



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 11:27 AM UTC

PDB ID : 7VPX / pdb_00007vpx
EMDB ID : EMD-32074
Title : The cryo-EM structure of the human pre-A complex
Authors : Zhang, X.; Zhan, X.; Shi, Y.
Deposited on : 2021-10-18
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

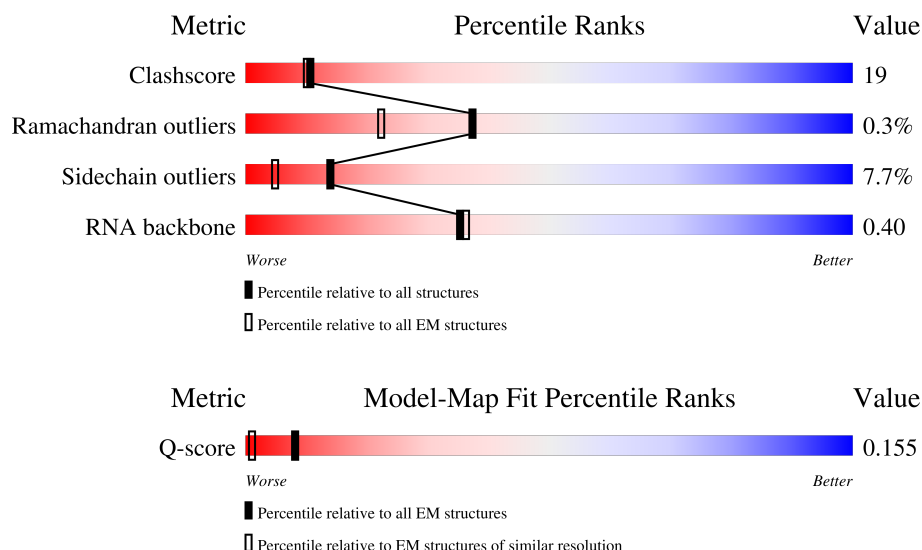
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	B	464	
2	D	639	
3	J	253	

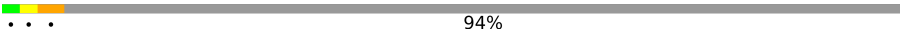
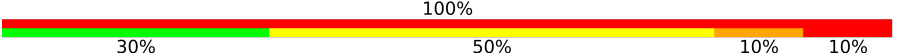
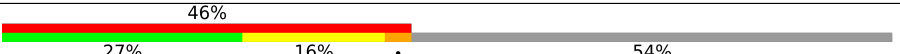
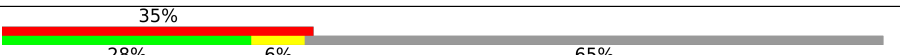
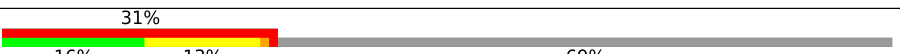
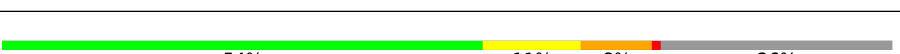
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Mol	Chain	Length	Quality of chain
4	H	188	
5	1	1304	
6	2	895	
7	3	1217	
8	4	424	
9	5	86	
10	A	793	
11	C	501	
12	E	1031	
13	F	255	
14	G	225	
15	a	118	
15	i	118	
16	b	86	
16	m	86	
17	c	92	
17	l	92	
18	d	76	
18	n	76	
19	e	126	
19	j	126	
20	f	240	
20	k	240	
21	g	119	
21	h	119	

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Mol	Chain	Length	Quality of chain
22	I	259	 94%
23	K	10	 30% 50% 10% 10%
24	L	164	 40% 37% 21%
25	O	437	 27% 16% 54%
26	M	282	 35% 28% 6% 65%
27	N	159	 31% 16% 13% 69%
28	6	110	 54% 11% 8% 26%

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
30	SJT	6	204	X	-	-	-

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 43240 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 Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	147	Total	C	N	O	S	0	0
			799	455	173	168	3		

- Molecule 2 is a protein called Splicing factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	122	Total	C	N	O	0	0
			604	360	122	122		

- Molecule 3 is a protein called DnaJ homolog subfamily C member 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	J	54	Total	C	N	O	0	0
			369	224	73	72		

- Molecule 4 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	130	Total	C	N	O	P	0	0
			2754	1233	478	915	128		

- Molecule 5 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1	815	Total	C	N	O	S	0	0
			6487	4163	1121	1164	39		

- Molecule 6 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	2	187	Total	C	N	O	S	0	0
			1325	835	245	243	2		

- Molecule 7 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	3	1180	Total	C	N	O	S	0	0
			9247	5872	1571	1759	45		

- Molecule 8 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	4	160	Total	C	N	O	0	0
			664	344	160	160		

- Molecule 9 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	5	66	Total	C	N	O	S	0	0
			539	342	93	99	5		

- Molecule 10 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	A	123	Total	C	N	O	0	0
			504	258	123	123		

- Molecule 11 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	425	Total	C	N	O	S	0	0
			2127	1191	470	462	4		

- Molecule 12 is a protein called Probable ATP-dependent RNA helicase DDX46.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	455	Total	C	N	O	S	0	0
			2153	1157	487	507	2		

- Molecule 13 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	F	162	Total	C	N	O	0	0
			666	342	162	162		

- Molecule 14 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	G	166	Total	C	N	O	0	0
			685	353	166	166		

- Molecule 15 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	a	90	Total	C	N	O	0	0
			372	192	90	90		
15	i	94	Total	C	N	O	S	0
			764	478	139	141	6	0

- Molecule 16 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	b	74	Total	C	N	O	0	0
			308	160	74	74		
16	m	74	Total	C	N	O	S	0
			576	373	95	103	5	0

- Molecule 17 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	c	79	Total	C	N	O	0	0
			319	161	79	79		
17	l	77	Total	C	N	O	S	0
			638	405	113	115	5	0

- Molecule 18 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	d	74	Total	C	N	O	0	0
			305	157	74	74		
18	n	73	Total	C	N	O	S	0
			568	358	102	102	6	0

- Molecule 19 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	e	83	Total	C	N	O	0	0
			341	175	83	83		
19	j	81	Total	C	N	O	S	0
			637	400	112	119	6	0

- Molecule 20 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	f	71	Total	C	N	O		0	0
			293	151	71	71			
20	k	86	Total	C	N	O	S	0	0
			692	435	126	124	7		

- Molecule 21 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	g	82	Total	C	N	O		0	0
			337	173	82	82			
21	h	81	Total	C	N	O	S	0	0
			641	408	112	118	3		

- Molecule 22 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	I	15	Total	C	N	O	P	0	0
			314	141	51	107	15		

- Molecule 23 is a RNA chain called 5SS.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	K	10	Total	C	N	O	P	0	0
			216	97	42	68	9		

- Molecule 24 is a RNA chain called U1 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L	164	Total	C	N	O	P	0	0
			3485	1555	607	1159	164		

- Molecule 25 is a protein called U1 small nuclear ribonucleoprotein 70 kDa.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	O	201	Total	C	N	O	S	0	0
			1643	1030	317	291	5		

- Molecule 26 is a protein called U1 small nuclear ribonucleoprotein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	M	98	Total	C	N	O	S	0	0
			787	506	134	143	4		

- Molecule 27 is a protein called U1 small nuclear ribonucleoprotein C.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	N	50	Total	C	N	O	S	0	0
			425	266	73	82	4		

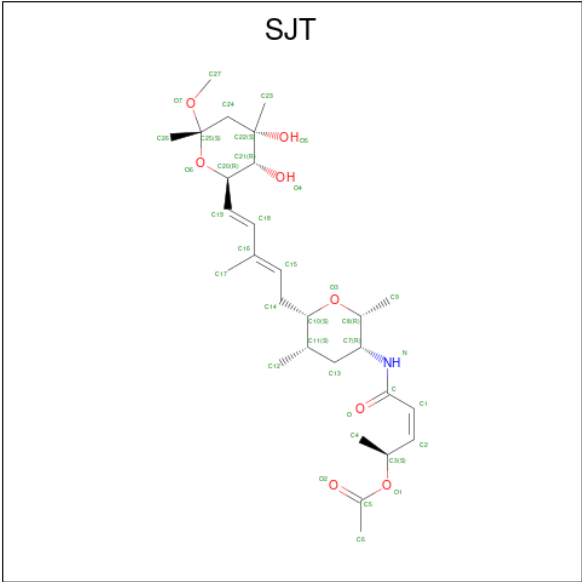
- Molecule 28 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	81	Total	C	N	O	S	0	0
			613	376	109	115	13		

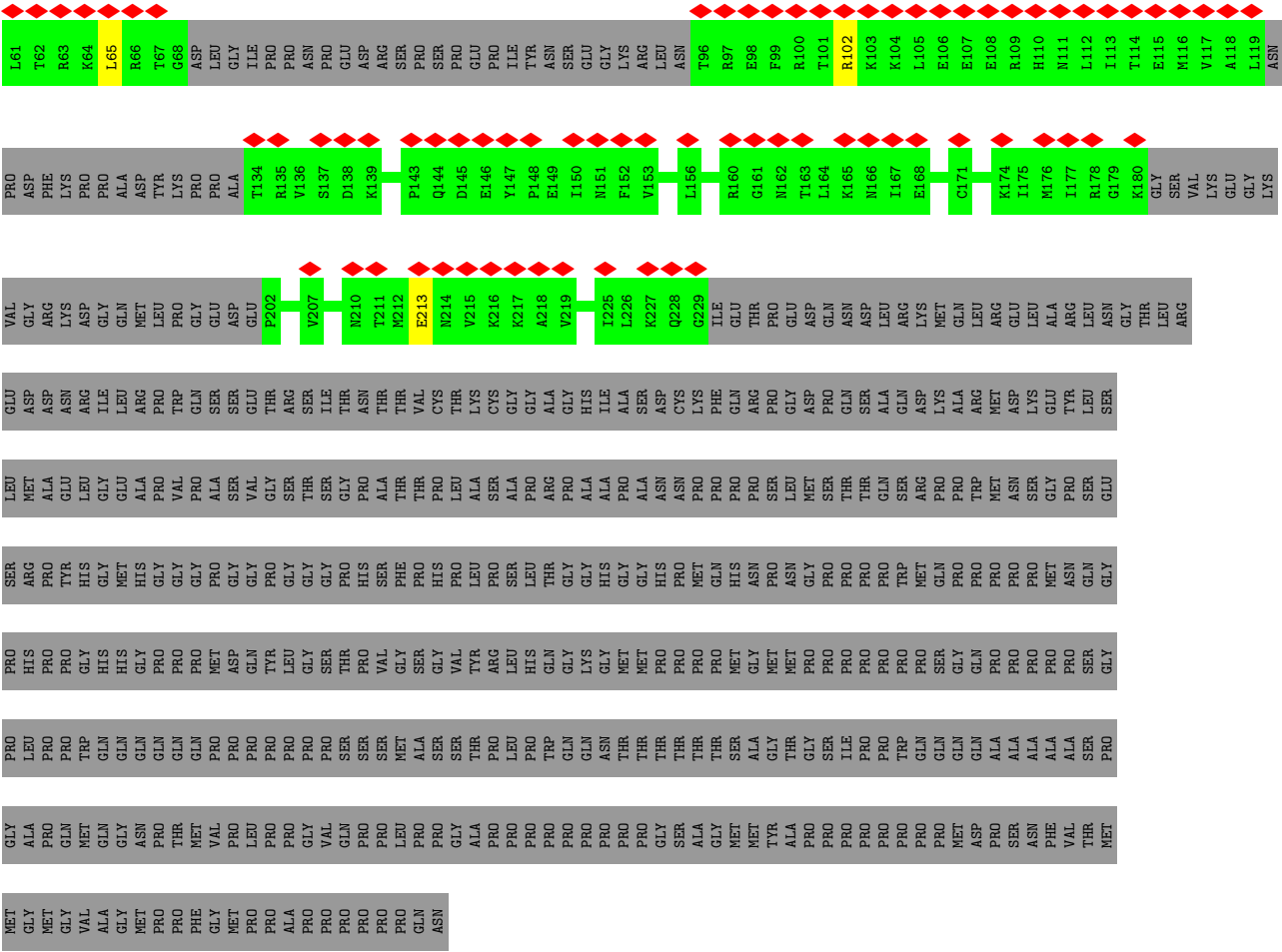
- Molecule 29 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
29	B	1	Total	Zn	0
			1	1	
29	C	1	Total	Zn	0
			1	1	
29	N	1	Total	Zn	0
			1	1	
29	6	3	Total	Zn	0
			3	3	

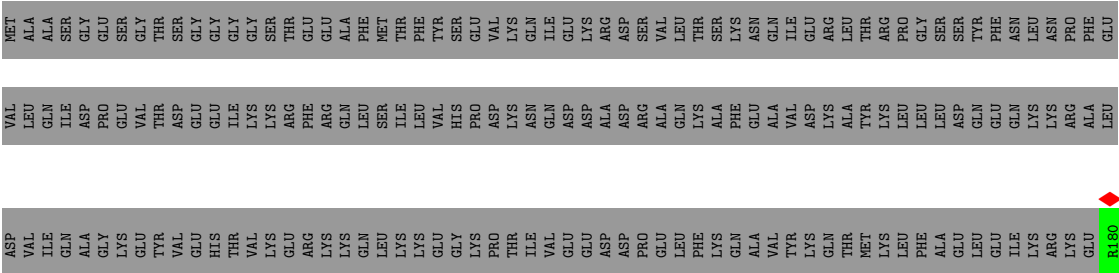
- Molecule 30 is spliceostatin A (form II) (CCD ID: SJT) (formula: C₂₈H₄₅NO₈) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
30	6	1	Total	C	N	O	0
			37	28	1	8	

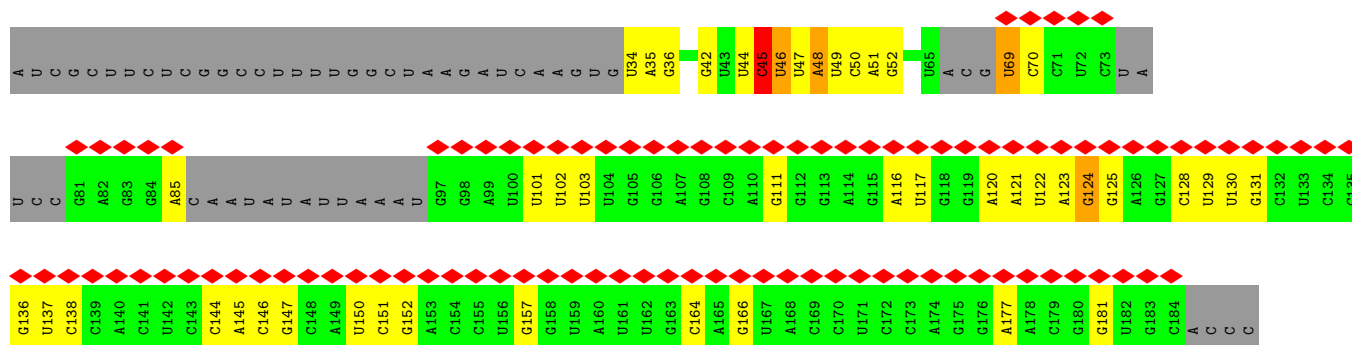


• Molecule 3: DnaJ homolog subfamily C member 8

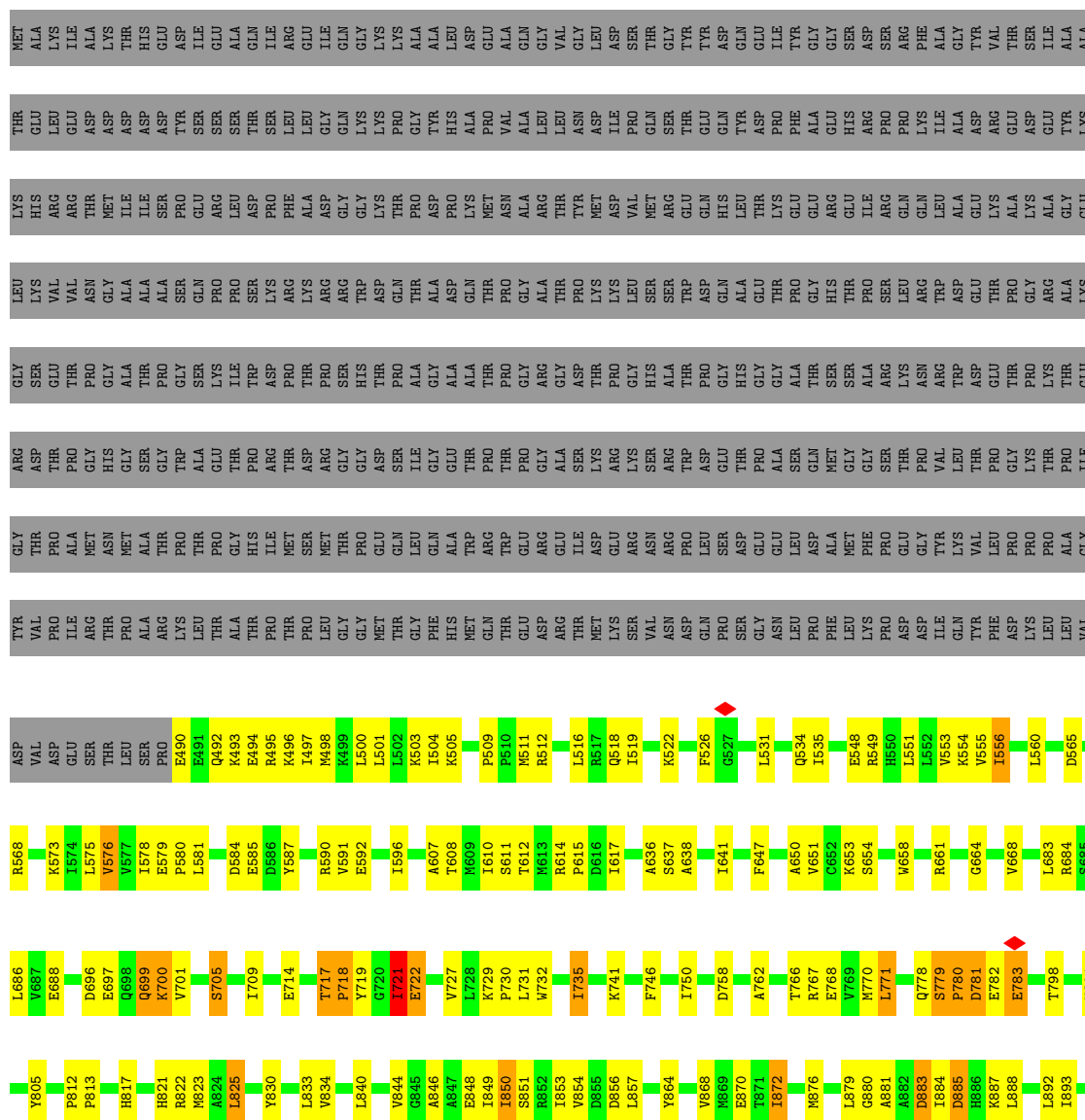


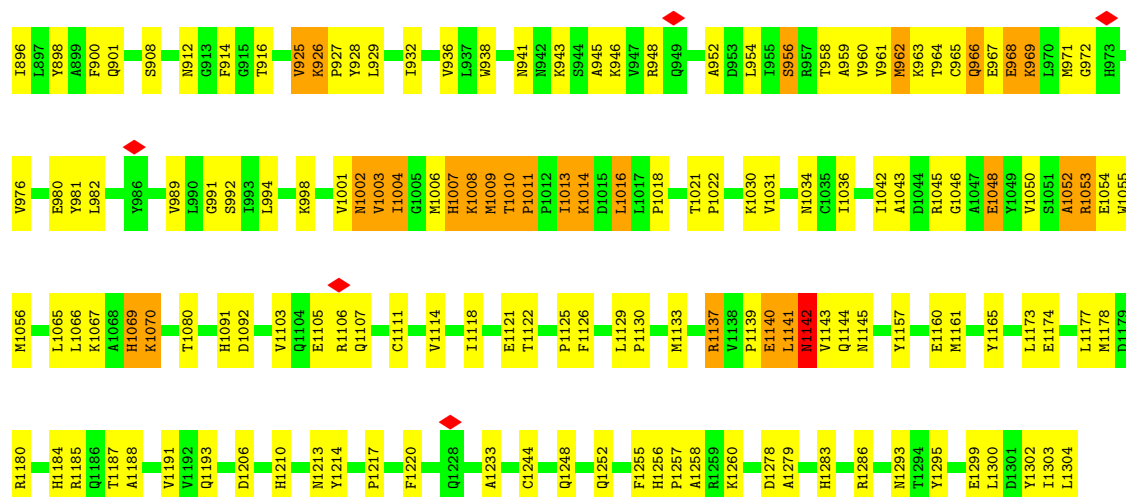
• Molecule 4: U2 snRNA



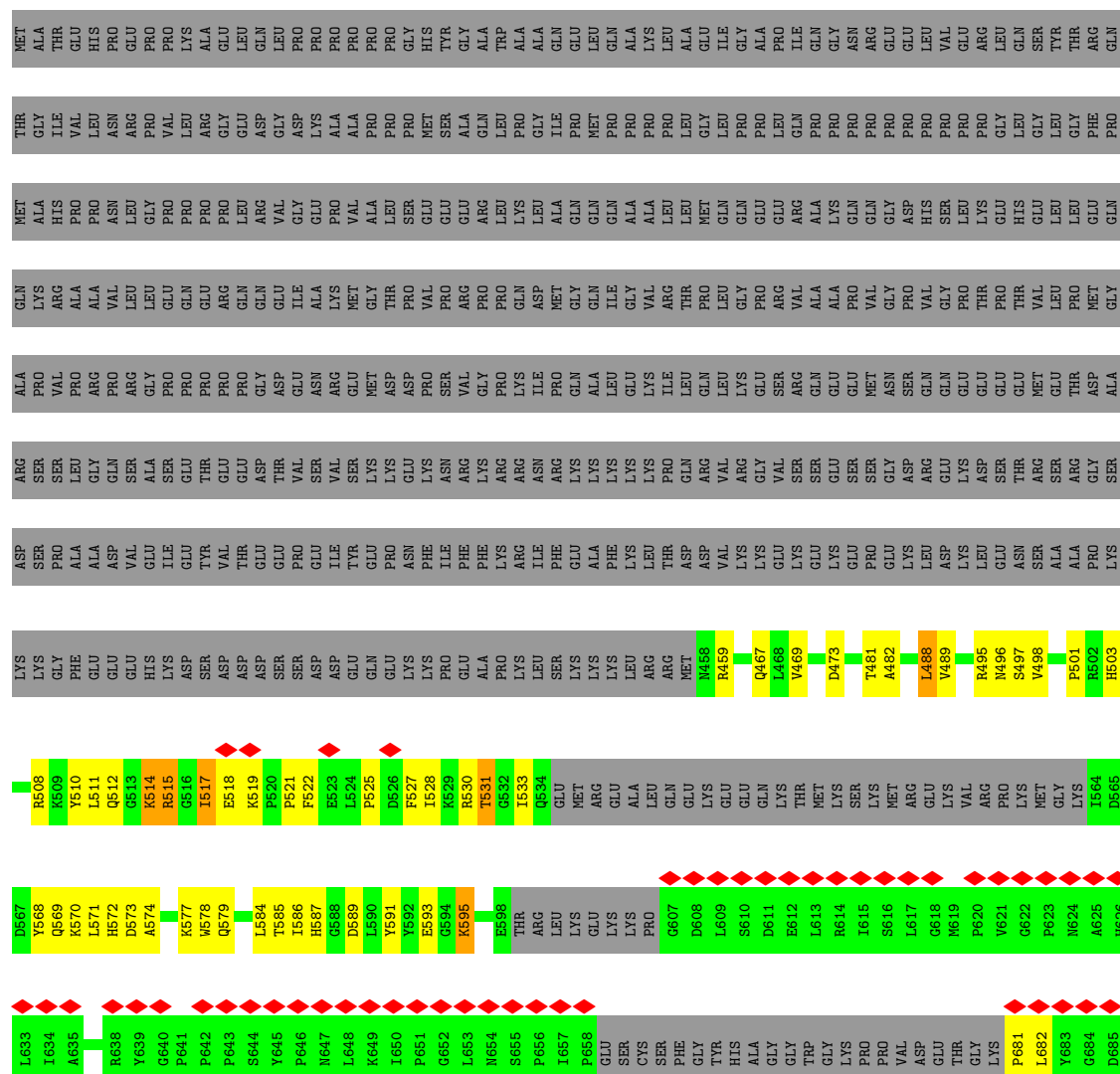


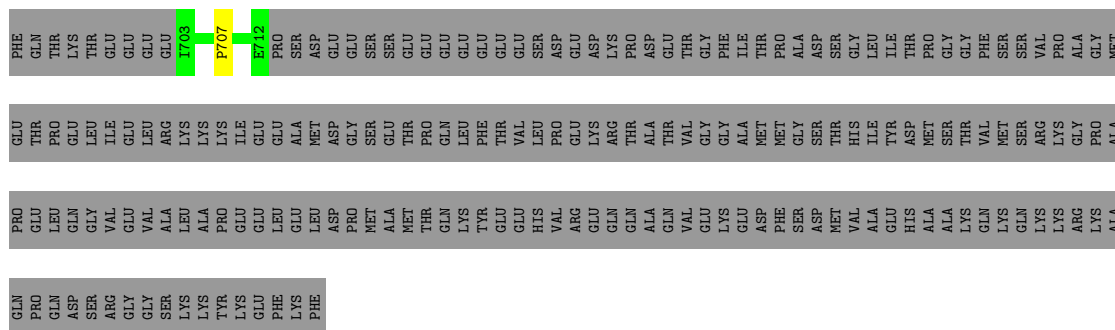
• Molecule 5: Splicing factor 3B subunit 1



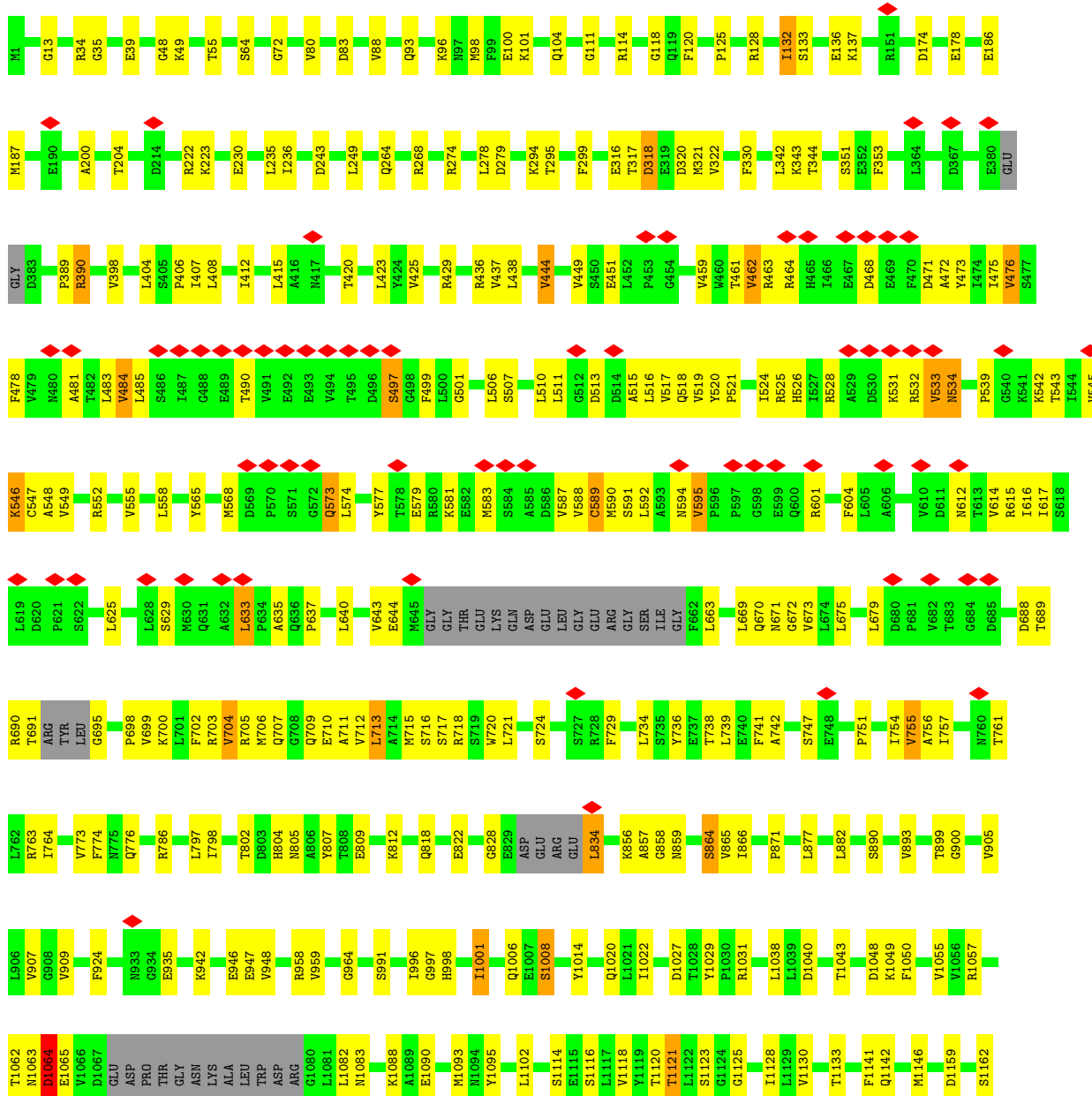


• Molecule 6: Splicing factor 3B subunit 2



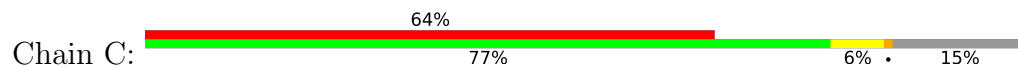


- Molecule 7: Splicing factor 3B subunit 3

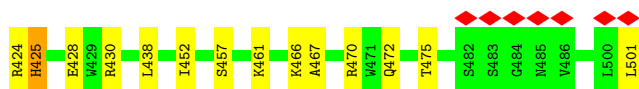


ILE	HIS	HIS	LEU	ALA	GLY	GLN	VAL	LEU	VAL	PHE	THR	THR	GLY	ARG	LYS	LYS	LEU	PRO	THR	ASP	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
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• Molecule 11: Splicing factor 3A subunit 3



GLY	ALA	HIS	ASP	LEU	SER	PHE	SER	SER	TRP	GLU	GLU	LEU	ALA	SER	LEU	GLY	LEU	ASP	ARG	LYS	LYS	LEU	ALA	GLY	LEU	GLY	THR	LEU	E279	E280	R281	A282	Q283	R284	L285	F286	S287	T288	K289	G290	K291	S292	L293	E294	S295	L296	D297	T298	S299	L300									
E181	Y182	K183	R184	Y185	L186	E187	M188	L189	L190	E191	Y192	E193	Q194	D195	Y196	T197	D198	R199	V200	K201	P202	L203	Q204	D205	Q206	N207	E208	L209	F210	G211	K212	I213	Q214	A215	E216	F217	E218	K219	K220	W221	E222	N223	G224	T225	F226	P227	G228	W229	PRO	LYS	GLU	THR	SER	ALA	LEU	THR	HIS	ALA	
S121	E122	E123	A124	Q125	N126	L127	V128	E129	F130	T131	D132	E133	E134	G135	Y136	G137	R138	Y139	L140	D141	L142	H143	D144	C145	Y146	L147	K148	Y149	I150	N151	L152	K153	A154	S155	E156	K157	L158	D159	Y160	I161	T162	Y163	L164	S165	I166	F167	D168	Q169	L170	F171	D172	I173	P174	K175	E176	K177	N178	A180	
M1	E2	T3	I4	L5	E6	Q7	Q8	R9	R10	Y11	H12	E13	E14	K15	E16	R17	L18	M19	D20	V21	M22	A23	K24	E25	M26	L27	T28	K29	K30	S31	T32	K33	L34	D35	Q36	I37	N38	S39	D40	H41	R42	T43	A44	M45	M46	Q47	D48	R49	Y50	M51	E52	V53	S54	G55	N56	L57	R58	D59	L60
Y61	D62	D63	K64	Q65	G66	L67	R68	K69	E70	E71	L72	N73	A74	I75	S76	G77	P78	N79	E80	F81	A82	E83	F84	N85	N86	R87	L88	K89	Q90	I91	L92	K93	F94	H95	R96	K97	H98	P99	N100	I101	I102	C103	V104	P105	M106	S107	V108	E109	F110	E111	E112	L113	L114	K115	A116	R117	N118	E119	M120



Chain E: 41% 41% 41% 56%



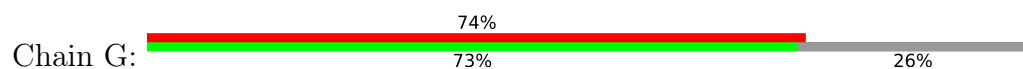
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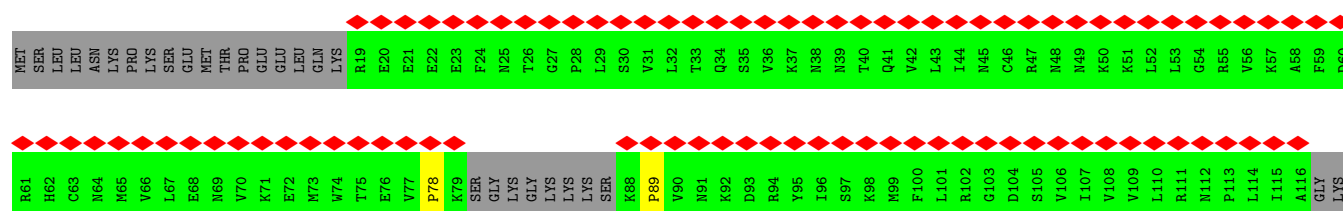
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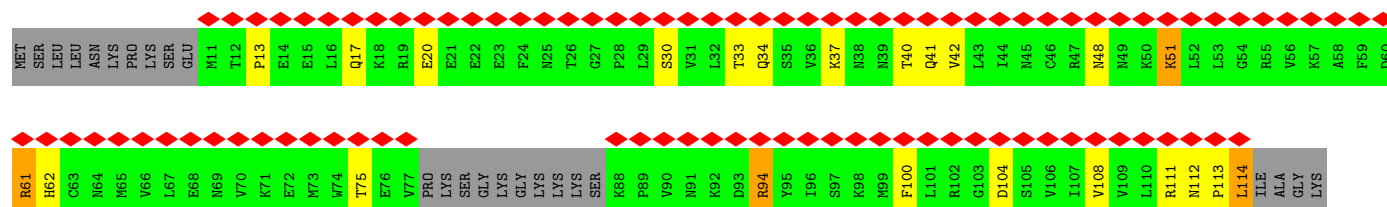
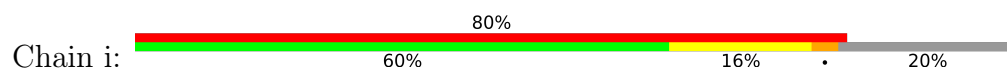
MET	ASP	I6	R7	P8	H9	H10	T11	I12	Y13	I14	M15	N16	M17	N18	D19	K20	I21	K22	K23	E24	E25	L26	K27	R28	S29	L30	Y31	A32	L33	F34	S35	Q36	F37	G38	H39	V40	V41	D42	I43	V44	A45	L46	K47	T48	H49	K50	H51	R52	O53	Q54	A55	F56	V57	I58	F59	K60	E61	L62	Q63
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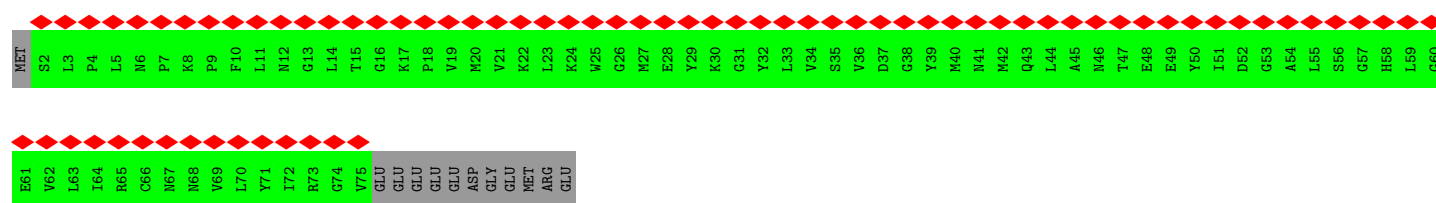
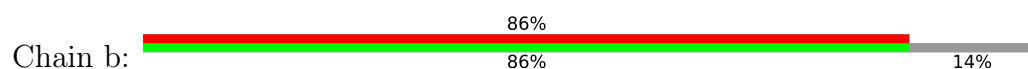
• Molecule 15: Small nuclear ribonucleoprotein Sm D2



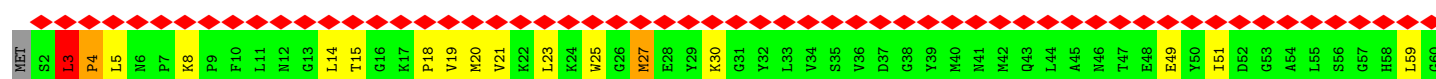
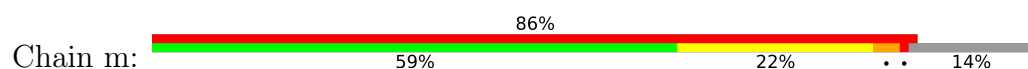
• Molecule 15: Small nuclear ribonucleoprotein Sm D2



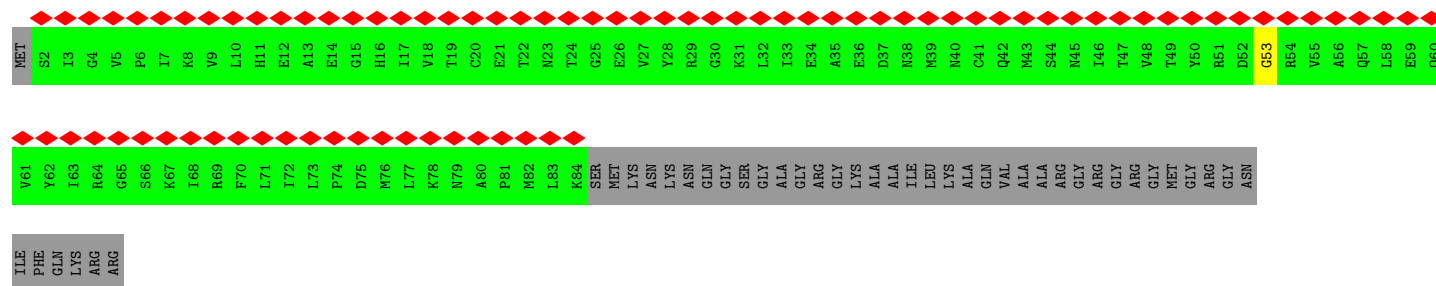
• Molecule 16: Small nuclear ribonucleoprotein F



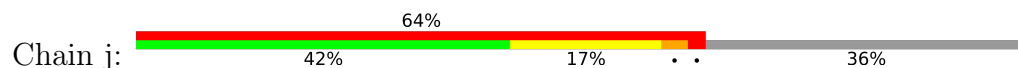
• Molecule 16: Small nuclear ribonucleoprotein F







• Molecule 19: Small nuclear ribonucleoprotein Sm D3



• Molecule 20: Small nuclear ribonucleoprotein-associated proteins B and B'

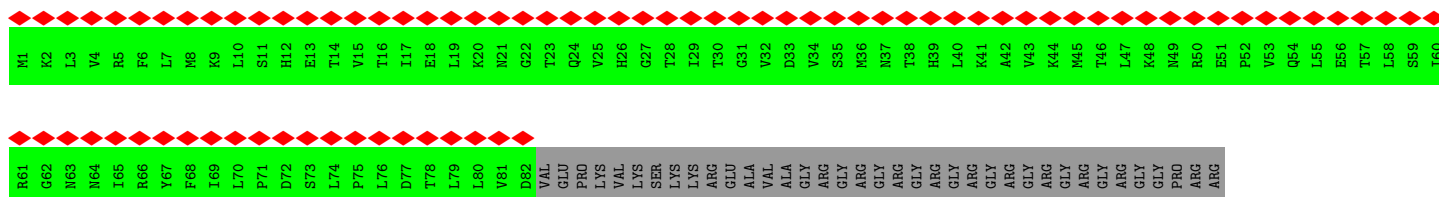


• Molecule 20: Small nuclear ribonucleoprotein-associated proteins B and B'

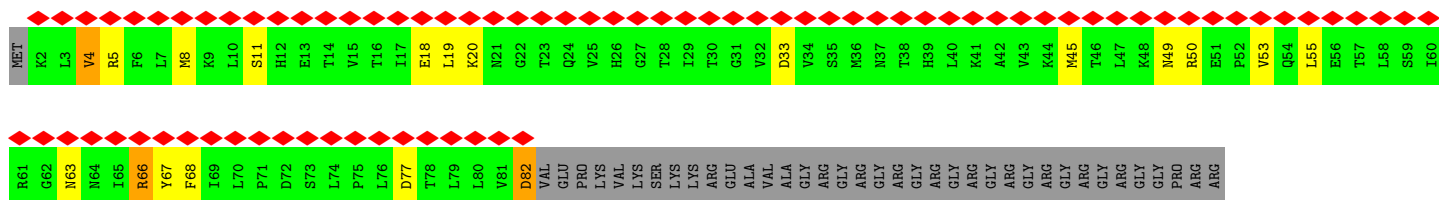


ARG	GLY	ALA	PRO	PRO	GLY	LEU	ALA	VAL	ARG	GLY	VAL	GLY	GLY	PRO	SER	GLN	GLN	VAL	MET	THR	PRO	GLN	GLY	ARG	THR	VAL	ALA	ALA	ALA	ALA	ILE	ARG	PRO	PRO	PRO	PRO	GLY	THR	GLY	GLY	MET	ARG								
PRO	GLN	ALA	PRO	ALA	GLY	LEU	ALA	VAL	ARG	GLY	VAL	GLY	GLY	PRO	SER	GLN	GLN	VAL	MET	THR	PRO	GLN	GLY	ARG	THR	VAL	ALA	ALA	ALA	ALA	ILE	ARG	ALA	GLY	ALA	THR	THR	PRO	GLN	TYR	PRO	PRO	GLY	ARG	GLY	PRO	PRO	PRO	MET	GLY

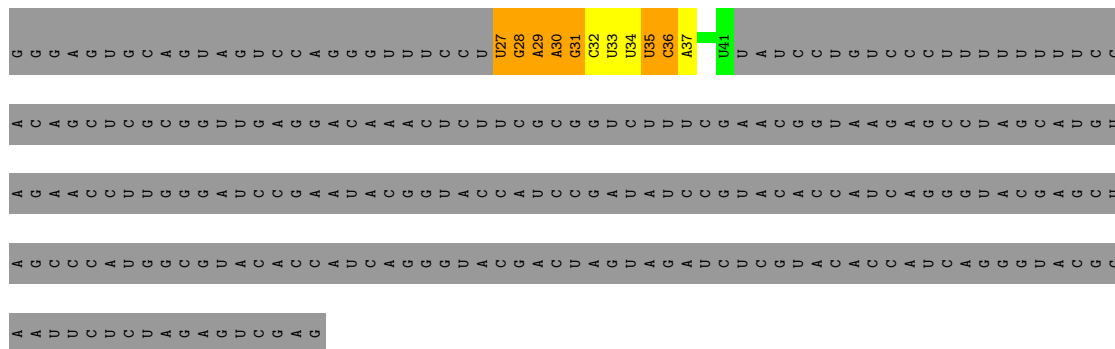
- Molecule 21: Small nuclear ribonucleoprotein Sm D1



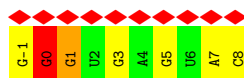
- Molecule 21: Small nuclear ribonucleoprotein Sm D1



- Molecule 22: pre-mRNA



- Molecule 23: 5SS



- Molecule 24: U1 snRNA

Chain L:

Chain 0:

- Molecule 26: U1 small nuclear ribonucleoprotein A

Chain M:

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	419522	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)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.684	Depositor
Minimum map value	-2.084	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.25	Depositor
Map size ($\text{\AA}$)	521.76, 521.76, 521.76	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.087, 1.087, 1.087	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	B	0.35	0/812	0.56	0/1060
2	D	0.64	0/600	1.25	0/830
3	J	1.02	0/374	1.38	0/507
4	H	0.19	0/3073	0.54	11/4779 (0.2%)
5	1	0.41	4/6609 (0.1%)	0.72	13/8946 (0.1%)
6	2	0.61	0/1364	0.81	0/1831
7	3	0.22	0/9435	0.54	2/12802 (0.0%)
8	4	0.15	0/670	0.36	0/850
9	5	0.46	1/555 (0.2%)	0.88	2/750 (0.3%)
10	A	0.17	0/507	0.37	0/640
11	C	0.51	2/2158 (0.1%)	0.71	5/2808 (0.2%)
12	E	0.53	0/2171	0.72	3/2779 (0.1%)
13	F	0.18	0/671	0.44	0/849
14	G	0.14	0/689	0.32	0/869
15	a	0.17	0/374	0.42	0/472
15	i	0.95	0/773	1.33	0/1039
16	b	0.17	0/311	0.42	0/395
16	m	0.83	1/588 (0.2%)	1.34	5/795 (0.6%)
17	c	0.16	0/319	0.41	0/399
17	l	0.82	0/646	1.42	6/867 (0.7%)
18	d	0.15	0/307	0.37	0/388
18	n	0.81	0/575	1.40	6/768 (0.8%)
19	e	0.18	0/343	0.37	0/433
19	j	0.72	0/645	1.22	4/870 (0.5%)
20	f	0.14	0/294	0.36	0/370
20	k	0.87	1/702 (0.1%)	1.33	5/936 (0.5%)
21	g	0.14	0/339	0.36	0/428
21	h	0.93	0/649	1.35	6/878 (0.7%)
22	I	0.50	2/349 (0.6%)	0.71	0/540
23	K	0.61	0/242	1.14	2/377 (0.5%)
24	L	0.53	1/3891 (0.0%)	0.83	15/6061 (0.2%)
25	O	1.47	13/1688 (0.8%)	1.33	12/2279 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	M	1.32	1/801 (0.1%)	1.22	2/1074 (0.2%)
27	N	0.70	0/437	1.33	2/587 (0.3%)
28	6	0.94	3/621 (0.5%)	1.51	16/833 (1.9%)
All	All	0.58	29/44582 (0.1%)	0.83	117/61089 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	1	0	1
15	i	0	1
25	O	0	1
All	All	0	3

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	C	419	PRO	N-CA	17.45	1.69	1.47
28	6	38	ARG	C-N	13.94	1.52	1.33
5	1	718	PRO	N-CA	11.30	1.66	1.47
28	6	30	CYS	C-O	-8.56	1.12	1.23
25	O	176	VAL	C-O	-7.94	1.15	1.24

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	3	1064	ASP	N-CA-CB	18.36	141.51	110.49
11	C	418	GLY	CA-C-N	16.07	139.93	119.84
11	C	418	GLY	C-N-CA	16.07	139.93	119.84
5	1	780	PRO	N-CA-C	14.94	133.41	113.40
28	6	38	ARG	CA-C-N	13.68	133.85	119.89

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	1	1002	ASN	Mainchain
25	O	56	PRO	Peptide
15	i	17	GLN	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	B	799	0	514	31	0
2	D	604	0	261	2	0
3	J	369	0	275	23	0
4	H	2754	0	1398	22	0
5	1	6487	0	6699	513	0
6	2	1325	0	1184	139	0
7	3	9247	0	9179	203	0
8	4	664	0	230	0	0
9	5	539	0	505	41	0
10	A	504	0	150	0	0
11	C	2127	0	1138	78	0
12	E	2153	0	1054	144	0
13	F	666	0	209	0	0
14	G	685	0	226	7	0
15	a	372	0	118	1	0
15	i	764	0	783	30	0
16	b	308	0	115	0	0
16	m	576	0	589	18	0
17	c	319	0	92	0	0
17	l	638	0	657	42	0
18	d	305	0	105	0	0
18	n	568	0	590	22	0
19	e	341	0	112	1	0
19	j	637	0	652	29	0
20	f	293	0	99	1	0
20	k	692	0	717	23	0
21	g	337	0	110	0	0
21	h	641	0	680	18	0
22	I	314	0	160	33	0
23	K	216	0	110	6	0
24	L	3485	0	1759	289	0
25	O	1643	0	1605	159	0
26	M	787	0	797	10	0
27	N	425	0	392	20	0
28	6	613	0	596	21	0
29	6	3	0	0	0	0
29	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	C	1	0	0	0	0
29	N	1	0	0	0	0
30	6	37	0	0	16	0
All	All	43240	0	33860	1429	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 1429 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)
6:2:574:ALA:HA	6:2:578:TRP:CE3	1.40	1.51
5:1:1114:VAL:HG21	30:6:204:SJT:C1	1.40	1.51
25:O:61:GLU:CB	25:O:65:GLU:HG2	1.41	1.50
24:L:92:C:H2'	24:L:93:G:C8	1.44	1.48
24:L:32:A:N3	25:O:135:VAL:HG22	1.22	1.47

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	B	141/464 (30%)	139 (99%)	2 (1%)	0	100	100
2	D	114/639 (18%)	113 (99%)	1 (1%)	0	100	100
3	J	52/253 (21%)	51 (98%)	1 (2%)	0	100	100
5	1	813/1304 (62%)	776 (95%)	33 (4%)	4 (0%)	24	60
6	2	177/895 (20%)	162 (92%)	14 (8%)	1 (1%)	21	56
7	3	1168/1217 (96%)	1119 (96%)	47 (4%)	2 (0%)	43	76
8	4	156/424 (37%)	153 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	5	64/86 (74%)	63 (98%)	1 (2%)	0	100	100
10	A	121/793 (15%)	121 (100%)	0	0	100	100
11	C	419/501 (84%)	397 (95%)	20 (5%)	2 (0%)	24	60
12	E	447/1031 (43%)	430 (96%)	16 (4%)	1 (0%)	43	76
13	F	160/255 (63%)	160 (100%)	0	0	100	100
14	G	160/225 (71%)	158 (99%)	2 (1%)	0	100	100
15	a	86/118 (73%)	84 (98%)	2 (2%)	0	100	100
15	i	90/118 (76%)	84 (93%)	6 (7%)	0	100	100
16	b	72/86 (84%)	71 (99%)	1 (1%)	0	100	100
16	m	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
17	c	77/92 (84%)	77 (100%)	0	0	100	100
17	l	75/92 (82%)	70 (93%)	5 (7%)	0	100	100
18	d	72/76 (95%)	72 (100%)	0	0	100	100
18	n	71/76 (93%)	69 (97%)	2 (3%)	0	100	100
19	e	81/126 (64%)	79 (98%)	2 (2%)	0	100	100
19	j	79/126 (63%)	75 (95%)	4 (5%)	0	100	100
20	f	67/240 (28%)	67 (100%)	0	0	100	100
20	k	84/240 (35%)	82 (98%)	2 (2%)	0	100	100
21	g	80/119 (67%)	79 (99%)	1 (1%)	0	100	100
21	h	79/119 (66%)	77 (98%)	2 (2%)	0	100	100
25	O	199/437 (46%)	182 (92%)	13 (6%)	4 (2%)	6	28
26	M	96/282 (34%)	94 (98%)	2 (2%)	0	100	100
27	N	48/159 (30%)	47 (98%)	1 (2%)	0	100	100
28	6	79/110 (72%)	71 (90%)	5 (6%)	3 (4%)	2	15
All	All	5499/10789 (51%)	5291 (96%)	191 (4%)	17 (0%)	37	70

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1	969	LYS
5	1	1052	ALA
5	1	1053	ARG
7	3	1064	ASP
25	O	59	ARG

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	B	47/382 (12%)	47 (100%)	0	100	100
3	J	24/226 (11%)	22 (92%)	2 (8%)	10	37
5	1	701/1104 (64%)	648 (92%)	53 (8%)	12	41
6	2	124/776 (16%)	116 (94%)	8 (6%)	15	47
7	3	1022/1051 (97%)	957 (94%)	65 (6%)	16	48
8	4	8/336 (2%)	8 (100%)	0	100	100
9	5	57/77 (74%)	56 (98%)	1 (2%)	51	77
10	A	4/709 (1%)	4 (100%)	0	100	100
11	C	83/446 (19%)	77 (93%)	6 (7%)	13	43
12	E	73/892 (8%)	64 (88%)	9 (12%)	4	21
13	F	6/218 (3%)	6 (100%)	0	100	100
14	G	7/195 (4%)	7 (100%)	0	100	100
15	a	4/110 (4%)	4 (100%)	0	100	100
15	i	89/110 (81%)	80 (90%)	9 (10%)	7	29
16	b	4/74 (5%)	4 (100%)	0	100	100
16	m	63/74 (85%)	56 (89%)	7 (11%)	6	25
17	c	1/84 (1%)	1 (100%)	0	100	100
17	l	72/84 (86%)	61 (85%)	11 (15%)	3	14
18	d	3/66 (4%)	3 (100%)	0	100	100
18	n	63/66 (96%)	54 (86%)	9 (14%)	3	16
19	e	3/101 (3%)	3 (100%)	0	100	100
19	j	71/101 (70%)	61 (86%)	10 (14%)	3	16
20	f	3/177 (2%)	3 (100%)	0	100	100
20	k	78/177 (44%)	69 (88%)	9 (12%)	5	24
21	g	3/101 (3%)	3 (100%)	0	100	100
21	h	76/101 (75%)	72 (95%)	4 (5%)	20	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	O	169/373 (45%)	153 (90%)	16 (10%)	8	31
26	M	85/240 (35%)	81 (95%)	4 (5%)	23	58
27	N	48/135 (36%)	41 (85%)	7 (15%)	3	15
28	6	69/95 (73%)	62 (90%)	7 (10%)	7	29
All	All	3060/8681 (35%)	2823 (92%)	237 (8%)	14	40

5 of 237 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	3	890	SER
19	j	24	THR
12	E	241	LYS
27	N	48	SER
28	6	61	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
7	3	164	ASN
25	O	133	HIS
7	3	594	ASN
25	O	80	GLN
20	k	22	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	I	15/259 (5%)	7 (46%)	4 (26%)
23	K	9/10 (90%)	2 (22%)	0
24	L	163/164 (99%)	51 (31%)	6 (3%)
4	H	126/188 (67%)	29 (23%)	2 (1%)
All	All	313/621 (50%)	89 (28%)	12 (3%)

5 of 89 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	H	35	A
4	H	36	G

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Mol	Chain	Res	Type
4	H	45	C
4	H	46	U
4	H	47	U

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	L	90	U
24	L	92	C
24	L	128	U
24	L	123	A
22	I	28	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 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	$\# Z > 2$
30	SJT	6	204	-	38,38,38	1.25	6 (15%)	51,55,55	1.77	11 (21%)

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
30	SJT	6	204	-	5/5/12/18	19/26/63/63	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	6	204	SJT	C17-C16	-3.21	1.44	1.50
30	6	204	SJT	C1-C	-3.09	1.41	1.48
30	6	204	SJT	O1-C3	-2.69	1.44	1.47
30	6	204	SJT	O1-C5	-2.50	1.29	1.35
30	6	204	SJT	C18-C16	-2.14	1.41	1.46

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	6	204	SJT	C2-C1-C	-5.90	108.80	122.67
30	6	204	SJT	C19-C18-C16	-5.13	115.28	126.32
30	6	204	SJT	C26-C25-C24	-4.04	109.69	113.36
30	6	204	SJT	O7-C25-C26	-3.46	111.01	113.61
30	6	204	SJT	C21-C20-C19	-3.28	108.56	112.75

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
30	6	204	SJT	C10
30	6	204	SJT	C22
30	6	204	SJT	C25
30	6	204	SJT	C8
30	6	204	SJT	C3

5 of 19 torsion outliers are listed below:

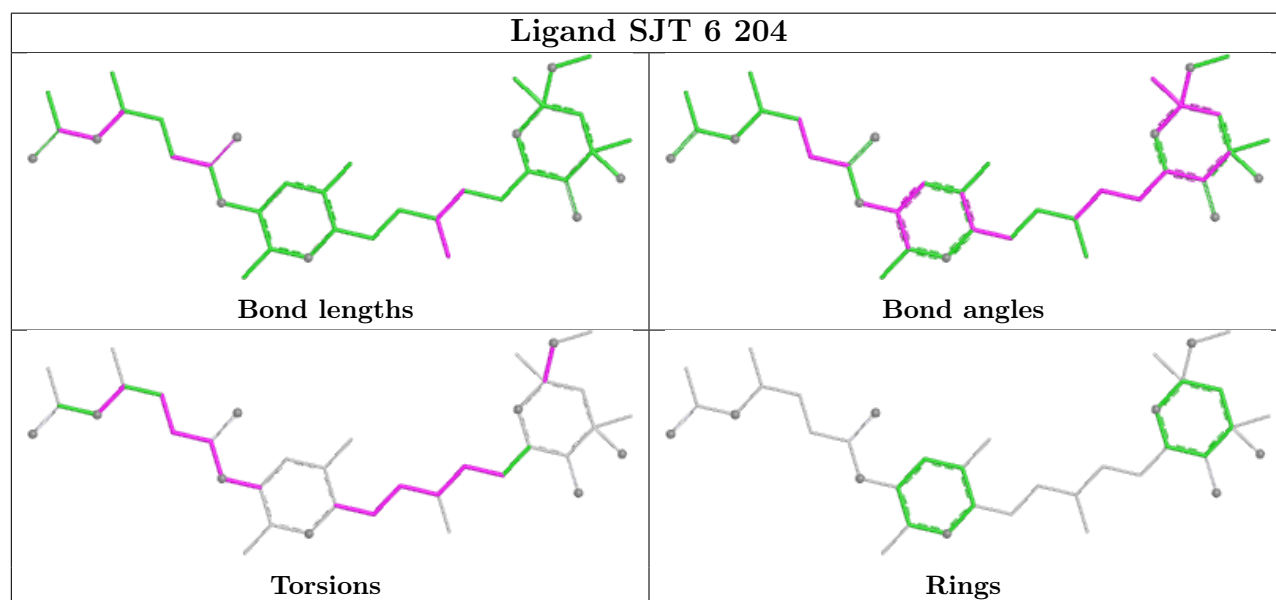
Mol	Chain	Res	Type	Atoms
30	6	204	SJT	C-C1-C2-C3
30	6	204	SJT	O-C-N-C7
30	6	204	SJT	C1-C-N-C7
30	6	204	SJT	C13-C7-N-C
30	6	204	SJT	O3-C10-C14-C15

There are no ring outliers.

1 monomer is involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	6	204	SJT	16	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.

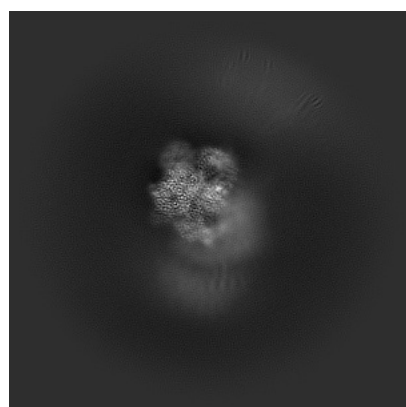
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32074. These allow visual inspection of the internal detail of the map and identification of artifacts.

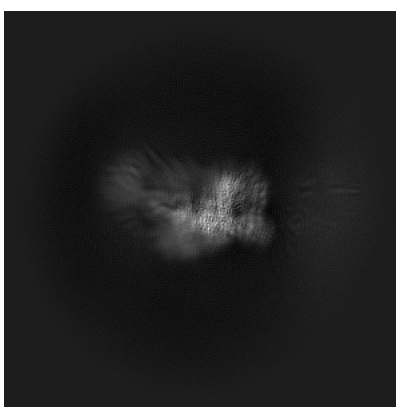
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

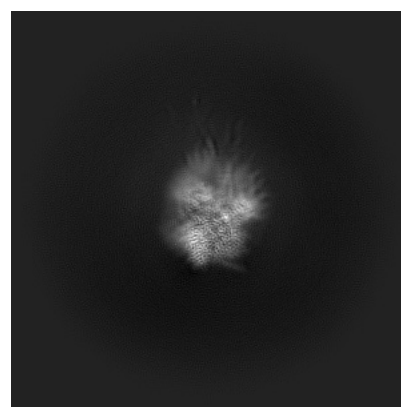
6.1.1 Primary map



X



Y

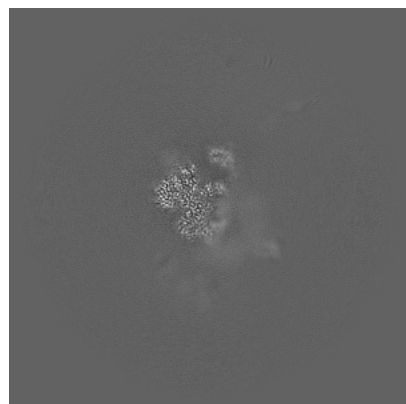


Z

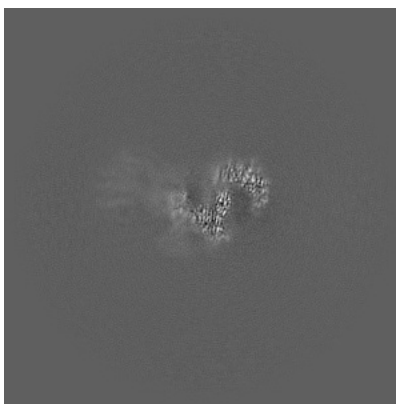
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 240



Y Index: 240



Z Index: 240

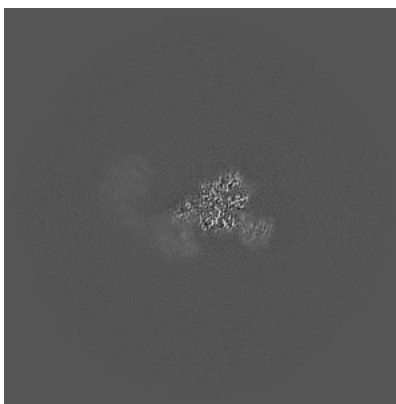
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

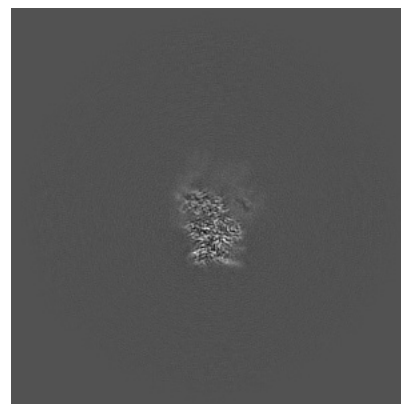
6.3.1 Primary map



X Index: 226



Y Index: 211

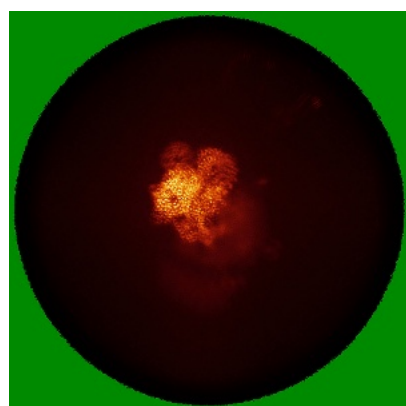


Z Index: 260

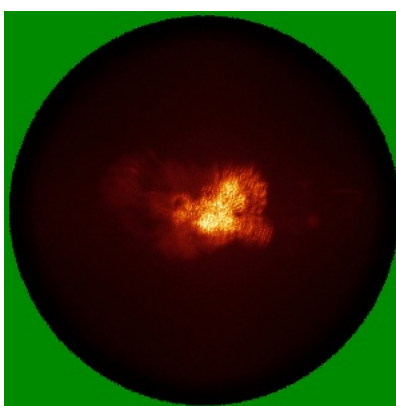
The images above show the largest variance slices of the map in three orthogonal directions.

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

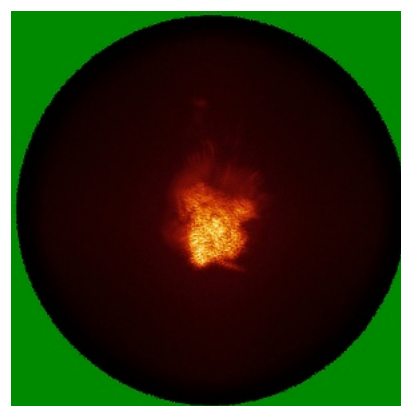
6.4.1 Primary map



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

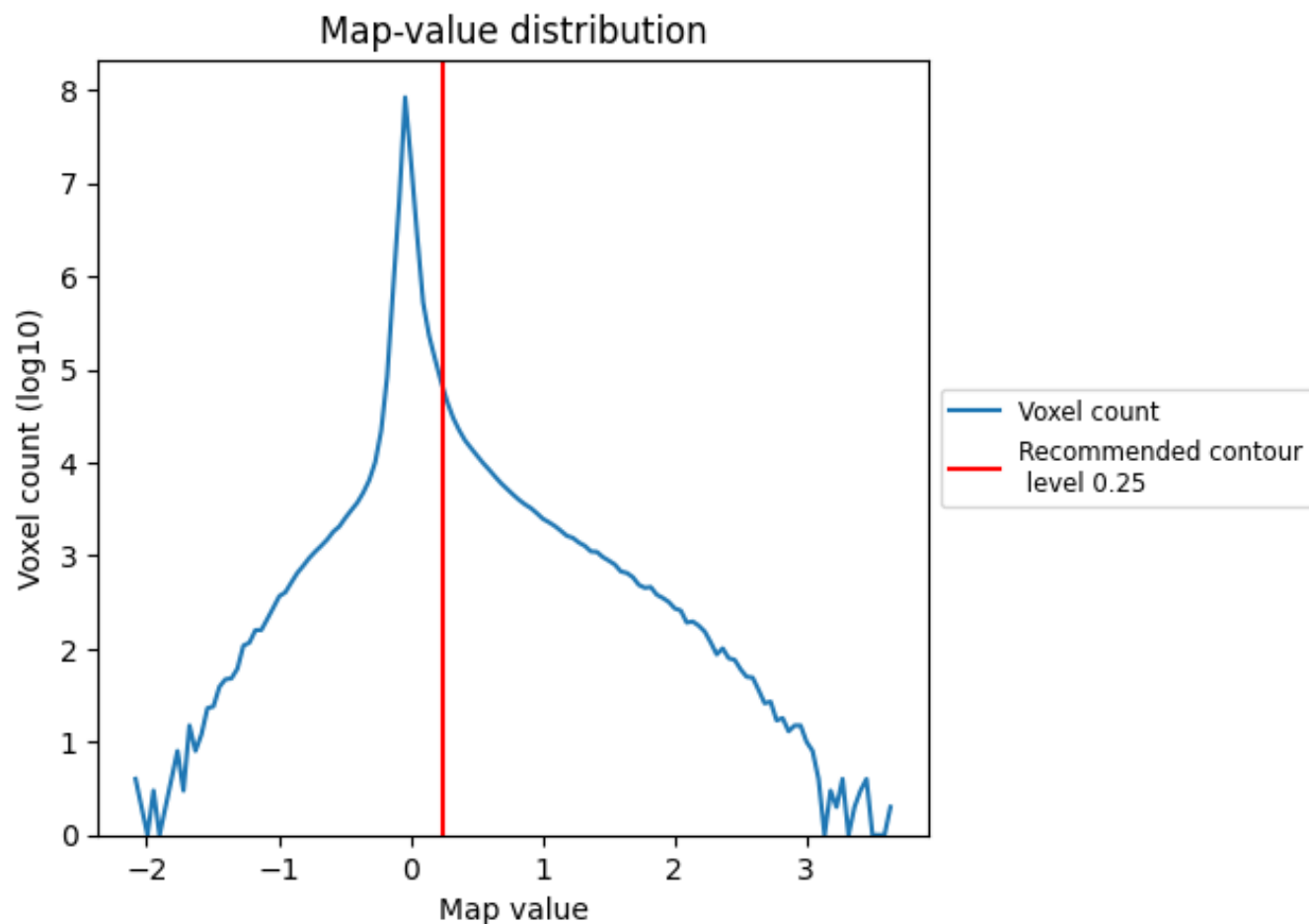
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

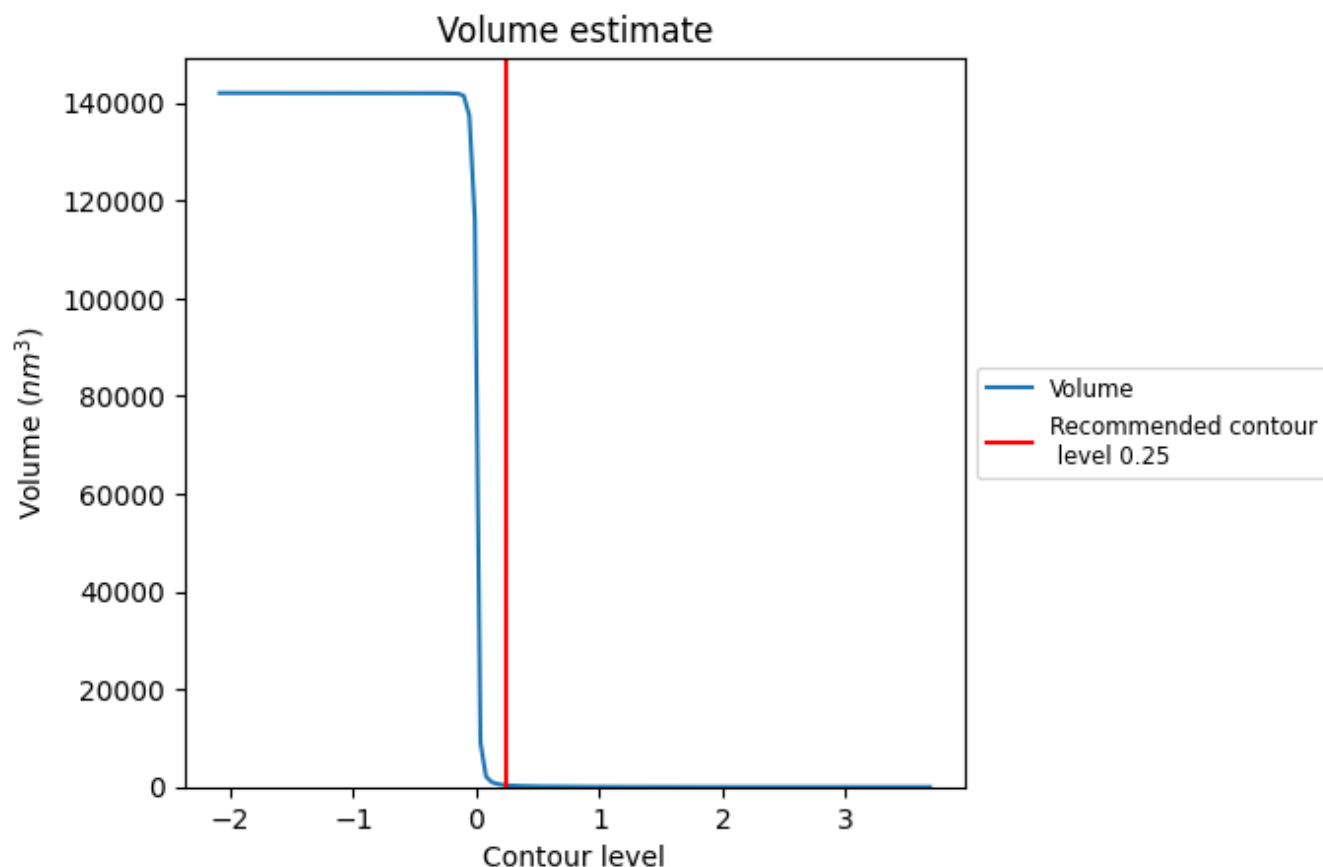
This section contains the results of statistical analysis of the map.

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.

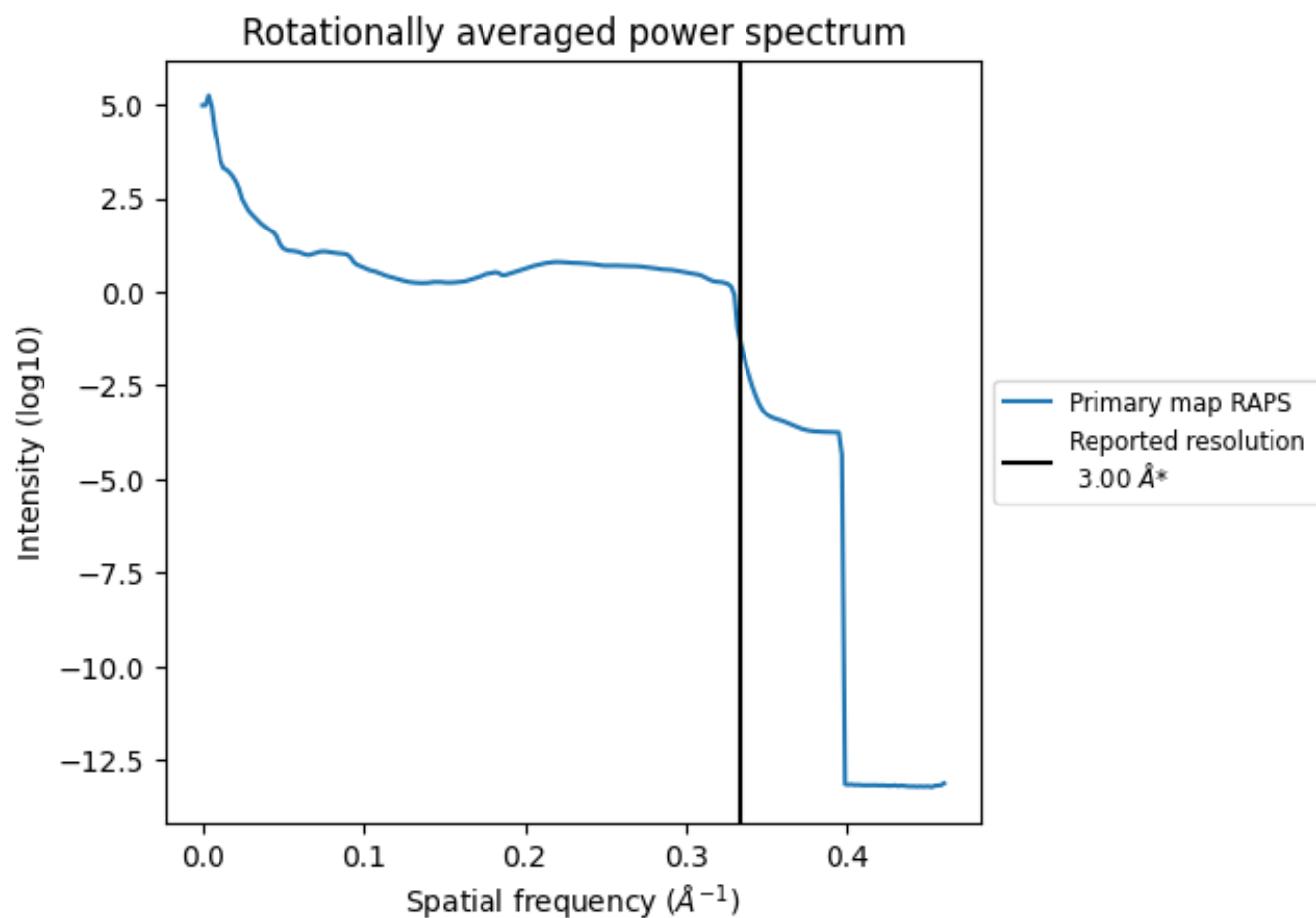
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 341 nm³; this corresponds to an approximate mass of 308 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 0.333 Å⁻¹

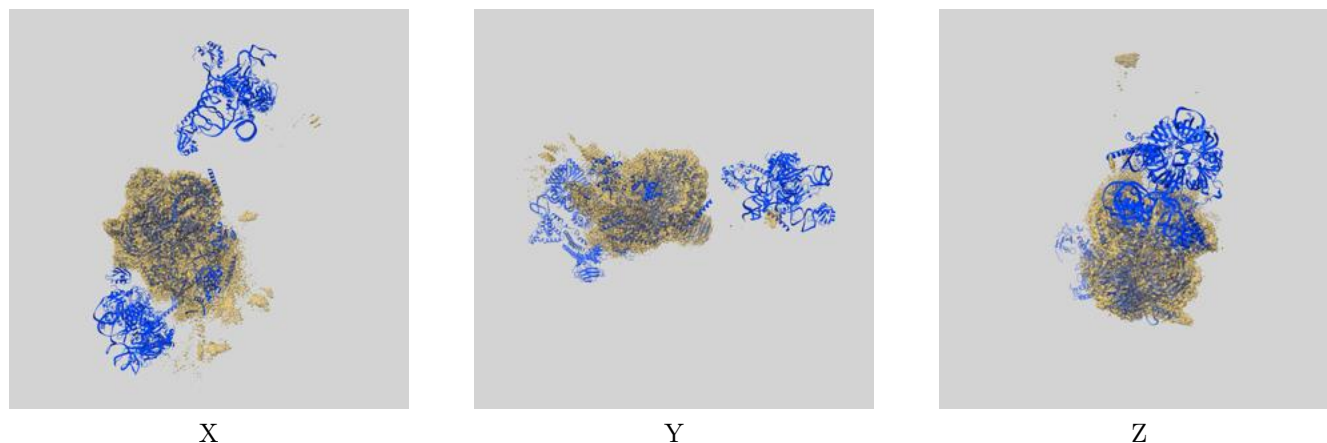
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

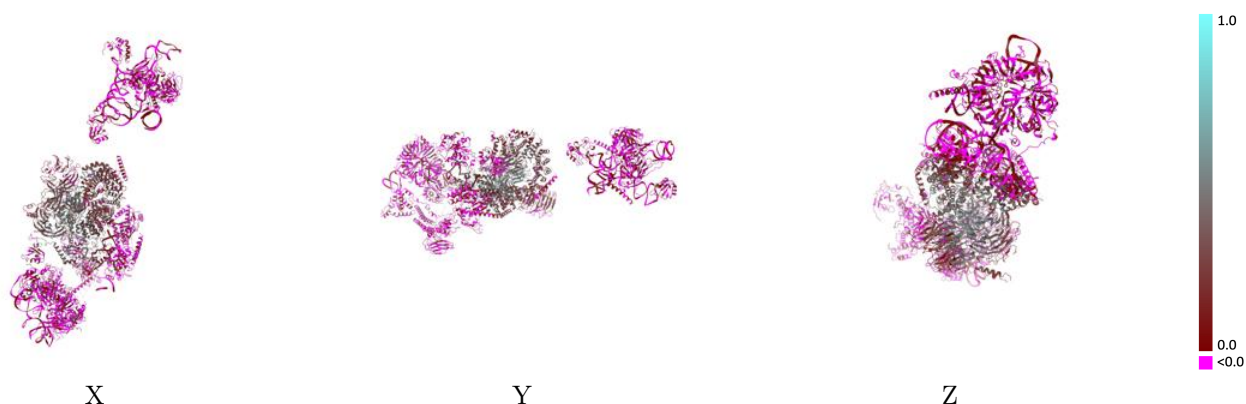
This section contains information regarding the fit between EMDB map EMD-32074 and PDB model 7VPX. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



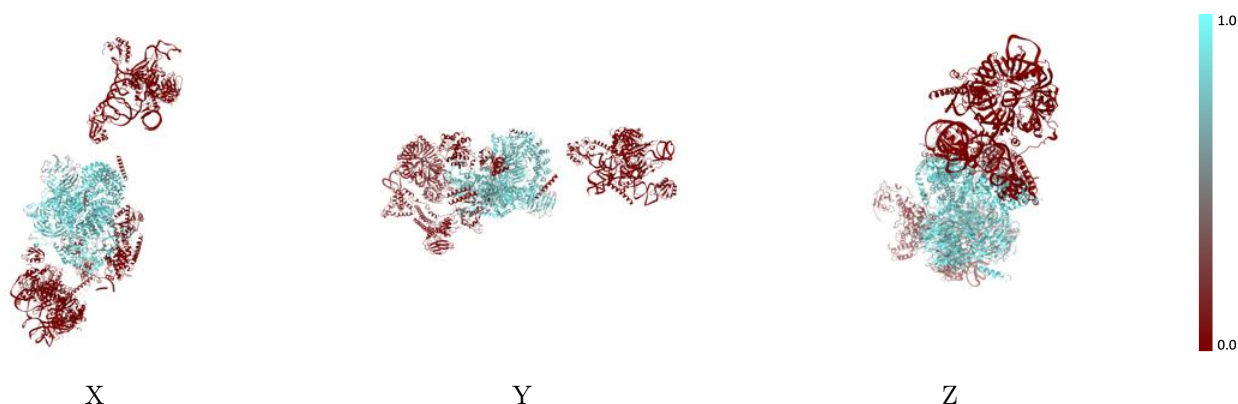
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



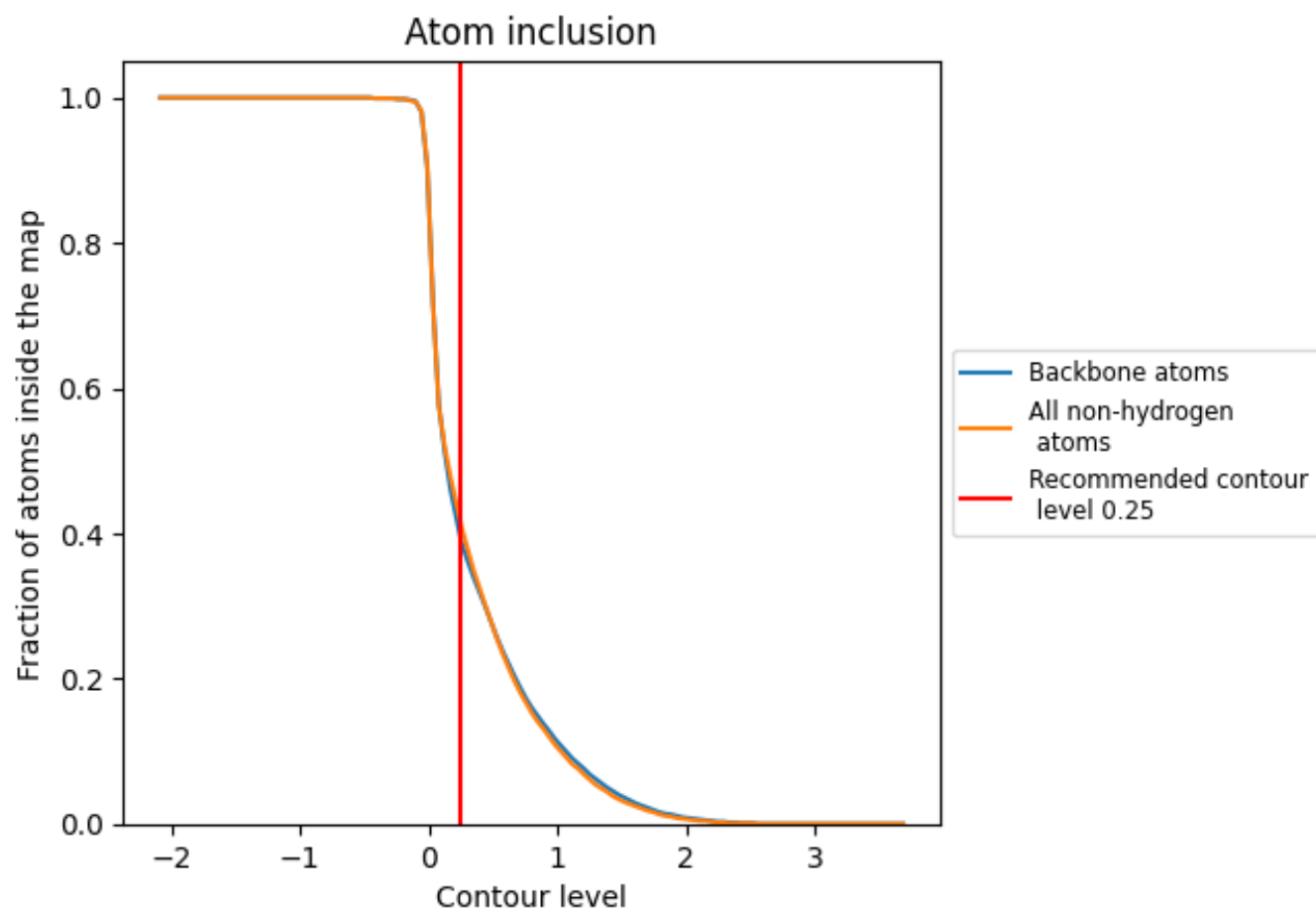
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 39% of all backbone atoms, 41% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4130	 0.1550
1	 0.8560	 0.3180
2	 0.6680	 0.2780
3	 0.8360	 0.3320
4	 0.1820	 -0.0130
5	 0.9150	 0.4810
6	 0.9070	 0.4080
A	 0.0000	 -0.0220
B	 0.3050	 0.0340
C	 0.3410	 0.1190
D	 0.3080	 0.0390
E	 0.1050	 0.0210
F	 0.0000	 0.0170
G	 0.0000	 -0.0200
H	 0.2320	 0.0690
I	 0.8540	 0.1490
J	 0.7150	 0.1100
K	 0.0000	 0.0440
L	 0.0000	 0.0100
M	 0.0000	 0.0120
N	 0.0000	 0.0110
O	 0.0000	 0.0030
a	 0.0000	 0.0040
b	 0.0000	 0.0060
c	 0.0000	 -0.0130
d	 0.0000	 0.0090
e	 0.0000	 0.0120
f	 0.0030	 -0.0260
g	 0.0030	 -0.0450
h	 0.0000	 -0.0010
i	 0.0000	 0.0050
j	 0.0000	 0.0260
k	 0.0000	 0.0060
l	 0.0000	 0.0120
m	 0.0000	 -0.0060
n	 0.0000	 -0.0180

