6	4	0.72	0/307	1.00	3/476 (0.6%)
7	G	0.62	2/1674 (0.1%)	1.41	35/2594 (1.3%)
8	H	0.85	26/3305 (0.8%)	1.41	60/5130 (1.2%)
9	I	0.65	0/3884	1.45	29/5301 (0.5%)
10	J	0.57	1/3851 (0.0%)	0.88	16/5227 (0.3%)
11	K	0.59	1/768 (0.1%)	0.98	2/1067 (0.2%)
12	L	0.53	0/3046	0.85	10/4115 (0.2%)
13	M	0.53	0/1119	0.90	6/1497 (0.4%)
14	N	0.66	0/1210	0.80	2/1622 (0.1%)
15	O	0.53	0/2344	0.80	2/3163 (0.1%)
16	P	0.74	1/967 (0.1%)	1.18	13/1285 (1.0%)
17	Q	0.40	0/6565	0.89	1/9143 (0.0%)
18	R	0.80	6/2091 (0.3%)	1.03	11/2809 (0.4%)
19	S	0.48	0/1268	0.75	1/1714 (0.1%)
20	T	0.78	0/2519	0.95	9/3433 (0.3%)
21	U	0.50	0/424	0.85	2/582 (0.3%)
22	V	0.43	0/2642	0.82	0/3602
23	W	0.43	0/4237	0.88	5/5723 (0.1%)
24	X	1.07	1/706 (0.1%)	2.08	23/941 (2.4%)
25	Y	1.00	1/3436 (0.0%)	1.52	24/4774 (0.5%)
26	Z	0.41	1/936 (0.1%)	0.76	0/1258
27	2	0.55	0/1030	1.16	10/1371 (0.7%)
28	z	0.94	2/513 (0.4%)	1.58	8/683 (1.2%)
29	b	0.77	0/797	1.05	4/1062 (0.4%)
29	i	0.72	0/700	1.03	4/933 (0.4%)
30	y	1.30	2/389 (0.5%)	1.65	5/540 (0.9%)
31	a	0.64	0/616	0.85	0/830

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	h	0.66	0/639	0.86	0/857
32	c	0.74	0/657	0.98	0/888
32	j	0.74	0/657	0.98	0/888
33	d	0.94	1/786 (0.1%)	1.10	2/1053 (0.2%)
33	k	0.95	0/696	1.07	1/935 (0.1%)
34	f	1.04	1/588 (0.2%)	1.08	0/795
34	m	1.05	1/584 (0.2%)	1.14	1/791 (0.1%)
35	e	0.84	0/660	1.06	1/886 (0.1%)
35	l	0.85	0/660	1.06	1/886 (0.1%)
36	g	0.71	0/584	0.95	1/779 (0.1%)
36	n	0.71	0/548	1.03	2/729 (0.3%)
37	v	0.47	0/710	1.03	3/987 (0.3%)
38	w	0.47	0/444	1.20	4/614 (0.7%)
39	u	0.51	0/1906	1.20	13/2653 (0.5%)
40	x	0.53	0/123	1.13	0/170
41	q	0.62	0/658	1.04	3/919 (0.3%)
41	r	0.57	0/653	1.00	3/912 (0.3%)
41	s	0.60	0/658	1.11	4/919 (0.4%)
41	t	0.62	0/653	0.94	3/912 (0.3%)
42	o	0.81	0/1299	2.06	56/1761 (3.2%)
43	p	0.78	0/774	1.71	12/1035 (1.2%)
44	l	0.40	0/2247	0.84	9/3024 (0.3%)
All	All	0.71	128/99052 (0.1%)	1.10	600/136538 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	21
3	C	0	9
4	E	0	1
9	I	0	7
10	J	0	5
14	N	0	4
15	O	0	1
16	P	0	3
18	R	0	7
20	T	0	3
23	W	0	2
27	2	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
33	d	0	1
33	k	0	1
All	All	0	66

The worst 5 of 128 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	y	38	PRO	N-CA	20.50	1.71	1.47
1	A	1724	PRO	N-CA	16.51	1.68	1.47
28	z	60	PRO	N-CA	16.09	1.68	1.47
1	A	1955	LYS	C-N	14.36	1.51	1.34
18	R	223	PRO	N-CA	13.60	1.67	1.47

The worst 5 of 600 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	y	37	ILE	CA-C-N	18.84	139.11	119.90
30	y	37	ILE	C-N-CA	18.84	139.11	119.90
1	A	1883	VAL	CA-C-N	-18.75	98.16	123.10
1	A	1883	VAL	C-N-CA	-18.75	98.16	123.10
7	G	1	G	C1'-C2'-O2'	-16.54	86.99	111.80

There are no chirality outliers.

5 of 66 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	170	ASP	Mainchain
1	A	377	GLU	Peptide
1	A	385	GLU	Peptide
1	A	55	ASP	Peptide
1	A	73	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16449	0	16378	1202	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1768	0	897	66	0
3	C	6791	0	6807	126	0
4	E	2338	0	2275	73	0
5	F	2075	0	1048	188	0
6	4	276	0	142	15	0
7	G	1510	0	760	217	0
8	H	2966	0	1505	292	0
9	I	3857	0	2738	157	0
10	J	3809	0	2900	42	0
11	K	772	0	342	19	0
12	L	3015	0	2570	90	0
13	M	1098	0	1082	39	0
14	N	1184	0	1190	27	0
15	O	2296	0	2284	77	0
16	P	953	0	939	37	0
17	Q	6562	0	2836	35	0
18	R	2073	0	2119	53	0
19	S	1236	0	1210	49	0
20	T	2454	0	2413	80	0
21	U	422	0	291	10	0
22	V	2632	0	1734	43	0
23	W	4129	0	4040	152	0
24	X	702	0	632	143	0
25	Y	3431	0	1662	41	0
26	Z	902	0	860	54	0
27	2	1013	0	1058	117	0
28	z	504	0	509	129	0
29	b	786	0	811	48	0
29	i	690	0	712	15	0
30	y	390	0	190	5	0
31	a	609	0	620	13	0
31	h	633	0	645	14	0
32	c	649	0	693	10	0
32	j	649	0	693	11	0
33	d	776	0	819	32	0
33	k	688	0	709	30	0
34	f	576	0	589	21	0
34	m	572	0	578	57	0
35	e	652	0	668	20	0
35	l	652	0	668	48	0
36	g	577	0	603	15	0
36	n	542	0	568	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	v	711	0	299	6	0
38	w	445	0	203	6	0
39	u	1907	0	845	3	0
40	x	124	0	51	0	0
41	q	659	0	296	19	0
41	r	654	0	294	9	0
41	s	659	0	296	20	0
41	t	654	0	294	16	0
42	o	1282	0	1305	30	0
43	p	760	0	783	12	0
44	l	2194	0	2137	321	0
45	A	36	0	6	9	0
46	C	32	0	12	2	0
47	C	1	0	0	0	0
47	F	6	0	0	0	0
47	Q	2	0	0	0	0
48	l	1	0	0	0	0
48	N	3	0	0	0	0
48	O	3	0	0	0	0
49	Q	31	0	12	5	0
All	All	96822	0	79620	3313	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 3313 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1596:VAL:CG2	44:1:275:LEU:HD22	1.14	1.61
27:2:48:ILE:HG23	34:m:5:LEU:CD2	1.31	1.60
1:A:1556:ASP:HA	28:z:103:TYR:CD2	1.34	1.59
1:A:1701:VAL:CG2	1:A:1718:TRP:CH2	1.76	1.58
27:2:48:ILE:CG2	34:m:5:LEU:HD21	1.30	1.56

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1980/2335 (85%)	1782 (90%)	181 (9%)	17 (1%)	14	46
3	C	856/972 (88%)	781 (91%)	71 (8%)	4 (0%)	24	57
4	E	297/357 (83%)	275 (93%)	22 (7%)	0	100	100
9	I	576/855 (67%)	557 (97%)	15 (3%)	4 (1%)	18	51
10	J	528/848 (62%)	487 (92%)	33 (6%)	8 (2%)	8	37
11	K	147/225 (65%)	137 (93%)	6 (4%)	4 (3%)	4	27
12	L	425/802 (53%)	408 (96%)	15 (4%)	2 (0%)	24	57
13	M	128/243 (53%)	117 (91%)	11 (9%)	0	100	100
14	N	141/144 (98%)	124 (88%)	16 (11%)	1 (1%)	18	51
15	O	283/420 (67%)	259 (92%)	23 (8%)	1 (0%)	30	61
16	P	107/229 (47%)	89 (83%)	15 (14%)	3 (3%)	4	26
17	Q	1308/1485 (88%)	1282 (98%)	26 (2%)	0	100	100
18	R	255/536 (48%)	228 (89%)	23 (9%)	4 (2%)	7	36
19	S	157/166 (95%)	147 (94%)	10 (6%)	0	100	100
20	T	310/514 (60%)	275 (89%)	29 (9%)	6 (2%)	6	33
21	U	68/2752 (2%)	60 (88%)	8 (12%)	0	100	100
22	V	444/908 (49%)	431 (97%)	12 (3%)	1 (0%)	43	72
23	W	507/579 (88%)	432 (85%)	69 (14%)	6 (1%)	10	41
24	X	83/254 (33%)	81 (98%)	2 (2%)	0	100	100
25	Y	667/1220 (55%)	642 (96%)	23 (3%)	2 (0%)	36	65
26	Z	97/758 (13%)	87 (90%)	10 (10%)	0	100	100
27	2	121/184 (66%)	113 (93%)	5 (4%)	3 (2%)	4	28
28	z	58/112 (52%)	55 (95%)	3 (5%)	0	100	100
29	b	98/240 (41%)	93 (95%)	2 (2%)	3 (3%)	3	25
29	i	84/240 (35%)	82 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	y	77/301 (26%)	75 (97%)	2 (3%)	0	100	100
31	a	75/126 (60%)	74 (99%)	1 (1%)	0	100	100
31	h	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
32	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
32	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
33	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
33	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
34	f	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
34	m	72/86 (84%)	69 (96%)	2 (3%)	1 (1%)	9	38
35	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
35	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
36	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
36	n	65/76 (86%)	63 (97%)	2 (3%)	0	100	100
37	v	142/146 (97%)	138 (97%)	4 (3%)	0	100	100
38	w	89/174 (51%)	87 (98%)	1 (1%)	1 (1%)	11	43
39	u	384/411 (93%)	372 (97%)	9 (2%)	3 (1%)	16	49
40	x	23/703 (3%)	22 (96%)	1 (4%)	0	100	100
41	q	130/504 (26%)	117 (90%)	7 (5%)	6 (5%)	2	17
41	r	129/504 (26%)	118 (92%)	9 (7%)	2 (2%)	7	36
41	s	130/504 (26%)	115 (88%)	7 (5%)	8 (6%)	1	12
41	t	129/504 (26%)	116 (90%)	9 (7%)	4 (3%)	3	25
42	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	39
43	p	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
44	l	263/586 (45%)	244 (93%)	19 (7%)	0	100	100
All	All	12396/23429 (53%)	11559 (93%)	741 (6%)	96 (1%)	18	49

5 of 96 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	PRO
1	A	1092	ILE
1	A	1136	ARG
1	A	1494	TYR
1	A	1503	TRP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1780/2108 (84%)	1674 (94%)	106 (6%)	17	45
3	C	760/866 (88%)	751 (99%)	9 (1%)	63	73
4	E	256/300 (85%)	255 (100%)	1 (0%)	84	81
9	I	199/749 (27%)	184 (92%)	15 (8%)	12	39
10	J	241/751 (32%)	239 (99%)	2 (1%)	73	77
12	L	218/709 (31%)	211 (97%)	7 (3%)	34	58
13	M	117/209 (56%)	115 (98%)	2 (2%)	53	69
14	N	130/130 (100%)	129 (99%)	1 (1%)	73	77
15	O	255/361 (71%)	253 (99%)	2 (1%)	73	77
16	P	101/203 (50%)	97 (96%)	4 (4%)	28	54
18	R	219/457 (48%)	216 (99%)	3 (1%)	59	71
19	S	129/134 (96%)	127 (98%)	2 (2%)	55	69
20	T	268/441 (61%)	264 (98%)	4 (2%)	57	70
21	U	21/2432 (1%)	19 (90%)	2 (10%)	8	32
22	V	98/838 (12%)	94 (96%)	4 (4%)	27	53
23	W	448/502 (89%)	440 (98%)	8 (2%)	51	68
24	X	67/230 (29%)	39 (58%)	28 (42%)	0	0
25	Y	32/1085 (3%)	28 (88%)	4 (12%)	4	22
26	Z	91/655 (14%)	87 (96%)	4 (4%)	25	52
27	2	106/157 (68%)	99 (93%)	7 (7%)	15	43
28	z	54/99 (54%)	47 (87%)	7 (13%)	4	21
29	b	83/177 (47%)	80 (96%)	3 (4%)	31	56
29	i	77/177 (44%)	74 (96%)	3 (4%)	28	54
31	a	68/101 (67%)	68 (100%)	0	100	100
31	h	70/101 (69%)	70 (100%)	0	100	100
32	c	77/101 (76%)	75 (97%)	2 (3%)	40	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	j	77/101 (76%)	75 (97%)	2 (3%)	40	62
33	d	90/110 (82%)	89 (99%)	1 (1%)	65	74
33	k	80/110 (73%)	79 (99%)	1 (1%)	61	72
34	f	63/74 (85%)	61 (97%)	2 (3%)	34	58
34	m	62/74 (84%)	58 (94%)	4 (6%)	15	43
35	e	74/84 (88%)	74 (100%)	0	100	100
35	l	74/84 (88%)	74 (100%)	0	100	100
36	g	64/66 (97%)	63 (98%)	1 (2%)	55	69
36	n	60/66 (91%)	59 (98%)	1 (2%)	53	69
42	o	139/218 (64%)	133 (96%)	6 (4%)	26	52
43	p	82/195 (42%)	79 (96%)	3 (4%)	30	56
44	1	233/520 (45%)	224 (96%)	9 (4%)	28	54
All	All	7063/15775 (45%)	6803 (96%)	260 (4%)	31	56

5 of 260 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	i	13	ILE
34	m	5	LEU
1	A	1944	HIS
1	A	1921	ASP
42	o	71	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 140 such sidechains are listed below:

Mol	Chain	Res	Type
29	b	22	GLN
33	d	34	GLN
35	l	65	HIS
3	C	245	HIS
3	C	208	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	82/117 (70%)	17 (20%)	4 (4%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	F	96/107 (89%)	46 (47%)	16 (16%)
6	4	13/46 (28%)	8 (61%)	3 (23%)
7	G	80/174 (45%)	63 (78%)	20 (25%)
8	H	133/188 (70%)	34 (25%)	10 (7%)
All	All	404/632 (63%)	168 (41%)	53 (13%)

5 of 168 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A

5 of 53 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	G	23	U
7	G	119	A
8	H	40	C
7	G	90	C
7	G	97	A

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	$\# Z > 2$
18	SEP	R	224	18	8,9,10	1.47	2 (25%)	7,12,14	1.71	1 (14%)
18	SEP	R	232	18	8,9,10	1.61	1 (12%)	7,12,14	1.00	1 (14%)

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
18	SEP	R	224	18	-	0/6/8/10	-
18	SEP	R	232	18	-	2/6/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	R	232	SEP	P-O1P	3.55	1.61	1.50
18	R	224	SEP	P-O2P	-2.48	1.45	1.54
18	R	224	SEP	P-O3P	-2.28	1.46	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	R	224	SEP	OG-CB-CA	-3.55	104.69	108.14
18	R	232	SEP	OG-CB-CA	2.37	110.46	108.14

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	R	232	SEP	N-CA-CB-OG
18	R	232	SEP	C-CA-CB-OG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	R	224	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 16 are monoatomic - leaving 3 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	$\# Z > 2$
45	IHP	A	3000	-	36,36,36	0.72	0	60,60,60	1.09	0
49	ATP	Q	1501	47	32,33,33	2.04	8 (25%)	48,52,52	1.87	16 (33%)
46	GTP	C	1500	47	33,34,34	1.08	2 (6%)	50,54,54	1.77	11 (22%)

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
45	IHP	A	3000	-	-	3/30/54/54	0/1/1/1
49	ATP	Q	1501	47	-	4/22/38/38	0/3/3/3
46	GTP	C	1500	47	-	2/22/38/38	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	Q	1501	ATP	PB-O3B	7.24	1.67	1.59
49	Q	1501	ATP	C6-N6	4.70	1.46	1.34
49	Q	1501	ATP	C4-N3	3.20	1.40	1.34
49	Q	1501	ATP	C2'-C3'	-2.78	1.45	1.53
46	C	1500	GTP	C5-N7	-2.32	1.34	1.39

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	C	1500	GTP	C5-C4-N3	-5.14	120.22	128.39
49	Q	1501	ATP	C5-C4-N3	-4.90	119.97	126.72
46	C	1500	GTP	C2-N3-C4	4.46	119.98	112.30
49	Q	1501	ATP	N3-C2-N1	-4.24	122.16	128.58
49	Q	1501	ATP	N3-C4-N9	3.74	133.53	127.17

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

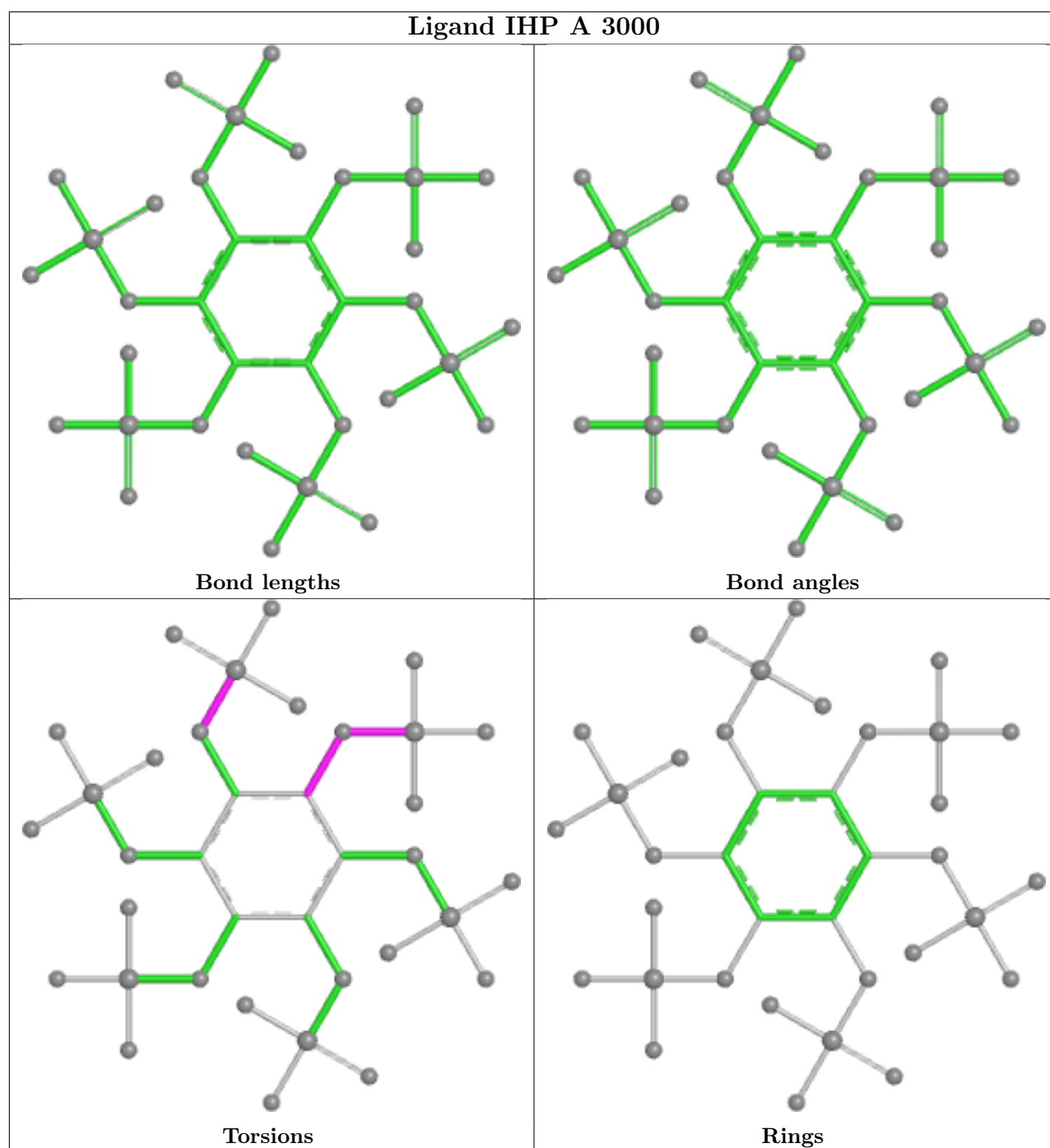
Mol	Chain	Res	Type	Atoms
49	Q	1501	ATP	C5'-O5'-PA-O1A
49	Q	1501	ATP	C5'-O5'-PA-O2A
49	Q	1501	ATP	C5'-O5'-PA-O3A
46	C	1500	GTP	O4'-C4'-C5'-O5'
46	C	1500	GTP	C5'-O5'-PA-O1A

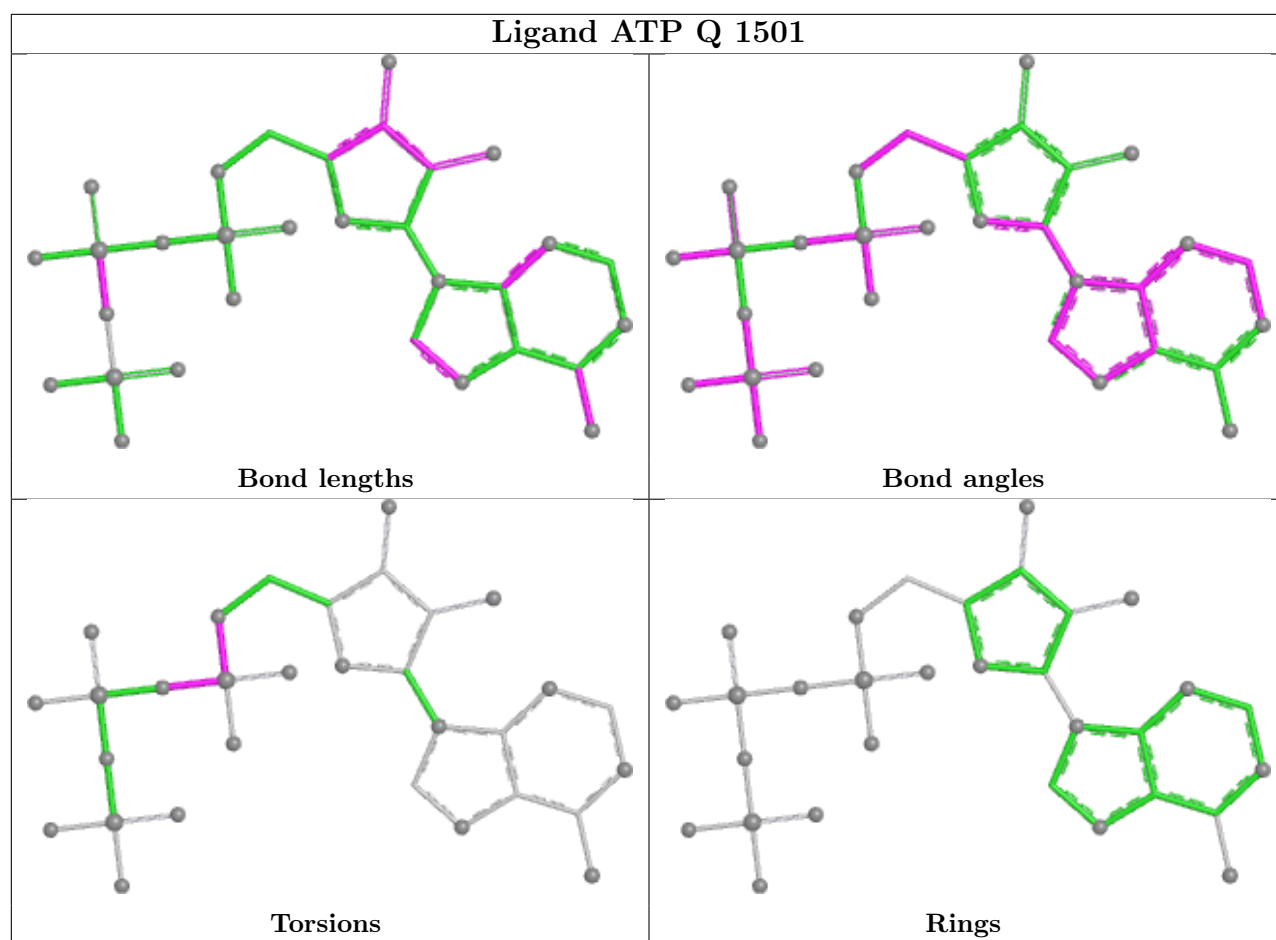
There are no ring outliers.

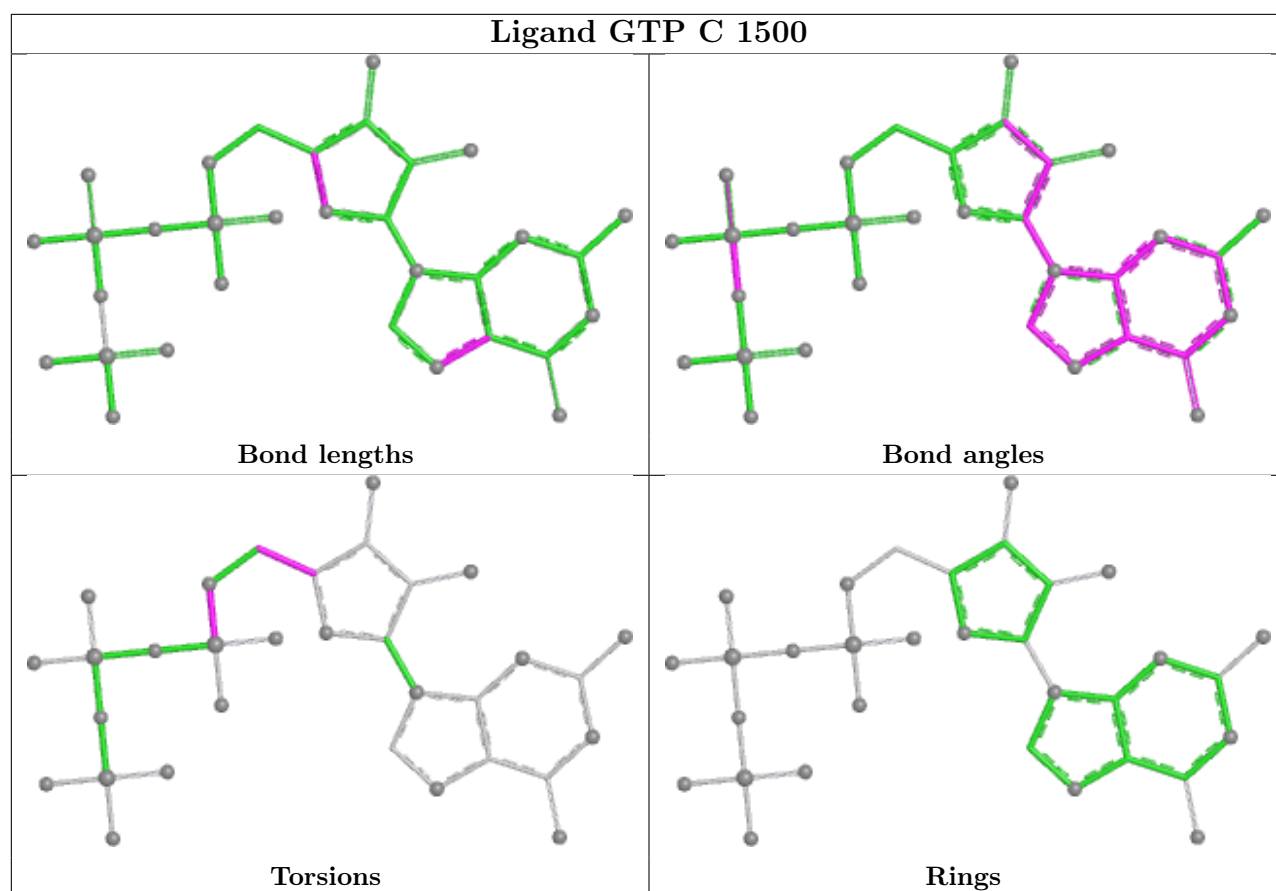
3 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	A	3000	IHP	9	0
49	Q	1501	ATP	5	0
46	C	1500	GTP	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.







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.

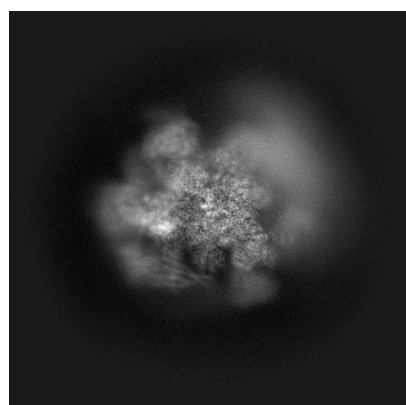
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32319. These allow visual inspection of the internal detail of the map and identification of artifacts.

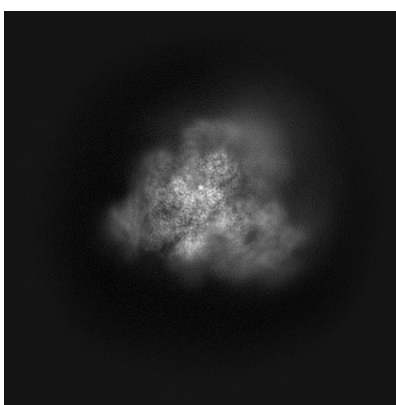
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

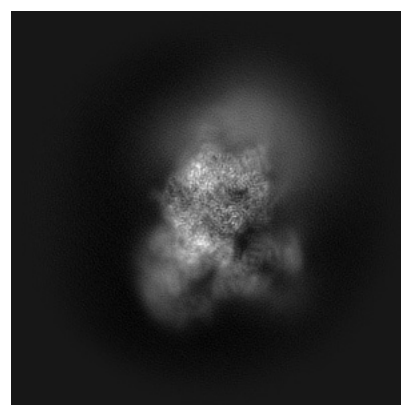
6.1.1 Primary map



X



Y

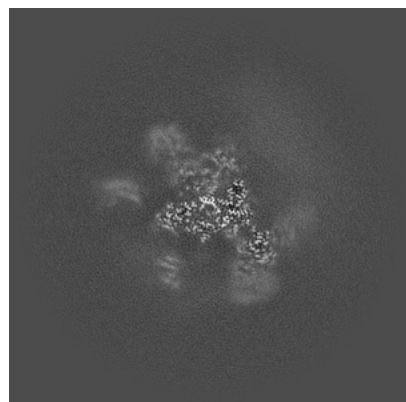


Z

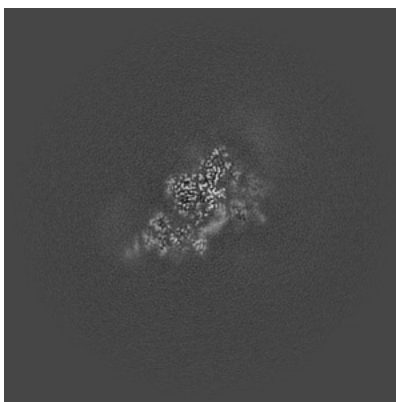
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

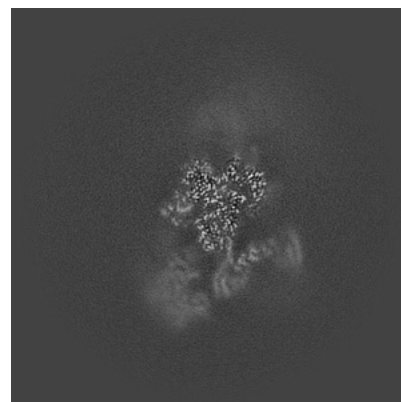
6.2.1 Primary map



X Index: 200



Y Index: 200

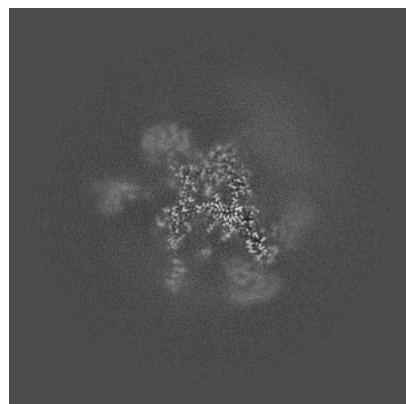


Z Index: 200

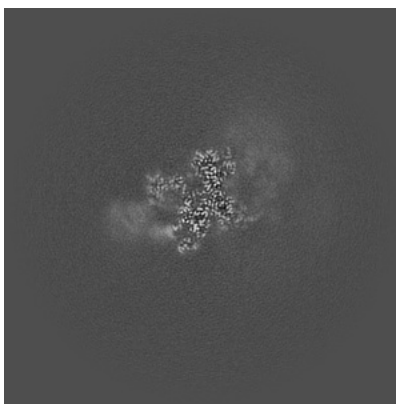
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

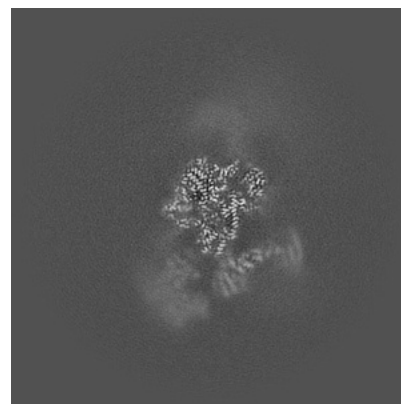
6.3.1 Primary map



X Index: 194



Y Index: 227

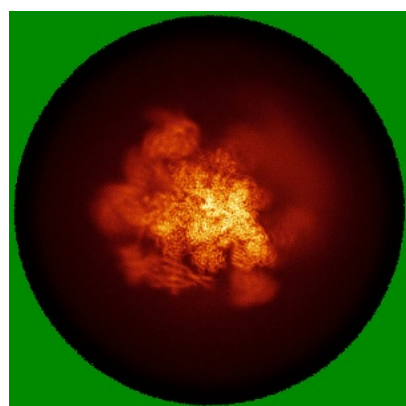


Z Index: 197

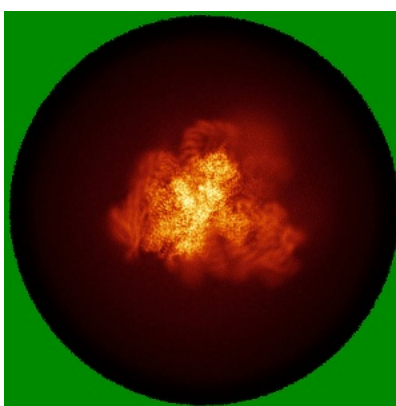
The images above show the largest variance slices of the map in three orthogonal directions.

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

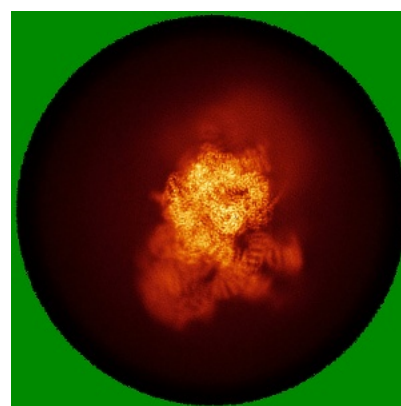
6.4.1 Primary map



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

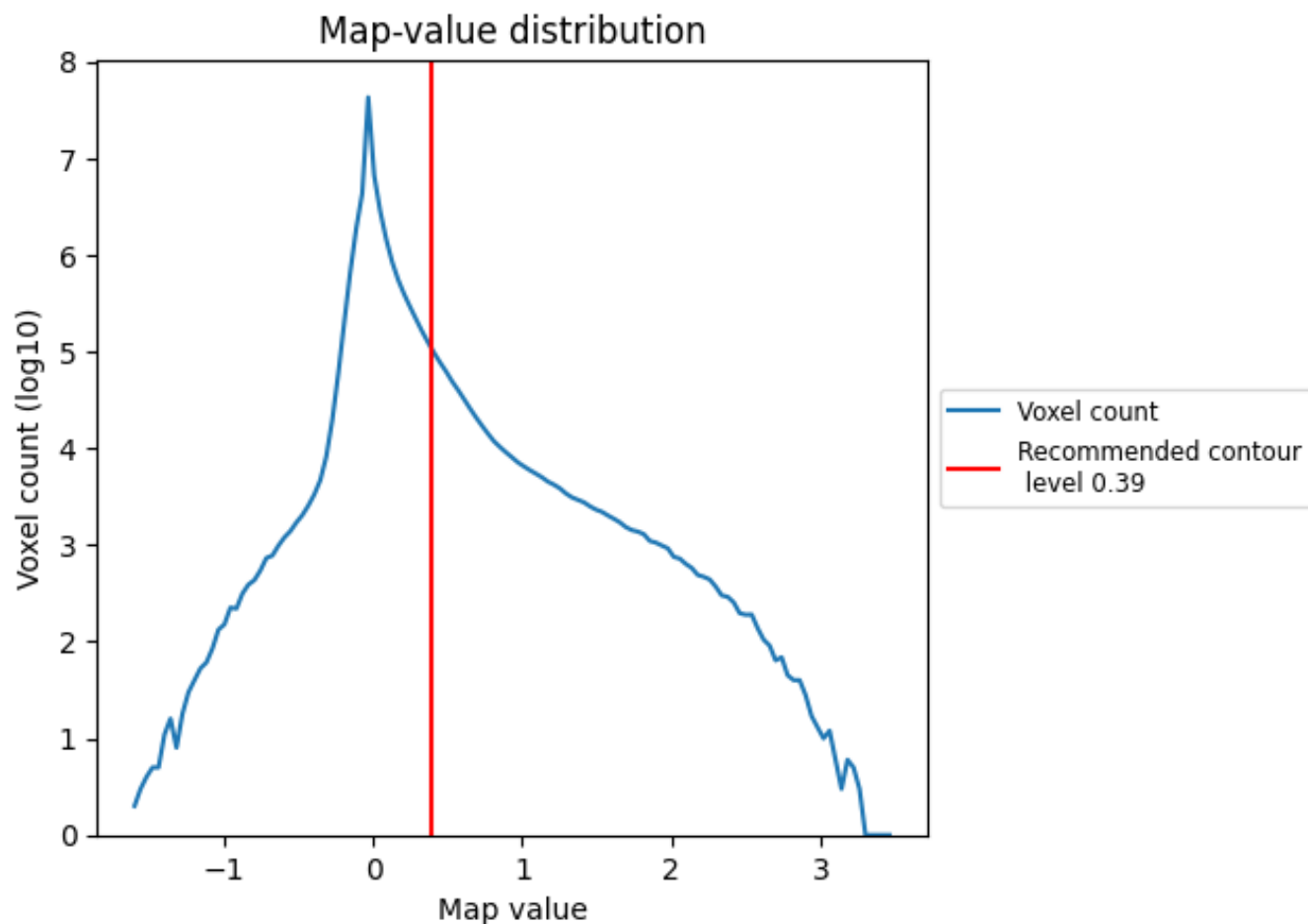
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

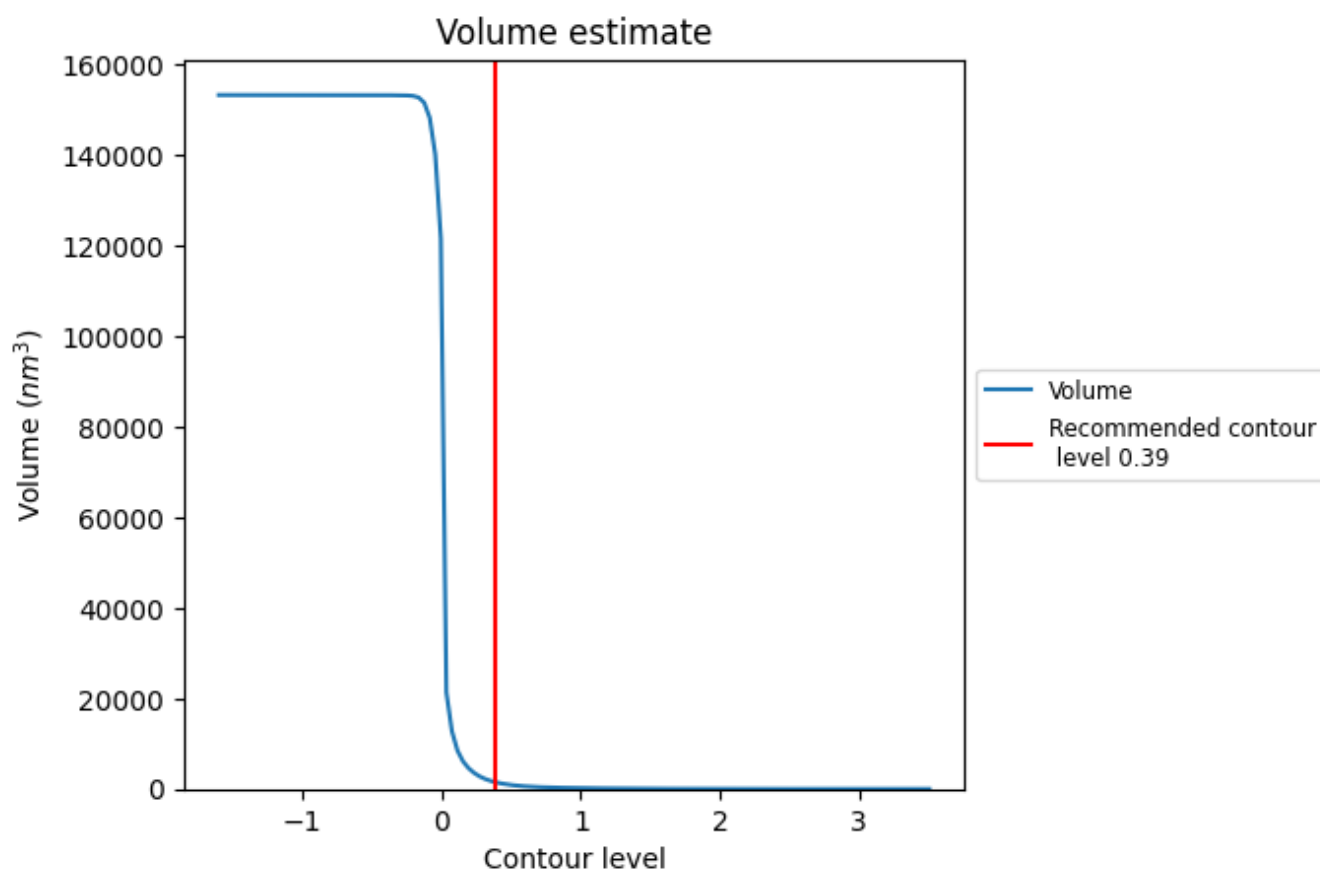
This section contains the results of statistical analysis of the map.

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.

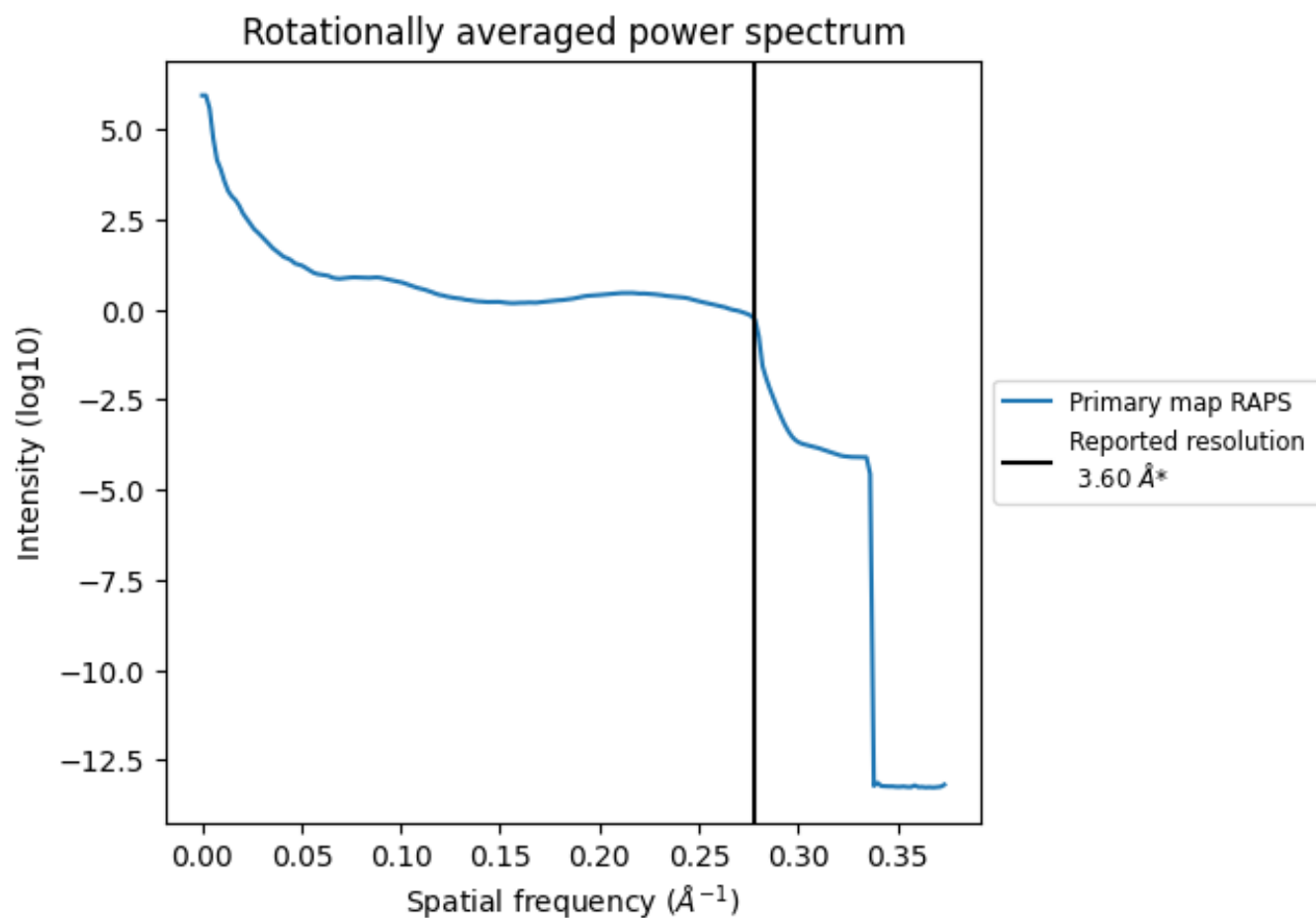
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1478 nm³; this corresponds to an approximate mass of 1335 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 0.278 Å⁻¹

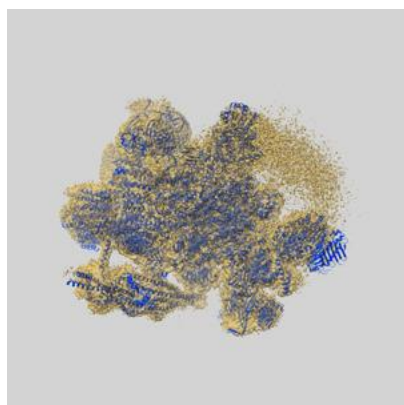
8 Fourier-Shell correlation ⓘ

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

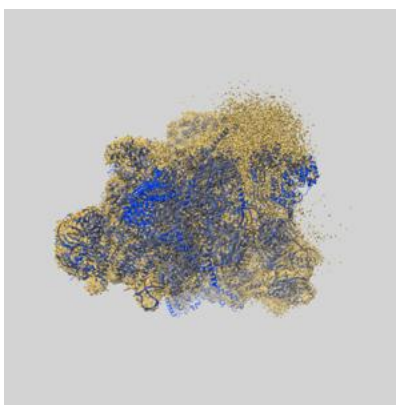
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32319 and PDB model 7W5A. Per-residue inclusion information can be found in section [3](#) on page [15](#).

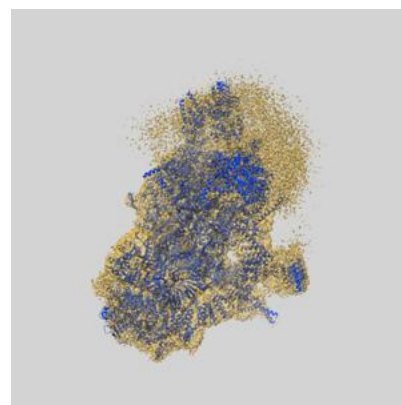
9.1 Map-model overlay [i](#)



X



Y



Z

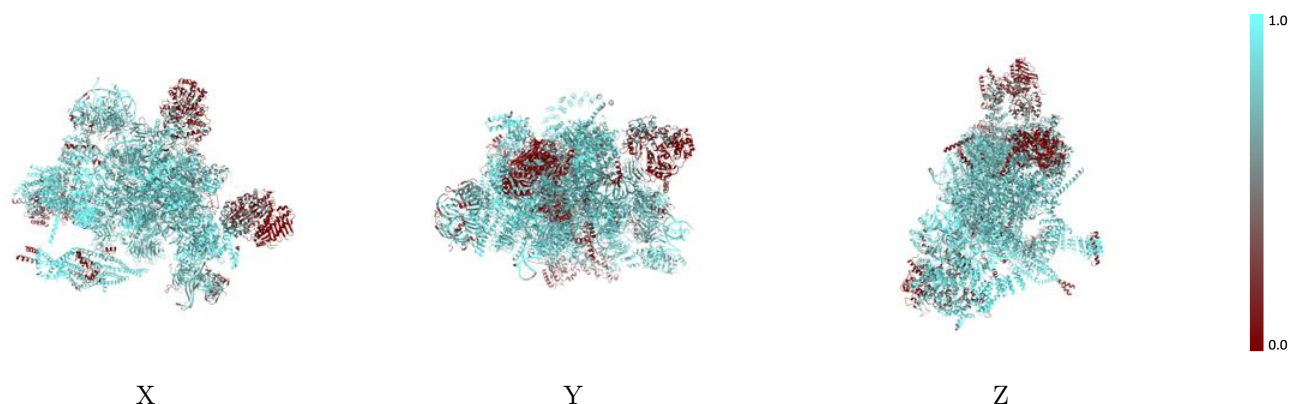
The images above show the 3D surface view of the map at the recommended contour level 0.39 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



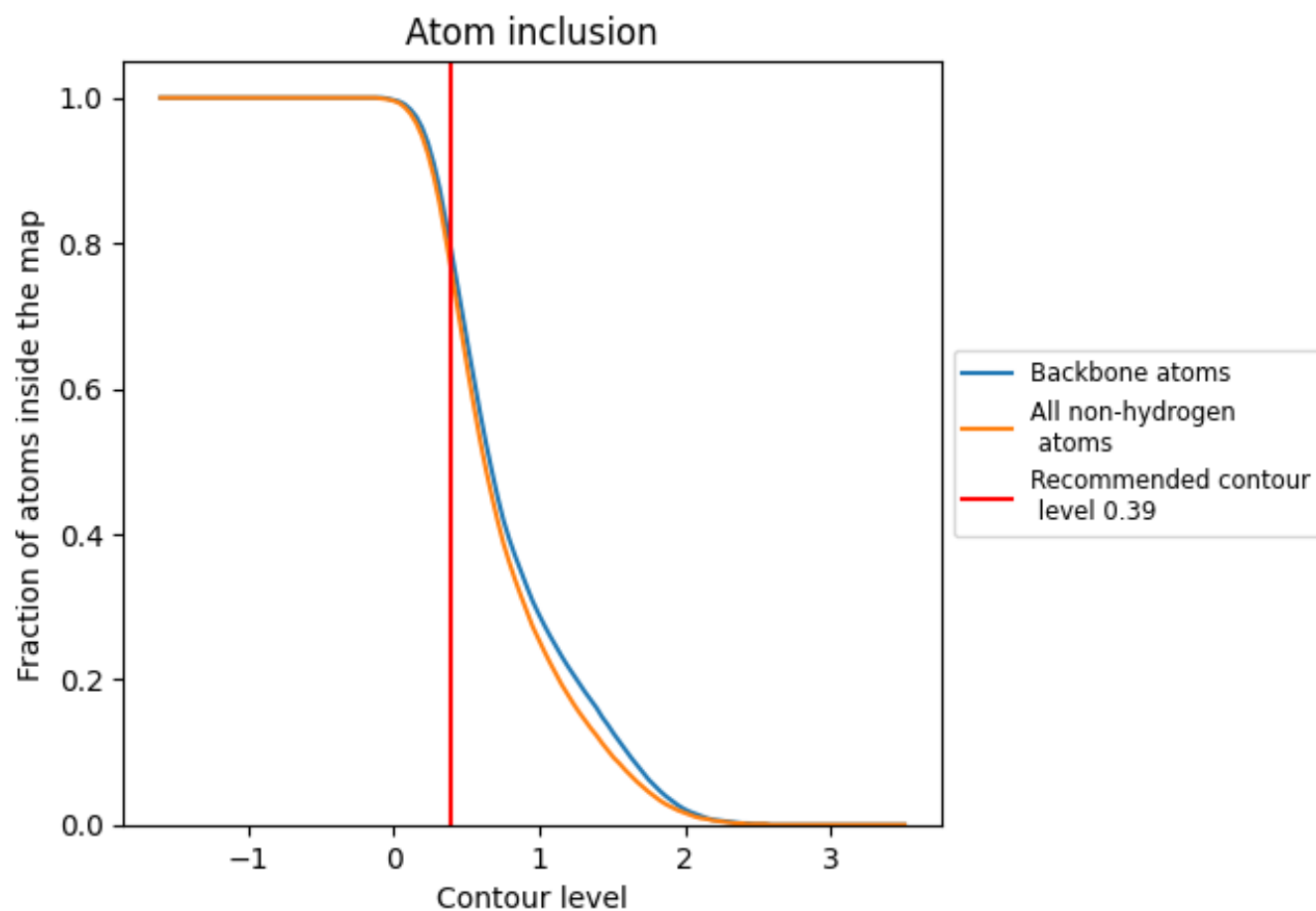
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.39).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 77% 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 (0.39) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7690	 0.2690
1	 0.2940	 0.2090
2	 0.7600	 0.2290
4	 0.9860	 0.4820
A	 0.9110	 0.4460
B	 0.9280	 0.3030
C	 0.8950	 0.3900
E	 0.9280	 0.4200
F	 0.9520	 0.3700
G	 0.7950	 0.2110
H	 0.9090	 0.1640
I	 0.9080	 0.2300
J	 0.8770	 0.3030
K	 0.9640	 0.2140
L	 0.8930	 0.3370
M	 0.8520	 0.3870
N	 0.9250	 0.4370
O	 0.8840	 0.3700
P	 0.8070	 0.3930
Q	 0.5250	 0.0520
R	 0.8550	 0.4010
S	 0.9260	 0.4110
T	 0.9550	 0.4950
U	 0.8850	 0.2950
V	 0.6440	 0.1890
W	 0.8190	 0.2890
X	 0.7270	 0.3180
Y	 0.2740	 0.0650
Z	 0.6840	 0.3220
a	 0.7370	 0.1700
b	 0.7180	 0.1150
c	 0.8310	 0.0590
d	 0.7320	 0.0270
e	 0.6020	 0.0550
f	 0.6110	 0.0080



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Chain	Atom inclusion	Q-score
g	 0.5610	 0.0960
h	 0.6810	 0.0850
i	 0.6090	 0.0580
j	 0.7920	 0.0500
k	 0.7260	 0.0950
l	 0.6630	 0.0860
m	 0.9060	 0.1440
n	 0.7140	 0.1320
o	 0.7790	 0.0570
p	 0.8830	 0.0900
q	 0.5660	 0.0450
r	 0.9270	 0.1650
s	 0.4870	 0.1010
t	 0.3980	 0.0490
u	 0.3010	 0.0250
v	 0.0110	 0.0060
w	 0.0130	 -0.0000
x	 0.0970	 0.0270
y	 0.8590	 0.1390
z	 0.1890	 0.1200