



wwPDB EM Validation Summary Report ⓘ

May 17, 2025 – 08:11 PM EDT

PDB ID : 8ETI / pdb_00008eti
EMDB ID : EMD-24395
Title : Fkbp39 associated 60S nascent ribosome State 1
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-17
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

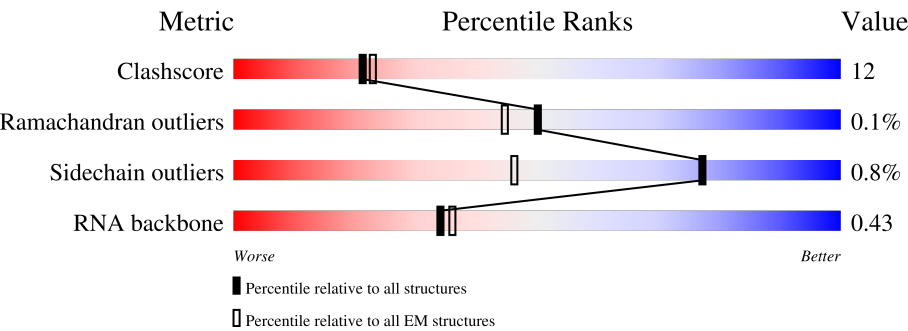
EMDB validation analysis : 0.0.1.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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	1	3497	<div><div>6%</div><div>21%19%5%55%</div></div>
2	2	165	<div><div>7%</div><div>39%41%12%8%</div></div>
3	3	302	<div><div>58%</div><div>48%15%37%</div></div>
4	4	217	<div><div>96%</div><div>62%33%</div></div>
5	5	387	<div><div>88%</div><div>57%31%12%</div></div>
6	6	300	<div><div>27%</div><div>7%13%7%73%</div></div>
7	A	295	<div><div>85%</div><div>76%10%14%</div></div>

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Mol	Chain	Length	Quality of chain
8	B	388	
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	J	333	
16	K	373	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	S	176	
24	V	139	
25	W	241	
26	X	141	
27	Y	126	
28	b	642	
29	d	113	
30	e	127	
31	f	108	
32	h	122	

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Mol	Chain	Length	Quality of chain
33	i	99	
34	j	91	
35	m	740	
36	n	607	
37	o	276	
38	r	260	
39	t	249	
40	u	192	
41	v	209	
42	x	306	
43	y	244	
44	z	117	
45	T	160	

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 90456 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA (1564-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1579	Total	C	N	O	P	0	0
			33816	15104	6144	10989	1579		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	501	G	U	conflict	GB 157310483
1	503	U	G	conflict	GB 157310483
1	2930	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	152	Total	C	N	O	P	0	0
			3229	1445	568	1064	152		

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	190	Total	C	N	O	S	0	0
			1576	999	299	272	6		

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	209	Total	C	N	O	S	0	0
			1762	1149	301	304	8		

- Molecule 5 is a protein called Ribosome biogenesis protein nsa1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	340	Total	C	N	O	S	0	0
			2686	1716	468	491	11		

- Molecule 6 is a RNA chain called RNA (125-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	81	Total	C	N	O	P	0	0
			1717	770	296	570	81		

- Molecule 7 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	254	Total	C	N	O	S	0	0
			1427	856	285	285	1		

- Molecule 8 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	332	Total	C	N	O	S	0	0
			2641	1676	488	468	9		

- Molecule 9 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	328	Total	C	N	O	S	0	0
			2571	1631	486	450	4		

- Molecule 10 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	D	391	Total	C	N	O	0	0
			1931	1149	391	391		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	170	Total	C	N	O	S	0	0
			1328	854	243	228	3		

- Molecule 12 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	239	Total	C	N	O	S	0	0
			1939	1247	355	334	3		

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	186	Total	C	N	O	S	0	0
			1464	938	264	260	2		

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	183	Total	C	N	O		0	0
			902	536	183	183			

- Molecule 15 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	113	Total	C	N	O		0	0
			564	338	113	113			

- Molecule 16 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	240	Total	C	N	O		0	0
			1190	710	240	240			

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	115	Total	C	N	O	S	0	0
			938	590	197	150	1		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	166	Total	C	N	O	S	0	0
			1401	877	291	230	3		

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	196	Total	C	N	O	S	0	0
			1557	999	297	257	4		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	147	Total	C	N	O	S	0	0
			1154	733	209	209	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	136	Total	C	N	O	S	0	0
			1057	664	205	187	1		

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	167	Total	C	N	O	S	0	0
			1395	900	262	228	5		

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	127	Total	C	N	O	0	0
			624	369	127	128		

- Molecule 25 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	W	173	Total	C	N	O	0	0
			850	504	173	173		

- Molecule 26 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	X	122	Total	C	N	O	0	0
			750	457	153	140		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 28 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	b	391	Total	C	N	O	0	0
			1939	1157	391	391		

- Molecule 29 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	d	97	Total	C	N	O	0	0
			483	289	97	97		

- Molecule 30 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	123	Total	C	N	O	S	0	0
			986	616	201	164	5		

- Molecule 31 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 32 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	h	120	Total	C	N	O	0	0
			994	626	193	175		

- Molecule 33 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	85	Total	C	N	O	S	0	0
			696	431	148	116	1		

- Molecule 34 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	j	71	Total	C	N	O	S	0	0
			563	346	121	90	6		

- Molecule 35 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	m	121	Total	C	N	O		0	0
			859	529	163	167			

- Molecule 36 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	369	Total	C	N	O	S	0	0
			2215	1369	430	415	1		

- Molecule 37 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	o	134	Total	C	N	O		0	0
			666	398	134	134			

- Molecule 38 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	r	166	Total	C	N	O		0	0
			823	490	166	167			

- Molecule 39 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	t	225	Total	C	N	O		0	0
			1115	664	225	226			

- Molecule 40 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	u	110	Total	C	N	O		0	0
			546	326	110	110			

- Molecule 41 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	v	161	Total	C	N	O	S	0	0
			1299	818	243	235	3		

- Molecule 42 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	x	303	Total	C	N	O	S	0	0
			2503	1570	460	465	8		

- Molecule 43 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	y	225	Total	C	N	O		0	0
			1107	657	225	225			

- Molecule 44 is a protein called UPF0642 protein C32H8.05.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	35	Total	C	N	O		0	0
			173	103	35	35			

- Molecule 45 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	T	23	Total	C	N	O		0	0
			175	111	31	33			

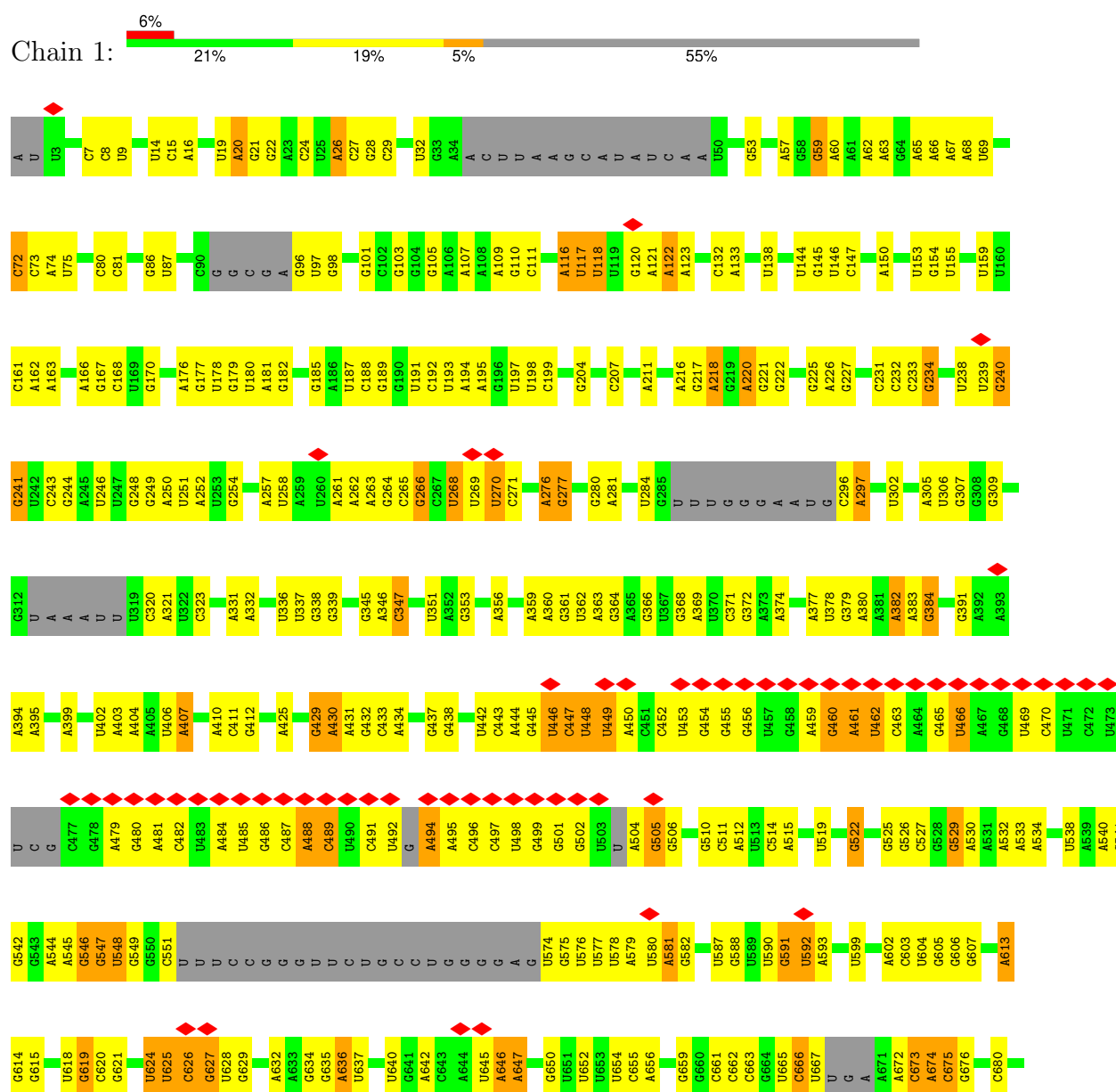
- Molecule 46 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
46	j	1	Total	Zn	0
			1	1	

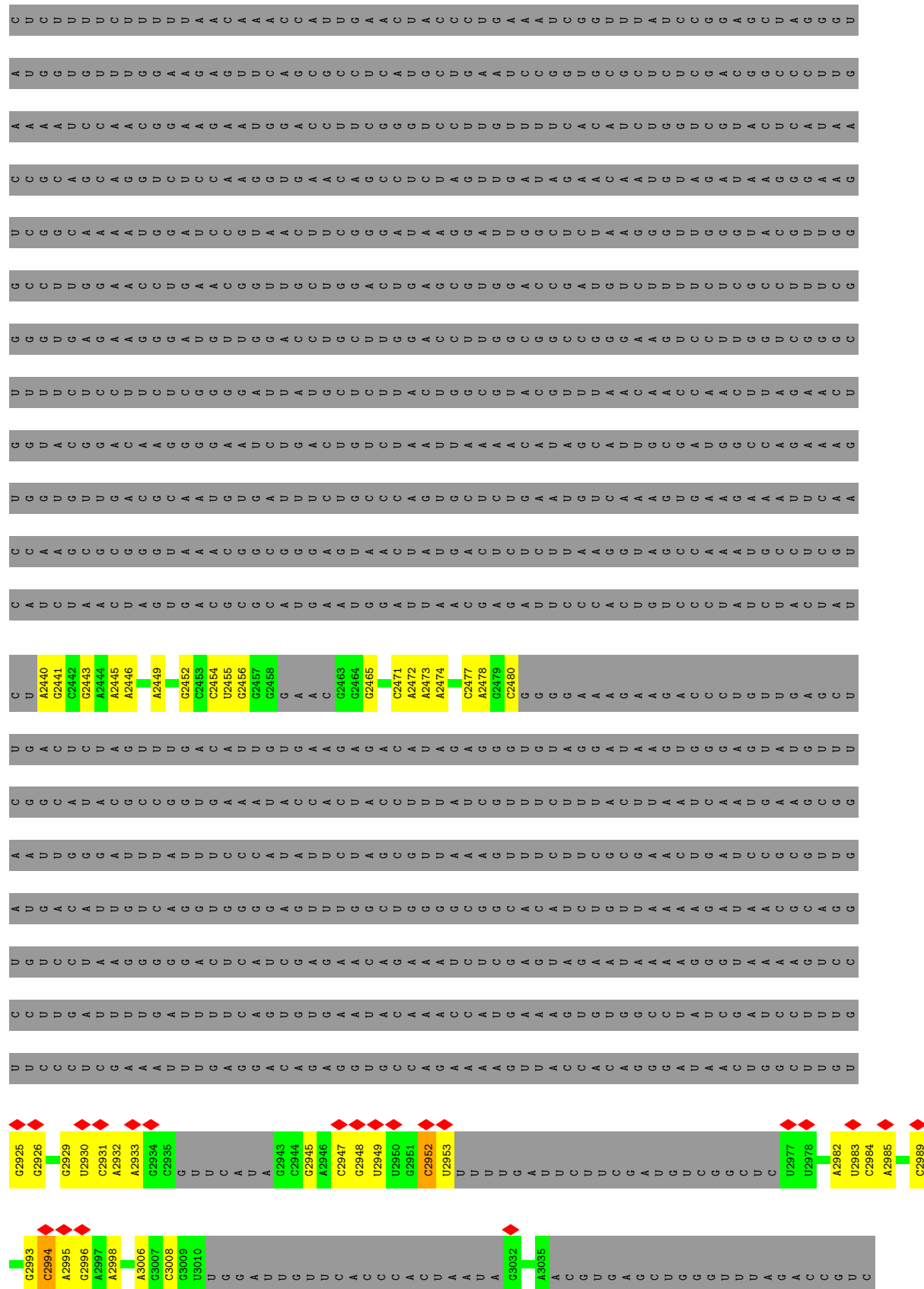
3 Residue-property plots

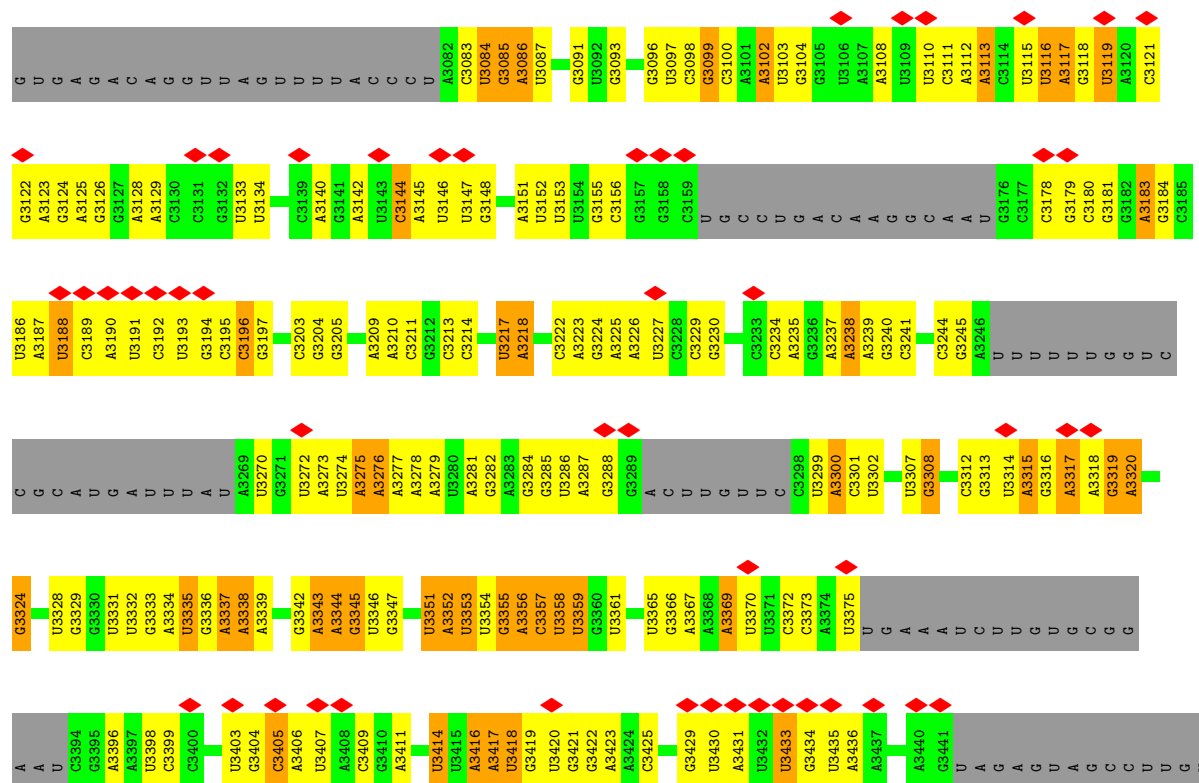
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: RNA (1564-MER)

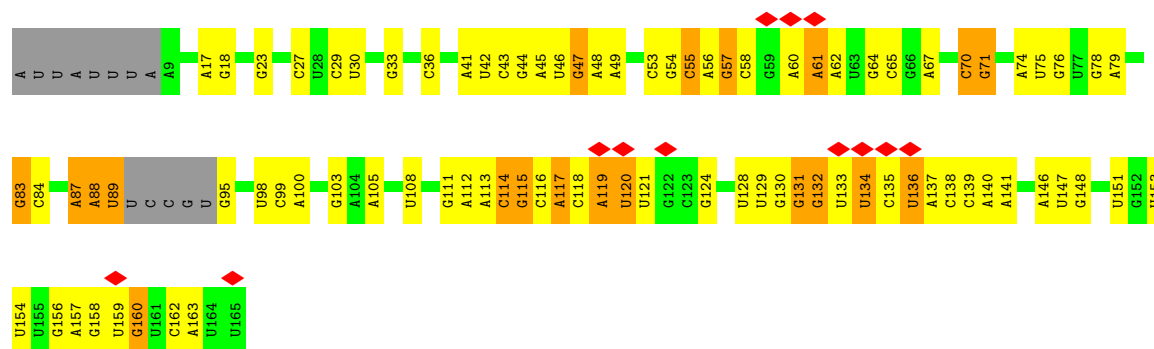
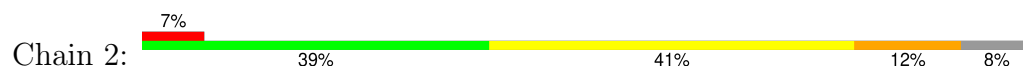






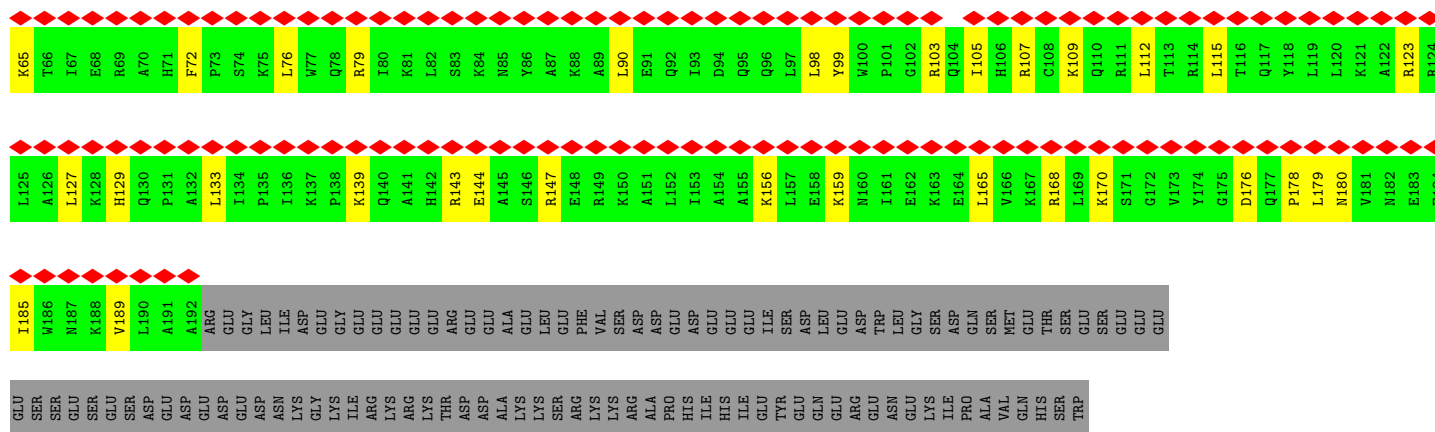


• Molecule 2: RNA (152-MER)

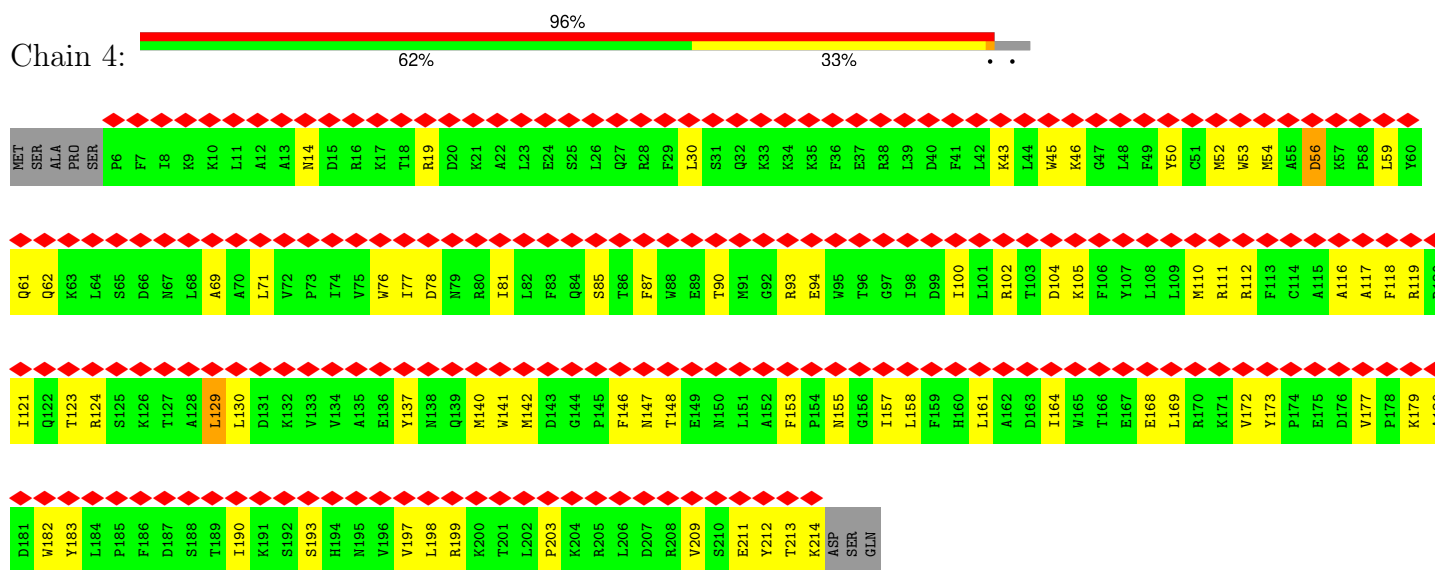


• Molecule 3: Protein mak16

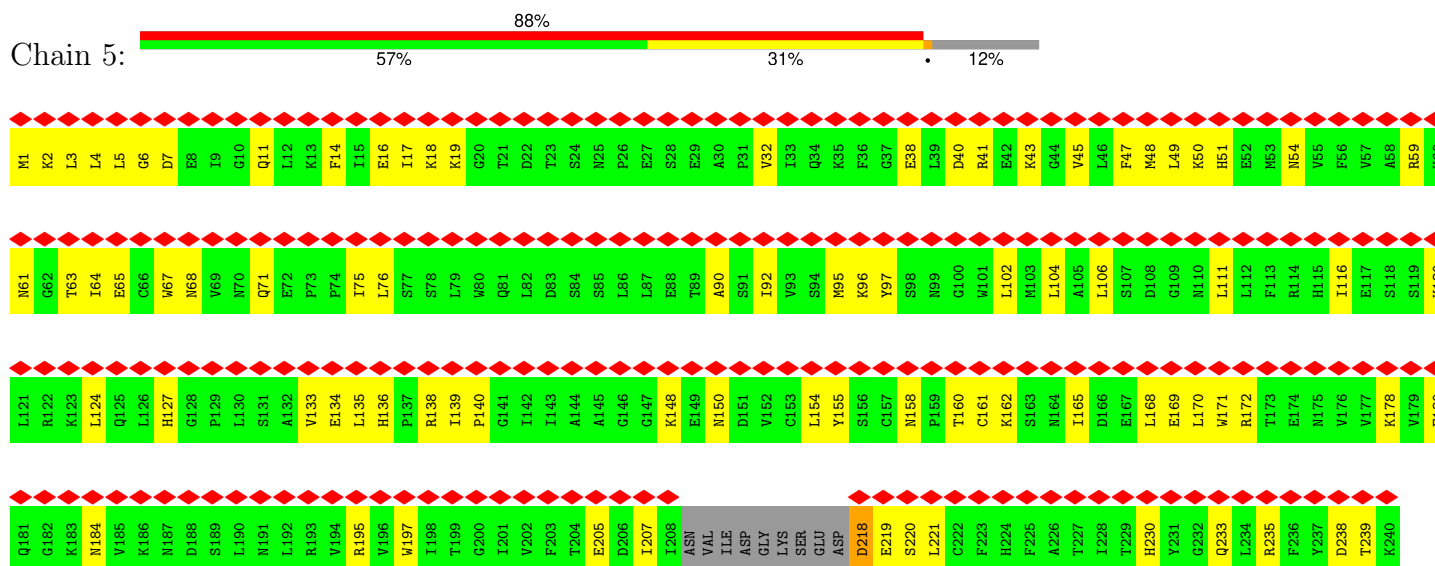


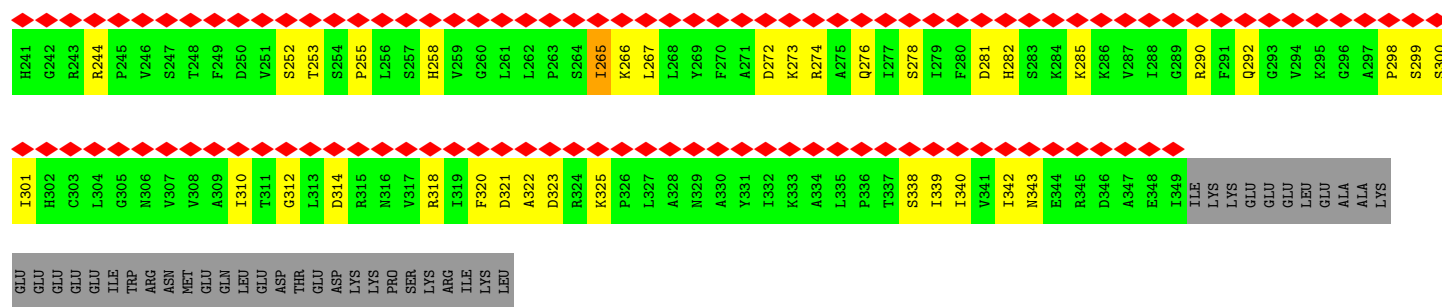


• Molecule 4: Ribosomal RNA-processing protein 1 homolog

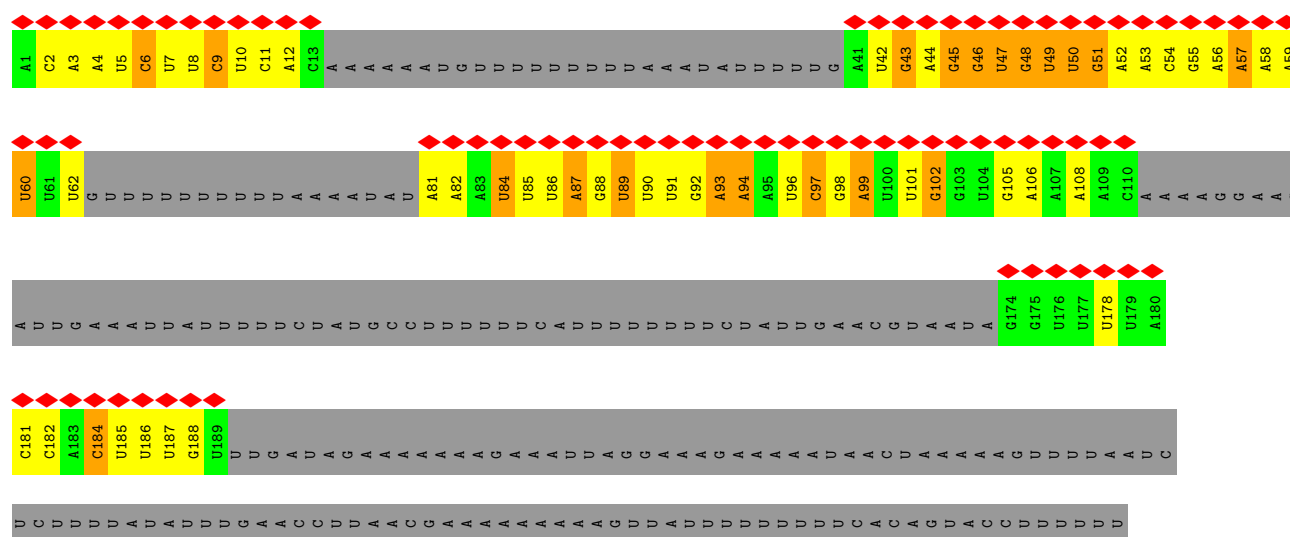


• Molecule 5: Ribosome biogenesis protein nsal

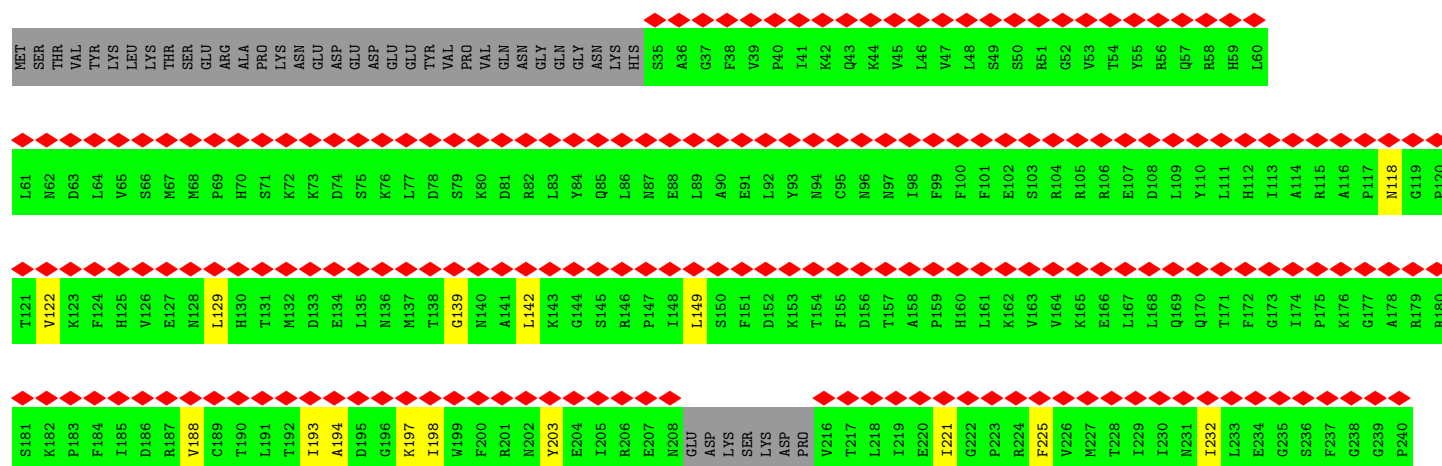
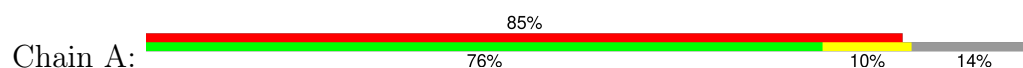


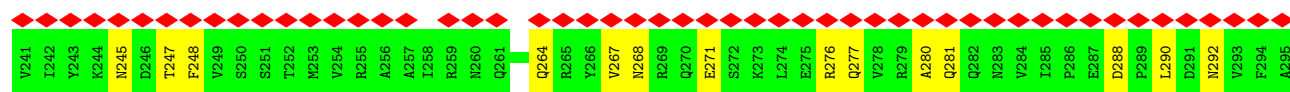


• Molecule 6: RNA (125-MER)

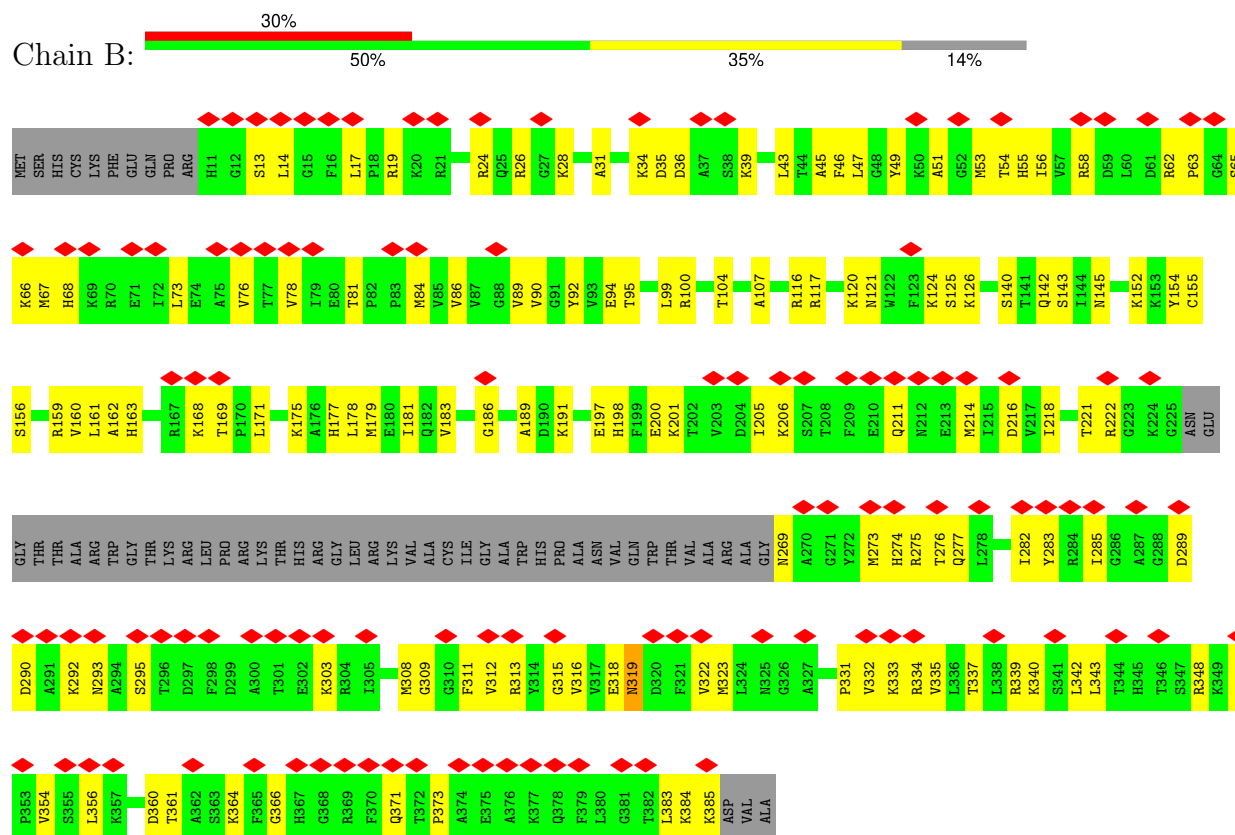


• Molecule 7: Ribosome biogenesis protein brx1

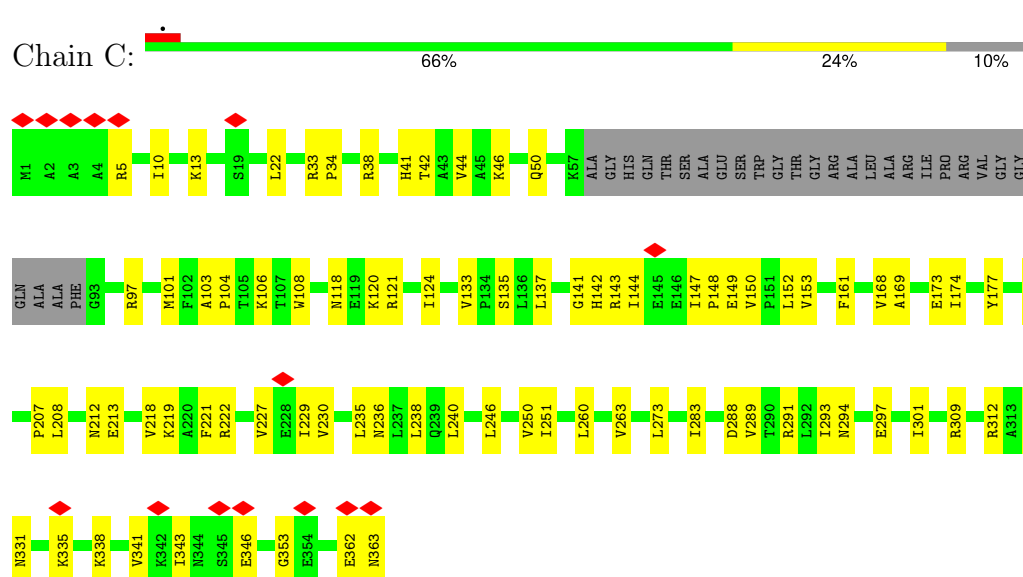




• Molecule 8: 60S ribosomal protein L3-A



• Molecule 9: 60S ribosomal protein L4-B

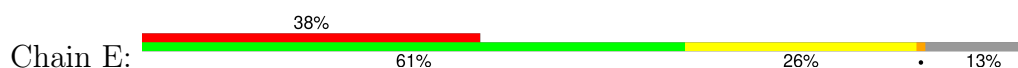


• Molecule 10: ATP-dependent RNA helicase has1



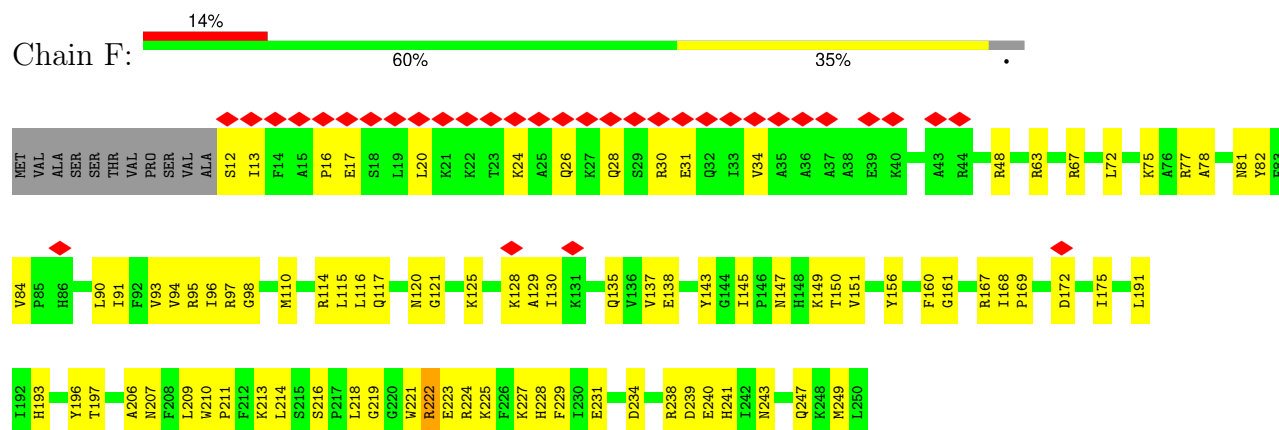
ARG	THR	ASP	LYS	GLU	ARG	ARG	THR	ALA	ARG	GLY	ASN	HIS	VAL	ASP	VAL	TYR	SER	GLN	ARG	SER	SER	ALA	ILE	SER	GLN	ASP	LYS	ARG	GLY	TRP	SER	ARG																													
S481	K482	N483	Y484	Y485	L486	Q487	Q488	Q487	Q488	A490	K491	D492	G493	Y494	R495	S496	Y497	L498	Q499	A500	Y501	A502	S503	Y504	S505	L506	K507	S508	I509	F510	D511	I512	N513	K514	L515	D516	A517	A518	K519	V520	A521	K522	S523	F524	G525	F526	A527	H528	P529	P530	N531	V532	N533	I534	THR	ILE	GLY	ALA	SER	GLY	
I421	H422	R423	V424	G425	ARG	THR	ALA	ARG	GLY	THR	LYS	THR	GLY	THR	G435	K436	S437	L438	M439	F440	L441	A442	P443	S444	E445	L446	G447	F448	L449	R450	Y451	L452	K453	T454	A455	K456	V457	S458	L459	N460	E461	F462	F464	E463	F464	P465	A466	N467	K468	V469	A470	N471	V472	Q473	S474	Q475	L476	E477	K478	L479	V480
L361	P362	L363	L364	D365	L366	H367	G368	K369	Q370	K371	Q372	Q373	R374	R375	T376	T377	T378	F379	F380	E381	L382	C383	N384	A385	E386	K387	G388	I389	L390	L391	C392	T393	N394	V395	A396	A397	R398	G399	L400	D401	I402	P403	P405	A404	V405	D406	V407	T408	V409	Q410	Y411	D412	P413	P414	D415	D416	P417	R418	D419	Y420	
SER	GLY	LYS	PRO	THR	SER	THR	VAL	GLY	LEU	E312	Q313	G314	V315	V316	V317	V318	S320	D321	K322	R323	F324	L325	L326	L327	F328	S329	F330	L331	K332	R333	N334	L335	K336	K337	K338	V339	T340	V341	F342	N343	S344	S345	C346	A347	S348	V349	K350	Y351	K352	A353	E354	L355	L356	N357	Y358	I359	D360				
V241	I242	D243	E244	A245	D246	R247	L248	L249	E250	I251	G252	F253	E254	D255	E256	M257	R258	Q259	I260	M261	K262	I263	L264	P265	S266	E267	N268	R269	Q270	L271	L272	LEU	PHE	SER	ALA	THR	GLN	THR	THR	LYS	VAL	GLU	ASP	LEU	ALA	ARG	ILE	SER	LEU	LYS	PRO	GLY	PRO	LEU	VAL	THR	ASN	VAL	ASP		
A181	K182	E183	L184	L185	K186	Y187	H188	H189	Q190	T191	F192	G193	I194	V195	I196	G197	G198	A199	N200	R201	R202	A203	E204	A205	D206	K207	L208	V209	K210	G211	V212	N213	L214	L215	V216	A217	T218	P219	G220	R221	L222	L223	D224	H225	L226	Q227	N228	T229	K230	G231	F232	V233	F234	R235	N236	L237	R238	S239	L240		
P121	P122	L123	L124	A125	G126	P127	D128	V129	L130	G131	A132	A133	K134	T135	G136	S137	G138	K139	T140	L141	A142	F143	L144	I145	P146	T147	I148	E149	M150	L151	Y152	A153	K155	F156	K157	P158	R159	N160	G161	T162	G163	V164	I165	I166	I167	S168	P169	T170	R171	E172	L173	A174	L175	Q176	I177	F178	G179	V180			
GLU	SER	GLU	LEU	ASP	ASN	GLU	GLU	GLU	GLU	GLU	GLU	GLU	VAL	ASN	LEU	ASN	ALA	SER	THR	SER	LEU	ASP	ILE	GLN	LYS	PHE	SER	ILE	ALA	GLU	GLN	L96	S97	E98	N99	I100	Q101	K102	A103	I104	K105	E106	M107	G108	F109	E110	T111	M112	T113	E114	I115	Q116	K117	R118	S119	I120					
MET	ALA	LYS	SER	GLU	LEU	LYS	ARG	LYS	HIS	GLN	SER	GLY	ASN	GLU	VAL	LYS	LYS	GLN	PRO	LEU	LYS	ASN	GLN	ASP	ALA	GLU	GLU	LEU	PRO	GLN	ASP	ASP	TYR	GLN	GLU	GLU	GLU	ASN	GLU	ASP	ALA	GLN	ASN	THR	SER	VAL	GLU	SER													

• Molecule 11: 60S ribosomal protein L6

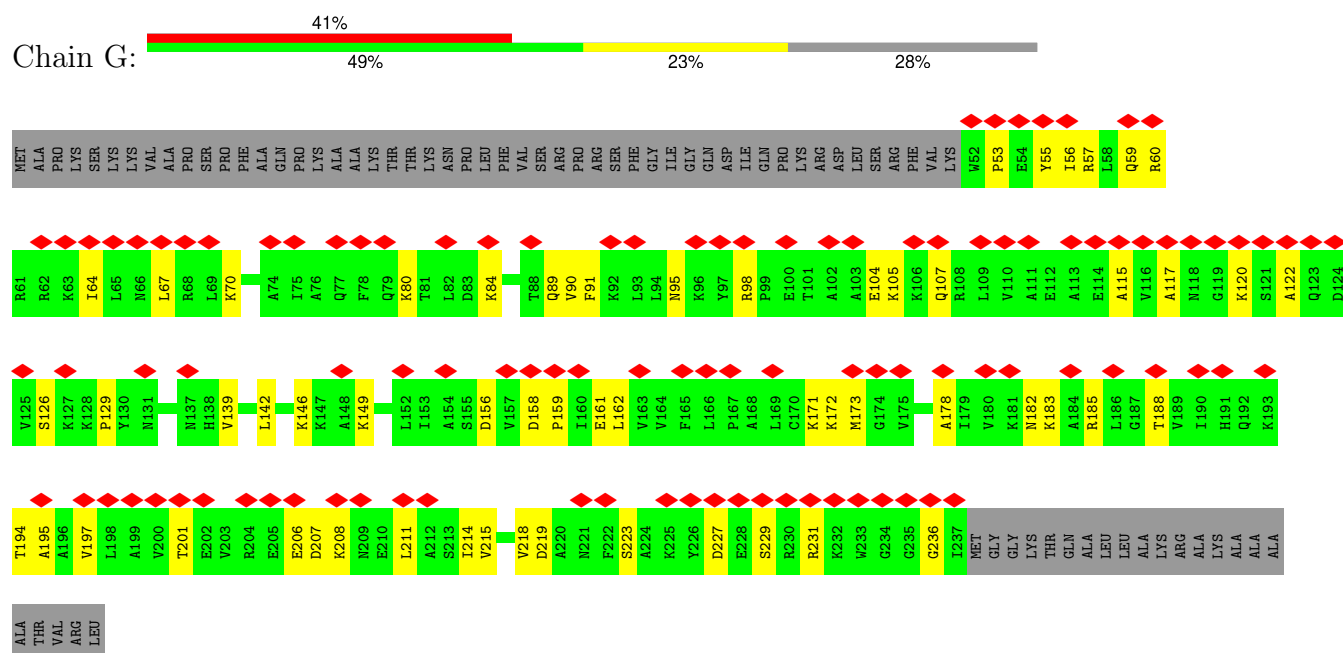


MET	SER	THR	VAL	LYS	VAL	ASN	GLY	ALA	LYS	ASN	HIS	VAL	LEU	PRO	ALA	GLY	ALA	ALA	ALA	ALA	K26	Y27	Y28	P29	A30	Y31	R32	E33	N34	V35	K38	R44	P45	T46	K47	L52	G55	L61	A62	G63	R64	V71	V72	E73	E77	D78	Y79	L80																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
V81	V82	T83	G84	P85	Y86	K87	V88	N89	G90	I93	R94	R95	V96	N97	V101	I102	A106	I109	D110	V111	S112	G113	V114	S115	V116	E117	K118	F119	T120	K121	A122	K126	Q127	K128	R129	S130	G131	P132	V133	K134	K135	D136	E137	A138	F139	F140	A141	E142	N143	A144	P145	K146	N147	A148																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
L149	P150	A151	E152	R153	I154	A155	D156	Q157	K158	A159	V160	D161	A162	K163	L164	L165	I168	I171	M174	K175	E176	Y177	L178	A179	L184	S185	F189	P190	H191	L192	F195																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		

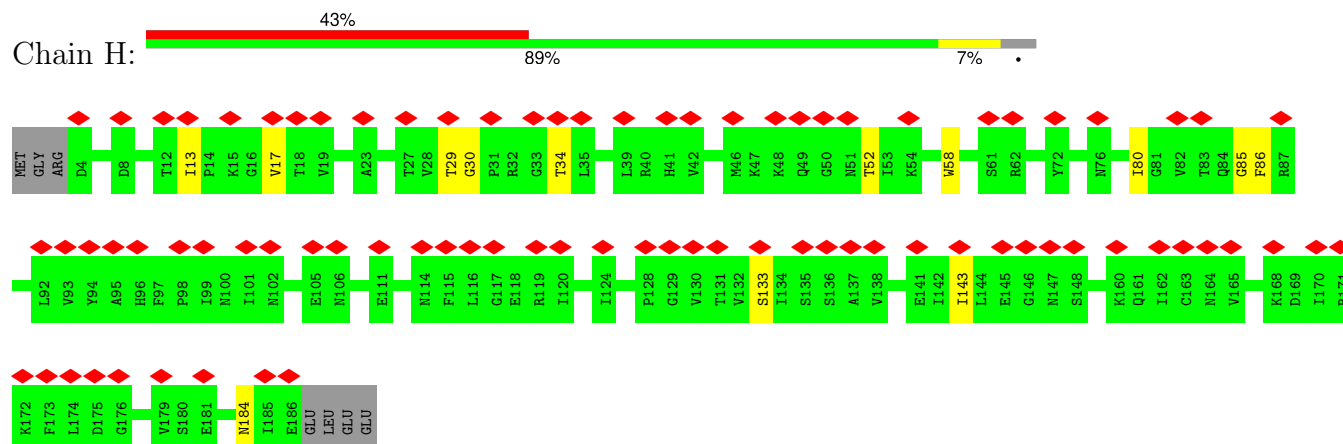
- Molecule 12: 60S ribosomal protein L7-B

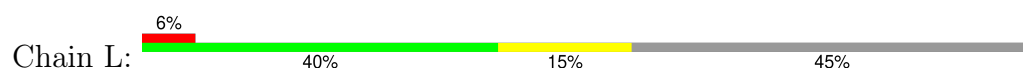


- Molecule 13: 60S ribosomal protein L8

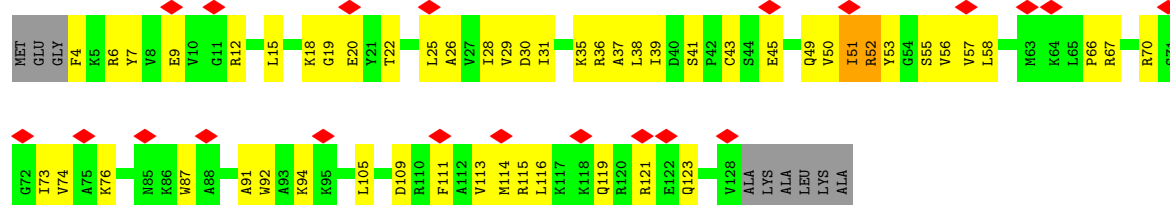


- Molecule 14: 60S ribosomal protein L9-A

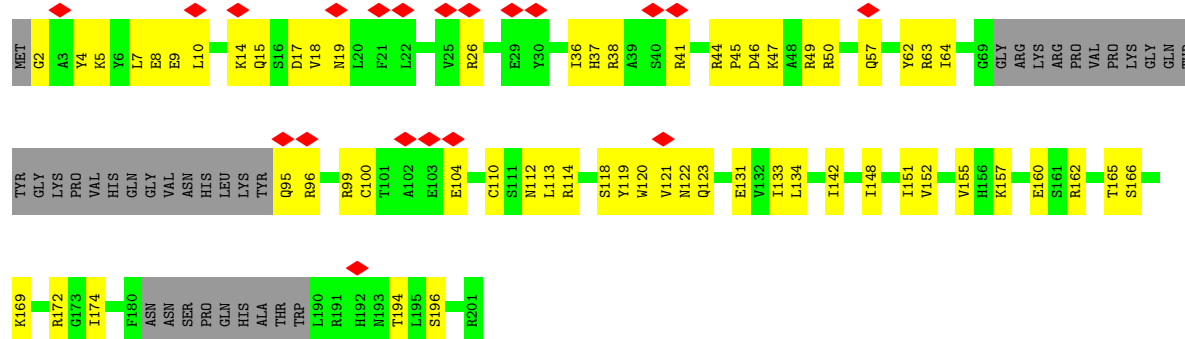




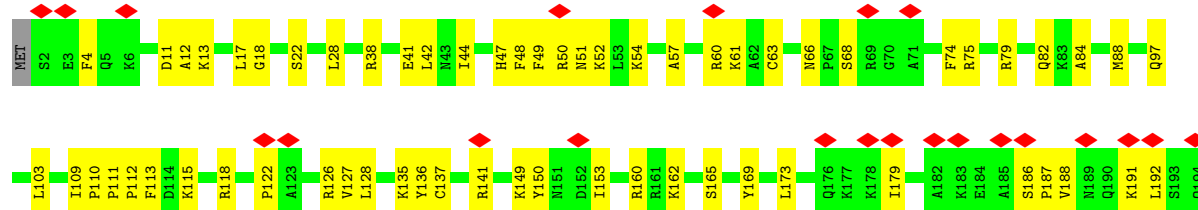
• Molecule 18: 60S ribosomal protein L14



• Molecule 19: 60S ribosomal protein L15-A

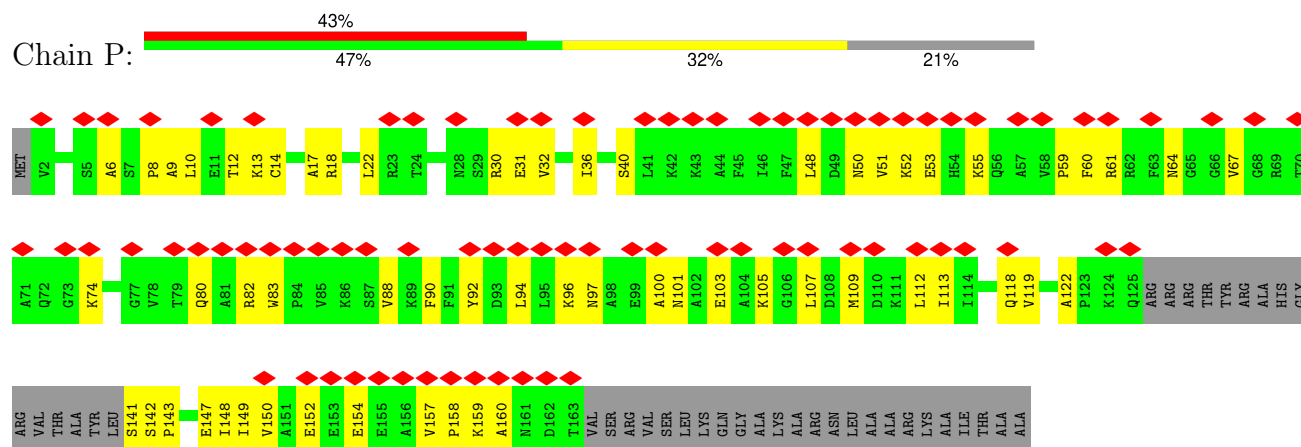


• Molecule 20: 60S ribosomal protein L16-B

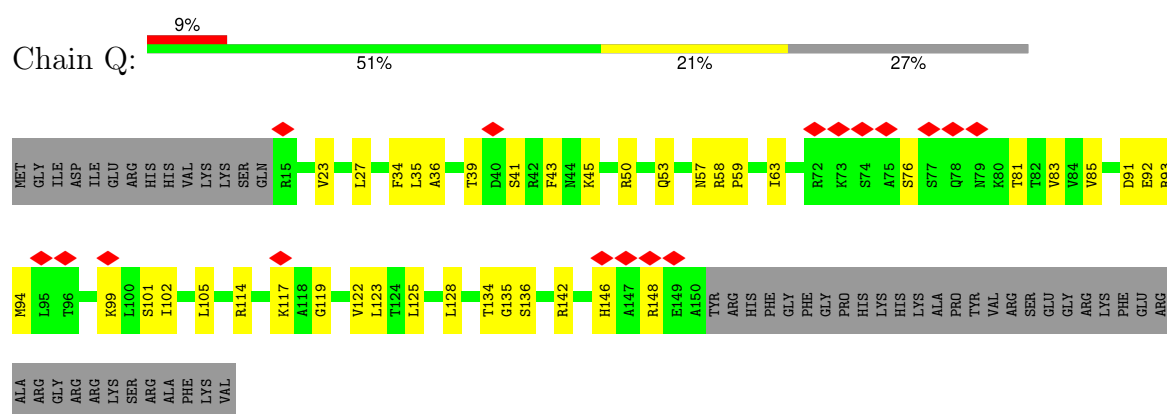




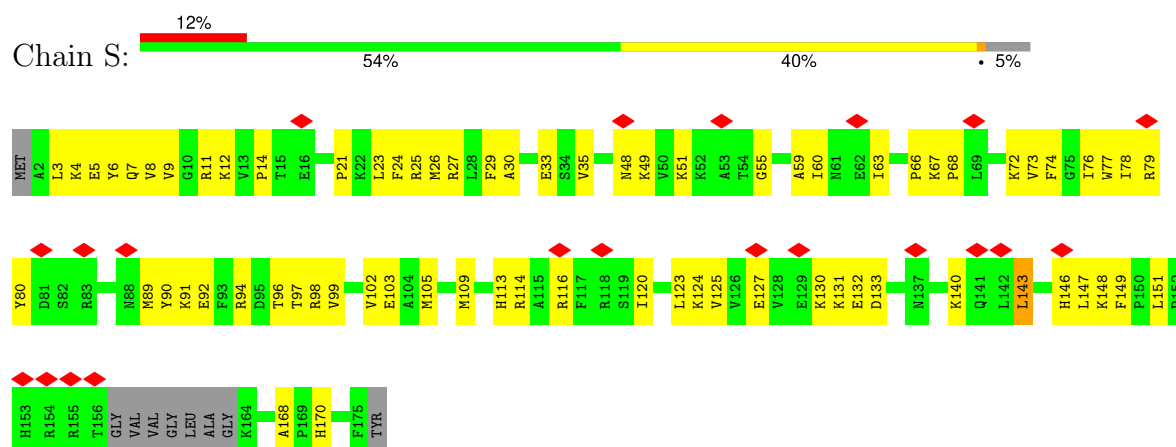
• Molecule 21: 60S ribosomal protein L17-A



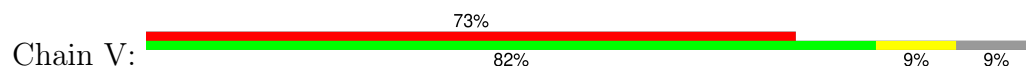
• Molecule 22: 60S ribosomal protein L18-A

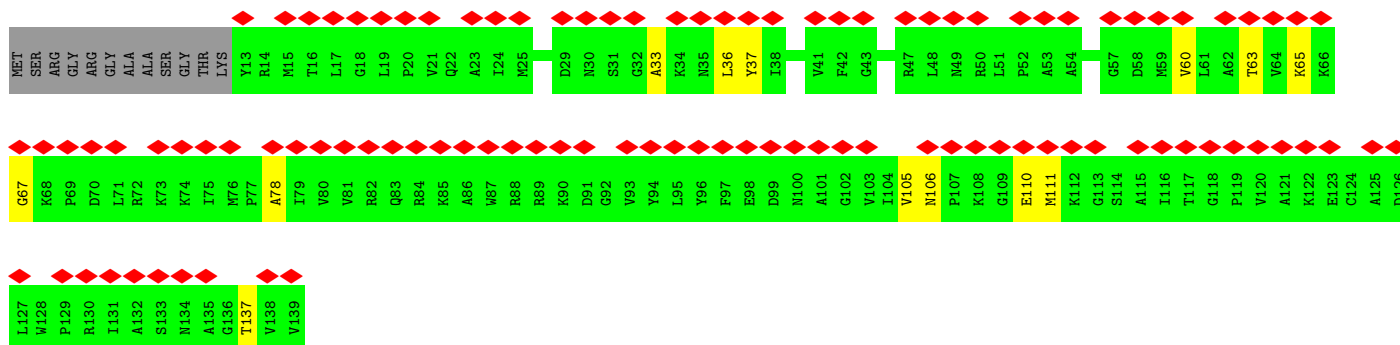


• Molecule 23: 60S ribosomal protein L20-A

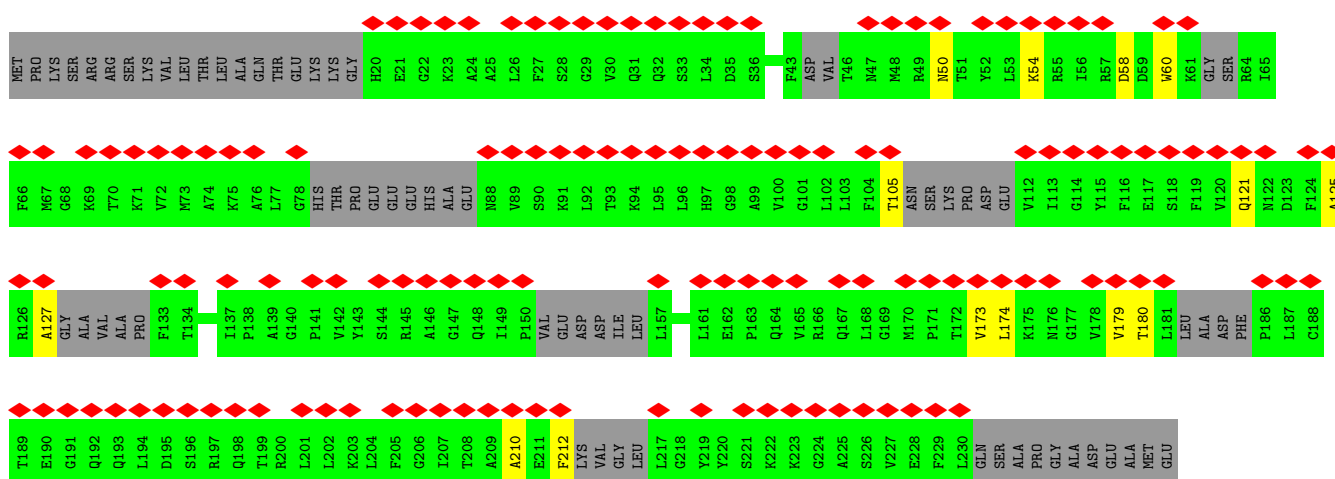


• Molecule 24: 60S ribosomal protein L23-A

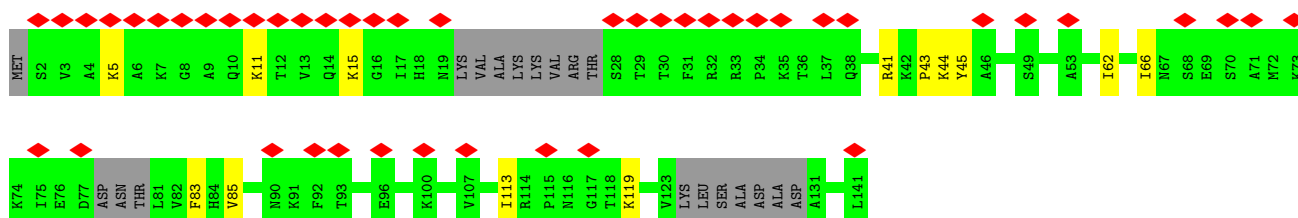
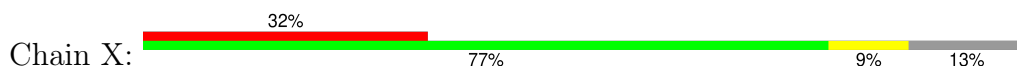




• Molecule 25: Ribosome assembly factor mrt4

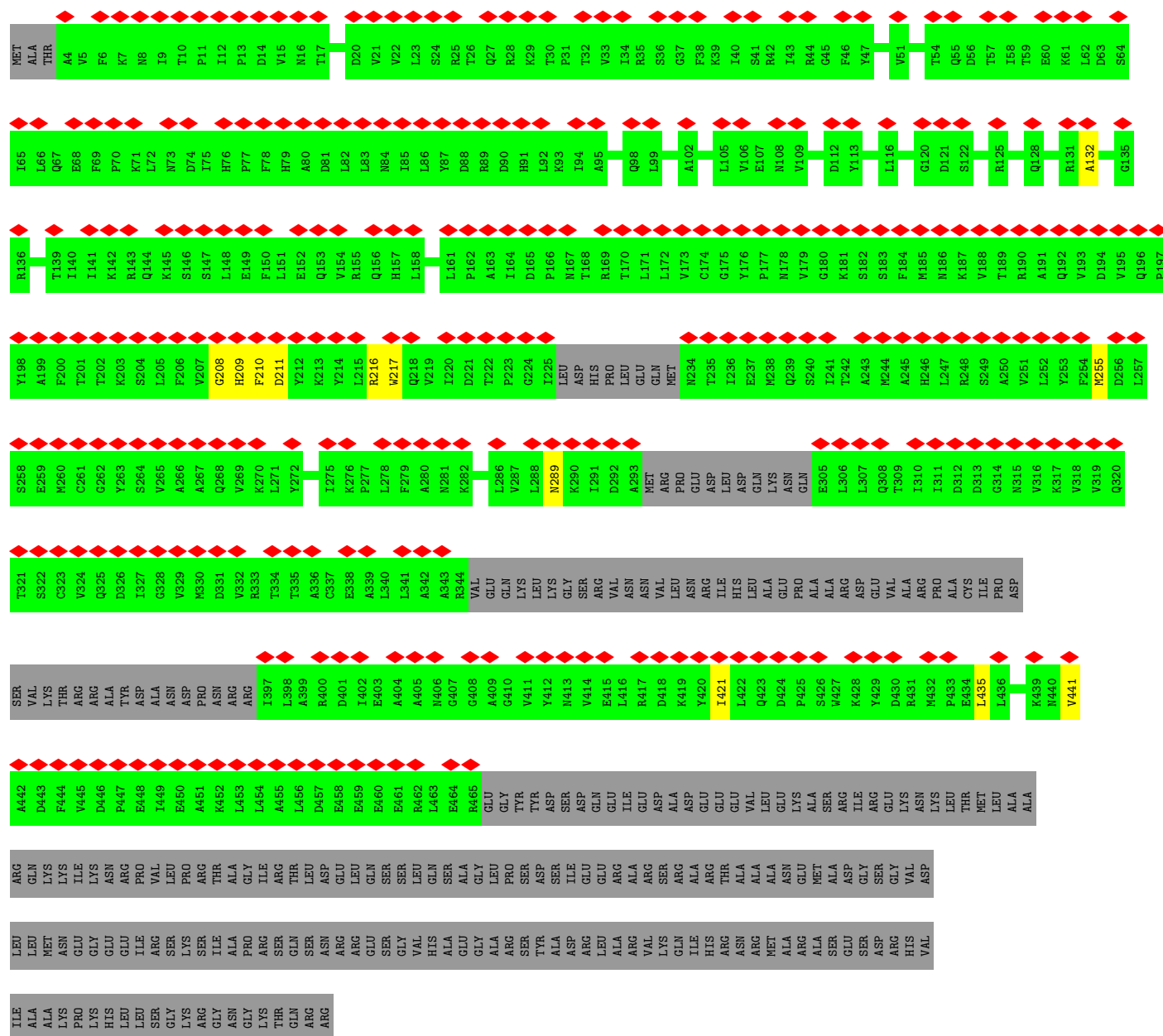


• Molecule 26: 60S ribosomal protein L25-A

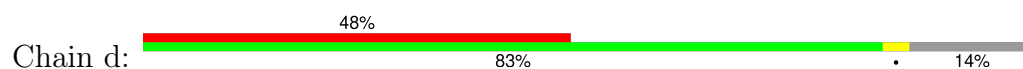


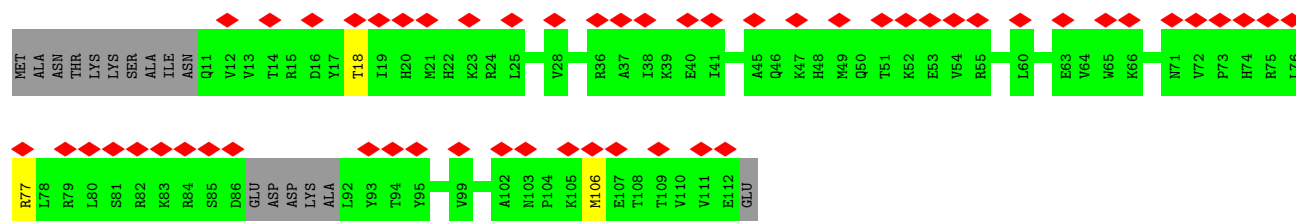
• Molecule 27: 60S ribosomal protein L26



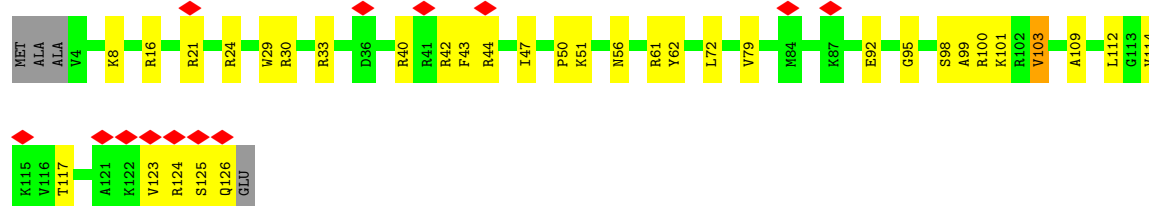


- Molecule 29: 60S ribosomal protein L31

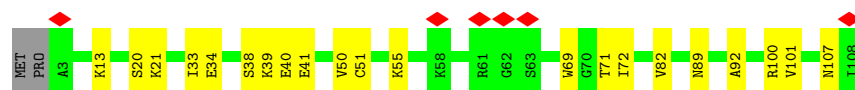
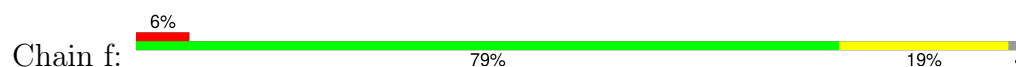




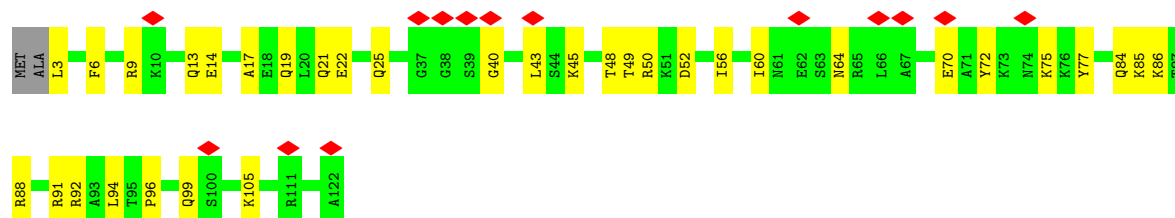
- Molecule 30: 60S ribosomal protein L32-A



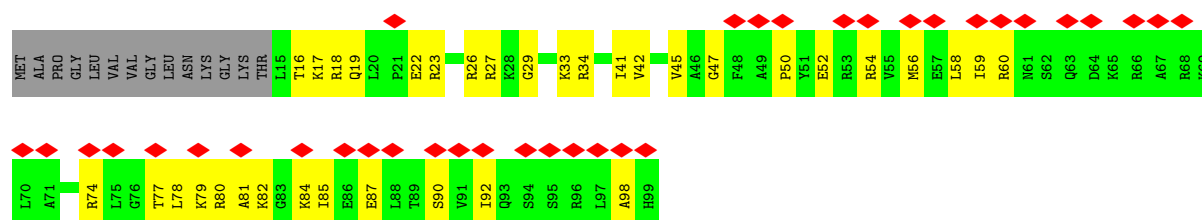
- Molecule 31: 60S ribosomal protein L33-B



- Molecule 32: 60S ribosomal protein L35



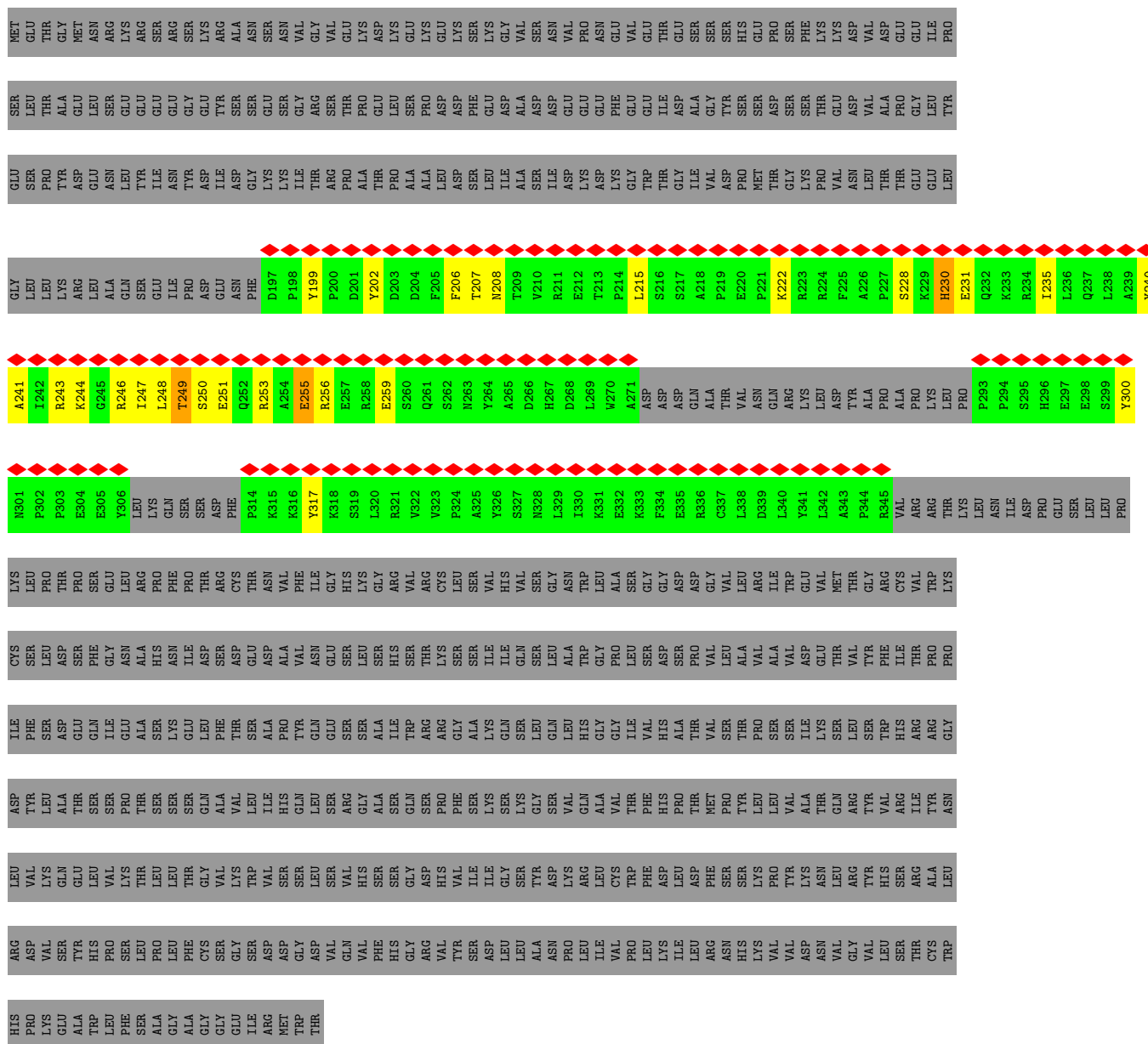
- Molecule 33: 60S ribosomal protein L36-B



- Molecule 34: 60S ribosomal protein L37-B

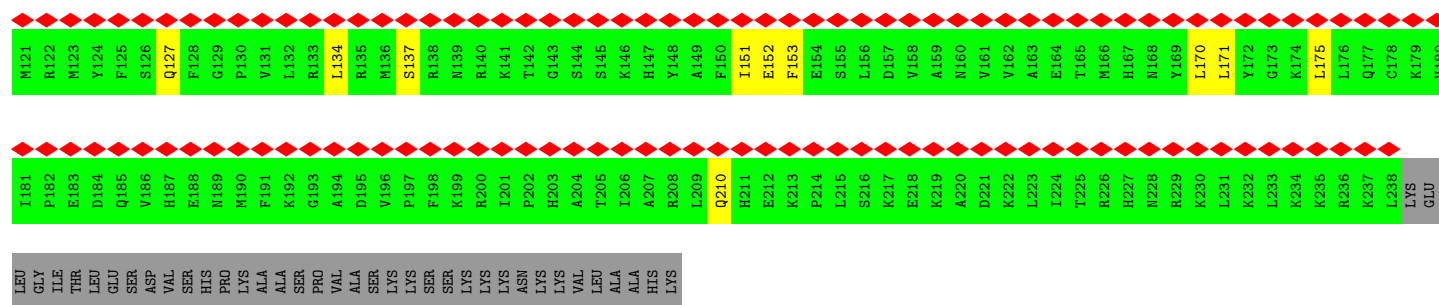


Chain m:  16%
13% 84%

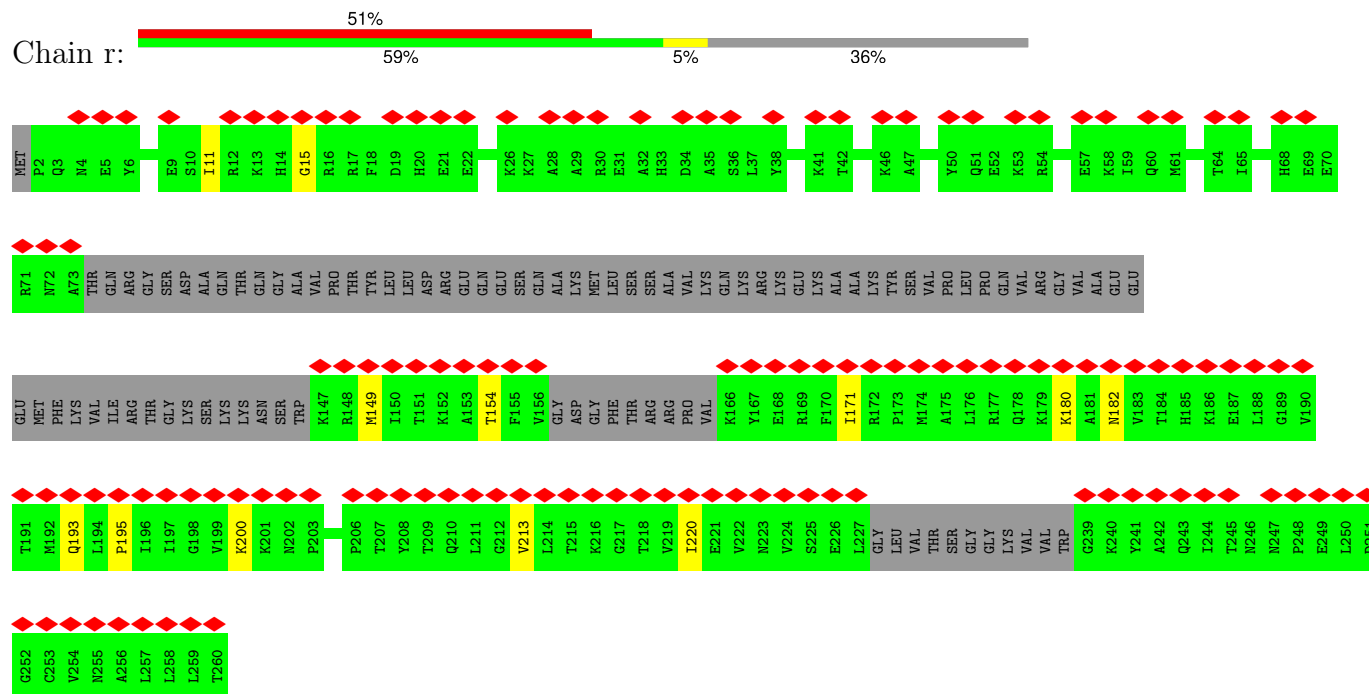


- Molecule 36: Pescadillo homolog

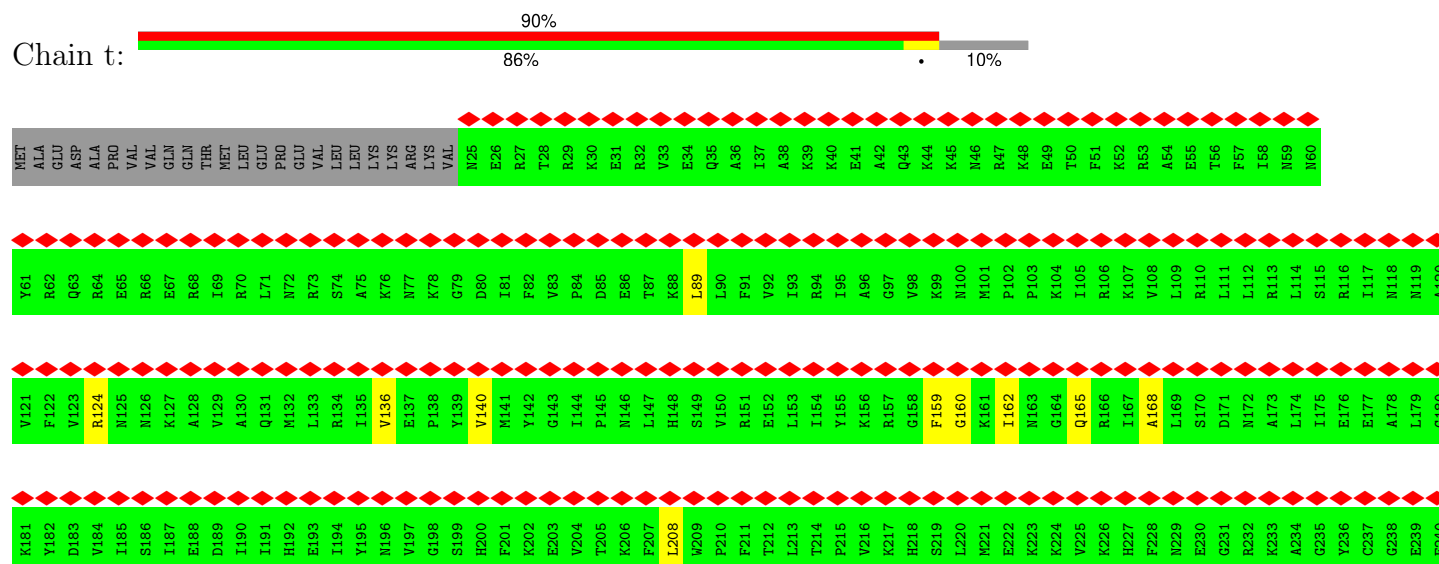


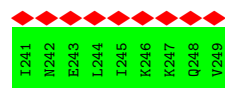


• Molecule 38: Ribosome biogenesis protein nsa2

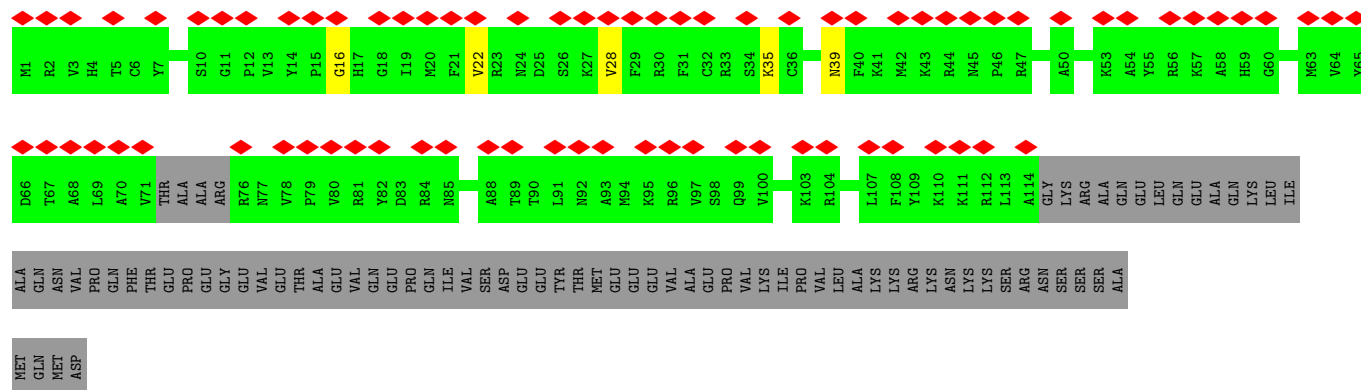
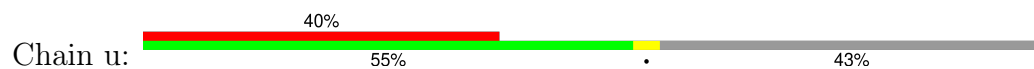


• Molecule 39: 60S ribosomal protein L7-A

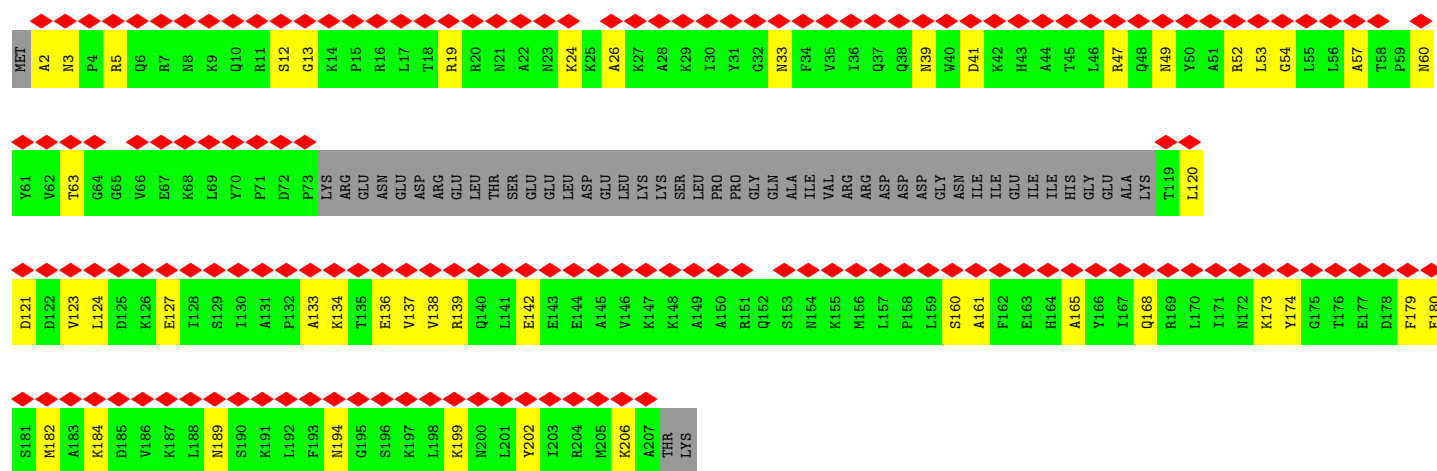
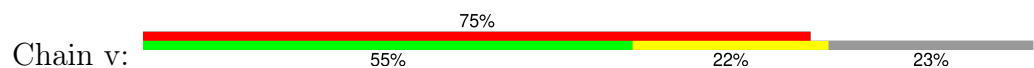




• Molecule 40: Ribosome biogenesis protein rlp24



• Molecule 41: Nucleolar protein 16

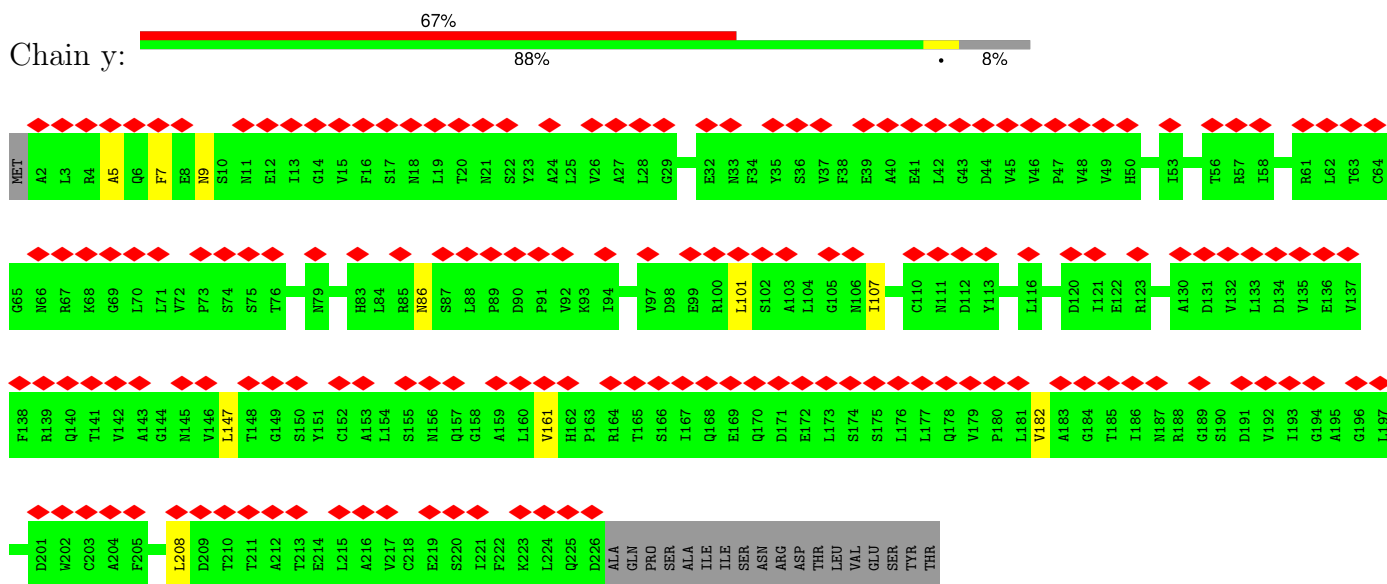


• Molecule 42: Brix domain-containing protein C4F8.04

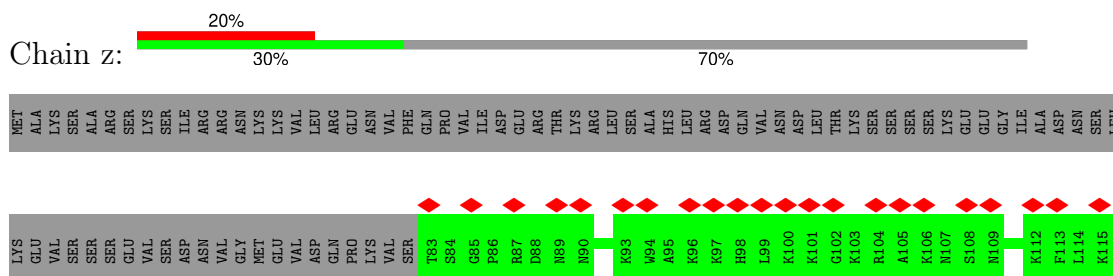




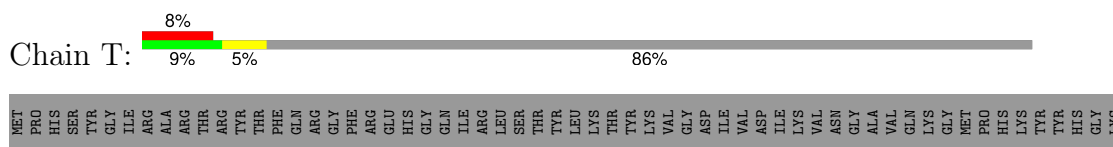
• Molecule 43: Eukaryotic translation initiation factor 6



• Molecule 44: UPF0642 protein C32H8.05



• Molecule 45: 60S ribosomal protein L21-A





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.491	Depositor
Minimum map value	-0.210	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.21	0/37838	0.26	0/58935
2	2	0.21	0/3608	0.25	0/5615
3	3	0.28	0/1607	0.39	0/2162
4	4	0.20	0/1809	0.40	0/2443
5	5	0.18	0/2739	0.41	0/3702
6	6	0.14	0/1916	0.34	0/2973
7	A	0.16	0/1431	0.40	0/1971
8	B	0.18	0/2694	0.41	0/3619
9	C	0.31	0/2617	0.46	0/3529
10	D	0.07	0/1928	0.23	0/2680
11	E	0.21	0/1356	0.50	0/1829
12	F	0.23	0/1977	0.42	0/2651
13	G	0.23	0/1487	0.43	0/2007
14	H	0.08	0/901	0.24	0/1252
15	J	0.06	0/563	0.20	0/786
16	K	0.09	0/1188	0.24	0/1654
17	L	0.31	0/956	0.50	0/1283
18	M	0.19	0/1024	0.48	0/1375
19	N	0.29	0/1429	0.40	0/1909
20	O	0.21	0/1588	0.43	0/2128
21	P	0.22	0/1176	0.42	0/1580
22	Q	0.25	0/1068	0.43	0/1434
23	S	0.20	0/1430	0.50	0/1921
24	V	0.06	0/623	0.23	0/862
25	W	0.07	0/841	0.30	0/1154
26	X	0.21	0/753	0.38	0/1021
27	Y	0.24	0/1008	0.42	0/1341
28	b	0.06	0/1935	0.21	0/2693
29	d	0.07	0/481	0.20	0/669
30	e	0.29	0/1000	0.45	0/1333
31	f	0.24	0/859	0.39	0/1152
32	h	0.25	0/1003	0.51	0/1333

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.26	0/703	0.52	0/931
34	j	0.25	0/575	0.42	0/761
35	m	0.19	0/873	0.43	0/1188
36	n	0.16	0/2233	0.40	0/3054
37	o	0.11	0/665	0.28	0/925
38	r	0.07	0/819	0.22	0/1134
39	t	0.07	0/1114	0.24	0/1550
40	u	0.07	0/544	0.23	0/756
41	v	0.19	0/1319	0.43	0/1769
42	x	0.20	0/2549	0.41	0/3416
43	y	0.06	0/1106	0.20	0/1536
44	z	0.06	0/172	0.19	0/238
45	T	0.15	0/182	0.35	0/252
All	All	0.20	0/95687	0.34	0/138506

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1	33816	0	17019	568	0
2	2	3229	0	1632	67	0
3	3	1576	0	1626	43	0
4	4	1762	0	1784	56	0
5	5	2686	0	2745	92	0
6	6	1717	0	866	45	0
7	A	1427	0	854	21	0
8	B	2641	0	2727	118	0
9	C	2571	0	2709	78	0
10	D	1931	0	874	5	0
11	E	1328	0	1408	44	0
12	F	1939	0	2030	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	G	1464	0	1558	51	0
14	H	902	0	392	7	0
15	J	564	0	259	3	0
16	K	1190	0	526	12	0
17	L	938	0	1009	31	0
18	M	1007	0	1072	46	0
19	N	1401	0	1439	48	0
20	O	1557	0	1652	59	0
21	P	1154	0	1169	47	0
22	Q	1057	0	1153	23	0
23	S	1395	0	1453	76	0
24	V	624	0	303	7	0
25	W	850	0	383	8	0
26	X	750	0	576	10	0
27	Y	998	0	1090	26	0
28	b	1939	0	867	8	0
29	d	483	0	208	2	0
30	e	986	0	1053	32	0
31	f	839	0	866	20	0
32	h	994	0	1087	28	0
33	i	696	0	763	31	0
34	j	563	0	578	23	0
35	m	859	0	691	28	0
36	n	2215	0	1603	43	0
37	o	666	0	298	8	0
38	r	823	0	367	6	0
39	t	1115	0	492	5	0
40	u	546	0	248	3	0
41	v	1299	0	1347	40	0
42	x	2503	0	2508	93	0
43	y	1107	0	514	6	0
44	z	173	0	76	0	0
45	T	175	0	165	9	0
46	j	1	0	0	0	0
All	All	90456	0	64039	1724	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 12.

The worst 5 of 1724 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)
1:1:1388:G:H1	3:3:26:ASN:HB2	1.28	0.96
23:S:109:MET:HG2	23:S:120:ILE:HD11	1.55	0.87
42:x:168:ASN:O	42:x:168:ASN:ND2	2.07	0.86
1:1:379:G:H22	1:1:382:A:H5''	1.42	0.84
8:B:331:PRO:HD2	8:B:334:ARG:HE	1.43	0.84

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	
3	3	188/302 (62%)	177 (94%)	11 (6%)	0	100	100
4	4	207/217 (95%)	198 (96%)	9 (4%)	0	100	100
5	5	336/387 (87%)	301 (90%)	35 (10%)	0	100	100
7	A	250/295 (85%)	237 (95%)	12 (5%)	1 (0%)	30	62
8	B	328/388 (84%)	314 (96%)	14 (4%)	0	100	100
9	C	324/363 (89%)	302 (93%)	22 (7%)	0	100	100
10	D	385/578 (67%)	364 (94%)	21 (6%)	0	100	100
11	E	168/195 (86%)	144 (86%)	23 (14%)	1 (1%)	22	54
12	F	237/250 (95%)	217 (92%)	19 (8%)	1 (0%)	30	62
13	G	184/259 (71%)	175 (95%)	9 (5%)	0	100	100
14	H	181/190 (95%)	175 (97%)	6 (3%)	0	100	100
15	J	111/333 (33%)	106 (96%)	5 (4%)	0	100	100
16	K	236/373 (63%)	228 (97%)	8 (3%)	0	100	100
17	L	113/208 (54%)	106 (94%)	7 (6%)	0	100	100
18	M	123/134 (92%)	115 (94%)	8 (6%)	0	100	100
19	N	160/201 (80%)	154 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	O	194/197 (98%)	186 (96%)	8 (4%)	0	100	100
21	P	143/187 (76%)	134 (94%)	9 (6%)	0	100	100
22	Q	134/187 (72%)	121 (90%)	12 (9%)	1 (1%)	19	51
23	S	163/176 (93%)	149 (91%)	14 (9%)	0	100	100
24	V	125/139 (90%)	120 (96%)	5 (4%)	0	100	100
25	W	155/241 (64%)	147 (95%)	8 (5%)	0	100	100
26	X	114/141 (81%)	104 (91%)	10 (9%)	0	100	100
27	Y	123/126 (98%)	120 (98%)	3 (2%)	0	100	100
28	b	383/642 (60%)	374 (98%)	9 (2%)	0	100	100
29	d	93/113 (82%)	91 (98%)	2 (2%)	0	100	100
30	e	121/127 (95%)	111 (92%)	10 (8%)	0	100	100
31	f	104/108 (96%)	93 (89%)	11 (11%)	0	100	100
32	h	118/122 (97%)	110 (93%)	8 (7%)	0	100	100
33	i	83/99 (84%)	81 (98%)	2 (2%)	0	100	100
34	j	69/91 (76%)	64 (93%)	5 (7%)	0	100	100
35	m	115/740 (16%)	107 (93%)	8 (7%)	0	100	100
36	n	365/607 (60%)	353 (97%)	12 (3%)	0	100	100
37	o	132/276 (48%)	132 (100%)	0	0	100	100
38	r	158/260 (61%)	153 (97%)	5 (3%)	0	100	100
39	t	223/249 (90%)	215 (96%)	8 (4%)	0	100	100
40	u	106/192 (55%)	104 (98%)	2 (2%)	0	100	100
41	v	157/209 (75%)	141 (90%)	16 (10%)	0	100	100
42	x	301/306 (98%)	289 (96%)	12 (4%)	0	100	100
43	y	223/244 (91%)	219 (98%)	4 (2%)	0	100	100
44	z	33/117 (28%)	32 (97%)	1 (3%)	0	100	100
45	T	21/160 (13%)	18 (86%)	3 (14%)	0	100	100
All	All	7487/10729 (70%)	7081 (95%)	402 (5%)	4 (0%)	50	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	A	118	ASN
11	E	136	ASP

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Mol	Chain	Res	Type
22	Q	76	SER
12	F	222	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	
3	3	167/271 (62%)	166 (99%)	1 (1%)	84	90
4	4	190/197 (96%)	187 (98%)	3 (2%)	58	74
5	5	301/345 (87%)	299 (99%)	2 (1%)	81	88
7	A	47/266 (18%)	47 (100%)	0	100	100
8	B	282/326 (86%)	279 (99%)	3 (1%)	70	80
9	C	276/297 (93%)	275 (100%)	1 (0%)	89	93
11	E	139/155 (90%)	138 (99%)	1 (1%)	81	88
12	F	201/210 (96%)	200 (100%)	1 (0%)	86	92
13	G	155/212 (73%)	154 (99%)	1 (1%)	84	90
17	L	97/167 (58%)	97 (100%)	0	100	100
18	M	108/113 (96%)	106 (98%)	2 (2%)	52	70
19	N	146/176 (83%)	146 (100%)	0	100	100
20	O	161/162 (99%)	160 (99%)	1 (1%)	84	90
21	P	120/149 (80%)	120 (100%)	0	100	100
22	Q	116/159 (73%)	115 (99%)	1 (1%)	75	84
23	S	149/154 (97%)	148 (99%)	1 (1%)	81	88
26	X	41/122 (34%)	41 (100%)	0	100	100
27	Y	110/111 (99%)	110 (100%)	0	100	100
30	e	105/107 (98%)	104 (99%)	1 (1%)	73	82
31	f	89/91 (98%)	89 (100%)	0	100	100
32	h	106/107 (99%)	106 (100%)	0	100	100
33	i	74/84 (88%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	j	58/71 (82%)	57 (98%)	1 (2%)	56	73
35	m	67/659 (10%)	64 (96%)	3 (4%)	23	50
36	n	102/532 (19%)	101 (99%)	1 (1%)	73	82
37	o	1/246 (0%)	1 (100%)	0	100	100
41	v	138/181 (76%)	138 (100%)	0	100	100
42	x	271/273 (99%)	266 (98%)	5 (2%)	54	71
45	T	20/139 (14%)	20 (100%)	0	100	100
All	All	3837/6082 (63%)	3808 (99%)	29 (1%)	77	85

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	M	52	ARG
42	x	178	ASN
23	S	143	LEU
42	x	45	LEU
22	Q	102	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
21	P	64	ASN
31	f	107	ASN
42	x	264	GLN
21	P	80	GLN
30	e	85	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1551/3497 (44%)	408 (26%)	25 (1%)
2	2	150/165 (90%)	35 (23%)	1 (0%)
6	6	77/300 (25%)	37 (48%)	0
All	All	1778/3962 (44%)	480 (26%)	26 (1%)

5 of 480 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	14	U
1	1	15	C
1	1	20	A
1	1	26	A
1	1	32	U

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1234	A
1	1	1338	G
1	1	3416	A
1	1	1333	A
1	1	1385	U

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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

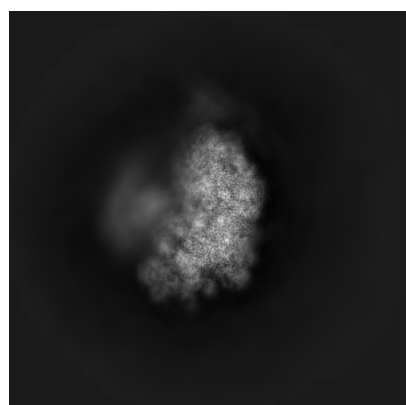
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24395. These allow visual inspection of the internal detail of the map and identification of artifacts.

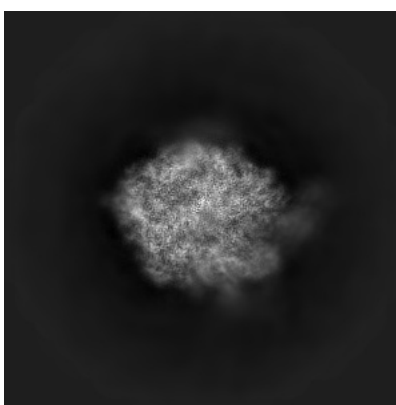
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

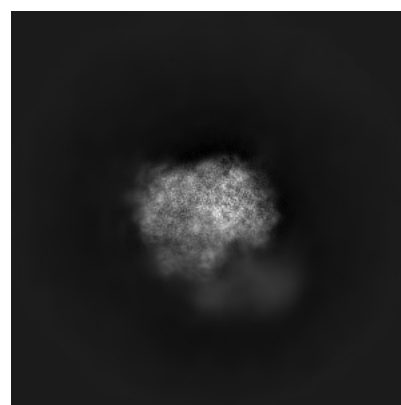
6.1.1 Primary map



X



Y

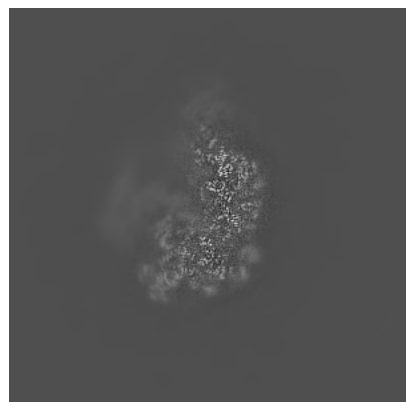


Z

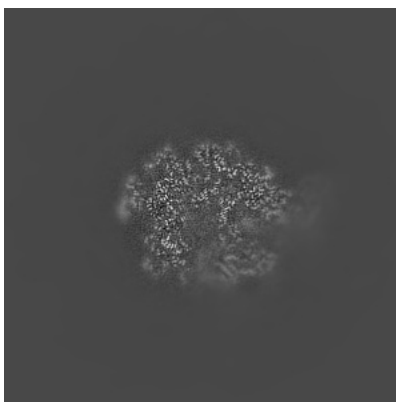
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

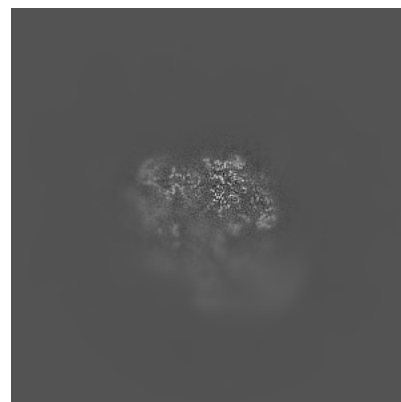
6.2.1 Primary map



X Index: 256



Y Index: 256

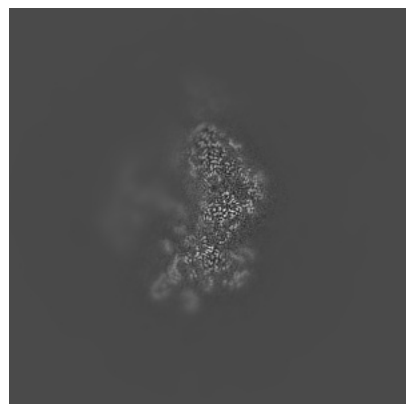


Z Index: 256

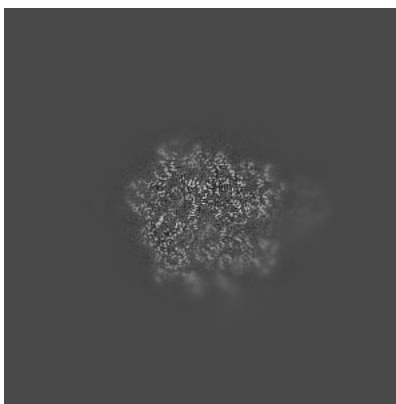
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

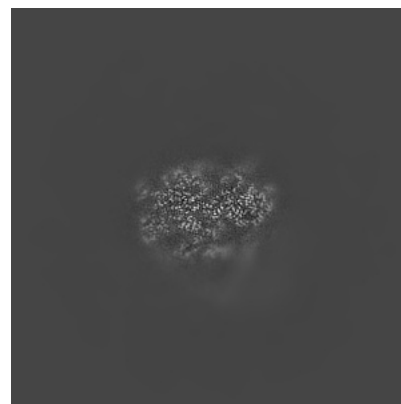
6.3.1 Primary map



X Index: 267



Y Index: 272

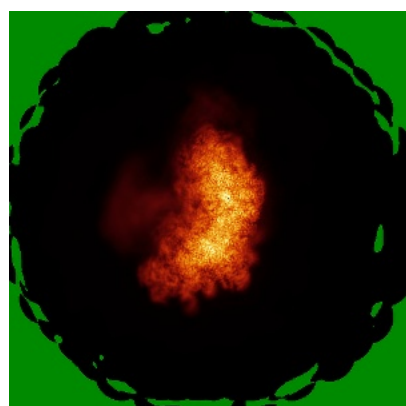


Z Index: 208

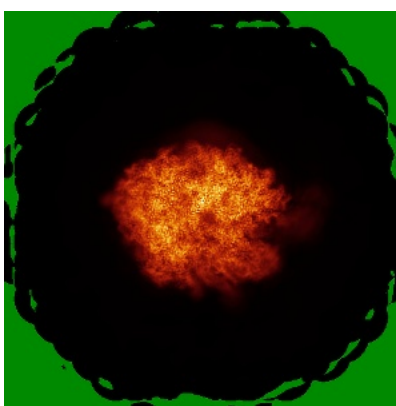
The images above show the largest variance slices of the map in three orthogonal directions.

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

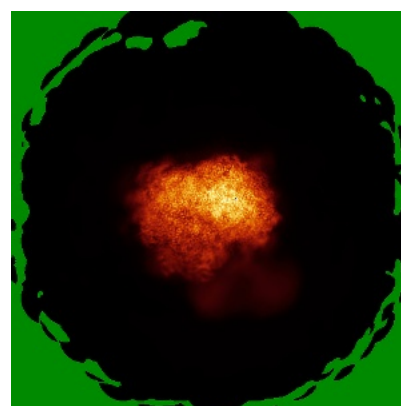
6.4.1 Primary map



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

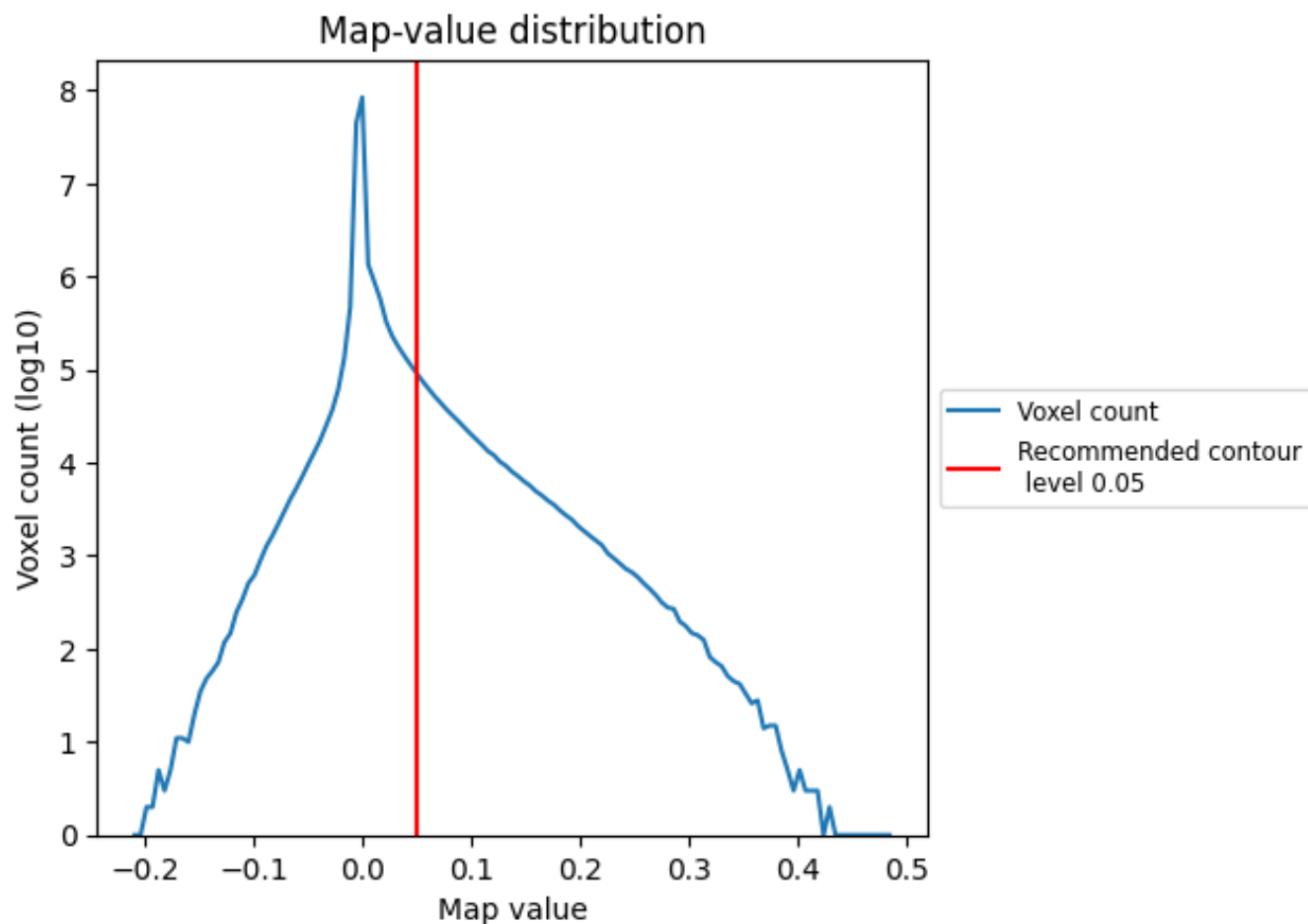
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

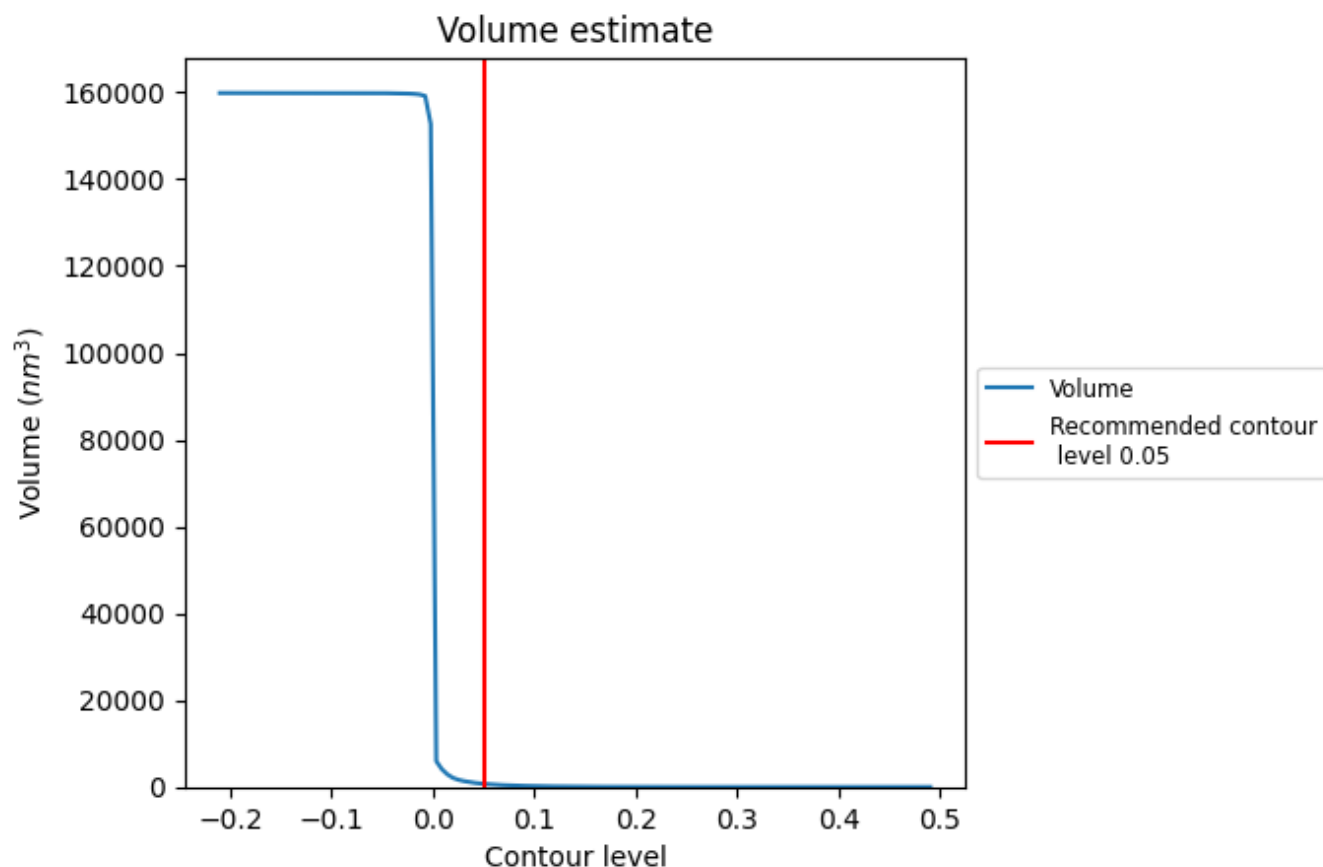
This section contains the results of statistical analysis of the map.

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.

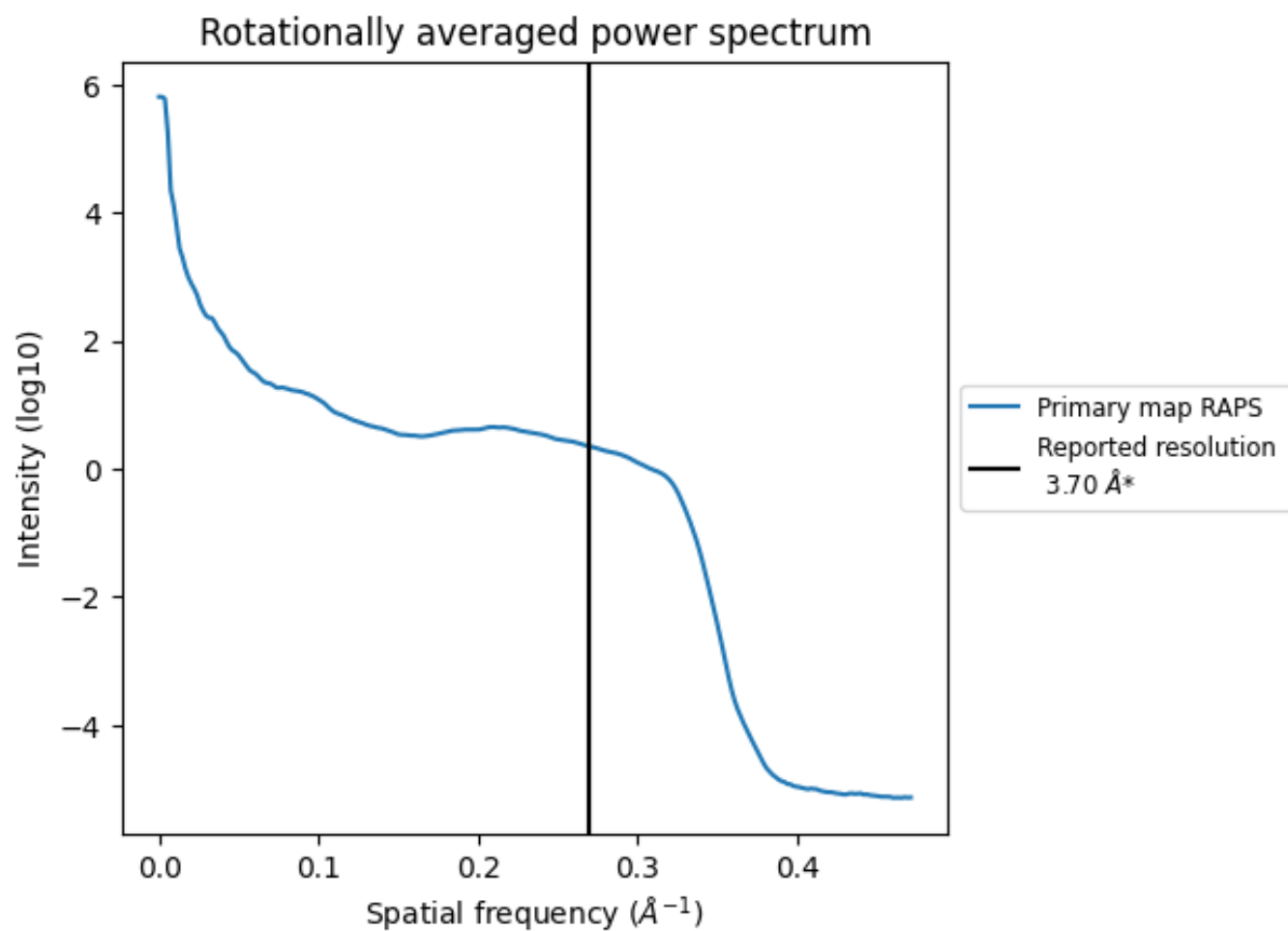
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 724 nm^3 ; this corresponds to an approximate mass of 654 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 0.270 Å⁻¹

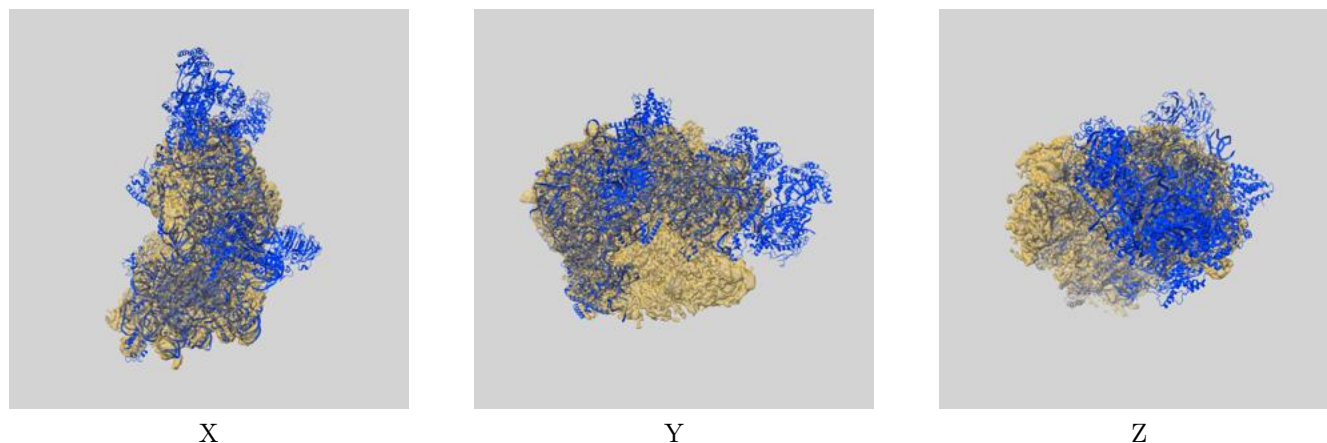
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

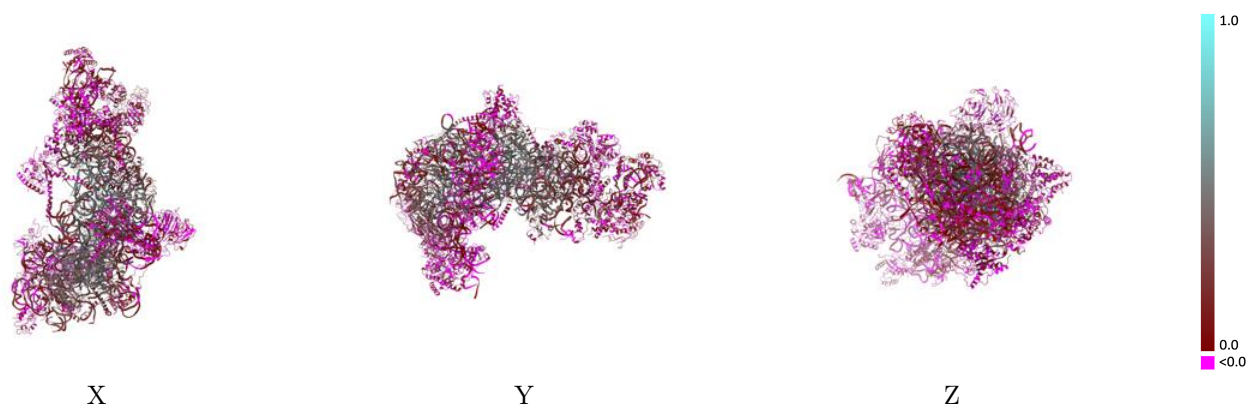
This section contains information regarding the fit between EMDB map EMD-24395 and PDB model 8ETI. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



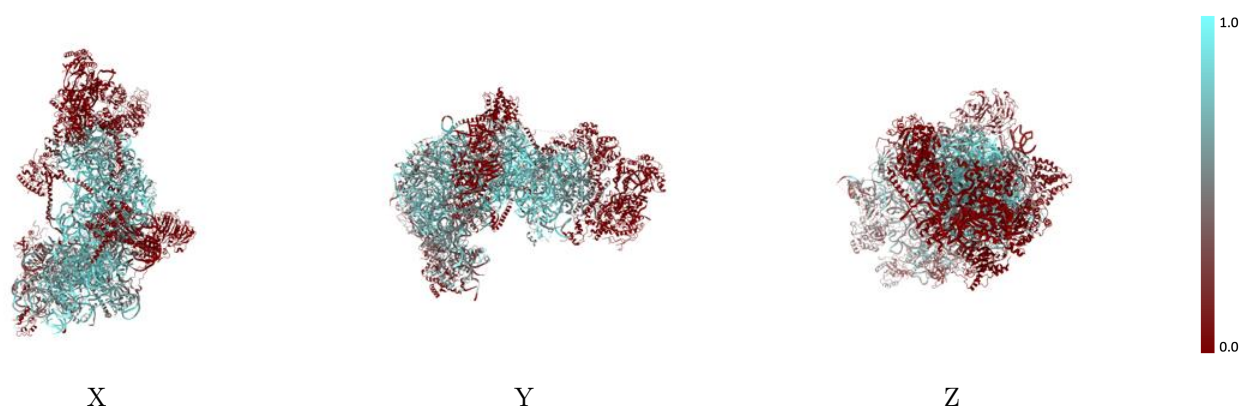
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



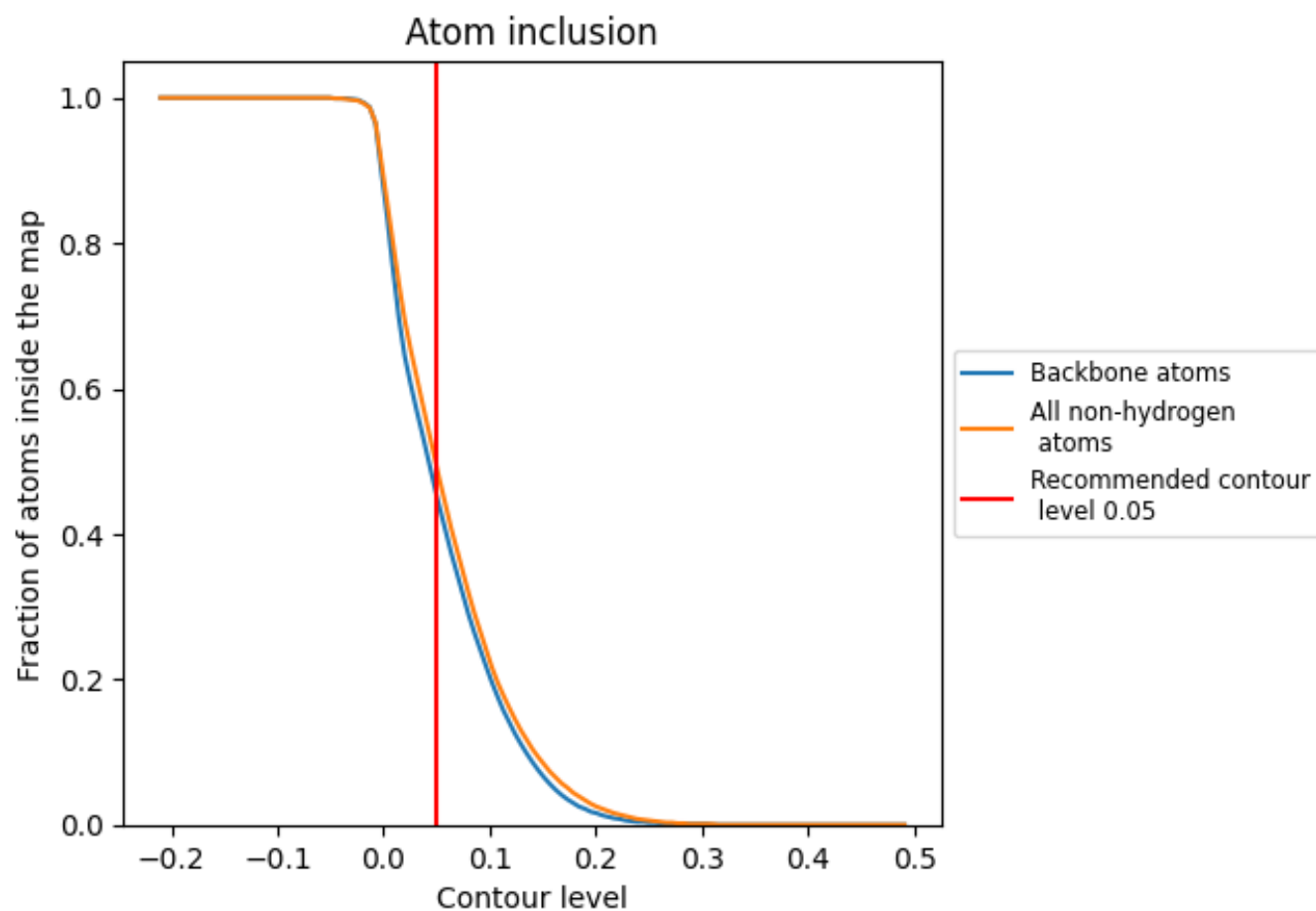
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 45% of all backbone atoms, 49% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4910	 0.1930
1	 0.7230	 0.2640
2	 0.7740	 0.3030
3	 0.0950	 0.0660
4	 0.0010	 0.0230
5	 0.0000	 -0.0020
6	 0.0000	 0.0910
A	 0.0270	 -0.0030
B	 0.5030	 0.1290
C	 0.7530	 0.4280
D	 0.0060	 -0.0100
E	 0.4450	 0.1270
F	 0.6640	 0.3560
G	 0.3650	 0.0980
H	 0.5180	 0.1110
J	 0.0000	 -0.0180
K	 0.0000	 0.0750
L	 0.7120	 0.3730
M	 0.6150	 0.2320
N	 0.6610	 0.2970
O	 0.6950	 0.3370
P	 0.3920	 0.0530
Q	 0.6840	 0.3500
S	 0.6120	 0.2970
T	 0.3370	 0.2730
V	 0.2520	 -0.0370
W	 0.2140	 0.0360
X	 0.4930	 0.1990
Y	 0.7460	 0.3550
b	 0.2390	 0.0380
d	 0.4680	 0.0530
e	 0.6940	 0.3750
f	 0.7710	 0.4090
h	 0.6420	 0.2830
i	 0.4360	 0.1280



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Chain	Atom inclusion	Q-score
j	 0.7590	 0.4040
m	 0.0010	 0.0230
n	 0.0030	 0.0640
o	 0.0000	 0.0840
r	 0.2390	 0.0300
t	 0.0000	 0.0550
u	 0.3210	 0.0090
v	 0.0280	 0.0140
x	 0.0080	 -0.0010
y	 0.2910	 -0.0090
z	 0.3580	 0.0840