



wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 01:29 PM JST

PDB ID : 6AHD
EMDB ID : EMD-9624
Title : The Cryo-EM Structure of Human Pre-catalytic Spliceosome (B complex) at 3.8 angstrom resolution
Authors : Zhan, X.; Yan, C.; Zhang, X.; Shi, Y.
Deposited on : 2018-08-17
Resolution : 3.80 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.dev113
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

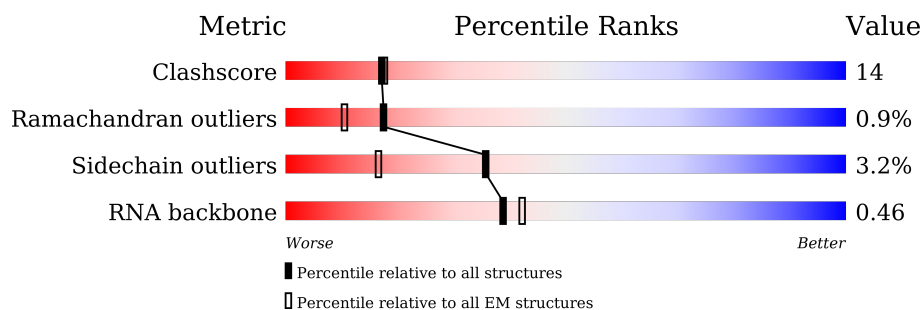
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	I	144	
3	B	117	
4	F	107	
5	G	274	
6	O	142	
7	C	972	

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Mol	Chain	Length	Quality of chain
8	N	941	
9	M	128	
10	L	499	
11	9	800	
12	J	683	
13	U	231	
13	a	231	
13	i	231	
14	V	119	
14	b	119	
14	j	119	
15	P	118	
15	c	118	
15	k	118	
16	Q	86	
16	d	86	
16	l	86	
17	R	92	
17	e	92	
17	m	92	
18	S	76	
18	f	76	
18	n	76	
19	T	126	
19	g	126	

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Mol	Chain	Length	Quality of chain
19	h	126	63% 63% 37%
20	E	357	80% 81% 16%
21	X	376	11% 19% 80%
22	W	177	19% 90% 6% 5%
23	A0	73	5% 71% 21% 8%
24	0	439	6% 9% 90%
25	Z	312	15% 54% 44%
26	8	199	8% 26% 72%
27	Y	513	88% 83% 5% 12%
28	H	188	58% 19% 20% 16% 42%
29	o	255	64% 63% 36%
30	p	225	42% 42% 58%
31	u	793	16% 15% 84%
32	v	464	20% 18% 80%
33	w	501	84% 83% 16%
34	q	95	95% 91% 5%
35	r	102	73% 70% 27%
36	s	139	53% 53% 47%
37	t	91	79% 78% 21%
38	x	80	88% 85% 12%
39	y	103	63% 63% 37%
40	z	96	64% 63% 36%
41	K	522	71% 7% 21%
42	1	1304	79% 57% 22% 20%
43	3	1217	96% 86% 10%

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Mol	Chain	Length	Quality of chain
44	5	125	<div>86%</div> <div> <div></div> <div>75%</div> <div>11%</div> <div>14%</div> </div>
45	6	110	<div>78%</div> <div> <div></div> <div>72%</div> <div>9%</div> <div>19%</div> </div>
46	7	86	<div>74%</div> <div> <div></div> <div>58%</div> <div>19%</div> <div>23%</div> </div>
47	2	895	<div>20%</div> <div> <div></div> <div>18%</div> <div>80%</div> </div>
48	4	424	<div>18%</div> <div> <div></div> <div>17%</div> <div>82%</div> </div>
49	D	2136	<div>52%</div> <div> <div></div> <div>76%</div> <div>20%</div> </div>

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
50	IHP	A	3000	-	-	X	-

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 85302 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	2209	Total	C	N	O	S	0	0
			17290	10998	3094	3128	70		

- Molecule 2 is a RNA chain called U4snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	136	Total	C	N	O	P	0	0
			2881	1288	498	959	136		

- Molecule 3 is a RNA chain called U5snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	115	Total	C	N	O	P	0	0
			2420	1084	403	818	115		

- Molecule 4 is a RNA chain called U6snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	94	Total	C	N	O	P	0	0
			1995	891	362	648	94		

- Molecule 5 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	77	Total	C	N	O	P	0	0
			1612	722	261	552	77		

- Molecule 6 is a protein called Thioredoxin-like protein 4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	O	141	Total	C	N	O	S	0	0
			1152	739	194	209	10		

- Molecule 7 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	818	Total	C	N	O	S	0	0
			6440	4117	1086	1205	32		

- Molecule 8 is a protein called Pre-mRNA-processing factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	781	Total	C	N	O	S	0	0
			4518	2759	876	878	5		

- Molecule 9 is a protein called NHP2-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	M	124	Total	C	N	O	S	0	0
			962	608	171	178	5		

- Molecule 10 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	376	Total	C	N	O	S	0	0
			2874	1788	524	550	12		

- Molecule 11 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	9	165	Total	C	N	O	S	0	0
			1087	669	205	212	1		

- Molecule 12 is a protein called U4/U6 small nuclear ribonucleoprotein Prp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	227	Total	C	N	O	S	0	0
			1273	724	283	263	3		

- Molecule 13 is a protein called SmB.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	a	86	Total	C	N	O	0	0
			344	172	86	86		
13	i	86	Total	C	N	O	0	0
			344	172	86	86		

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Mol	Chain	Residues	Atoms				AltConf	Trace
13	U	64	Total	C	N	O	0	0
			256	128	64	64		

- Molecule 14 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	b	82	Total	C	N	O	0	0
			328	164	82	82		
14	j	82	Total	C	N	O	0	0
			328	164	82	82		
14	V	82	Total	C	N	O	0	0
			334	170	82	82		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
15	c	97	Total	C	N	O	0	0
			388	194	97	97		
15	k	85	Total	C	N	O	0	0
			340	170	85	85		
15	P	74	Total	C	N	O	0	0
			300	152	74	74		

- Molecule 16 is a protein called SmE.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	d	74	Total	C	N	O	0	0
			296	148	74	74		
16	l	74	Total	C	N	O	0	0
			296	148	74	74		
16	Q	71	Total	C	N	O	0	0
			292	150	71	71		

- Molecule 17 is a protein called SmF.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	e	79	Total	C	N	O	0	0
			316	158	79	79		
17	m	79	Total	C	N	O	0	0
			316	158	79	79		
17	R	78	Total	C	N	O	0	0
			314	158	78	78		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	f	74	Total	C	N	O	0	0
			296	148	74	74		
18	n	68	Total	C	N	O	0	0
			272	136	68	68		
18	S	73	Total	C	N	O	0	0
			298	152	73	73		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
19	g	81	Total	C	N	O	0	0
			324	162	81	81		
19	h	80	Total	C	N	O	0	0
			320	160	80	80		
19	T	71	Total	C	N	O	0	0
			288	146	71	71		

- Molecule 20 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	E	299	Total	C	N	O	0	0
			1196	598	299	299		

- Molecule 21 is a protein called WW domain-binding protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	X	75	Total	C	N	O	0	0
			378	228	75	75		

- Molecule 22 is a protein called Peptidyl-prolyl cis-trans isomerase H.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	W	169	Total	C	N	O	0	0
			844	506	169	169		

- Molecule 23 is a protein called Ubiquitin-like protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A0	73	Total	C	N	O	S	0	0
			581	375	93	109	4		

- Molecule 24 is a protein called Microfibrillar-associated protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	0	45	Total	C	N	O	0	0
			225	135	45	45		

- Molecule 25 is a protein called Pre-mRNA-splicing factor 38A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Z	176	Total	C	N	O	0	0
			883	531	176	176		

- Molecule 26 is a protein called Zinc finger matrin-type protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	8	56	Total	C	N	O	0	0
			277	165	56	56		

- Molecule 27 is a protein called WD40 repeat-containing protein SMU1.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Y	453	Total	C	N	O	0	0
			2258	1352	453	453		

- Molecule 28 is a RNA chain called U2snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	H	109	Total	C	N	O	P	0	0
			2311	1032	396	774	109		

- Molecule 29 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	o	162	Total	C	N	O	0	0
			648	324	162	162		

- Molecule 30 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	p	94	Total	C	N	O	0	0
			376	188	94	94		

- Molecule 31 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	u	124	Total	C	N	O	0	0
			496	248	124	124		

- Molecule 32 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	v	94	Total	C	N	O	0	0
			376	188	94	94		

- Molecule 33 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	w	423	Total	C	N	O	0	0
			1693	847	423	423		

- Molecule 34 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	q	90	Total	C	N	O	0	0
			360	180	90	90		

- Molecule 35 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	r	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 36 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	s	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 37 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	t	72	Total	C	N	O	0	0
			288	144	72	72		

- Molecule 38 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	x	70	Total	C	N	O	0	0
			280	140	70	70		

- Molecule 39 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	y	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 40 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	z	61	Total	C	N	O	0	0
			244	122	61	61		

- Molecule 41 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	414	Total	C	N	O	S	0	0
			1821	969	423	428	1		

- Molecule 42 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	1	1048	Total	C	N	O	0	0
			4192	2096	1048	1048		

- Molecule 43 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	3	1168	Total	C	N	O	0	0
			4672	2336	1168	1168		

- Molecule 44 is a protein called SF3b14a, Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	5	108	Total	C	N	O	0	0
			432	216	108	108		

- Molecule 45 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	6	89	Total	C	N	O	0	0
			356	178	89	89		

- Molecule 46 is a protein called SF3b5, Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	7	66	Total	C	N	O	0	0
			264	132	66	66		

- Molecule 47 is a protein called SF3b145, Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	2	182	Total	C	N	O	0	0
			728	364	182	182		

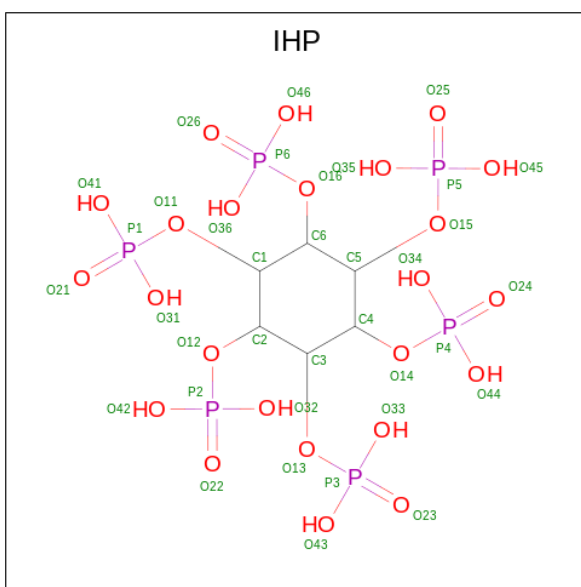
- Molecule 48 is a protein called SF3b49, Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	4	78	Total	C	N	O	0	0
			312	156	78	78		

- Molecule 49 is a protein called Brr2, U5 small nuclear ribonucleoprotein 200 kDa helicase.

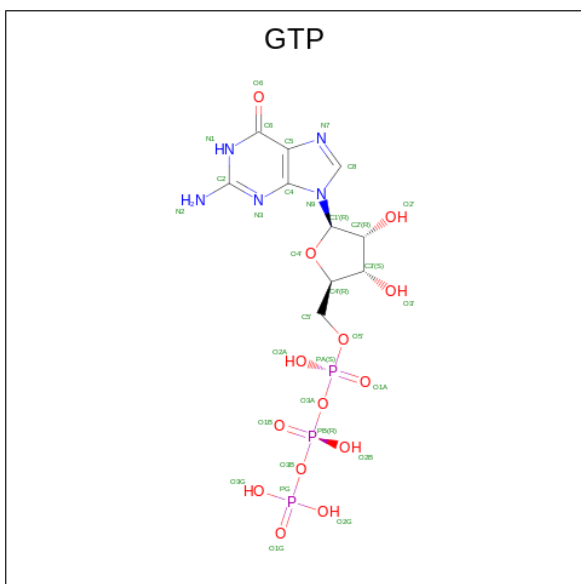
Mol	Chain	Residues	Atoms				AltConf	Trace
49	D	1699	Total	C	N	O	0	0
			6796	3398	1699	1699		

- Molecule 50 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: C₆H₁₈O₂₄P₆).



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

- Molecule 51 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

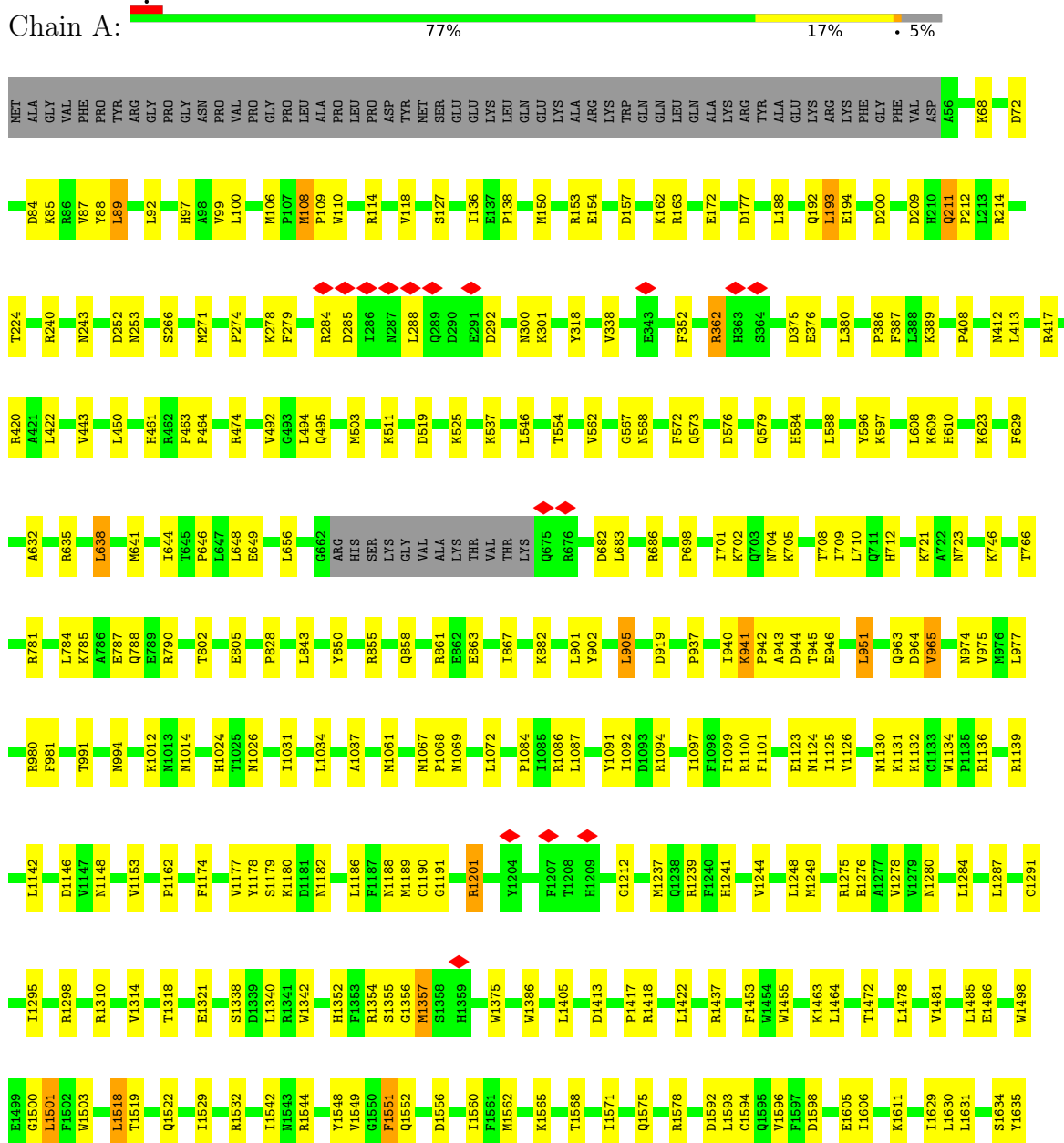
- Molecule 52 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

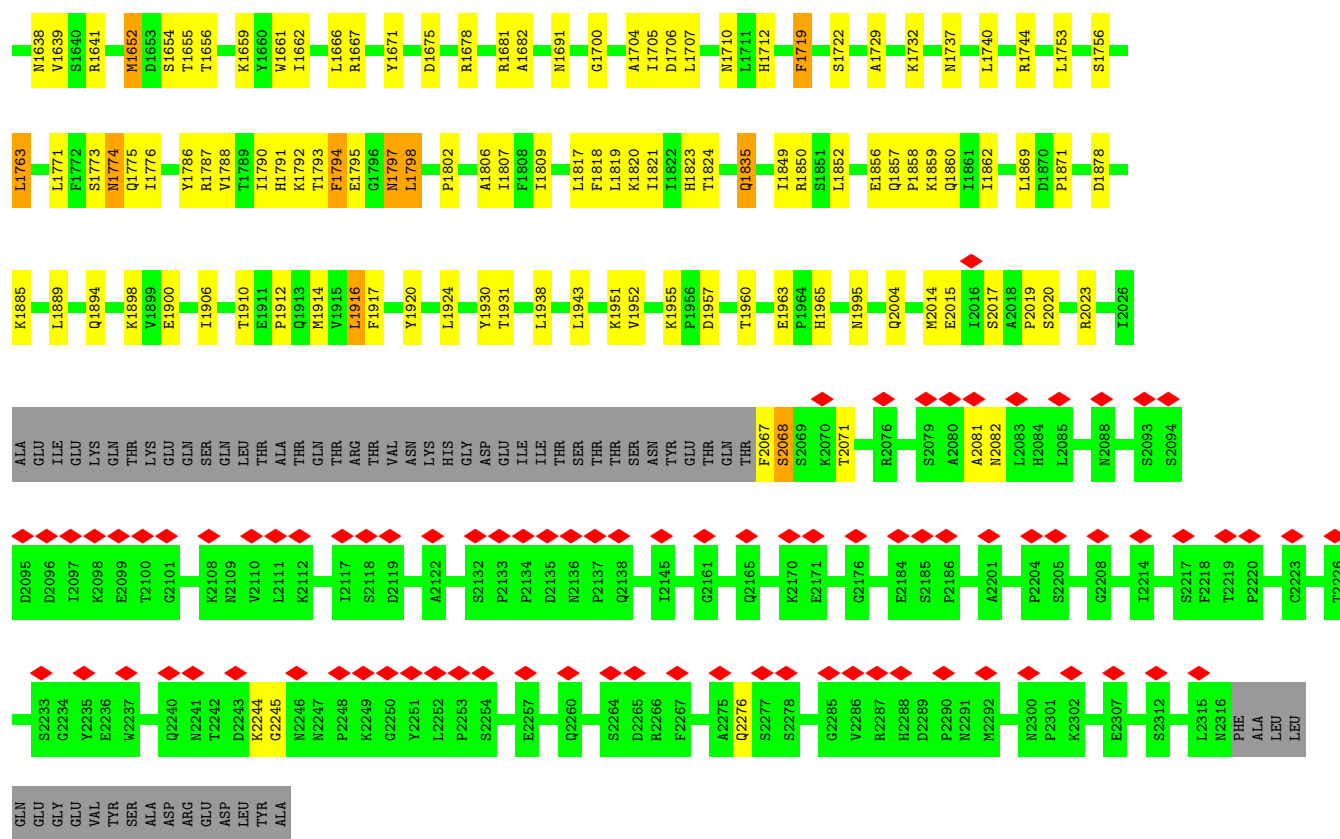
Mol	Chain	Residues	Atoms		AltConf
52	C	1	Total	Mg	0
			1	1	

3 Residue-property plots

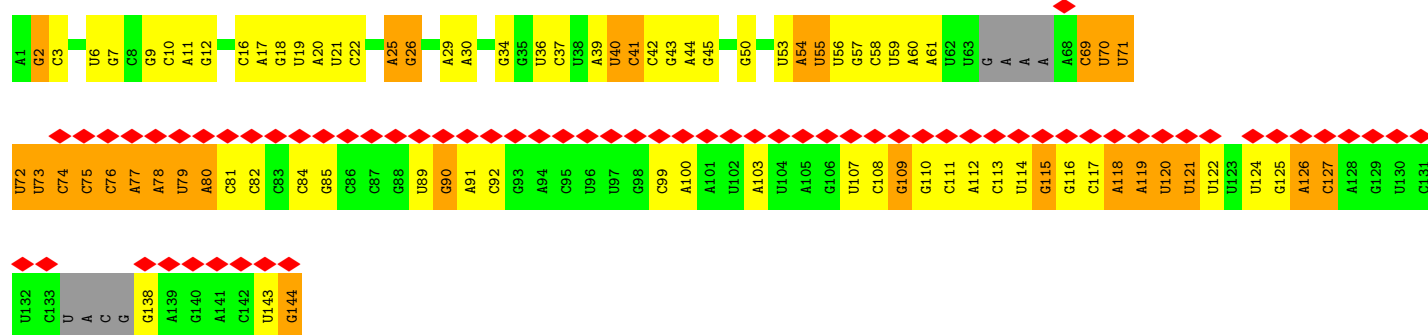
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Pre-mRNA-processing-splicing factor 8

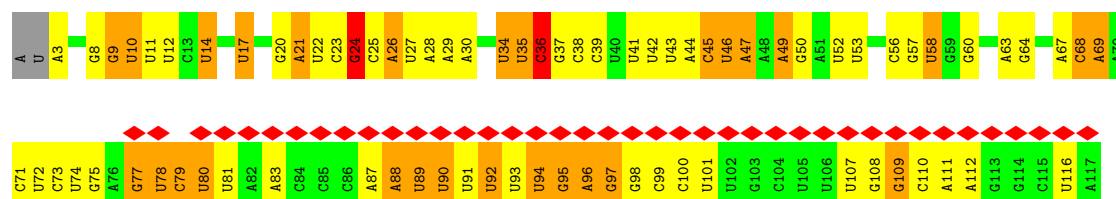


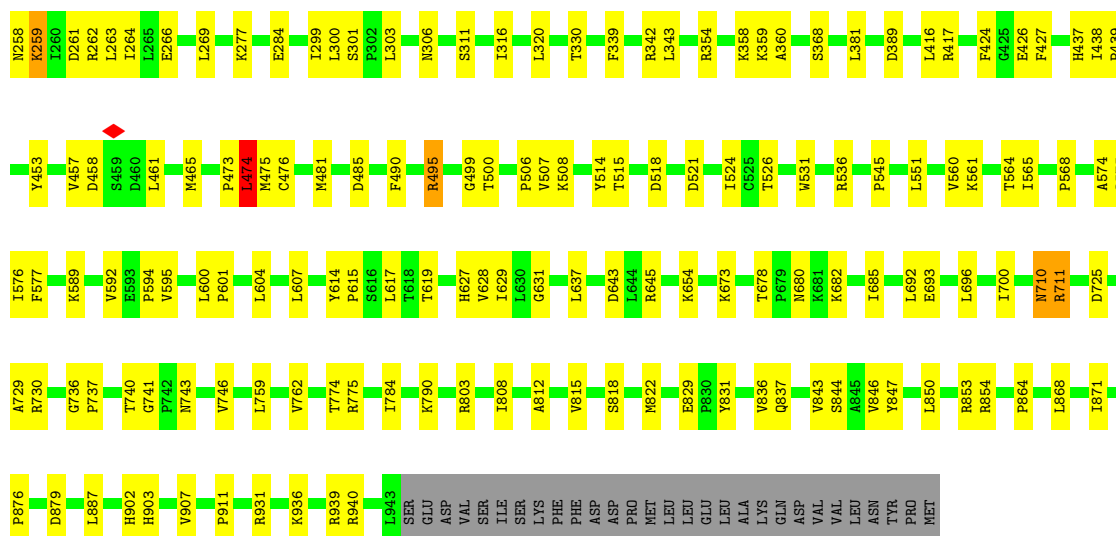


• Molecule 2: U4snRNA

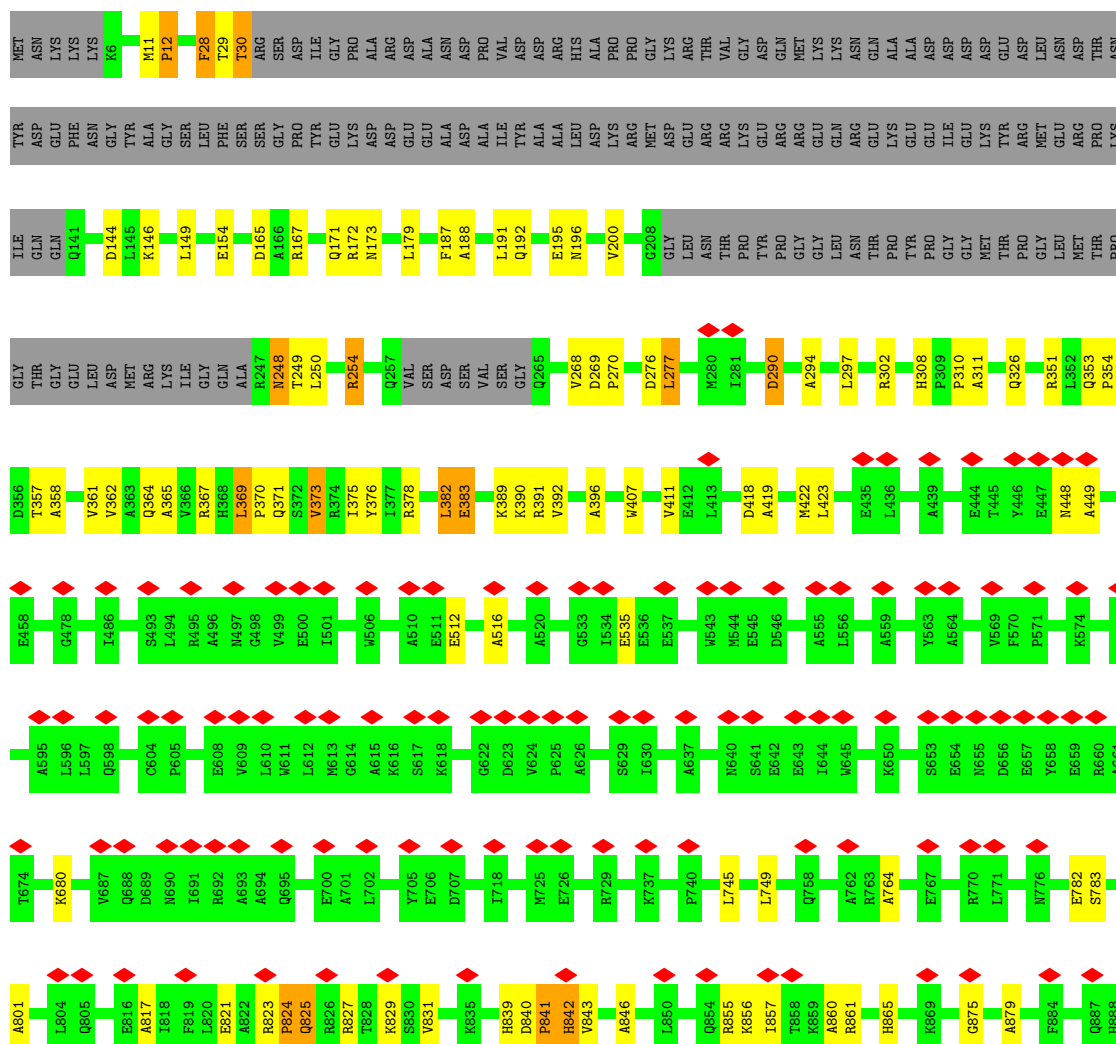


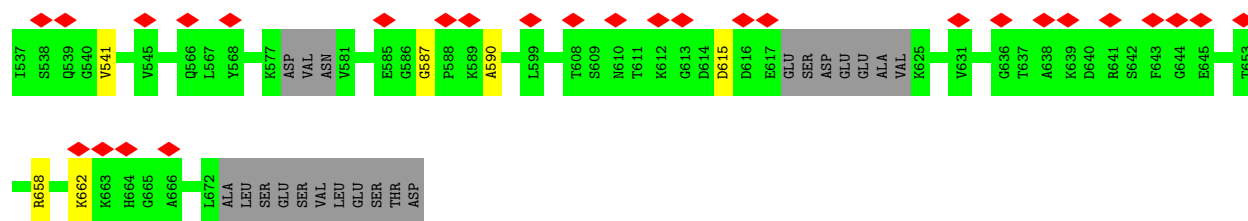
• Molecule 3: U5snRNA



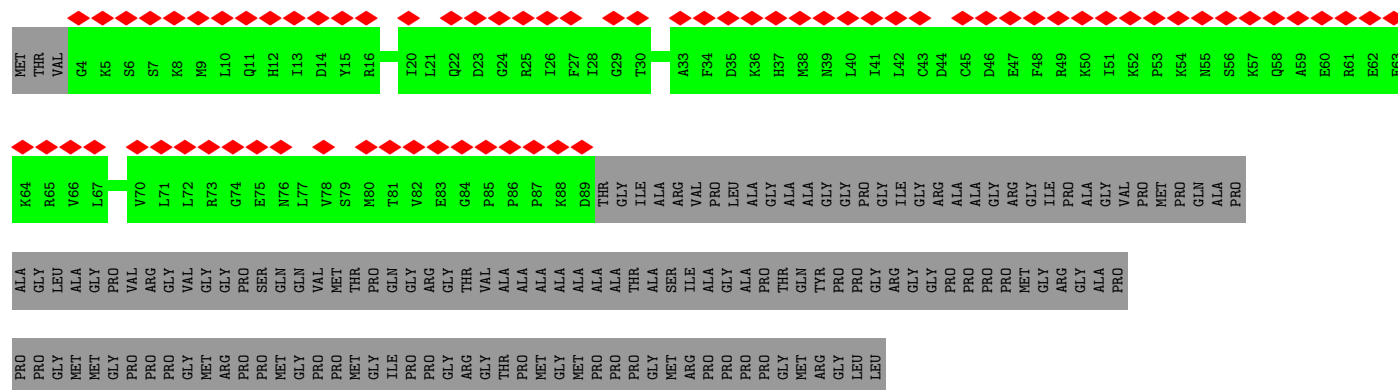


• Molecule 8: Pre-mRNA-processing factor 6

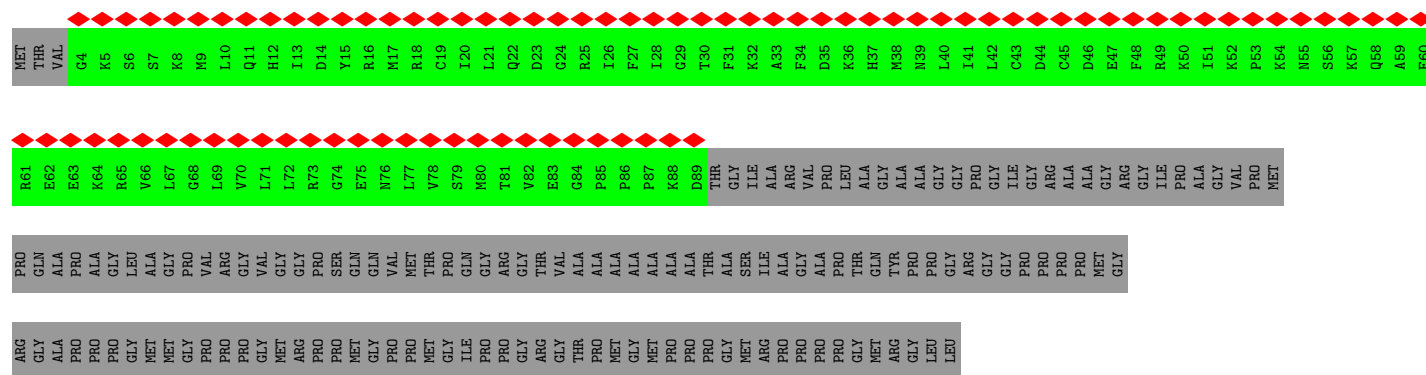




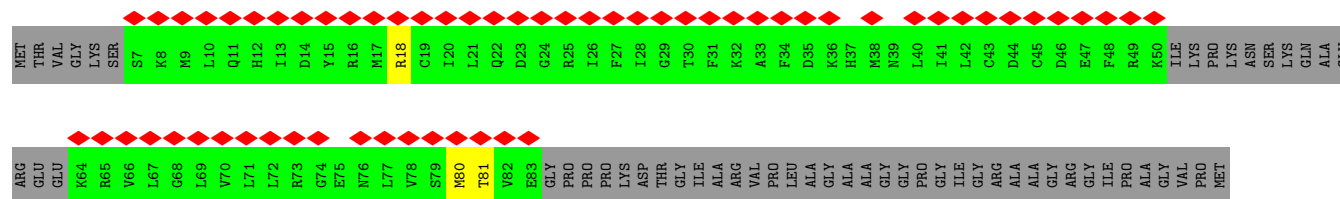
• Molecule 13: SmB

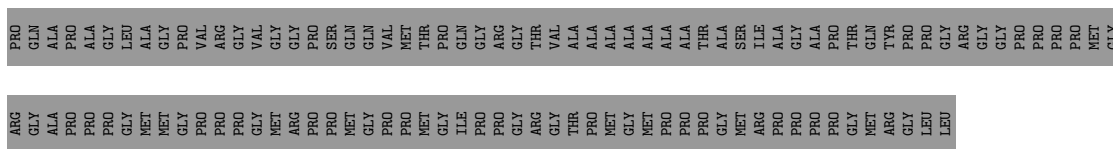


• Molecule 13: SmB

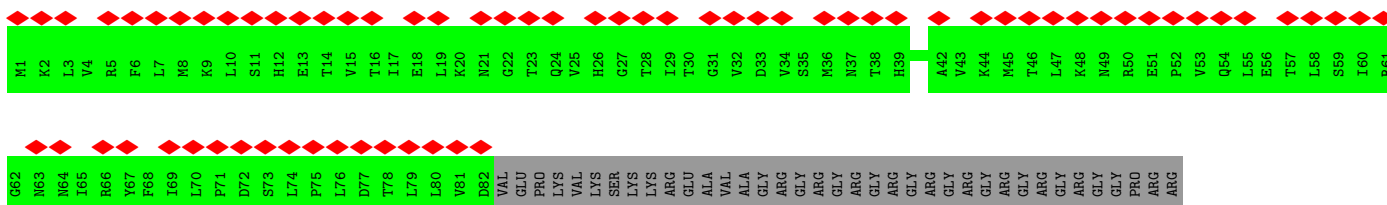


• Molecule 13: SmB

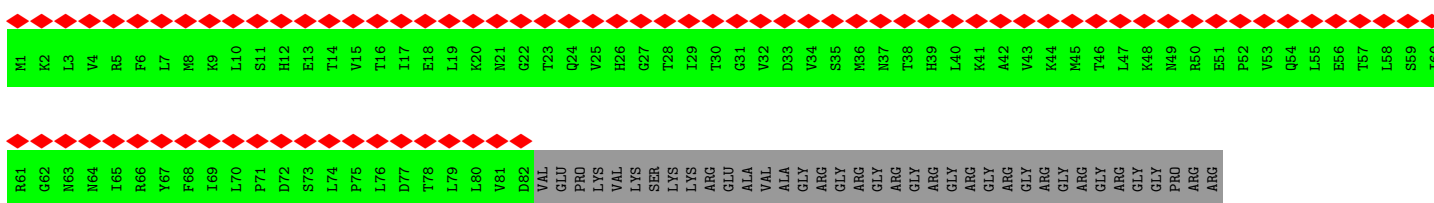




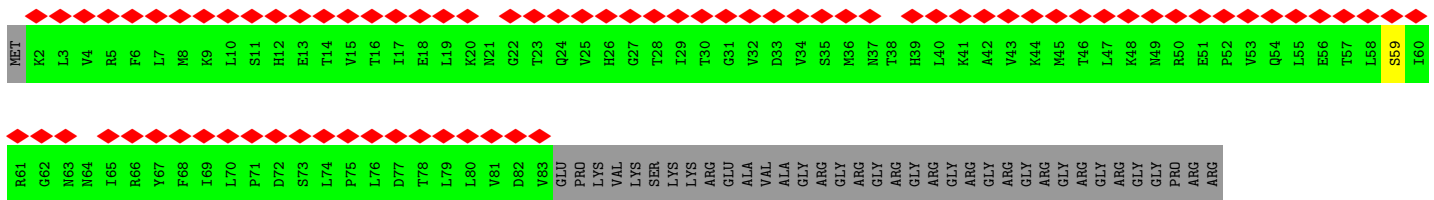
- Molecule 14: Small nuclear ribonucleoprotein Sm D1



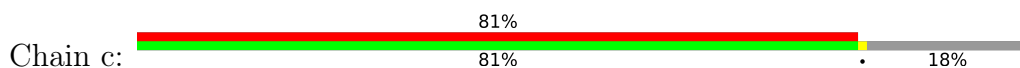
- Molecule 14: Small nuclear ribonucleoprotein Sm D1



- Molecule 14: Small nuclear ribonucleoprotein Sm D1



- Molecule 15: Small nuclear ribonucleoprotein Sm D2



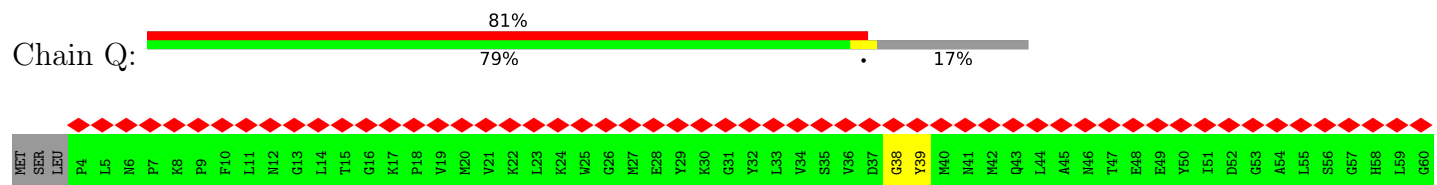
- Molecule 15: Small nuclear ribonucleoprotein Sm D2

- Molecule 15: Small nuclear ribonucleoprotein Sm D2

- Molecule 16: SmE

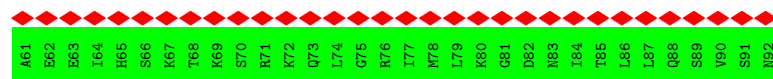
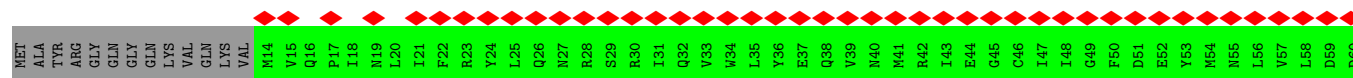
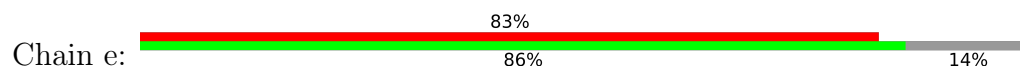
- Molecule 16: SmE

- Molecule 16: SmE

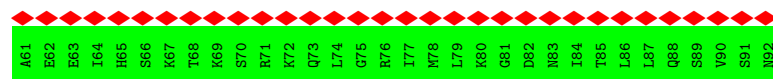
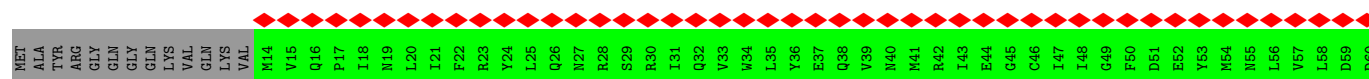
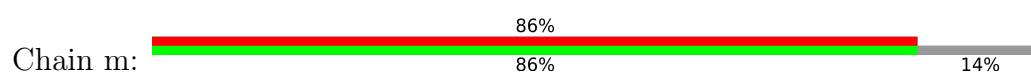




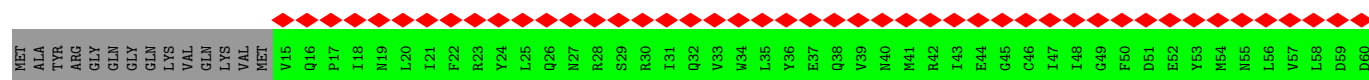
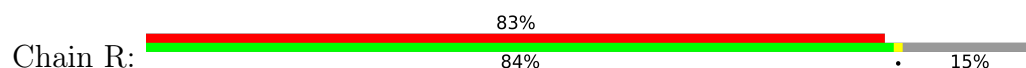
• Molecule 17: SmF



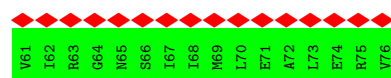
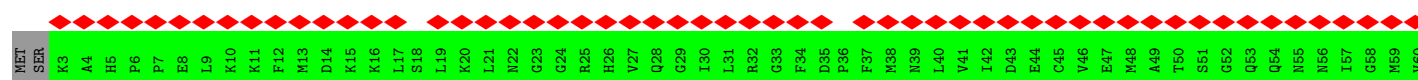
• Molecule 17: SmF



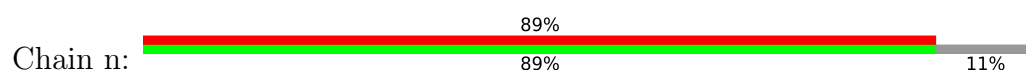
• Molecule 17: SmF

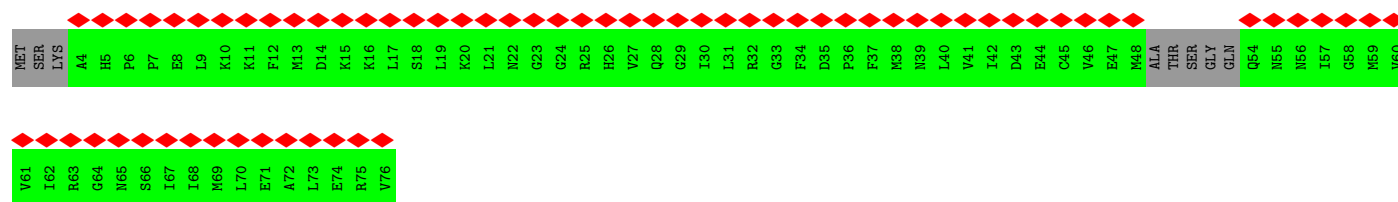


• Molecule 18: Small nuclear ribonucleoprotein G

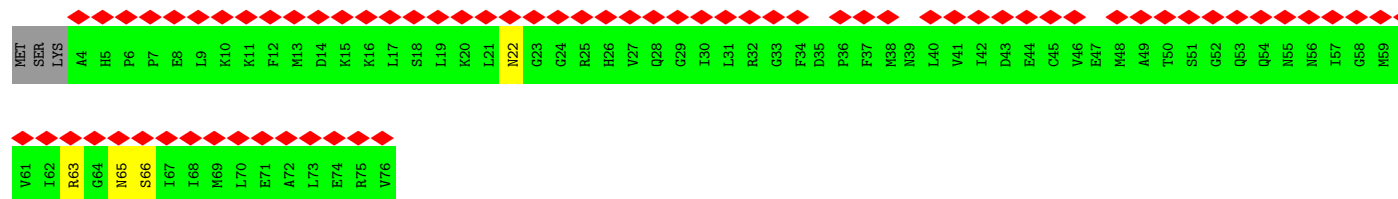
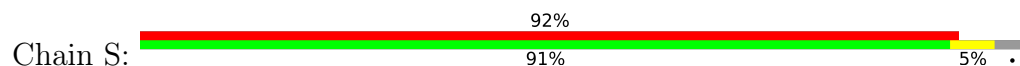


• Molecule 18: Small nuclear ribonucleoprotein G

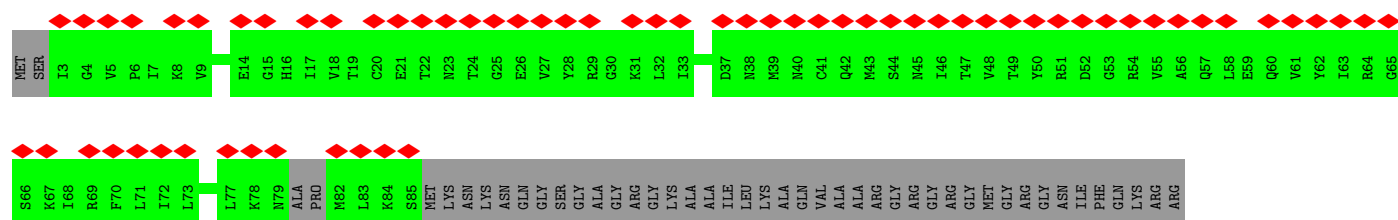




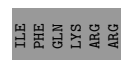
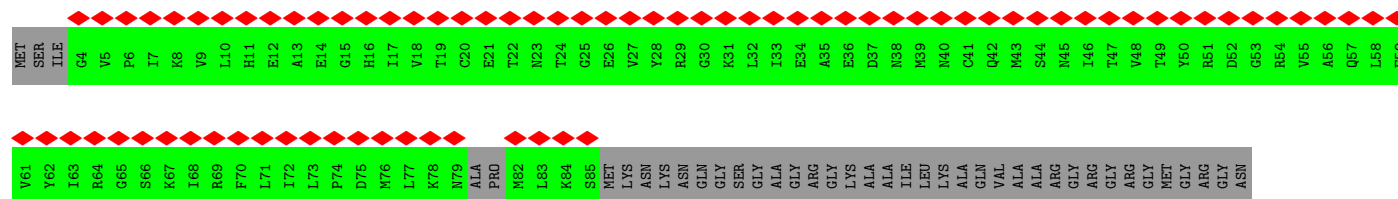
• Molecule 18: Small nuclear ribonucleoprotein G



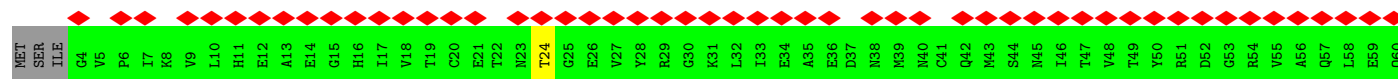
• Molecule 19: Small nuclear ribonucleoprotein Sm D3



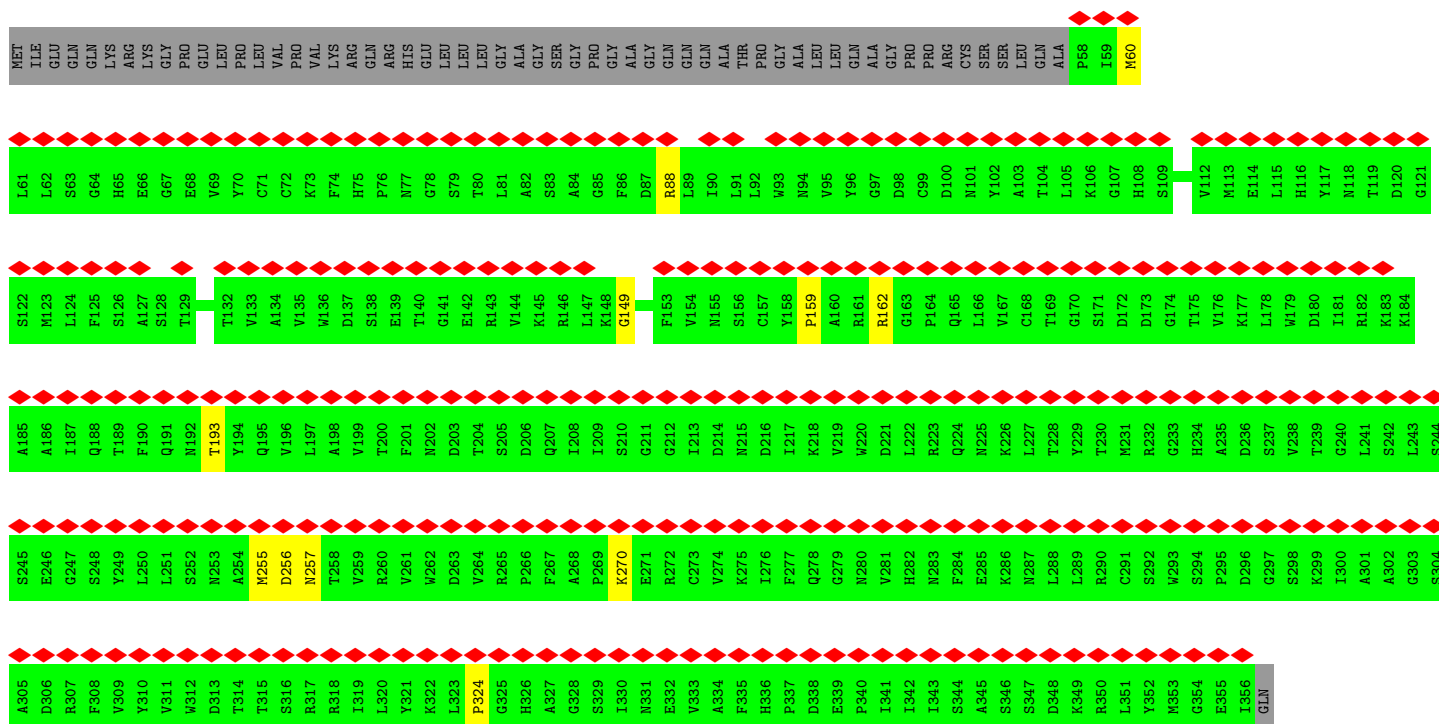
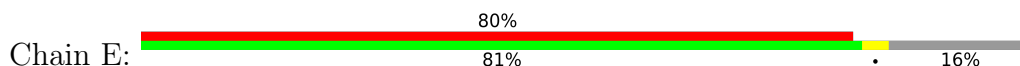
• Molecule 19: Small nuclear ribonucleoprotein Sm D3



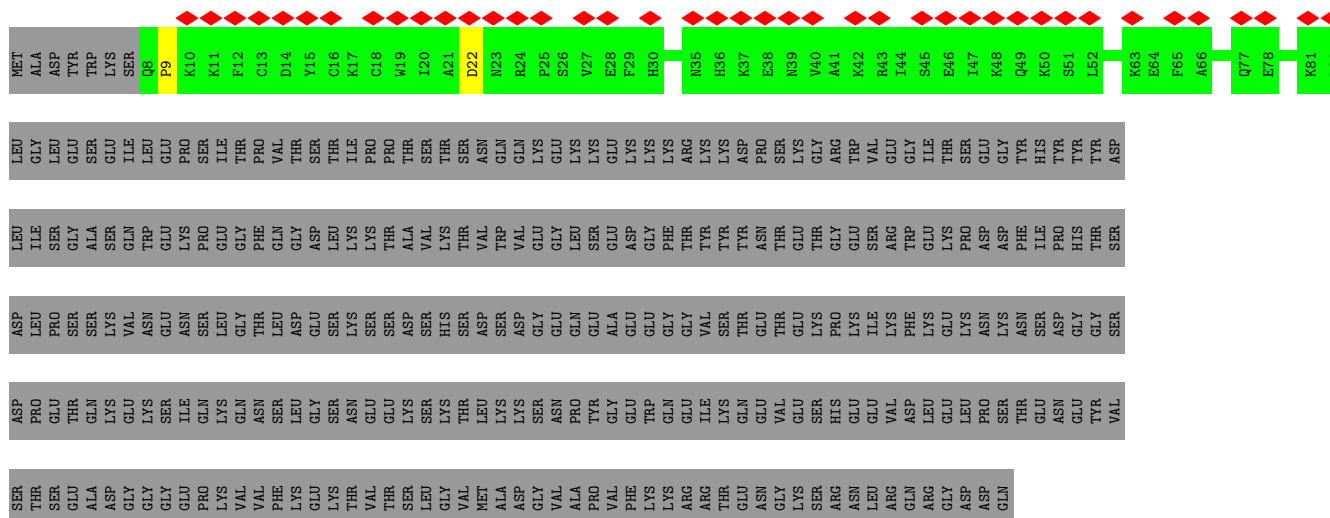
• Molecule 19: Small nuclear ribonucleoprotein Sm D3

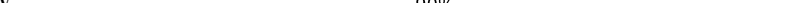


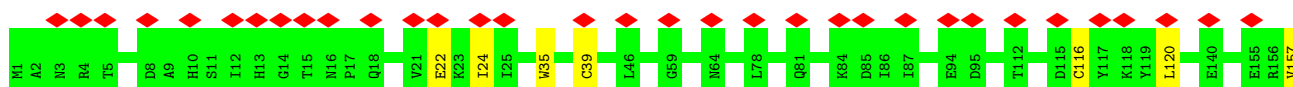
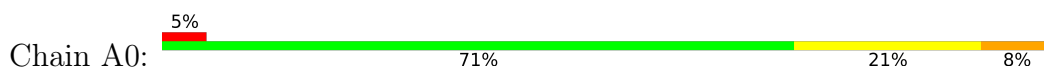
- Molecule 20: U5 small nuclear ribonucleoprotein 40 kDa protein.

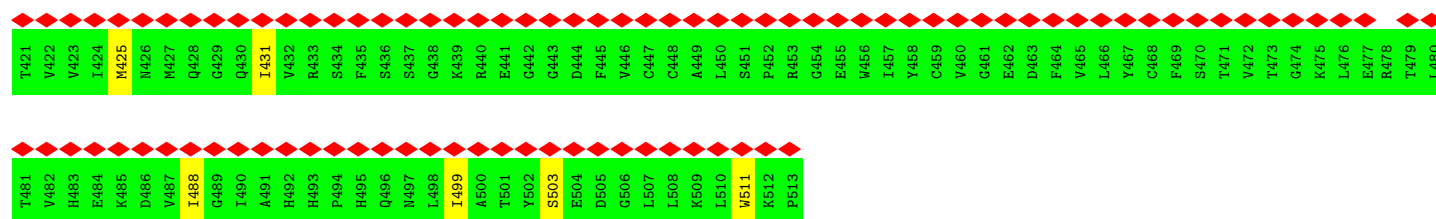


- Molecule 21: WW domain-binding protein 4

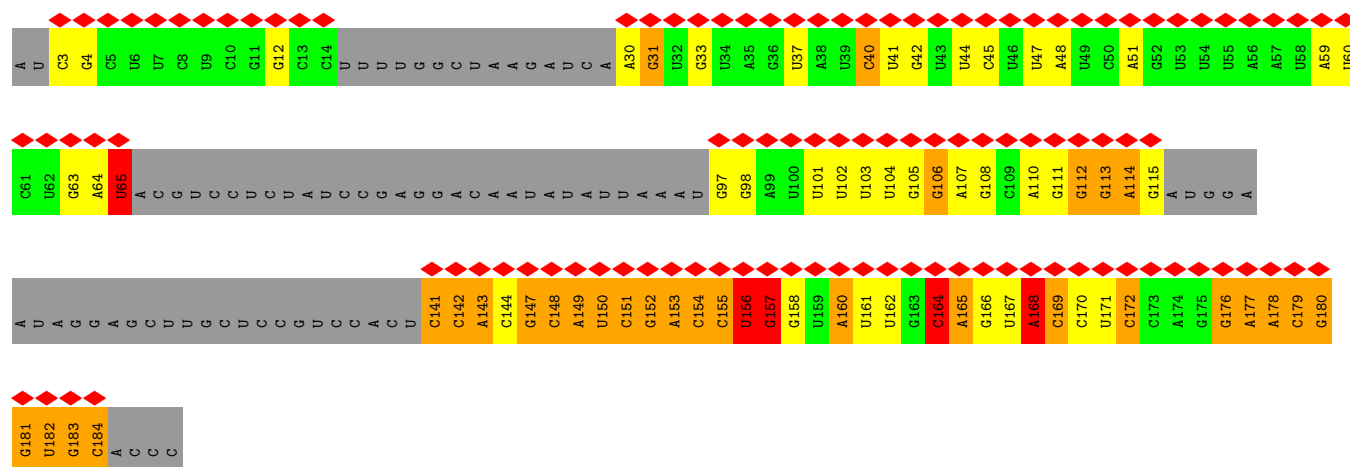


- Chain W:  19% 90% 6% 5%

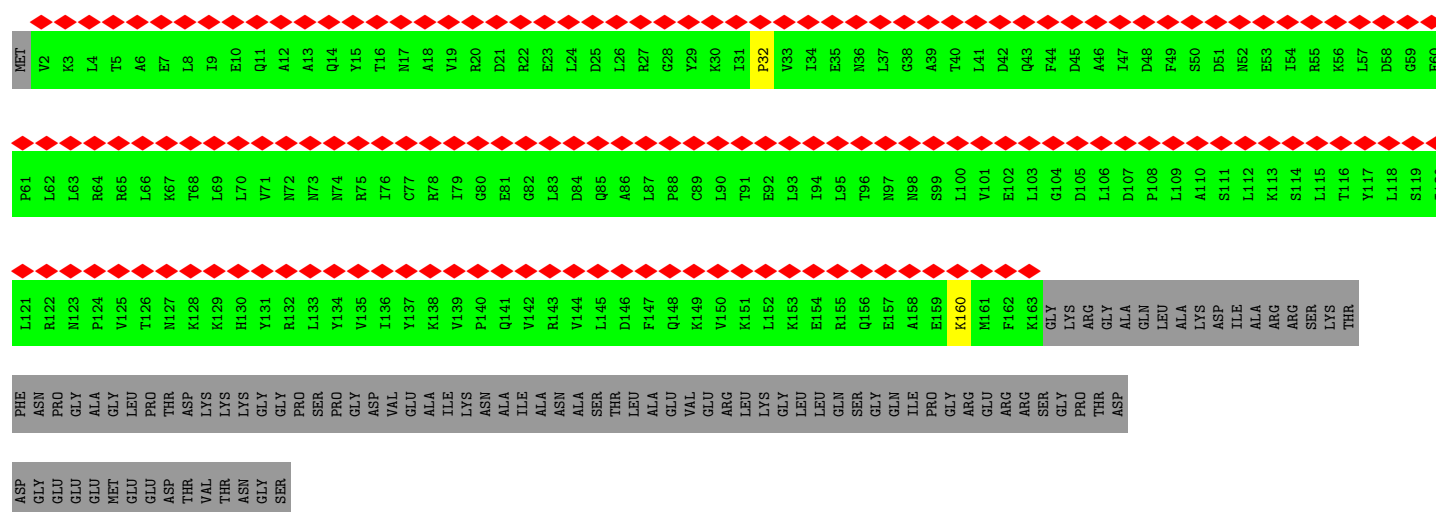




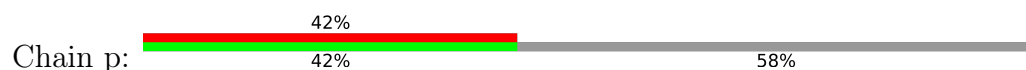
• Molecule 28: U2snRNA



• Molecule 29: U2 small nuclear ribonucleoprotein A'



• Molecule 30: U2 small nuclear ribonucleoprotein B''



ILE	LEU	GLY	VAL	LEU	VAL	PHI	THR	LEU	PRO	LEU	THR	ASP	GLN	VAL	SER	VAL	ILE	VAL	VAL	LYS	LYS	LYS	ILE	HIS	GLU	THR	GLY	MET	PRO	ALA	LYS	LYS	GLN	LYS	LEU	LYS	ASP	SER	ASN	ALA	ALA	LEU	TYR	TYR	ASN	MET	ASN	GLY	VAL	ALA	VAL	LYS
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- Molecule 32: Splicing factor 3A subunit 2

[illegible]

K121	Q122	R123	D124	S125	E126	M127	GLY	GLN	GLN	SER	LEU	LEU	PHE	GLN	GLN	ASP	Y138	P139	E140	I141	A142	E143	G144	I145	M146	P147	R148	H149	R150	F151	M152	M153	A154	Y155	E156	Q157	R158	I159	E160	P161	P162	D163	R164	R165	W166	Q167	Y168	L169	L170	M171	A172	A173	E174	Y175	Y176	E177	T178	I179	M180
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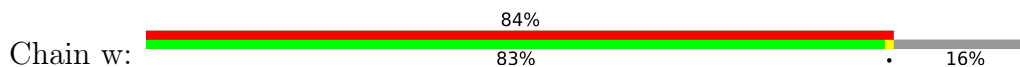
F181	K182	V183	P184	S185	R186	E187	I188	D189	K190	A191	E192	G193	K194	PHE	TRP	T197	H198	W199	N200	R201	E202	T203	K204	Q205	F206	T207	L208	Q209	F210	H211	F212	K213	M214	E215	K216	T217	F218	A219	P220	P221	S222	L223	PRO	ALA	GLY	PRO	PRO	GLY	GLY	VAL	LYS	ARG	PRO	PRO	PRO	PRO	LEU	MET	ASN
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LEU	PRO	PRO	ARG	PRO	PRO	LEU	LEU	GLU	SER	LEU	PRO	PRO	PRO	PRO	PRO	GLY	GLY	LEU	PRO	PRO	THR	PRO	PRO	ALA	SER	SER	GLY	PRO	PRO	GLY	PRO	PRO	PRO	GLN	LEU	PRO	PRO	PRO	ALA	GLY	GLY	VAL	HIS	PRO	PRO	ALA	ALA	VAL	VAL	HIS	PRO	PRO	PRO	ALA	ALA	SER	GLY
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[illegible][illegible]

VAL	HIS	PRO	GLN	PRO	PRO	GLY	VAL	HIS	PRO	SER	ASN	PRO	GLY	VAL	HIS	PRO	PRO	THR	PRO	MET	PRO	PRO	MET	LEU	ARG	PRO	PRO	LEU	PRO	SER	GLU	GLY	GLY	ASN	ILE	PRO	PRO	PRO	PRO	THR	ASN
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- Molecule 33: Splicing factor 3A subunit 3

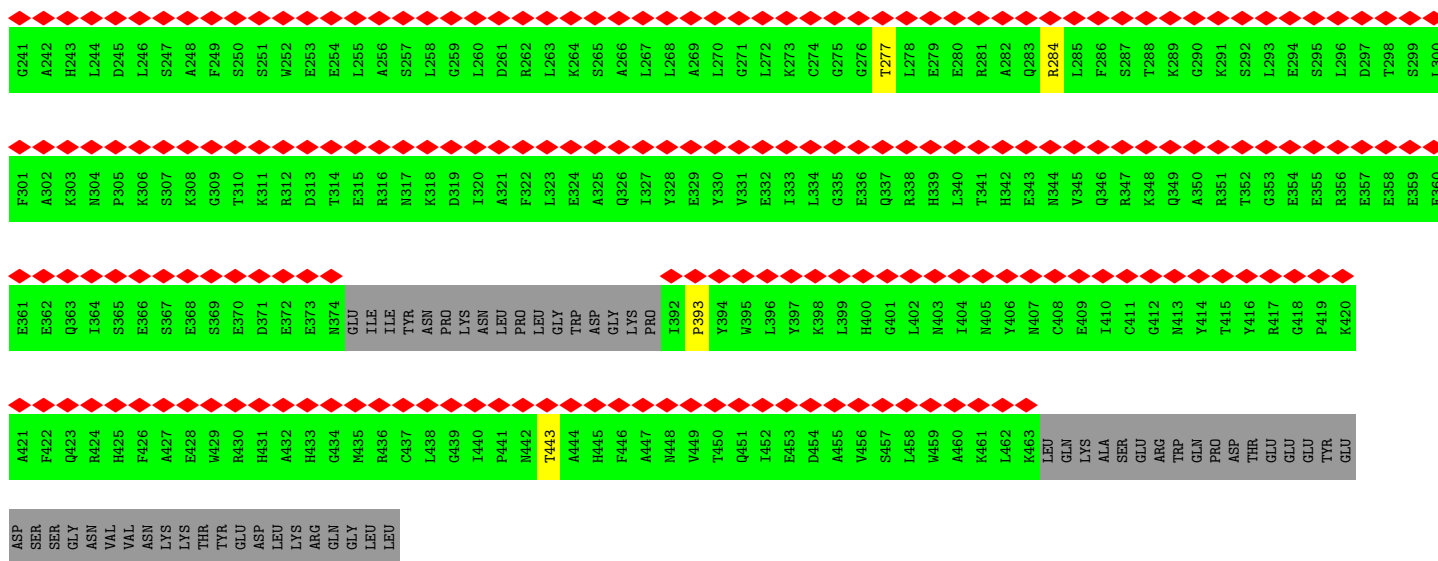


M1	E2	T3	I4	L5	E6	Q7	Q8	R9	R10	Y11	H12	E13	E14	K15	E16	R17	L18	M19	D20	V21	M22	A23	K24	E25	M26	L27	T28	K29	K30	S31	T32	L33	R34	D36	Q36	L37	N38	S39	D40	H41	R42	T43	R44	A46	M46	Q47	D48	R49	Y50	M51	E52	V53	S54	G55	N56	L57	R58	D59	E60
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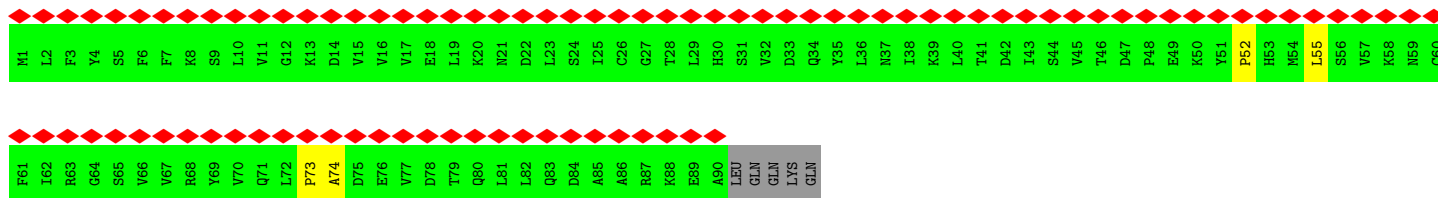
Y61	D62	D63	D64	D65	G66	L67	R68	K69	E70	E71	L72	N73	A74	L75	S76	G77	F78	N79	H80	F81	A82	S83	F84	Y85	N86	R87	L88	K89	Q90	I91	K92	E93	F94	H95	R96	K97	H98	PRO	ASN	GLU	ILE	CYS	VAL	PRO	PRO	MET	SER	VAL	GLU	F110	E111	E112	L113	L114	K115	A116	R117	E118	N119	P120
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S121	E122	E123	A124	Q125	N126	L127	V128	E129	F130	T131	D132	E133	E134	G135	V136	G137	R138	V139	L140	D141	L142	H143	ASP	CYS	TYR	LEU	LYS	V149	I150	N151	L152	K153	A154	S155	E156	K157	L158	D159	V160	I161	T162	V163	L164	S165	I166	F167	D168	Q169	L170	F171	D172	I173	P174	K175	E176	R177	K178	N179	A180
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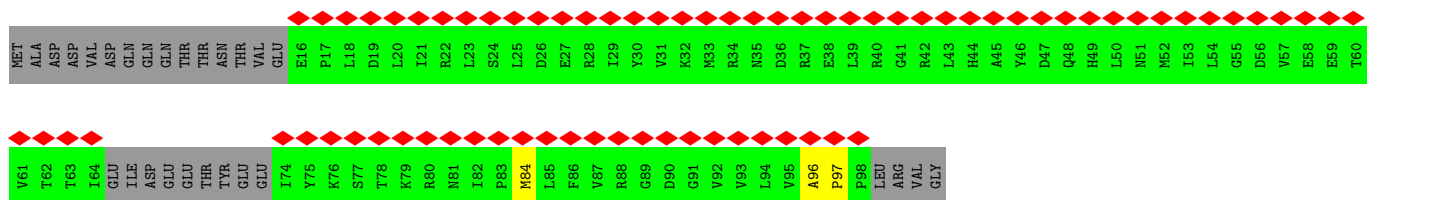
E181	Y182	R183	R184	Y185	L186	E187	M188	L189	L190	E191	Y192	Q194	D195	Y196	T197	D198	R199	V200	K201	P202	L203	L204	Q205	Q206	E207	N208	L209	F210	GLY	LYS	ILE	GLN	ALA	GLU	PHE	E218	K219	K220	W221	E222	N223	Q224	T225	F226	P227	Q228	W229	P230	K231	E232	T233	Q234	S235	A236	L237	T238	H239	A240
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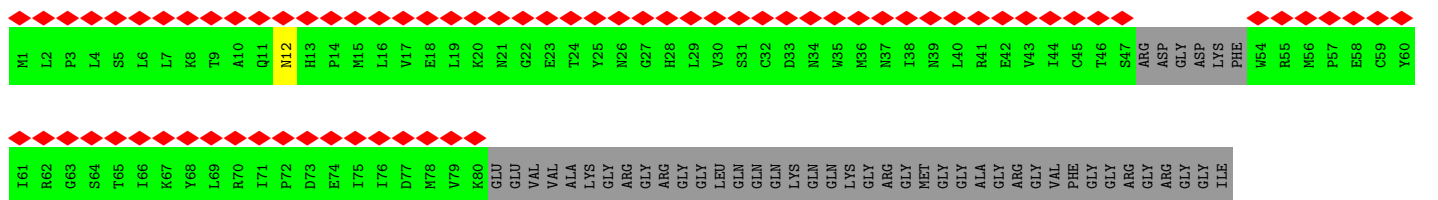
• Molecule 34: U6 snRNA-associated Sm-like protein LSm2



• Molecule 35: U6 snRNA-associated Sm-like protein LSm3




• Molecule 36: U6 snRNA-associated Sm-like protein LSm4



PRO GLY THR GLY ARG GLN PRO GLU LYS LYS PRO PRO GLY ARG GLN ALA LYS LYS GLN

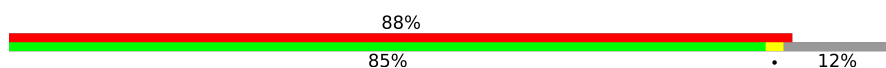
- Molecule 37: U6 snRNA-associated Sm-like protein LSm5

Chain t: 

MET ALA ALA ASN ALA THR THR ASN PRO S10 Q11 L12 L13 P14 L15 E16 L17 V18 D19 K20 C21 T22 G23 S24 R25 T26 T27 T28 V29 K30 K31 K32 D33 K34 E35 I36 V37 G38 T39 L40 L41 O42 F43 D44 D45 F46 V47 M48 M49 V50 L51 E52 D53 V54 T55 E56 F57 E58 I59 THR

PRO GLU GLY R64 R65 I66 T67 K68 L69 D70 Q71 I72 L73 L74 N75 G76 N77 N78 I79 T80 M81 L82 V83 P84 G85 GLY GLY P80 GLU VAL

- Molecule 38: U6 snRNA-associated Sm-like protein LSm6

Chain x: 

MET SER LEU ARG ALA GLN T7 P8 S9 D10 F11 L12 K13 Q14 I15 I16 G17 R18 P19 V20 V21 V22 K23 L24 M25 S26 G27 V28 D29 D30 R31 G32 V33 L34 A35 C36 L37 D38 G39 Y40 M41 N42 I43 A44 L45 E46 Q47 T48 E49 E50 Y51 Y52 N53 G54 Q55 L56 K57 N58 K59 Y60

G61 D62 A63 F64 I65 R66 G67 N68 N69 V70 L71 Y72 I73 S74 T75 Q76 LYS ARG ARG MET

- Molecule 39: U6 snRNA-associated Sm-like protein LSm7

Chain y: 

MET ALA ASP LYS LYS LYS LYS LYS S11 I12 L13 L14 L15 S16 K17 Y18 I19 D20 K21 T22 T23 R24 V25 K26 F27 Q28 G29 G30 R31 E32 A33 S34 G35 I36 L37 G38 G39 F40 D41 P42 L43 L44 N45 N46 V47 L48 D49 G50 T51 I52 E53 Y54 W55 ARG ASP PRO ASP

GLN THR LEU THR ASP T68 R69 Q70 L71 G72 L73 V74 V75 C76 R77 G78 T79 S80 V81 V82 L83 I84 C85 P86 Q87 ASP GLY MET GLU ALA ILE PRO ASN PRO PHE ILE GLN GLN ASP ALA

- Molecule 40: U6 snRNA-associated Sm-like protein LSm8

Chain z: 

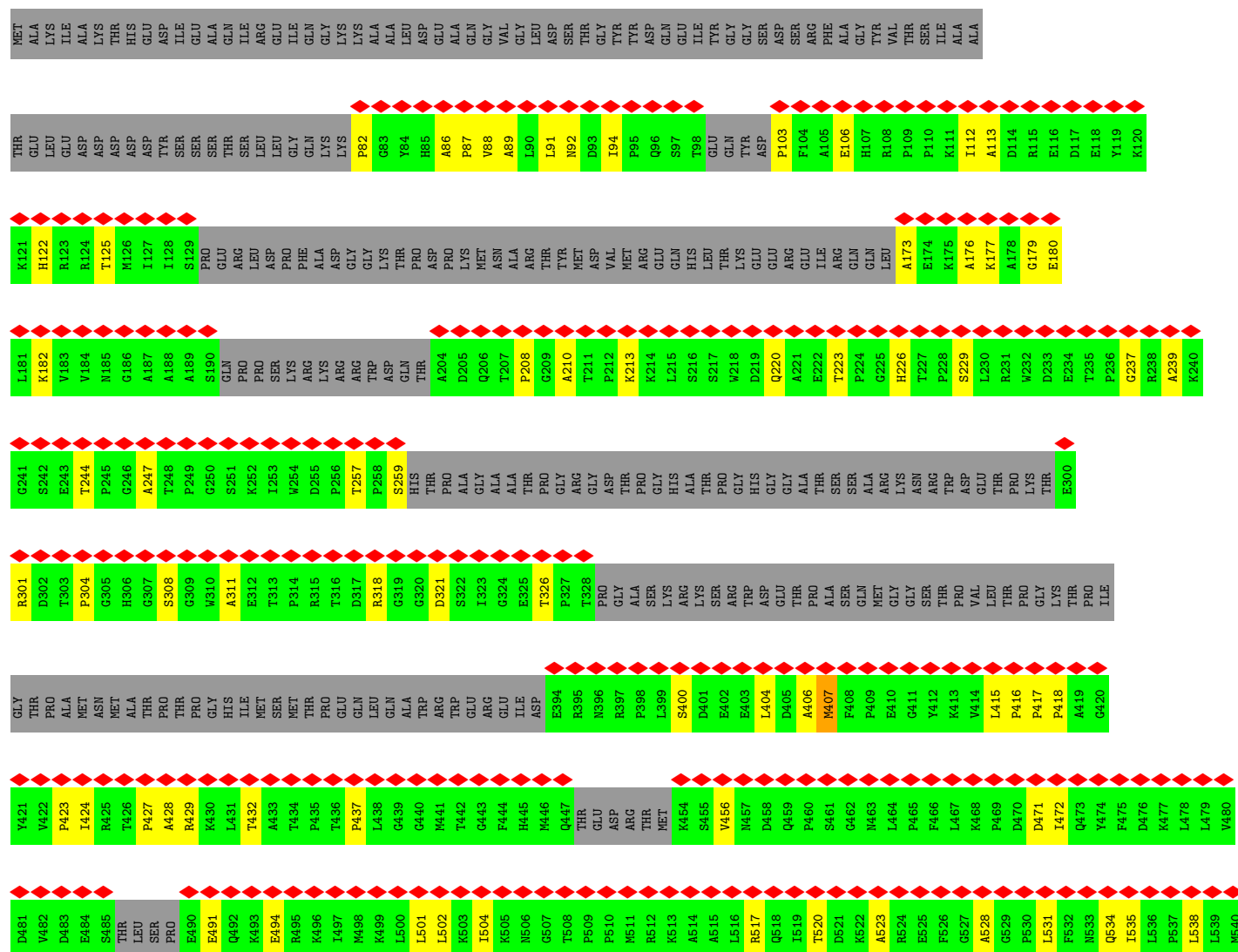
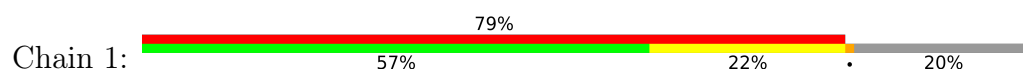
MET THR SER A4 L5 E6 N7 Y8 I9 N10 N11 T12 V13 A14 V15 I16 T17 S18 D19 G20 R21 M22 I23 V24 G25 T26 Q27 L28 K28 G29 F30 D31 Q32 T33 I34 N35 L36 I37 L38 D39 E40 S41 H42 E43 ARG VAL PHE SER SER SER GLN GLY VAL E53 Q54 V55 V56 L57 G58 L59 Y60

I61 V62 R63 G64 D65 N66 V67 A68 V69 I70 G71 E72 T73 ASP GLU GLU THR ASP SER LEU LEU LEU GLY ASN ILE ARG ALA GLU PRO LEU ASN SER VAL ALA HIS

- Molecule 41: U4/U6 small nuclear ribonucleoprotein Prp4

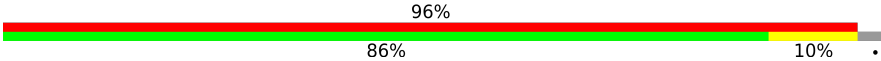
Chain K: 

- Molecule 42: Splicing factor 3B subunit 1

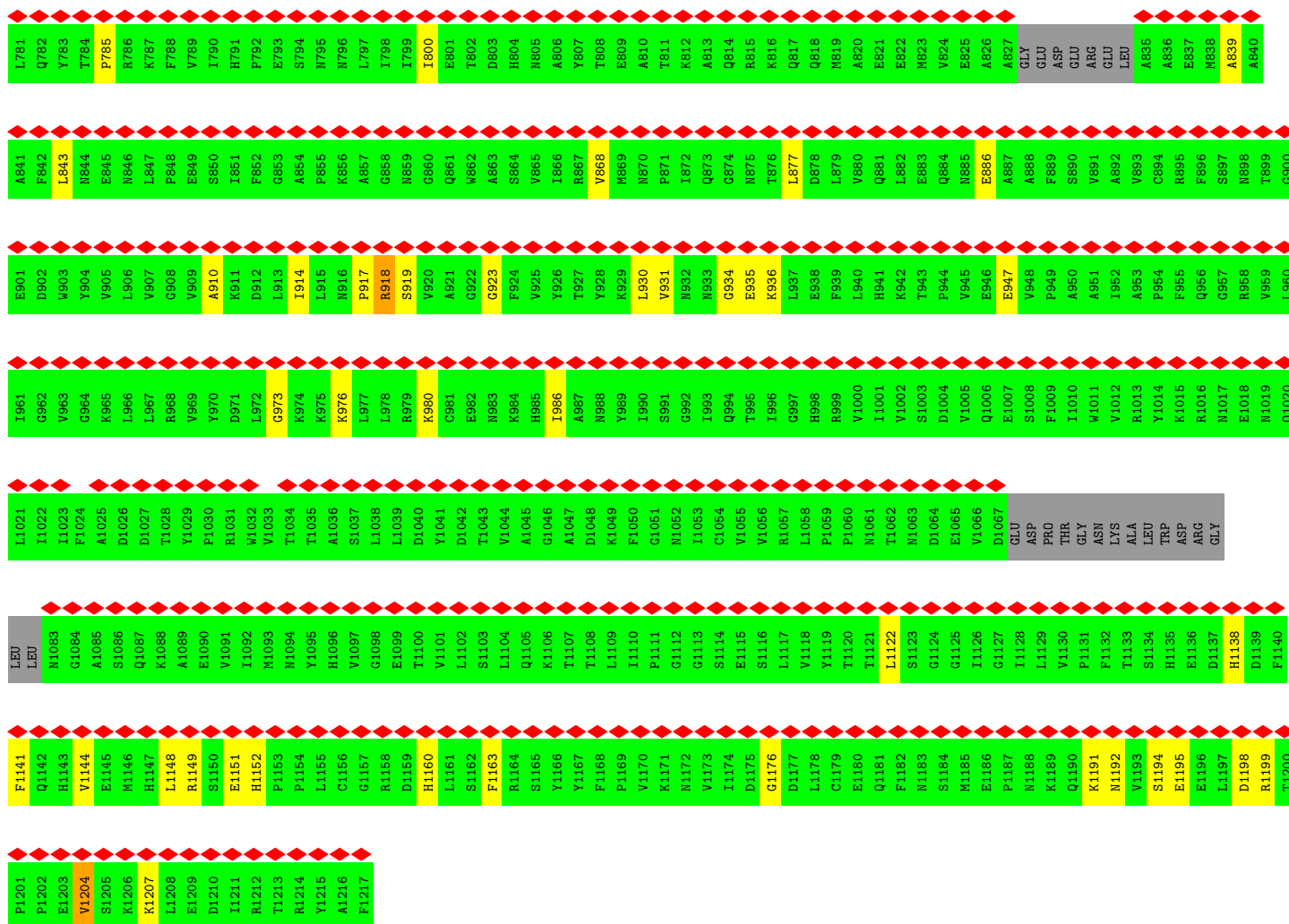


V1261	R1262	G1203	C1204	E1205	D1206	S1207	L1208	N1209	H1210	L1211	L1212	N1213	Y1214	V1215	W1216	P1217	N1218	V1219	F1220	E1221	T1222	S1223	P1224	H1225	V1226	I1227	Q1228	A1229	M1230	M1231	G1232	A1233	L1234	E1235	G1236	L1237	R1238	V1239	A1240	I1241	G1242	P1243	C1244	R1245	M1246	L1247	Q1248	Y1249	C1250	L1251	Q1252	G1253	L1254	F1255	H1256	P1257	R1258	L1259	K1260		
L1141	N1142	D1163	Q1164	M1145	G1146	V1147	L1148	K1149	S1150	L1151	S1152	F1153	L1154	F1155	E1156	Y1157	I1158	G1159	E1160	M1161	G1162	K1163	D1164	Y1165	I1166	Y1167	A1168	V1169	T1170	P1171	L1172	L1173	E1174	D1175	A1176	L1177	M1178	D1179	R1180	D1181	L1182	V1183	H1184	R1185	Q1186	T1187	V1188	A1189	S1189	A1190	V1191	V1192	Q1193	H1194	L1195	S1196	L1197	G1198	V1199	Y1200	
F1081	G1082	Y1083	I1084	A1085	K1086	A1087	I1088	G1089	P1090	H1091	D1092	V1093	L1094	A1095	T1096	L1097	L1098	N1099	M1100	L1101	K1102	A1043	Q1104	E1105	R1106	Q1107	N1108	R1109	V1110	C1111	T1112	T1113	V1114	A1115	T1116	A1117	I1118	V1119	A1120	E1121	T1122	C1123	S1124	P1125	F1126	T1127	K1128	L1129	M1129	P1130	A1131	L1132	M1133	I1073	N1134	E1135	Y1136	R1137	V1138	P1139	E1140
T1021	P1022	I1023	L1024	K1025	N1026	R1027	H1028	E1029	K1030	V1031	Q1032	E1033	N1034	C1035	T1036	D1037	L1038	V1039	G1040	R1041	L1042	A1043	D1044	R1045	G1046	A1047	E1048	Y1049	V1050	S1051	A1052	R1053	E1054	W1055	M1056	R1057	I1058	C1059	F1060	E1061	L1062	L1063	E1064	L1065	L1066	K1067	A1068	H1069	K1070	K1071	A1072	I1073	R1074	L1075	A1076	T1077	V1078	N1079	T1080		
Q901	E902	K903	T904	T905	E906	D907	S908	V909	M910	L911	N912	G913	F914	G915	T916	V917	V918	N919	A920	L921	G922	K923	R924	V925	K926	P927	Y928	L929	Q930	Q931	C932	C933	G934	T935	V936	L937	W938	R939	L940	N941	N942	K943	S944	A945	V947	R948	Q949	Q950	A951	A952	D953	L954	P955	S956	R957	T958	A959	V960			
A841	N842	K843	V844	G845	A846	A847	E848	T849	I850	S851	R852	L853	V854	D855	D856	L857	K858	D859	E860	A861	E862	Q863	Y864	R865	K866	M867	V868	M869	E870	I872	E873	K874	I875	M876	G877	N878	L879	G880	A881	A882	D883	I884	D885	H886	K887	L888	E889	E890	Q891	L892	T893	D894	G895	I896	L897	Y898	A899	F900			
D781	E782	E783	M784	K785	K786	I787	V788	L789	K790	V791	V792	K793	Q794	C795	C796	G797	T798	D799	G800	V801	A802	Q803	N804	Y805	I806	K807	T808	E809	I810	L811	P812	P813	F814	F815	K816	H817	R818	W819	Q820	H821	R822	M823	A824	L825	D826	R827	R828	N829	Y830	R831	Q832	L833	V834	D835	T836	V837	V838	E839	L840		
I721	E722	S723	F724	D725	S726	V727	L728	K729	P730	L731	V732	K733	G734	I735	R736	Q737	H738	R739	G740	P741	G742	L743	A744	R745	L746	L747	K748	A749	I750	G751	Y752	L753	I754	P755	L756	M757	D758	A759	E760	Y761	A762	M763	Y764	Y765	T766	R767	E768	V769	M770	L771	L772	L773	I774	R775	E776	F777	Q778	S779	P780		
R661	H662	T663	G664	K665	K666	I667	V668	Q669	Q670	I671	A672	I673	L674	M675	G676	C677	A678	I679	M680	P681	H682	L683	R684	R685	N686	V687	T688	I689	A690	E691	H692	G693	L694	V695	D696	E697	Q698	Q699	K700	V701	R702	T703	I704	S705	A706	L707	A708	I709	A710	A711	L712	K713	E714	A715	A716	T717	P718	Y719	G720		
A601	K602	A603	A604	G605	L606	A607	T608	M609	I610	S611	T612	M613	R614	P615	D616	I617	D618	N619	M620	D621	E622	Y623	V624	R625	N626	T627	T628	A629	R630	A631	F632	A633	V634	V635	A636	S637	A638	L639	G640	I641	P642	S643	L644	L645	D646	F647	L648	K649	A650	V651	C652	K653	S654	K655	I656	S657	Q658	A660			
S541	P542	T543	L544	E545	D546	Q547	E548	R549	H550	L551	L552	V553	K554	V555	I556	D557	R558	I559	L560	Y561	K562	L563	D564	D565	L566	V567	R568	P569	Y570	V571	H572	K573	I574	L575	V576	V577	I578	E579	P580	L581	L582	I583	D584	E585	D586	Y587	Y588	A589	R590	V591	E592	G593	R594	E595	I596	I597	S598	N599	L600		

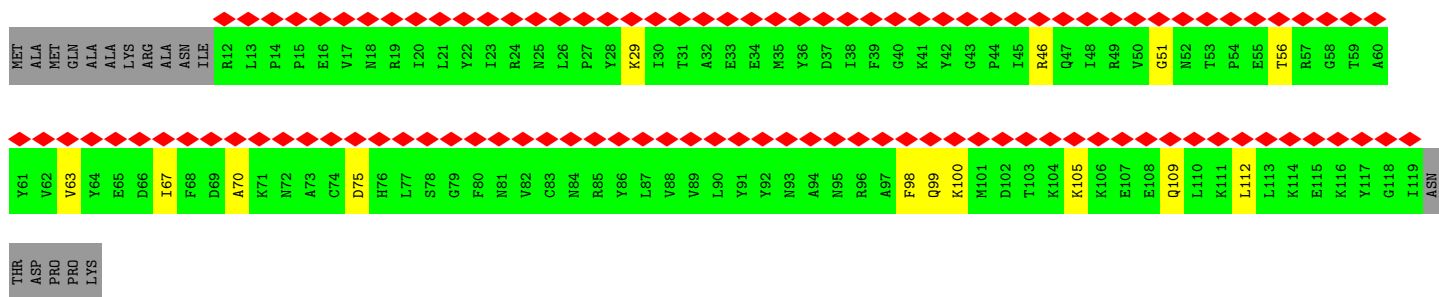
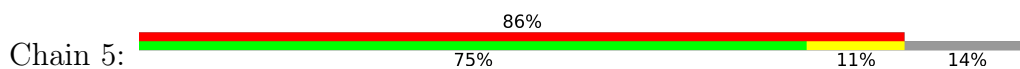
- Molecule 43: Splicing factor 3B subunit 3

Chain 3: 

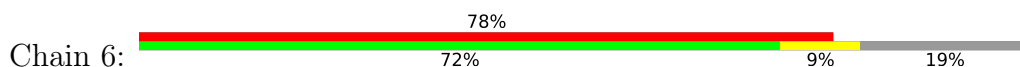
L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780
GLY	F662	F663	Y664	L665	N666	I667	G668	L669	Q670	N671	G672	V673	L674	L675	R676	T677	V678	L679	D680	P681	V682	T683	G684	D685	L686	S687	D688	T689	R690	T691	ARG	TYR	LEU	G695	S696	R697	P698	V699	K700	L701	F702	R703	V704	R705	M706	Q707	G708	Q709	E710	A711	V712	L713	A714	M715	S716	S717	R718	S719	W720
R601	S602	R603	F604	L605	A606	V607	G608	L609	V610	D611	N612	T613	V614	R615	L616	I617	S618	L619	D620	P621	S622	D623	C624	L625	Q626	P627	L628	S629	M630	Q631	A632	L633	P634	A635	Q636	P637	E638	S639	L640	C641	L642	V643	E644	M645	GLY	GLY	THR	GLU	LYS	GLN	ASP	GLU	LEU	GLY	ARG	GLY	SER	ILE	
K541	K542	L483	T544	V545	K546	C547	A548	V549	N550	Q551	R552	Q553	V554	V555	T556	A557	T558	D559	G560	G561	E562	L563	V564	Y565	F566	E567	M568	D569	P570	S571	G572	Q573	L574	N575	E576	F577	T578	E579	R580	L581	C582	L583	L584	K585	E586	M587	S588	A589	D590	S591	L592	A593	N594	V595	P596	F597	G598	E599	Q600
A481	T482	L483	V484	L485	S486	L487	G488	E489	T490	V491	E492	E493	V494	T495	D496	S497	F498	F499	L500	G501	T502	T503	P504	T505	L506	S507	C508	S509	L510	L511	G512	D513	D514	A515	L516	V517	Q518	V519	Y520	P521	D522	G523	L524	R525	H526	I527	R528	A529	G531	R532	L533	A534	N535	E536	K537	T538	P539	G540	
P421	Q422	L423	Y424	V425	A426	C427	G428	R429	G430	P431	R432	S433	S434	L435	R436	V437	L438	R439	HIS	G441	L442	E443	V444	S445	E446	M447	A448	V449	S450	L451	L452	P453	G454	N455	P456	N457	A458	V459	W460	T461	V462	R463	R464	H465	L466	E467	D468	E469	F470	D471	A472	Y473	L474	L475	V476	S477	F478	V479	N480
I361	A362	H363	L364	G365	D366	D367	D368	E369	E370	F371	E372	F373	S374	S375	A376	R377	PRO	LEU	GLU	GLU	GLY	ASP	T384	F385	F386	F387	Q388	P389	R390	P391	L392	K393	N394	L395	V396	L397	V398	D399	E400	L401	D402	S403	L404	S405	P406	L407	L408	F409	C410	Q411	L412	A413	D414	L415	A416	N417	E418	D419	T420
F301	L302	A303	Q304	T305	E306	Q307	G308	D309	T310	F311	K312	S313	T314	L315	E316	T317	D318	E319	D320	K321	V322	T323	E324	I325	K326	L327	K328	Y329	F330	D331	T332	V333	P334	V335	A336	A337	A338	K339	C340	V341	L342	K343	T344	G345	L346	L347	F348	V349	A350	S351	E352	F353	G354	N355	H356	Y357	L358	Y359	Q360
G241	S242	D243	G244	P245	S246	G247	V248	L249	T250	C251	S252	E253	N254	Y255	T256	T257	Y258	K259	N260	F261	G262	D263	Q264	P265	D266	L267	R268	C269	P270	I271	P272	R273	R274	R275	N276	D277	L278	D279	D280	P281	E282	R283	G284	M285	T286	F287	V288	C289	S290	A291	T292	H293	G294	T295	K296	S297	N298	F299	F300
M181	F182	A183	C184	L185	E186	M187	D188	Y189	E190	E191	A192	D193	N194	D195	P196	T197	G198	E199	A200	A201	A202	M203	T204	N205	Q206	T207	L208	T209	F210	Y211	E212	L213	D214	L215	G216	L217	N218	H219	V220	V221	R222	K223	V224	S225	E226	P227	L228	E229	H231	G232	M233	F234	L235	T236	T237	V238	P239	Q240	
L121	A122	V123	D124	K125	K126	G127	R128	A129	V130	M131	I132	S133	A134	I135	E136	K137	Q138	K139	L140	V141	Y142	I143	S144	G145	N146	D147	A148	A149	F150	R151	L152	T153	I154	S155	S156	L157	L158	E159	A160	H161	K162	A163	N164	T165	L166	V167	Y168	H169	V170	V171	G172	V173	D174	V175	G176	F177	E178	N179	P180
V61	I62	R63	S64	L65	M66	A67	F68	R69	L70	T71	G72	G73	T74	K75	D76	Y77	I78	V79	V80	G81	V82	S83	D84	G85	R86	I87	V88	I89	L90	E91	Y92	Q93	P94	S95	K96	N97	M98	F99	E100	K101	I102	H103	Q104	E105	T106	F107	G108	K109	V110	G111	C112	R113	L114	T115	V116	P117	G118	Q119	F120

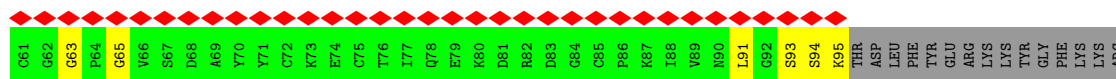


• Molecule 44: SF3b14a, Splicing factor 3B subunit 6



• Molecule 45: PHD finger-like domain-containing protein 5A





P1298	S1230	L1153	L1072	N978	L762	T642	L559	R490	HIS	TTR	GLU	SER
T1299	E1231	Y1154	E1073	F979	E767	E643	A560	A491	PHE	GLN	CYS	ALA
L3001	V1232	L1155		Q980	Q768	E644	T561	A492	ASN	HIS	LEU	ASN
L1302	I1233	L1156		Q981	C769		Y562	A493	ASN	GLU	GLN	VAL
D1303	H1235	H1158		A988	K770		G563	E494	LYS	THR	LEU	LEU
L1304	H1236	E1159					I564	T495	GLU	LYS	VAL	SER
Q1305	E1237	E1159		Y991	K775	I649	T565	D496	C428	GLU	LEU	GLY
P1306	Y1238	E1163		Y992	D776	G650	V566	E497	Q429	GLU	LEU	LEU
L1307	F1239	L1164		I993	L777	L651	A567	N498	L430	LEU	GLY	MET
P1308	L1240	I1165		T994		S652	E568	L499	P431	ILE	PHE	SER
L1309	L1241	R1166		N995	Y780	A653	L569	L500	D432	ASN	THR	LYS
K1242	K1242			D996	A783	N657	T570	P504	R436	ARG	PHE	LYS
A1243	A1243	G1171		Y1001		A662	G571			ARG	ILE	ASP
K1244	K1244	K1172		N1002	M789		Q574	A507	R439	ARG	ILE	LEU
Y1245	Y1245	T1173		Q1003	T790	D668	L575	G508	R440	GLU	VAL	PRO
A1246	A1246			L1004	R791	P669	C576	K509	G441	ARG	LEU	ARG
Q1247	Q1247			L1005	W792	A670	K577	T510	E444	VAL	ARG	ASP
D1248	D1248			K1006	D793	K671	E578	N511		GLN	ILE	ASP
E1249	E1249			P1007	R794	G672	E579	V512	A449	SER	HIS	ASP
H1250	H1250			T1008	T795	L673	I580	A513	L450	ALA	ALA	PHE
L1251	L1251			L1009	F674	Y675	S581	L514		MET	THR	THR
I1252	I1252			E1011	N678		A582	M515		MET	LEU	GLN
T1253	T1253			I1012			T583	C516		ASP	LEU	GLN
				I1013	A802		W584	M517		GLU	CYS	GLN
V1256	V1256	L1186		L1014	D803		I585	L518		THR	LEU	LEU
P1257	P1257	L1190		F1015		T688	I586	R519		THR	LEU	SER
F1258	F1258	Q1191		R1016	I806	Y689	V587	E520	E458	MET	LEU	ARG
F1259	F1259	P1192		V1017	V810	V690		I521	E459	ASP	ALA	PHE
E1260	E1260	I1193		F1018				G522	Q460	SER	LEU	TTR
P1261	P1261	T1194		D941	G818		E591	K523	L461	ASP	ALA	ASP
F1262	F1262	T1194		D942		K695	K592	H524	P462	GLN	GLN	ALA
L1263	L1263	L1195		L943	K829	K696	W593	I525	L463	SER	GLY	ALA
Q1264	Q1264	S1196		K944			G600	N526	V464	GLY	GLU	ILE
Y1266	Y1266	T1197		G945	Y834		G601	M526	E465	GLY	ALA	VAL
				D946	S835	K718	E602	M527	K466	LEU	GLY	SER
				P947	P836	N719	R603	D528	L467	ALA	GLU	GLN
				L948	E837		T604	G529	P468	ARG	ARG	LYS
				L949	K838		Y605	I531	K469	ILE	ILE	ALA
				D950	G839		T606	N532	Y470	GLN	MET	ASP
				Q951	R840		Q607	V533	A471	VAL	VAL	LEU
				L954			L608	D534	Q472	GLU	GLU	LEU
							V609	D535	A473	ASP	ASP	ALA
				V957	E843	D740	R610	D535	G474	LEU	PRO	LEU
				H958	G845	M741	L611	F536	F475	VAL	GLU	THR
				T959	A846	C742	L612	K537	E476	PHE	LEU	ALA
				A960	E744	L743	I613	I538	G477	THR	SER	SER
				A961	M852	L745	L614	I539	F478	LYS	LYS	ASP
				L962	R858	D746	D615	M544	K479	GLY	PHE	ASP
				D965	T863	T747	D623		T480	SER	LEU	ARG
									L481			
				D972	L869	F751	V627	E550	N482			
				D973		E754	L628	M551	R483			
				K974		A757	E629	V552	I484			
				T976	S872		A630	G553	Q485			
				Q977	H873		L631	S554	S486			
					G874		V632	F555	K487			
							A633	G556	L488			
							R634		Y489			

D125	VAL	A2005	V2065	V2066	L1945	N1885	M1825	L1755	L1685	Y1619	K1557	A1489	G1422	A1360
LYS	V2067	D2006	V2066	V2067	A1946	D1886	Y1826	T1756	Q1686	L1620	P1558	L1490	N1423	E1361
GLU	T2068	V2007	V2067	V2068	Q1947	P1887	T1827	M1764	M1687	H1621	F1562	S1491	I1424	F1362
ALA	A2008	A2008	V2068	T2068	M1948	H1888	T1828	T1765	V1688	G1623	V1563	A1497	I1425	I1363
THR	G2009	A2008	V2069	T2069	V1949	V1889	I1829	Q1766	A1691	L1624	P1564	K1498	I1426	I1364
ASP	D2070	F2010	D2070	T2070	T1950	K1890	E1830	M1767	N1692	S1625	S1565	A1501	S1427	L1365
ASP	A2071	C2011	A2071	Q1951	Q1951	T1891	I1831	N1767	R1693	P1626	S1566	H1502	T1428	R1366
ASP	K2072	N2012	K2072	A1952	A1952	T1892	F1832	M1769	P1694	E1627	K1567	W1503	K1431	L1367
ASP	S2073	R2013	S2073	M1953	M1953	L1893	M1834	L1773	Q1696	R1629	Q1568	L1504	L1368	L1369
S2074	S2073	Y2014	S2074	W1954	W1954	L1894	S1835	Q1774	L1695	E1628	T1569	G1505	Q1370	Q1370
S2075	S2075	P2015	S2075	S1955	S1955	L1895	L1836	Q1775	Q1696	R1630	R1570	C1506	S1371	S1371
L2076	L2076	N2016	L2076	L1956	L1956	A1897	M1837	G1776	D1698	V1632	T1572	S1507	E1373	E1373
L2077	L2077	I2017	L2077	D1957	D1957	H1898	A1838	I1776	E1699	E1633	I1574	A1508	G1374	G1374
S2078	S2078	E2018	S2078	S1958	S1958	L1899	K1839	S1777	G1700	E1633	I1574	T1509	R1375	R1375
I2079	I2079	L2019	I2079	Y1959	Y1959	S1900	T1840	H1778	A1701	Q1634	D1575	S1510	Q1441	C1376
K2080	K2080	S2020	K2080	L1960	L1960	R1901	K1841	R1779	C1702	L1635	I1576	F1512	R1442	T1380
L2081	L2081	Y2021	L2081	K1961	K1961	M1902	V1842	H1780	V1703	F1636	L1577	M1513	R1443	F1381
L2082	L2082	E2022	L2082	Q1962	Q1962	L1903	R1843	L1781	C1706	S1637	T1578	F1514	N1444	M1382
T2083	T2083	V2023	T2083	L1963	L1963	Q1904	G1844	S1782	Q1707	S1638	T1579	H1515	V1445	E1383
L2084	L2084	V2024	L2084	P1964	P1964	L1904	G1844	S1782	G1708	G1639	T1579	P1516	Q1446	A1384
Q2085	Q2085	D2025	Q2085	H1965	H1965	S1905	I1846	H1784	S1709	A1640	C1580	M1517	N1447	L1385
Q2086	Q2086	K2026	Q2086	F1966	F1966	A1906	I1846	H1784	S1709	A1640	C1580	M1517	N1447	L1385
K2087	K2087	D2027	K2087	T1967	T1967	E1907	E1847	L1785	D1712	V1644	D1583	P1520	N1449	E1387
A2088	A2088	S2028	A2088	S1968	S1968	L1908	I1848	S1786	F1713	V1644	D1583	P1520	N1449	E1387
K2089	K2089	I2029	K2089	E1969	E1969	Q1909	I1849	E1787	F1714	V1644	D1583	P1520	N1449	E1387
V2090	V2090	R2030	V2090	H1970	H1970	S1910	S1850	L1788	K1715	L1650	Q1585	V1521	L1450	Q1388
K2091	K2091	S2031	K2091	I1971	I1971	D1911	M1851	V1789	K1716	C1651	Q1586	P1522	F1451	V1389
L2092	L2092	G2032	L2092	K1972	K1972	E1913	A1852	E1790	F1717	W1652	Q1587	L1523	V1452	M1391
D2093	D2093	P2033	D2093	A1973	A1973	E1914	E1854	T1792	L1718	W1652	Q1588	E1524	D1454	D1392
P2094	P2094	G2034	P2094	C1974	C1974	I1915	Y1855	L1793	E1719	G1653	F1589	Q1528	E1455	W1393
V2095	V2095	V2035	V2095	T1975	T1975	L1916	Y1855	L1793	E1720	G1654	F1589	Q1528	E1455	W1393
A2096	A2096	V2036	A2096	D1976	D1976	S1917	M1857	D1795	P1721	M1655	F1589	Q1528	E1455	W1393
P2097	P2097	V2037	P2097	K1977	K1977	K1918	I1858	L1796	L1722	V1656	F1589	Q1528	E1455	W1393
A2098	A2098	L2038	A2098	G1978	G1978	A1919	I1859	E1797	E1725	A1657	F1589	Q1528	E1455	W1393
T2099	T2099	V2039	T2099	V1979	V1979	I1920	P1859	Q1798	E1725	A1657	F1589	Q1528	E1455	W1393
G2100	G2100	Q2040	G2100	E1980	E1980	R1921	H1862	K1800	L1728	I1663	F1589	Q1528	E1455	W1393
A2101	A2101	L2041	A2101	S1981	S1981	I1922	H1862	K1800	L1728	I1663	F1589	Q1528	E1455	W1393
H2102	H2102	E2042	H2102	V1982	V1982	I1923	H1863	C1801	D1729	M1664	F1589	Q1528	E1455	W1393
N2103	N2103	R2043	N2103	F1983	F1983	Q1924	E1864	I1802	H1730	M1664	F1589	Q1528	E1455	W1393
Y2104	Y2104	E2044	Y2104	D1984	D1984	A1925	D1865	S1803	C1731	M1664	F1589	Q1528	E1455	W1393
L2105	L2105	E2045	L2105	I1985	I1985	C1926	M1866	I1804	M1732	T1666	D1596	Q1536	L1467	R1400
L2106	L2106	E2046	L2106	M1986	M1986	V1927	M1867	I1804	H1733	Q1667	D1596	Q1536	L1467	R1400
Y2107	Y2107	V2047	Y2107	E1987	E1987	D1928	L1868	I1804	H1733	Q1667	D1596	Q1536	L1467	R1400
F2108	F2108	T2048	F2108	M1988	M1988	V1929	L1869	E1807	I1740	G1671	S1605	L1540	I1470	L1401
M2109	M2109	G2049	M2109	E1989	E1989	L1930	R1869	E1807	I1740	G1671	S1605	L1540	I1470	L1401
S2110	S2110	P2050	S2110	D1990	D1990	S1931	Q1870	M1808	V1741	M1670	S1605	L1540	I1470	L1401
D2111	D2111	V2051	D2111	E1991	E1991	S1932	L1871	D1809	T1742	M1670	S1605	L1540	I1470	L1401
A2112	A2112	T2052	A2112	I1992	I1992	S1933	L1872	V1810	K1743	K1672	S1605	L1540	I1470	L1401
Y2113	Y2113	A2053	Y2113	R1993	R1993	G1934	Q1873	A1811	E1746	I1673	S1607	L1541	C1471	K1403
M2114	M2114	P2054	M2114	N1994	N1994	W1935	K1874	P1812	M1747	H1674	S1607	L1541	C1471	K1403
G2115	G2115	L2055	G2115	A1995	A1995	L1936	V1875	L1813	M1747	A1675	T1608	M1542	S1472	K1404
C2116	C2116	F2056	C2116	L1996	L1996	S1937	P1876	M1814	K1748	A1675	T1608	M1542	S1472	K1404
D2117	D2117	P2057	D2117	L1997	L1997	F1938	H1877	V1677	Q1749	V1676	L1609	A1543	R1473	V1405
Q2118	Q2118	Q2058	Q2118	Q1998	Q1998	A1939	K1878	D1678	D1750	D1678	L1610	A1543	R1473	V1405
E2119	E2119	K2059	E2119	L1999	L1999	L1940	L1879	Y1679	A1751	I1673	L1612	K1552	Y1476	T1408
L2120	L2120	R2060	L2120	T2000	T2000	A1941	M1881	D1752	V1752	I1681	L1614	K1553	Y1476	T1408
K2121	K2121	E2061	K2121	D2001	D2001	A1942	P1882	D1753	D1753	Y1682	L1614	K1553	Y1476	T1408
F2122	F2122	G2062	F2122	S2123	S2123	M1943	K1883	Y1754	Y1754	V1684	G1616	K1556	I1487	V1488
S2123	S2123	W2064	S2123	I2004	I2004	E1944	F1884	L1824	Y1754	V1684	G1616	K1556	I1487	V1488

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	137853	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.251	Depositor
Minimum map value	-0.129	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.03	Depositor
Map size (\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 (\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, MG, GTP

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	0.47	0/17735	0.64	10/23951 (0.0%)
2	I	0.52	0/3214	0.97	7/4998 (0.1%)
3	B	0.47	0/2698	1.05	25/4195 (0.6%)
4	F	0.50	1/2230 (0.0%)	1.02	9/3468 (0.3%)
5	G	0.65	6/1793 (0.3%)	0.93	2/2783 (0.1%)
6	O	0.50	0/1180	0.65	1/1594 (0.1%)
7	C	0.38	0/6584	0.63	1/8942 (0.0%)
8	N	0.44	0/4568	0.60	2/6320 (0.0%)
9	M	0.36	0/974	0.60	0/1316
10	L	0.36	0/2912	0.60	0/3924
11	9	0.77	0/1091	0.91	3/1478 (0.2%)
12	J	0.50	0/1278	0.61	0/1657
13	U	0.22	0/254	0.48	0/314
13	a	0.50	0/343	0.69	0/427
13	i	0.50	0/343	0.69	0/427
14	V	0.22	0/333	0.47	0/416
14	b	0.57	0/327	0.67	0/407
14	j	0.56	0/327	0.68	0/407
15	P	0.23	0/298	0.48	0/370
15	c	0.69	0/387	0.72	0/482
15	k	0.70	0/338	0.73	0/419
16	Q	0.24	0/291	0.49	0/363
16	d	0.77	0/295	0.76	0/367
16	l	0.78	0/295	0.76	0/367
17	R	0.22	0/313	0.49	0/390
17	e	0.65	0/315	0.75	0/392
17	m	0.64	0/315	0.75	0/392
18	S	0.24	0/297	0.51	0/371
18	f	0.54	0/295	0.61	0/367
18	n	0.55	0/270	0.63	0/334
19	T	0.23	0/287	0.49	0/358
19	g	0.47	0/322	0.55	0/399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	h	0.47	0/318	0.56	0/394
20	E	0.67	0/1195	0.71	0/1492
21	X	0.24	0/379	0.35	0/530
22	W	0.25	0/853	0.47	0/1188
23	A0	0.38	0/591	0.84	2/799 (0.3%)
24	0	0.22	0/224	0.29	0/312
25	Z	0.23	0/888	0.40	0/1241
26	8	0.22	0/276	0.43	0/383
27	Y	0.24	0/2265	0.45	0/3156
28	H	0.85	11/2576 (0.4%)	1.43	55/4003 (1.4%)
29	o	0.63	0/647	1.42	0/807
30	p	0.61	0/375	1.20	0/467
31	u	0.22	0/493	0.42	0/611
32	v	0.21	0/373	0.58	1/461 (0.2%)
33	w	0.25	0/1688	0.47	0/2102
34	q	0.42	0/359	0.67	0/447
35	r	0.47	0/294	0.75	0/364
36	s	0.34	0/294	0.61	0/364
37	t	0.43	0/286	0.59	0/354
38	x	0.43	0/279	0.72	0/347
39	y	0.38	0/258	0.61	0/319
40	z	0.41	0/242	0.64	0/299
41	K	0.27	0/1818	0.63	0/2308
42	1	1.04	4/4184 (0.1%)	0.83	2/5216 (0.0%)
43	3	0.85	0/4664	0.76	0/5816
44	5	0.79	0/431	0.79	0/537
45	6	0.73	0/355	0.68	0/442
46	7	1.01	0/263	0.77	0/327
47	2	0.74	0/722	0.72	0/892
48	4	0.62	0/311	0.64	0/387
49	D	0.30	0/6795	0.58	0/8492
All	All	0.54	22/87198 (0.0%)	0.75	120/117252 (0.1%)

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	12
7	C	0	6
8	N	0	8

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Mol	Chain	#Chirality outliers	#Planarity outliers
15	c	0	1
15	k	0	1
23	A0	0	2
33	w	0	1
42	1	0	11
43	3	0	11
44	5	0	1
46	7	0	1
47	2	0	3
49	D	0	1
All	All	0	59

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	1	407	MET	N-CA	12.36	1.71	1.46
42	1	406	ALA	C-N	7.99	1.52	1.34
28	H	142	C	C1'-N1	7.29	1.59	1.48
42	1	1243	PRO	N-CA	-7.11	1.35	1.47
28	H	182	U	C1'-N1	6.93	1.59	1.48

The worst 5 of 120 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	H	167	U	C5-C4-O4	11.72	132.93	125.90
23	A0	8	ASP	CB-CG-OD1	10.83	128.05	118.30
42	1	406	ALA	C-N-CA	10.26	147.36	121.70
28	H	164	C	N1-C2-O2	-10.13	112.82	118.90
8	N	277	LEU	CA-CB-CG	9.42	136.96	115.30

There are no chirality outliers.

5 of 59 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	MET	Peptide
1	A	211	GLN	Peptide
1	A	408	PRO	Peptide
1	A	463	PRO	Peptide
1	A	802	THR	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	17290	0	16495	383	0
2	I	2881	0	1461	123	0
3	B	2420	0	1226	94	0
4	F	1995	0	1006	61	0
5	G	1612	0	821	192	0
6	O	1152	0	1123	21	0
7	C	6440	0	6465	127	0
8	N	4518	0	3121	96	0
9	M	962	0	1012	12	0
10	L	2874	0	2856	46	0
11	9	1087	0	921	252	0
12	J	1273	0	903	32	0
13	U	256	0	70	2	0
13	a	344	0	93	0	0
13	i	344	0	93	0	0
14	V	334	0	92	1	0
14	b	328	0	89	0	0
14	j	328	0	89	0	0
15	P	300	0	80	4	0
15	c	388	0	102	0	0
15	k	340	0	87	0	0
16	Q	292	0	93	6	0
16	d	296	0	87	0	0
16	l	296	0	87	0	0
17	R	314	0	86	3	0
17	e	316	0	85	0	0
17	m	316	0	85	0	0
18	S	298	0	89	5	0
18	f	296	0	84	0	0
18	n	272	0	75	0	0
19	T	288	0	84	1	0
19	g	324	0	89	0	0
19	h	320	0	88	0	0
20	E	1196	0	337	2	0
21	X	378	0	190	1	0
22	W	844	0	426	16	0
23	A0	581	0	567	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	0	225	0	98	2	0
25	Z	883	0	414	6	0
26	8	277	0	114	2	0
27	Y	2258	0	1064	38	0
28	H	2311	0	1170	141	0
29	o	648	0	167	0	0
30	p	376	0	102	0	0
31	u	496	0	118	0	0
32	v	376	0	85	0	0
33	w	1693	0	454	0	0
34	q	360	0	95	0	0
35	r	296	0	76	0	0
36	s	296	0	77	0	0
37	t	288	0	78	0	0
38	x	280	0	81	0	0
39	y	260	0	75	0	0
40	z	244	0	71	0	0
41	K	1821	0	759	50	0
42	1	4192	0	1110	173	0
43	3	4672	0	1260	62	0
44	5	432	0	114	6	0
45	6	356	0	105	7	0
46	7	264	0	70	8	0
47	2	728	0	183	8	0
48	4	312	0	87	3	0
49	D	6796	0	1778	106	0
50	A	36	0	6	9	0
51	C	32	0	12	0	0
52	C	1	0	0	0	0
All	All	85302	0	50580	1753	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 14.

The worst 5 of 1753 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:1790:ILE:HD13	11:9:266:PHE:CE2	1.27	1.66
11:9:352:GLU:HG3	11:9:357:ALA:CB	1.28	1.59
1:A:1790:ILE:HD13	11:9:266:PHE:CD2	1.40	1.54
42:1:407:MET:N	42:1:407:MET:CA	1.71	1.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1790:ILE:CD1	11:9:266:PHE:CE2	1.92	1.46

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2203/2335 (94%)	2043 (93%)	150 (7%)	10 (0%)	25	58
6	O	139/142 (98%)	125 (90%)	13 (9%)	1 (1%)	19	52
7	C	814/972 (84%)	756 (93%)	54 (7%)	4 (0%)	25	58
8	N	773/941 (82%)	685 (89%)	78 (10%)	10 (1%)	10	39
9	M	122/128 (95%)	118 (97%)	4 (3%)	0	100	100
10	L	372/499 (74%)	351 (94%)	21 (6%)	0	100	100
11	9	155/800 (19%)	141 (91%)	13 (8%)	1 (1%)	22	55
12	J	221/683 (32%)	207 (94%)	12 (5%)	2 (1%)	14	45
13	U	60/231 (26%)	57 (95%)	3 (5%)	0	100	100
13	a	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
13	i	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
14	V	80/119 (67%)	76 (95%)	4 (5%)	0	100	100
14	b	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
14	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
15	P	70/118 (59%)	68 (97%)	2 (3%)	0	100	100
15	c	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
15	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
16	Q	69/86 (80%)	67 (97%)	2 (3%)	0	100	100
16	d	72/86 (84%)	69 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	l	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
17	R	76/92 (83%)	70 (92%)	6 (8%)	0	100	100
17	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
17	m	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
18	S	71/76 (93%)	67 (94%)	4 (6%)	0	100	100
18	f	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
18	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
19	T	69/126 (55%)	69 (100%)	0	0	100	100
19	g	77/126 (61%)	75 (97%)	2 (3%)	0	100	100
19	h	76/126 (60%)	75 (99%)	1 (1%)	0	100	100
20	E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	3	26
21	X	73/376 (19%)	70 (96%)	3 (4%)	0	100	100
22	W	167/177 (94%)	158 (95%)	9 (5%)	0	100	100
23	A0	71/73 (97%)	68 (96%)	3 (4%)	0	100	100
24	0	43/439 (10%)	42 (98%)	1 (2%)	0	100	100
25	Z	174/312 (56%)	158 (91%)	15 (9%)	1 (1%)	22	55
26	8	54/199 (27%)	47 (87%)	7 (13%)	0	100	100
27	Y	445/513 (87%)	432 (97%)	12 (3%)	1 (0%)	44	74
29	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	10	39
30	p	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
31	u	118/793 (15%)	106 (90%)	6 (5%)	6 (5%)	1	17
32	v	88/464 (19%)	63 (72%)	16 (18%)	9 (10%)	0	7
33	w	413/501 (82%)	367 (89%)	41 (10%)	5 (1%)	11	40
34	q	88/95 (93%)	77 (88%)	7 (8%)	4 (4%)	2	19
35	r	70/102 (69%)	64 (91%)	3 (4%)	3 (4%)	2	20
36	s	70/139 (50%)	63 (90%)	6 (9%)	1 (1%)	9	37
37	t	68/91 (75%)	63 (93%)	4 (6%)	1 (2%)	8	37
38	x	68/80 (85%)	64 (94%)	2 (3%)	2 (3%)	3	26
39	y	61/103 (59%)	56 (92%)	5 (8%)	0	100	100
40	z	57/96 (59%)	52 (91%)	4 (7%)	1 (2%)	7	34
41	K	406/522 (78%)	343 (84%)	62 (15%)	1 (0%)	44	74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	1	1032/1304 (79%)	844 (82%)	166 (16%)	22 (2%)	5	32
43	3	1152/1217 (95%)	1053 (91%)	89 (8%)	10 (1%)	14	45
44	5	106/125 (85%)	84 (79%)	19 (18%)	3 (3%)	4	27
45	6	87/110 (79%)	76 (87%)	10 (12%)	1 (1%)	12	42
46	7	64/86 (74%)	55 (86%)	7 (11%)	2 (3%)	3	25
47	2	170/895 (19%)	151 (89%)	15 (9%)	4 (2%)	5	29
48	4	76/424 (18%)	75 (99%)	1 (1%)	0	100	100
49	D	1697/2136 (79%)	1604 (94%)	82 (5%)	11 (1%)	22	55
All	All	13852/21253 (65%)	12701 (92%)	1024 (7%)	127 (1%)	17	45

5 of 127 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	C	474	LEU
8	N	842	HIS
12	J	541	VAL
20	E	193	THR
27	Y	383	CYS

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	1775/2108 (84%)	1742 (98%)	33 (2%)	52	69
6	O	126/130 (97%)	123 (98%)	3 (2%)	44	62
7	C	719/866 (83%)	710 (99%)	9 (1%)	65	76
8	N	196/792 (25%)	185 (94%)	11 (6%)	17	43
9	M	108/111 (97%)	108 (100%)	0	100	100
10	L	299/424 (70%)	292 (98%)	7 (2%)	45	63
11	9	81/681 (12%)	54 (67%)	27 (33%)	0	1
12	J	72/599 (12%)	67 (93%)	5 (7%)	13	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	X	2/333 (1%)	2 (100%)	0	100	100
22	W	10/148 (7%)	10 (100%)	0	100	100
23	A0	60/66 (91%)	56 (93%)	4 (7%)	13	38
25	Z	6/293 (2%)	6 (100%)	0	100	100
27	Y	11/450 (2%)	11 (100%)	0	100	100
41	K	29/442 (7%)	17 (59%)	12 (41%)	0	0
All	All	3494/7443 (47%)	3383 (97%)	111 (3%)	36	56

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	L	161	ASN
41	K	139	VAL
11	9	260	GLU
41	K	138	SER
41	K	86	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1894	GLN
7	C	837	GLN
23	A0	67	ASN
11	9	291	ASN
6	O	70	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	I	133/144 (92%)	54 (40%)	5 (3%)
28	H	105/188 (55%)	22 (20%)	3 (2%)
3	B	114/117 (97%)	43 (37%)	6 (5%)
4	F	90/107 (84%)	32 (35%)	5 (5%)
5	G	76/274 (27%)	44 (57%)	15 (19%)
All	All	518/830 (62%)	195 (37%)	34 (6%)

5 of 195 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	I	2	G
2	I	9	G
2	I	11	A
2	I	12	G
2	I	18	G

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	G	153	C
5	G	155	U
28	H	164	C
4	F	35	A
4	F	28	A

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 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
51	GTP	C	1500	52	26,34,34	1.40	3 (11%)	32,54,54	1.79	8 (25%)
50	IHP	A	3000	-	36,36,36	0.82	0	54,60,60	1.20	2 (3%)

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
51	GTP	C	1500	52	-	6/18/38/38	0/3/3/3
50	IHP	A	3000	-	-	6/30/54/54	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	C	1500	GTP	C5-C6	-5.03	1.37	1.47
51	C	1500	GTP	C2-N3	2.38	1.38	1.33
51	C	1500	GTP	O4'-C4'	-2.00	1.40	1.45

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	C	1500	GTP	PB-O3B-PG	-5.03	115.58	132.83
51	C	1500	GTP	PA-O3A-PB	-4.55	117.22	132.83
50	A	3000	IHP	C6-C5-C4	3.80	118.73	110.41
51	C	1500	GTP	C3'-C2'-C1'	3.17	105.76	100.98
51	C	1500	GTP	C5-C6-N1	2.94	119.14	113.95

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
50	A	3000	IHP	C2-O12-P2-O42
50	A	3000	IHP	C3-O13-P3-O23
51	C	1500	GTP	C3'-C4'-C5'-O5'
51	C	1500	GTP	C4'-C5'-O5'-PA
51	C	1500	GTP	O4'-C4'-C5'-O5'

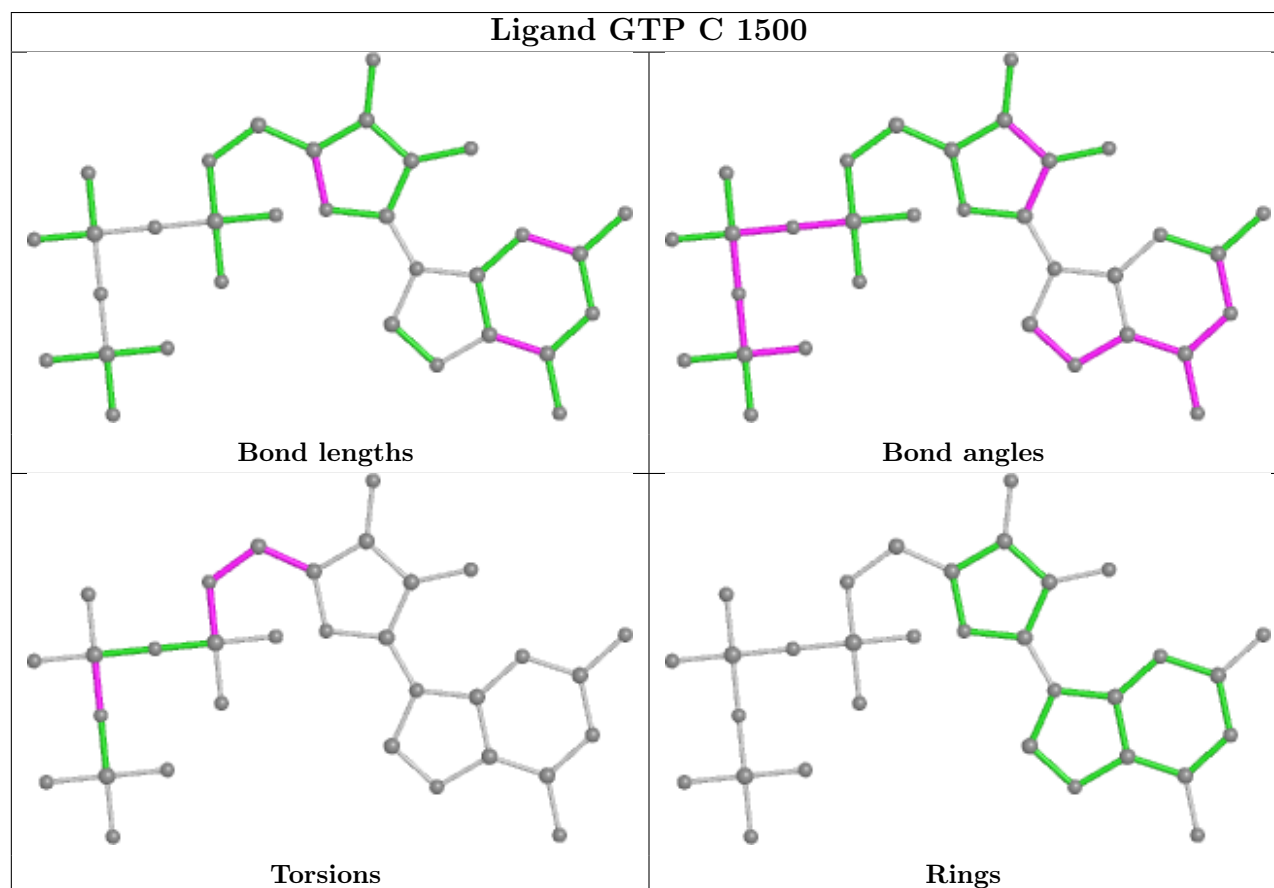
There are no ring outliers.

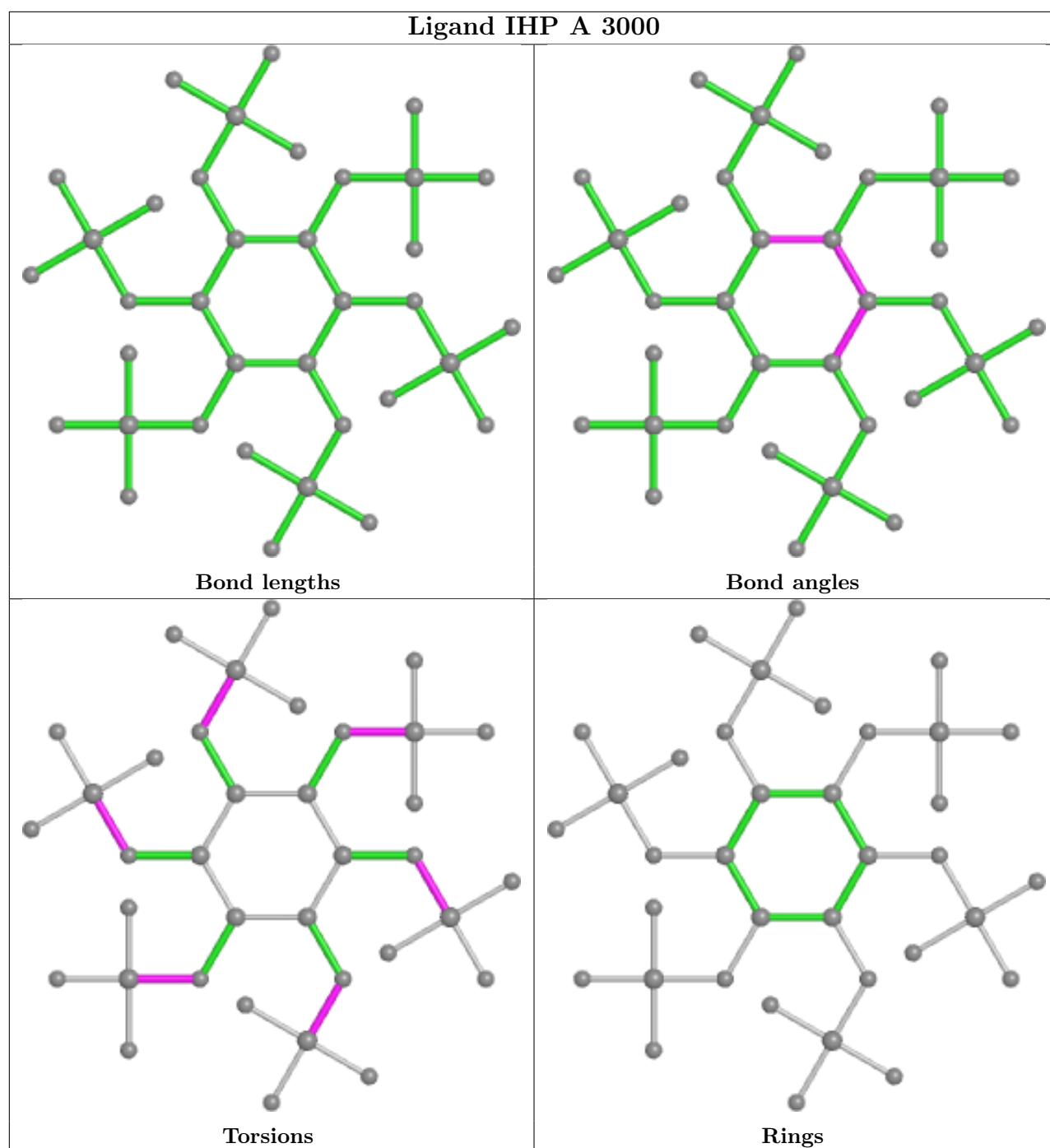
1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
50	A	3000	IHP	9	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.

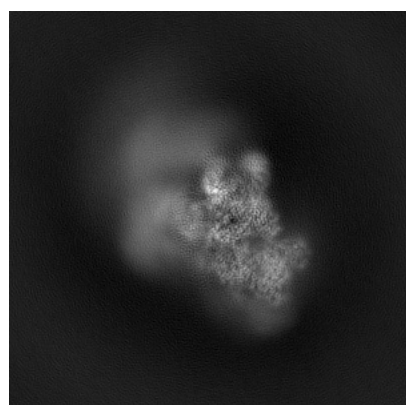
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9624. These allow visual inspection of the internal detail of the map and identification of artifacts.

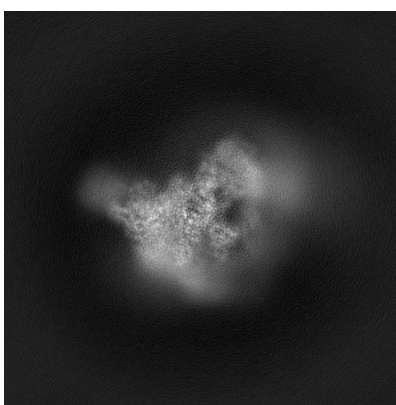
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

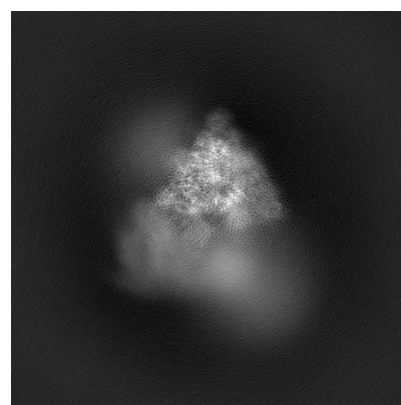
6.1.1 Primary map



X



Y

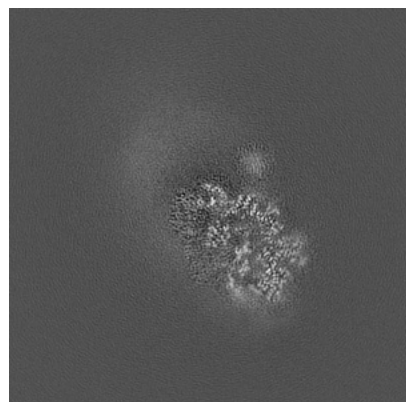


Z

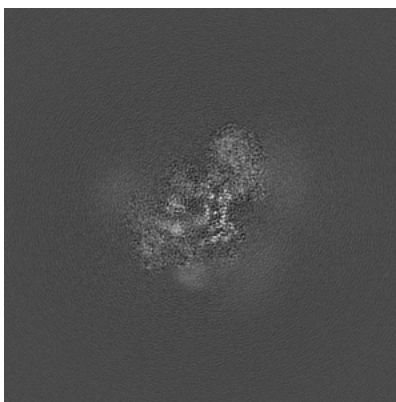
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

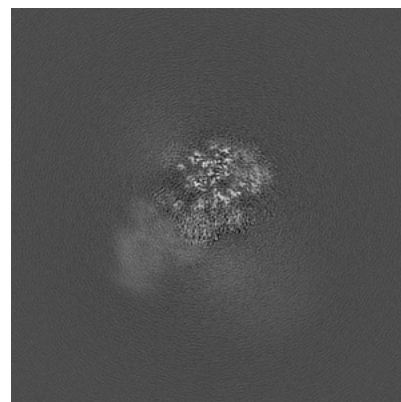
6.2.1 Primary map



X Index: 200



Y Index: 200

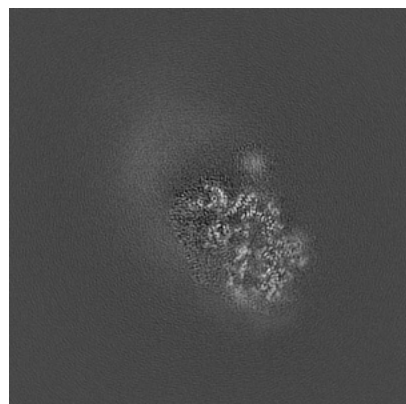


Z Index: 200

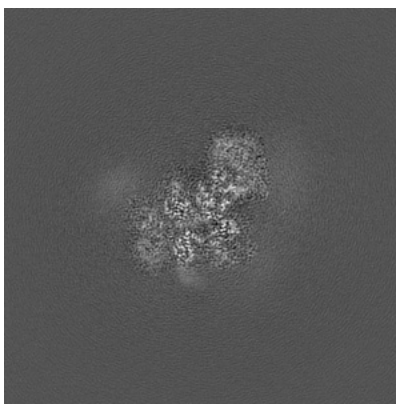
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

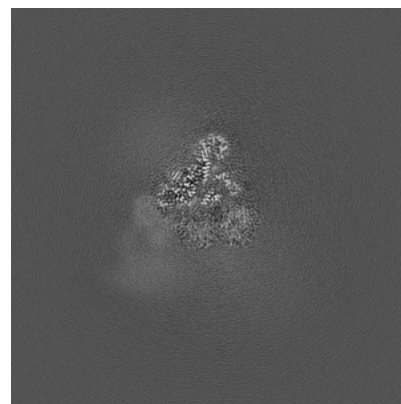
6.3.1 Primary map



X Index: 201



Y Index: 207

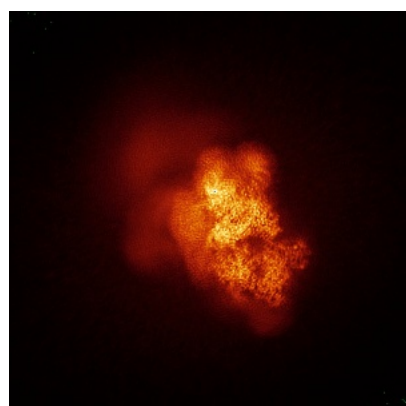


Z Index: 181

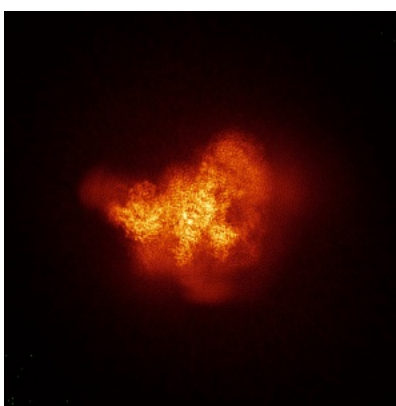
The images above show the largest variance slices of the map in three orthogonal directions.

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

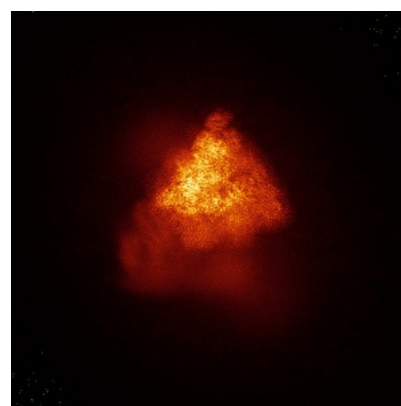
6.4.1 Primary map



X



Y

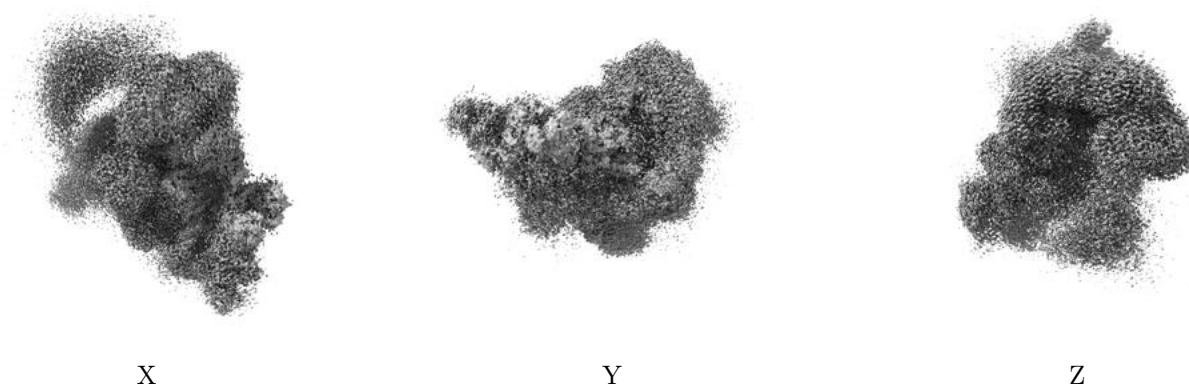


Z

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

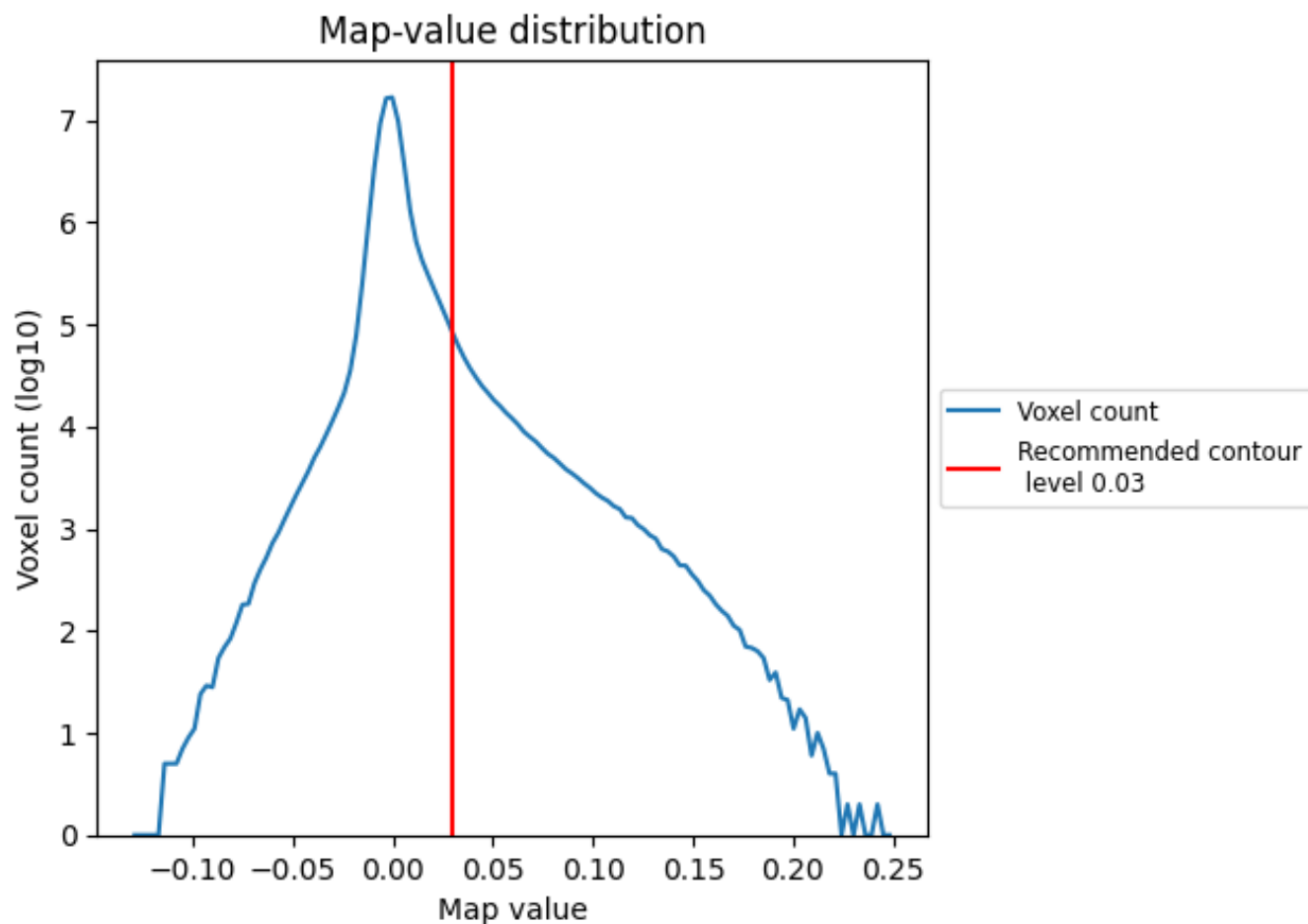
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

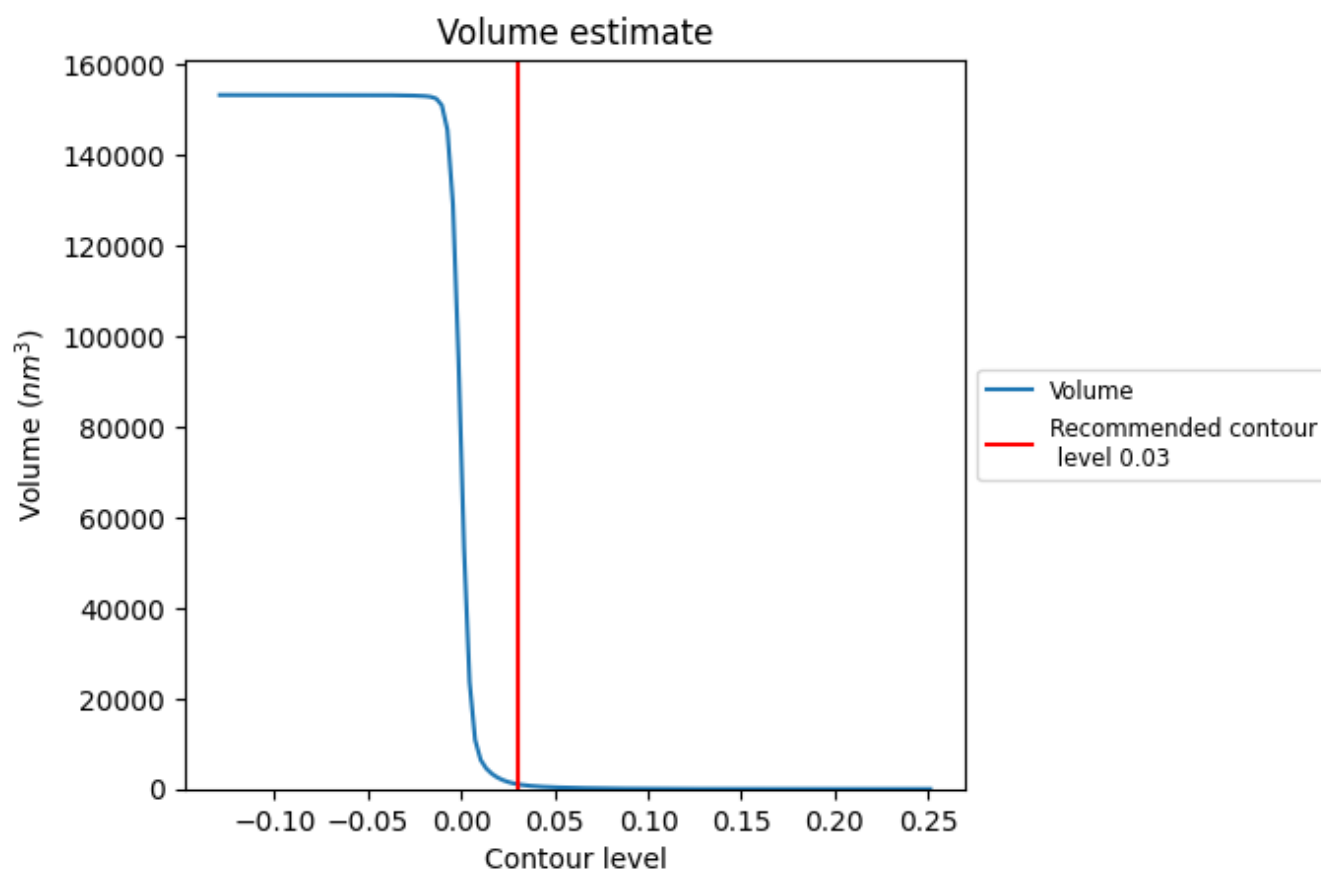
This section contains the results of statistical analysis of the map.

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.

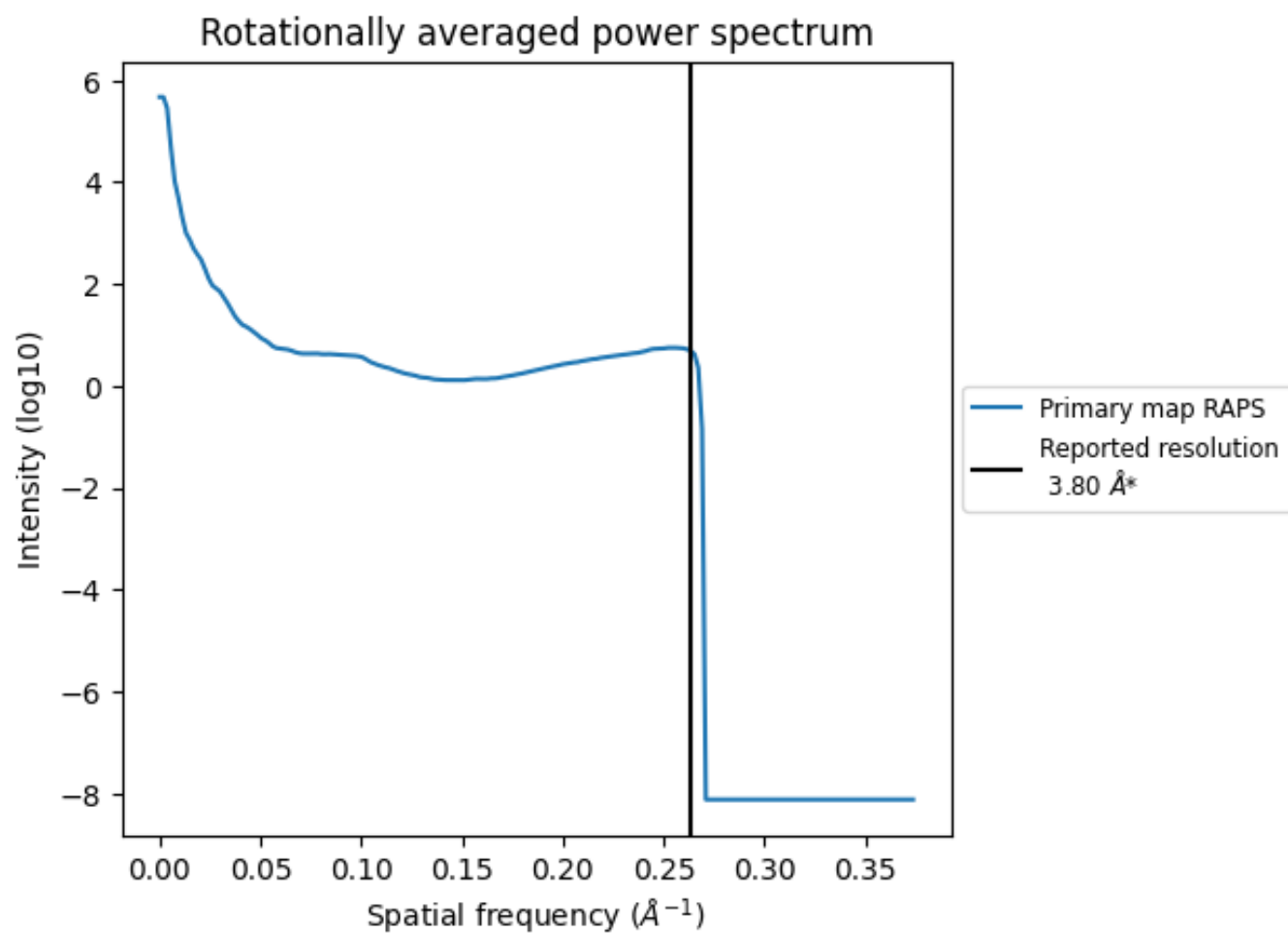
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1073 nm³; this corresponds to an approximate mass of 969 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 0.263 \AA^{-1}

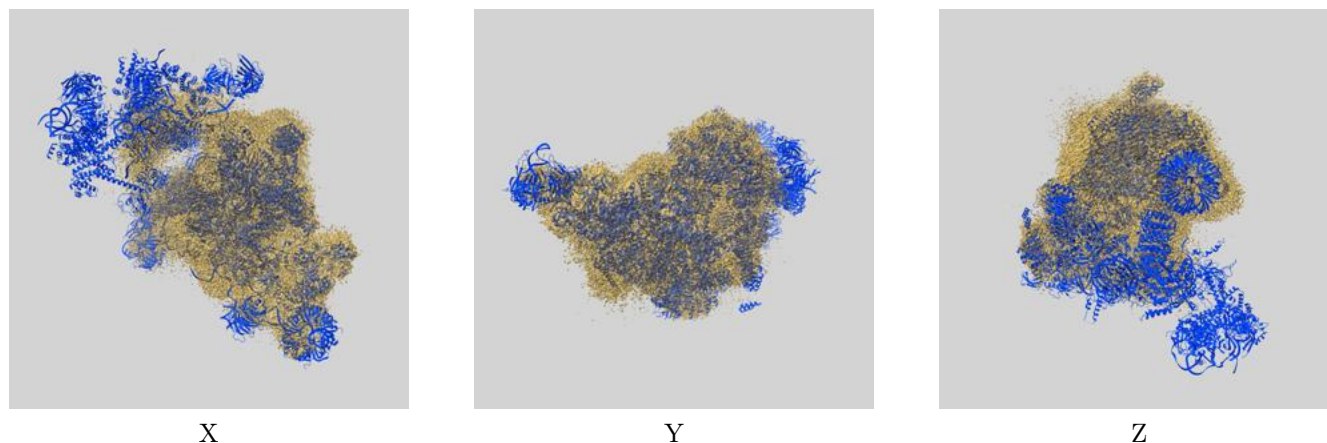
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

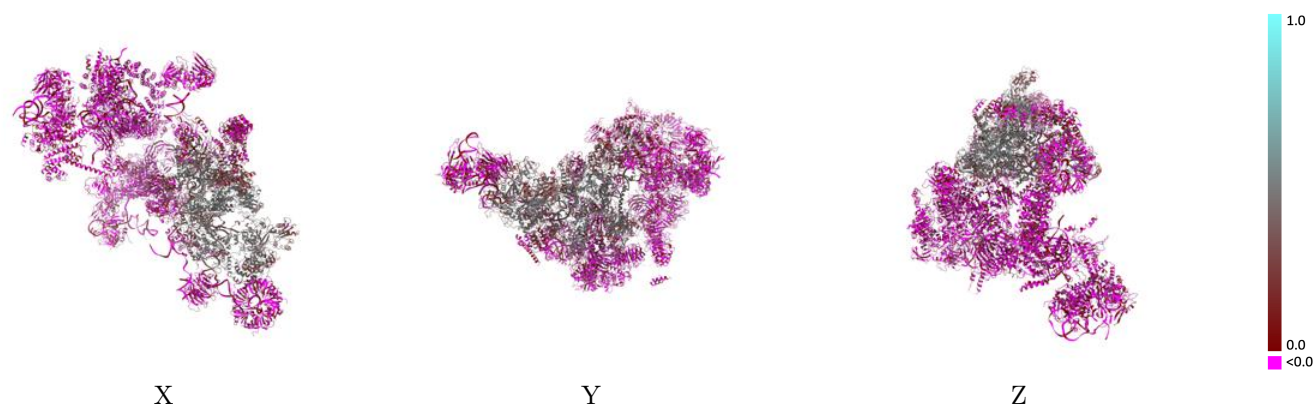
This section contains information regarding the fit between EMDB map EMD-9624 and PDB model 6AHD. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



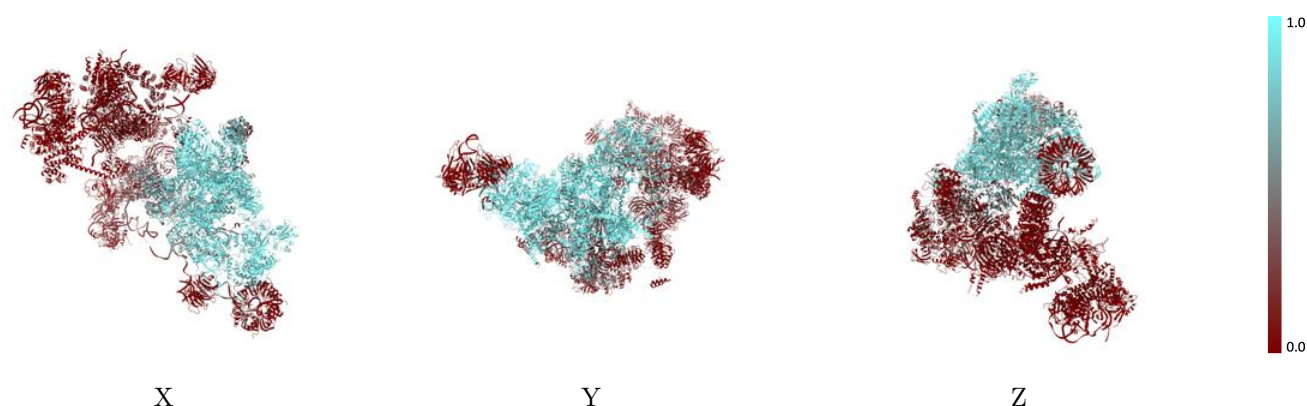
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



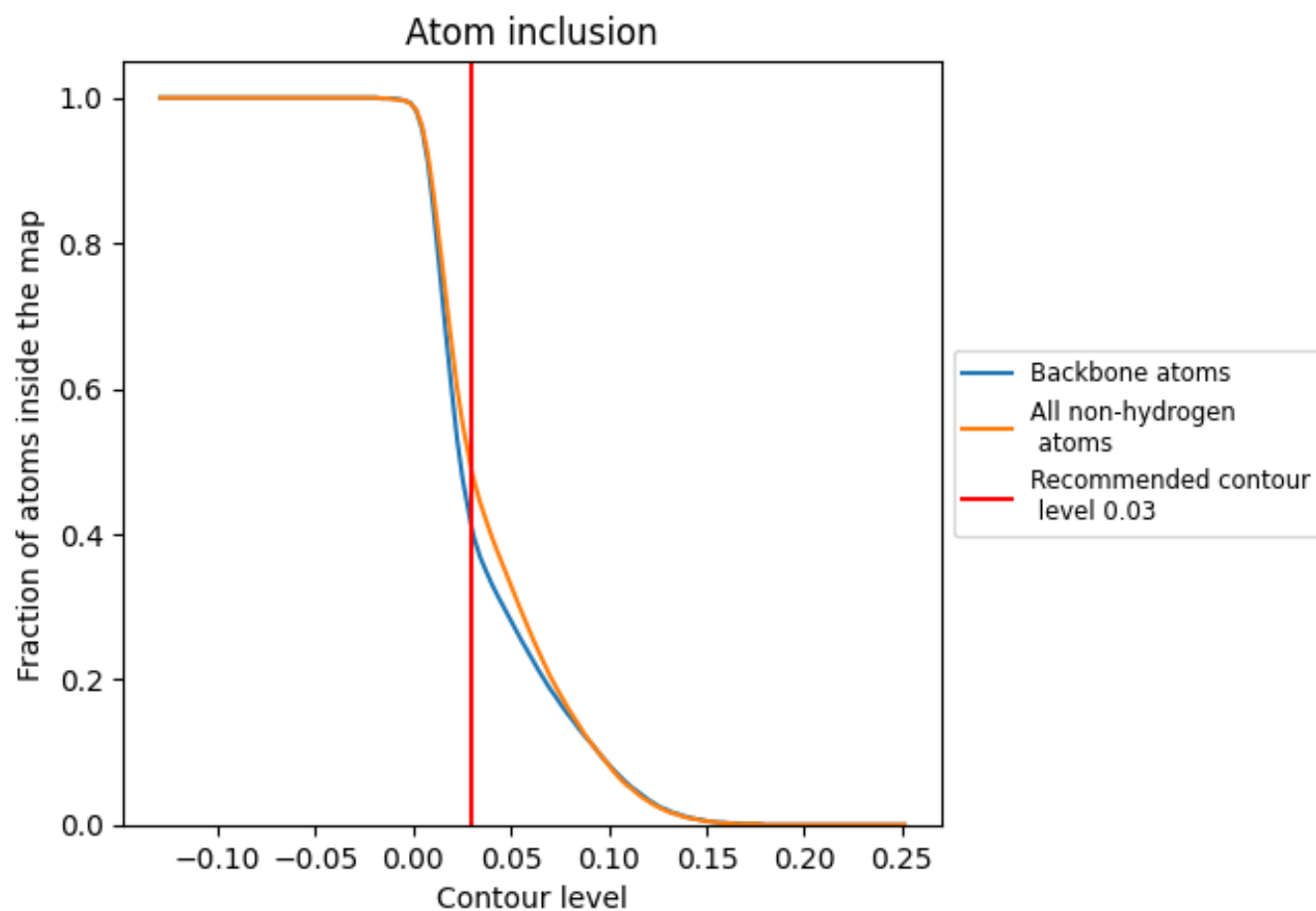
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 41% of all backbone atoms, 48% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4850	 0.1890
0	 0.4620	 0.0350
1	 0.0200	 -0.0020
2	 0.0510	 0.0150
3	 0.0100	 -0.0120
4	 0.0450	 0.0080
5	 0.0000	 -0.0120
6	 0.0450	 0.0060
7	 0.0490	 -0.0460
8	 0.6250	 0.1170
9	 0.8110	 0.3010
A	 0.8920	 0.4270
A0	 0.7330	 0.3980
B	 0.6270	 0.2100
C	 0.9040	 0.3920
D	 0.2710	 0.0170
E	 0.0430	 0.0270
F	 0.4840	 0.1360
G	 0.3250	 0.0910
H	 0.0290	 0.0170
I	 0.5260	 0.1780
J	 0.7910	 0.2650
K	 0.8960	 0.2760
L	 0.8380	 0.3490
M	 0.8950	 0.4130
N	 0.7580	 0.2080
O	 0.9210	 0.4500
P	 0.0270	 -0.0080
Q	 0.0170	 -0.0430
R	 0.0380	 0.0530
S	 0.0570	 0.0580
T	 0.0520	 0.0070
U	 0.0510	 0.0040
V	 0.0360	 0.0450
W	 0.6680	 0.0810



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Chain	Atom inclusion	Q-score
X	 0.4710	 0.0330
Y	 0.0260	 0.0100
Z	 0.6690	 0.1560
a	 0.1280	 -0.0110
b	 0.1250	 0.0190
c	 0.0410	 0.0080
d	 0.0100	 -0.0090
e	 0.0220	 0.0010
f	 0.0340	 -0.0570
g	 0.1850	 0.0140
h	 0.0000	 -0.0180
i	 0.0000	 0.0150
j	 0.0000	 -0.0030
k	 0.0000	 -0.0090
l	 0.0000	 -0.0360
m	 0.0000	 0.0330
n	 0.0000	 -0.0400
o	 0.0000	 0.0220
p	 0.0000	 -0.0370
q	 0.0000	 0.0190
r	 0.0000	 0.0090
s	 0.0000	 -0.0050
t	 0.0000	 0.0350
u	 0.0000	 0.0260
v	 0.0000	 0.0080
w	 0.0010	 0.0110
x	 0.0070	 0.0140
y	 0.0000	 -0.0360
z	 0.0000	 -0.0230