



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 10:48 am BST

PDB ID : 7QGG / pdb_00007qgg
EMDB ID : EMD-13954
Title : Neuronal RNA granules are ribosome complexes stalled at the pre-translocation state
Authors : Pulk, A.; Kipper, K.; Mansour, A.
Deposited on : 2021-12-08
Resolution : 2.86 Å(reported)
Based on initial model : 6OLE

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

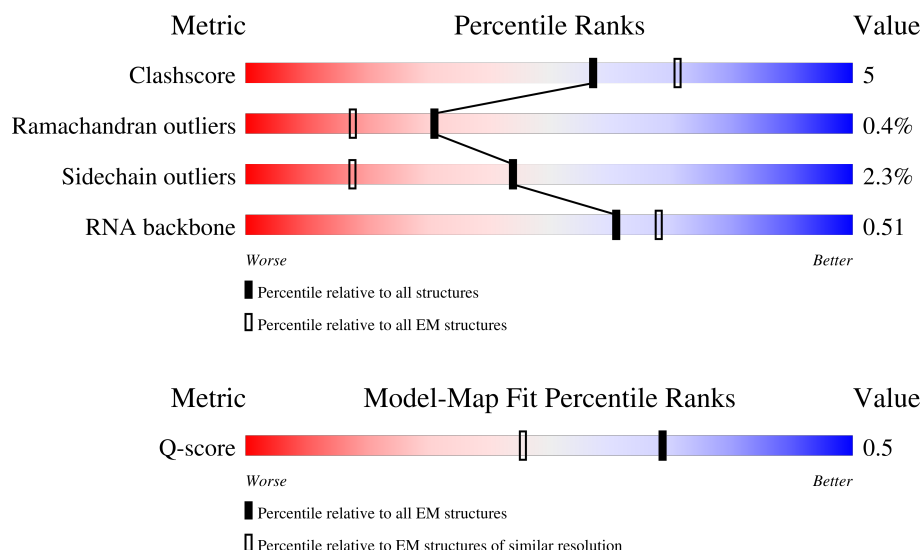
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.86 Å.

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



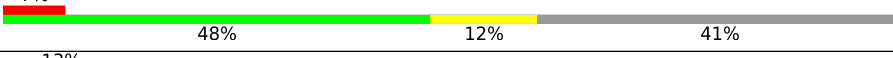
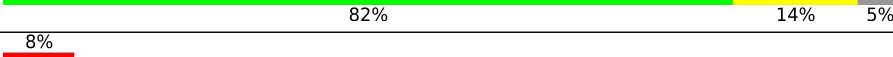
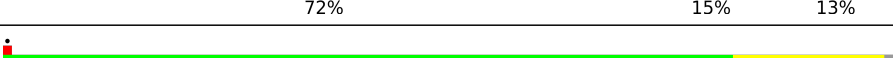
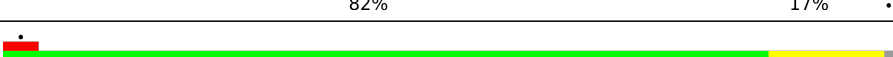
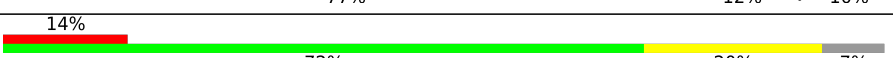
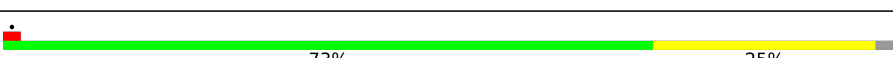
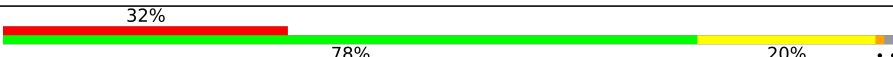
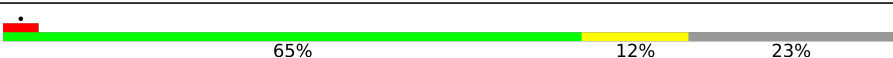
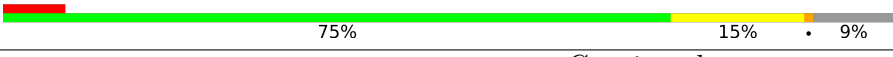
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12017 (2.36 - 3.36)

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	S2	1872	
2	SA	295	
3	SB	264	

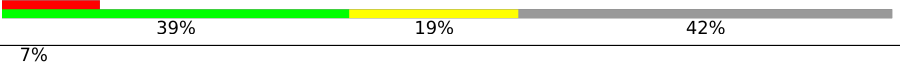
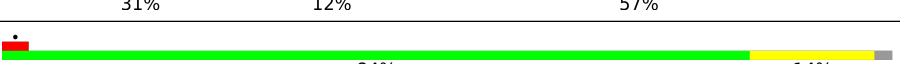
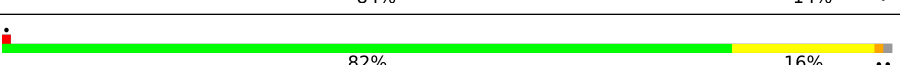
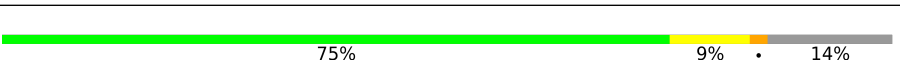
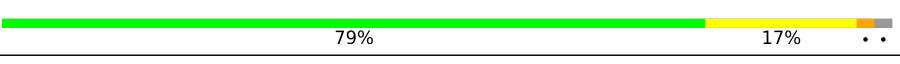
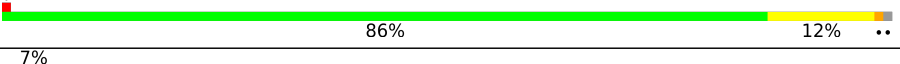
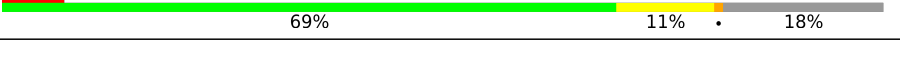
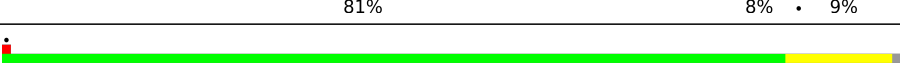
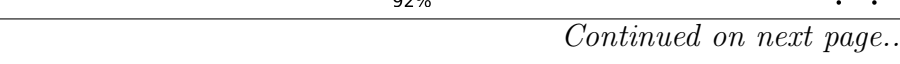
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Mol	Chain	Length	Quality of chain
4	SD	243	
5	SE	263	
6	SF	204	
7	SH	194	
8	SI	208	
9	SK	165	
10	SL	158	
11	SP	145	
12	SQ	146	
13	SR	135	
14	SS	152	
15	ST	145	
16	SU	119	
17	SV	83	
18	SX	143	
19	Sa	115	
20	Sc	69	
21	Sd	56	
22	Sg	317	
23	SC	293	
24	SG	249	
25	SJ	194	
26	SM	132	
27	SN	151	
28	SO	151	

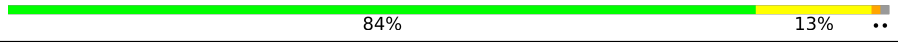
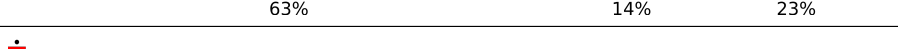
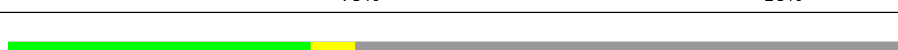
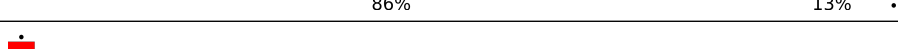
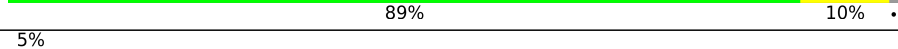
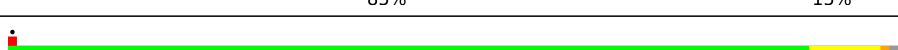
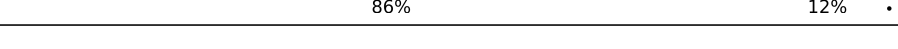
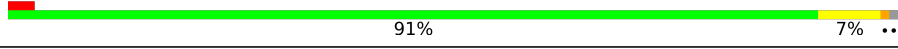
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Mol	Chain	Length	Quality of chain
29	SW	130	
30	SY	133	
31	SZ	125	
32	Sb	84	
33	Se	59	
34	Sf	156	
35	A	257	
36	B	403	
37	C	421	
38	D	157	
39	E	121	
40	F	297	
41	G	298	
42	H	260	
43	I	266	
44	J	192	
45	K	214	
46	L	178	
47	M	211	
48	N	214	
49	O	204	
50	P	203	
51	Q	184	
52	R	188	
53	S	196	

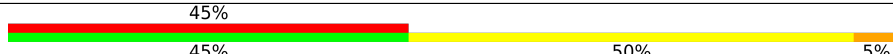
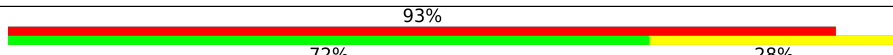
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Mol	Chain	Length	Quality of chain
54	T	176	
55	U	160	
56	V	128	
57	W	140	
58	X	157	
59	Y	156	
60	Z	145	
61	a	136	
62	b	148	
63	c	156	
64	d	115	
65	e	125	
66	f	135	
67	g	110	
68	h	117	
69	i	123	
70	j	105	
71	k	97	
72	l	70	
73	m	51	
74	n	128	
75	o	25	
76	p	106	
77	q	92	
78	r	137	

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Mol	Chain	Length	Quality of chain
79	t	4803	
80	u	76	
81	v	76	
82	w	20	
83	Cz	217	
84	y	4	

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
1	6MZ	S2	1835	-	X	-	-

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 218574 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 (1872-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	S2	1714	Total	C	N	O	P	0	0
			36502	16306	6533	11950	1713		

- Molecule 2 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	214	Total	C	N	O	S	0	0
			1693	1076	297	312	8		

- Molecule 3 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 4 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SD	226	Total	C	N	O	S	0	0
			1756	1119	316	314	7		

- Molecule 5 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SE	259	Total	C	N	O	S	0	0
			2059	1316	383	352	8		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 7 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 8 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	204	Total	C	N	O	S	0	0
			1673	1050	329	289	5		

- Molecule 9 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 10 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SL	150	Total	C	N	O	S	0	0
			1220	776	228	210	6		

- Molecule 11 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SP	130	Total	C	N	O	S	0	0
			1073	681	205	180	7		

- Molecule 12 is a protein called Rps16 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SQ	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 13 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SR	134	Total	C	N	O	S	0	0
			1079	676	201	198	4		

- Molecule 14 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 15 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	ST	143	Total	C	N	O	S	0	0
			1115	698	217	198	2		

- Molecule 16 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SU	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 17 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SV	82	Total	C	N	O	S	0	0
			626	382	118	121	5		

- Molecule 18 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 19 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Sa	103	Total	C	N	O	S	0	0
			826	515	172	134	5		

- Molecule 20 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 21 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 22 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Sg	312	Total	C	N	O	S	0	0
			2429	1531	423	463	12		

- Molecule 23 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SC	225	Total	C	N	O	S	1	0
			1755	1134	303	309	9		

- Molecule 24 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 25 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SJ	185	Total	C	N	O	S	1	0
			1533	974	309	248	2		

- Molecule 26 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SM	118	Total	C	N	O	S	0	0
			912	574	160	171	7		

- Molecule 27 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 28 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SO	137	Total	C	N	O	S	0	0
			1024	627	200	191	6		

- Molecule 29 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 30 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SY	131	Total	C	N	O	S	1	0
			1073	678	212	178	5		

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SZ	73	Total	C	N	O	S	0	0
			579	372	106	100	1		

- Molecule 32 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sb	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 33 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Se	57	Total	C	N	O	S	0	0
			452	281	99	71	1		

- Molecule 34 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sf	67	Total	C	N	O	S	0	0
			547	345	102	93	7		

- Molecule 35 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	A	252	Total	C	N	O	S	0	0
			1930	1209	395	320	6		

- Molecule 36 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B	397	Total	C	N	O	S	0	0
			3204	2041	603	546	14		

- Molecule 37 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	C	363	Total	C	N	O	S	0	0
			2889	1817	575	481	16		

- Molecule 38 is a RNA chain called RNA (157-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
38	D	157	Total	C	N	O	P	0	0
			3337	1489	587	1104	157		

- Molecule 39 is a RNA chain called RNA (121-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
39	E	119	Total	C	N	O	P	0	0
			2541	1132	454	836	119		

- Molecule 40 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	F	294	Total	C	N	O	S	0	0
			2399	1511	442	432	14		

- Molecule 41 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	G	243	Total	C	N	O	S	0	0
			1960	1251	375	330	4		

- Molecule 42 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	H	225	Total	C	N	O	S	0	0
			1865	1199	357	301	8		

- Molecule 43 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	I	241	Total	C	N	O	S	0	0
			1935	1232	372	327	4		

- Molecule 44 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	J	191	Total	C	N	O	S	0	0
			1528	961	285	276	6		

- Molecule 45 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	K	208	Total	C	N	O	S	0	0
			1692	1074	327	278	13		

- Molecule 46 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	L	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 47 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	M	205	Total	C	N	O	S	0	0
			1659	1036	342	276	5		

- Molecule 48 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	N	139	Total	C	N	O	S	0	0
			1142	732	221	182	7		

- Molecule 49 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	O	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 50 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	P	197	Total	C	N	O	S	0	0
			1611	1038	316	252	5		

- Molecule 51 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Q	158	Total	C	N	O	S	0	0
			1282	804	248	221	9		

- Molecule 52 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	R	187	Total	C	N	O	S	0	0
			1516	949	314	249	4		

- Molecule 53 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S	188	Total	C	N	O	S	0	0
			1572	974	337	252	9		

- Molecule 54 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	T	176	Total	C	N	O	S	0	0
			1458	929	284	234	11		

- Molecule 55 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	U	158	Total	C	N	O	S	0	0
			1293	821	251	215	6		

- Molecule 56 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	V	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 57 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	W	134	Total	C	N	O	S	0	0
			993	625	187	176	5		

- Molecule 58 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	X	61	Total	C	N	O	S	0	0
			511	327	100	82	2		

- Molecule 59 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Y	120	Total	C	N	O	S	0	0
			984	630	185	168	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Z	134	Total	C	N	O	S	0	0
			1116	700	227	186	3		

- Molecule 61 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	a	134	Total	C	N	O	S	0	0
			1103	712	207	181	3		

- Molecule 62 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	b	147	Total	C	N	O	S	0	0
			1165	736	240	185	4		

- Molecule 63 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	c	95	Total	C	N	O	S	0	0
			781	487	171	120	3		

- Molecule 64 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	d	101	Total	C	N	O	S	0	0
			785	498	138	142	7		

- Molecule 65 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	e	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 66 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	f	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 67 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	g	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 68 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	h	116	Total	C	N	O	S	0	0
			920	575	190	149	6		

- Molecule 69 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	i	122	Total	C	N	O	S	0	0
			1015	643	204	167	1		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	j	104	Total	C	N	O	S	0	0
			849	531	180	133	5		

- Molecule 71 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	k	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	l	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	m	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 74 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	n	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 75 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	o	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 76 is a protein called Ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	p	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 77 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	q	91	Total	C	N	O	S	0	0
			708	444	135	122	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
q	87	GLU	LYS	conflict	UNP A0A6J2LF66

- Molecule 78 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	r	131	Total	C	N	O	S	0	0
			1059	655	224	175	5		

- Molecule 79 is a RNA chain called RNA (4803-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
79	t	3679	Total	C	N	O	P	0	0
			78855	35119	14410	25647	3679		

- Molecule 80 is a RNA chain called RNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
80	u	76	Total	C	N	O	P	0	0
			1613	720	283	535	75		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	34	C	G	conflict	GB 1851728667
u	35	C	A	conflict	GB 1851728667
u	36	G	A	conflict	GB 1851728667
u	37	U	A	conflict	GB 1851728667

- Molecule 81 is a RNA chain called RNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
81	v	76	Total	C	N	O	P	0	0
			1618	721	287	534	76		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	?	-	A	deletion	GB 1879656365
v	12	C	U	conflict	GB 1879656365
v	14	C	A	conflict	GB 1879656365
v	16	A	U	conflict	GB 1879656365
v	34	C	G	conflict	GB 1879656365
v	35	C	A	conflict	GB 1879656365
v	36	G	A	conflict	GB 1879656365

- Molecule 82 is a RNA chain called RNA (5'-D(P*($\emptyset$)P*($\emptyset$)P*($\emptyset$)P*($\emptyset$))-R(P*UP*UP*AP*CP*GP*GP*CP*GP*GP*UP*($\emptyset$)P*($\emptyset$)P*($\emptyset$)P*($\emptyset$)P*($\emptyset$))-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
82	w	20	Total	C	N	O	P	0	0
			423	189	72	142	20		

- Molecule 83 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 84 is a protein called ALA-ALA-LYS-ALA.

Mol	Chain	Residues	Atoms				AltConf	Trace
84	y	4	Total	C	N	O	0	0
			24	15	5	4		

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

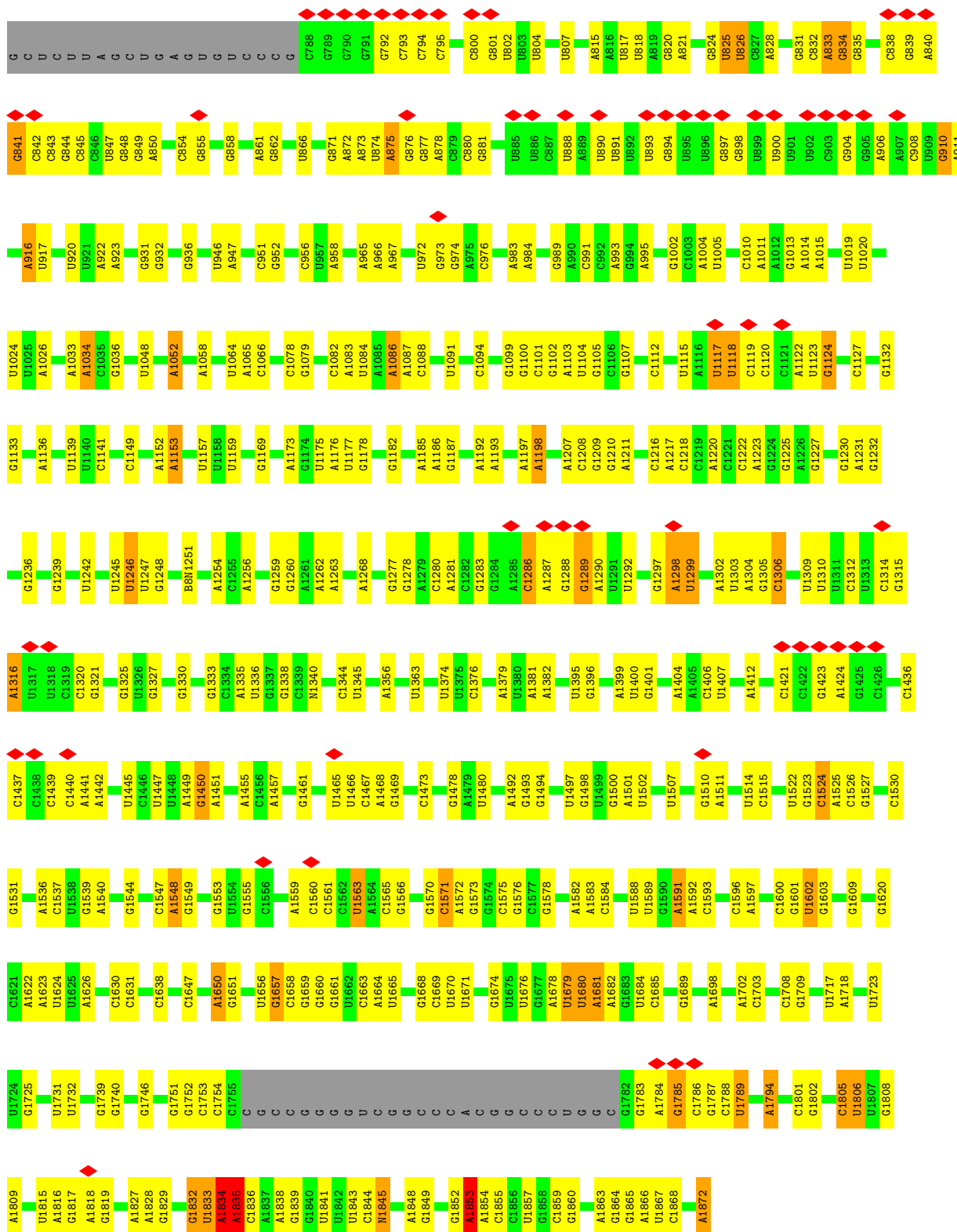
Mol	Chain	Residues	Atoms		AltConf
85	S2	3	Total 3	Mg 3	0
85	B	1	Total 1	Mg 1	0
85	D	6	Total 6	Mg 6	0
85	E	9	Total 9	Mg 9	0
85	Z	1	Total 1	Mg 1	0
85	t	13	Total 13	Mg 13	0

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	S2	1	Total 1	Zn 1	0
86	Sa	1	Total 1	Zn 1	0
86	Sf	1	Total 1	Zn 1	0
86	k	1	Total 1	Zn 1	0
86	p	1	Total 1	Zn 1	0
86	q	1	Total 1	Zn 1	0

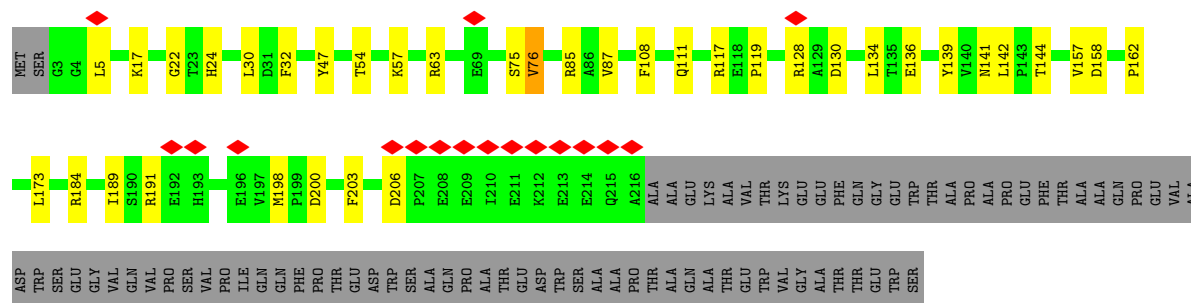
- Molecule 87 is water.

Mol	Chain	Residues	Atoms		AltConf
87	S2	5	Total 5	O 5	0
87	SS	1	Total 1	O 1	0
87	Sf	1	Total 1	O 1	0
87	u	1	Total 1	O 1	0

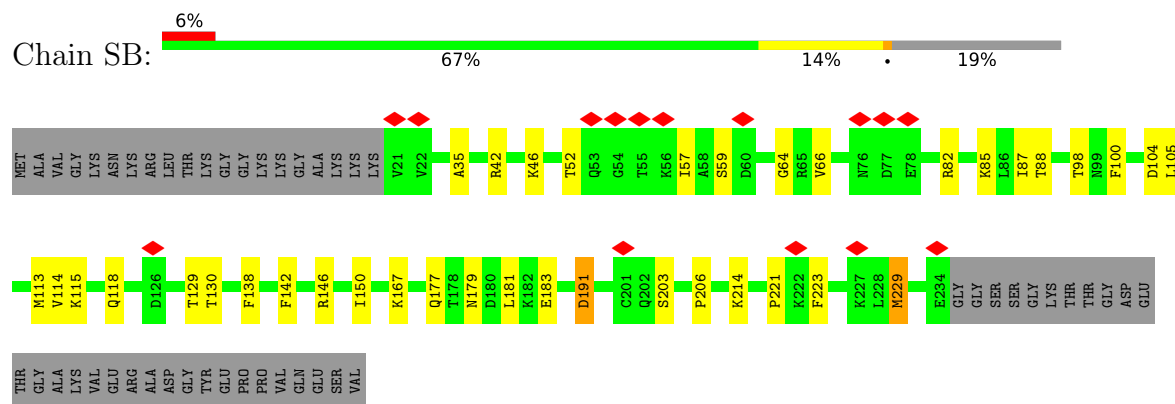


• Molecule 2: 40S ribosomal protein SA

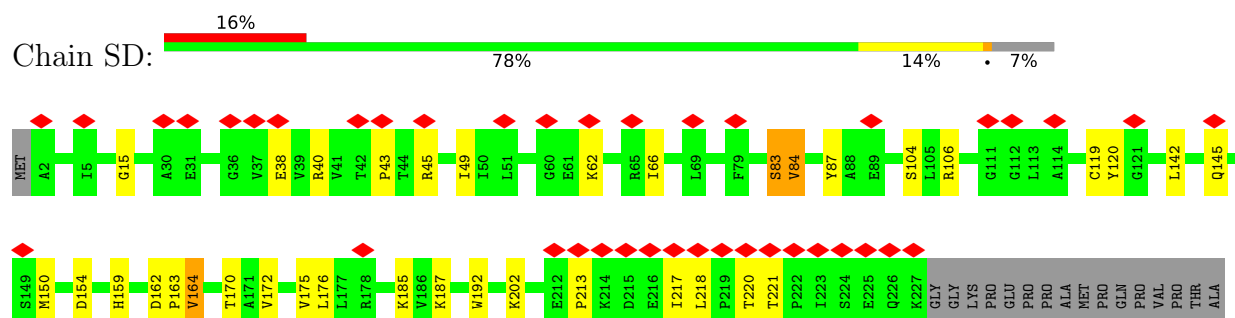




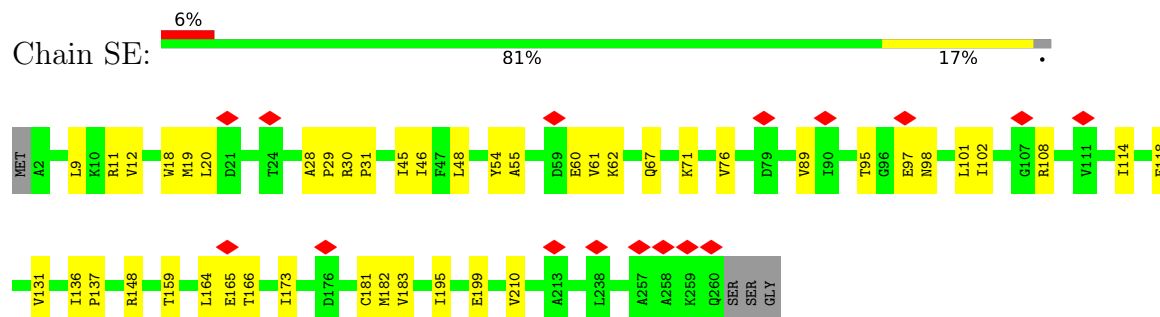
- Molecule 3: 40S ribosomal protein S3a



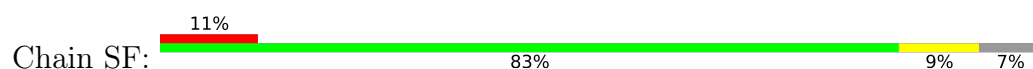
- Molecule 4: 40S ribosomal protein S3

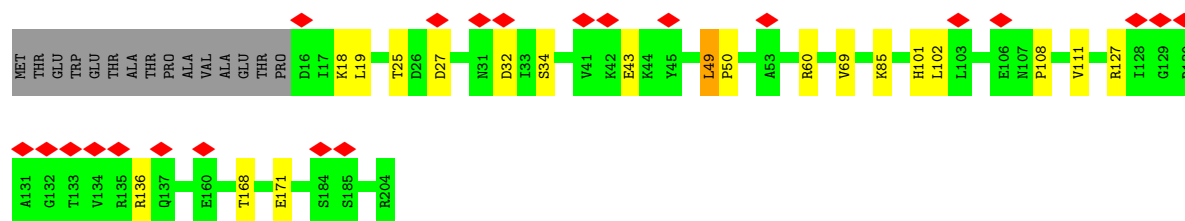


- Molecule 5: 40S ribosomal protein S4, X isoform

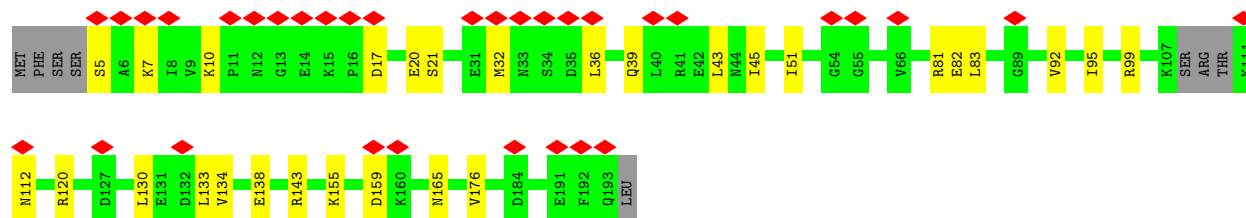
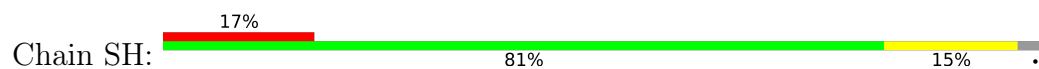


- Molecule 6: 40S ribosomal protein S5

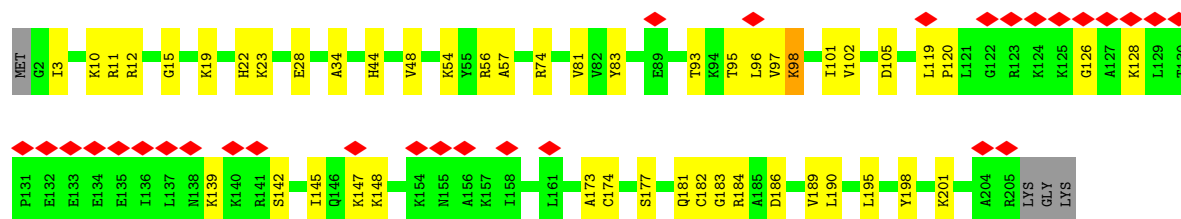
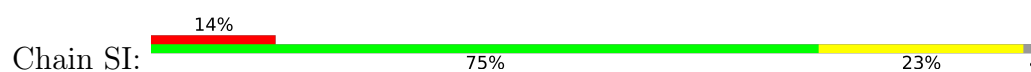




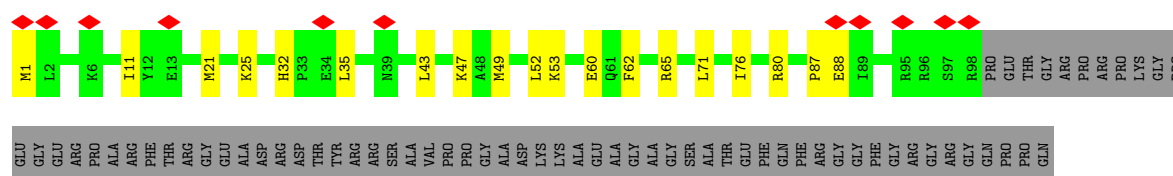
• Molecule 7: 40S ribosomal protein S7



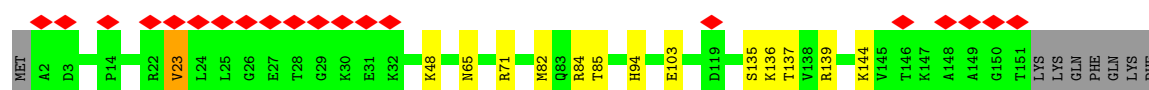
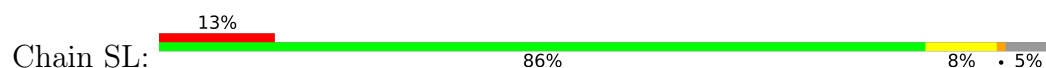
• Molecule 8: 40S ribosomal protein S8



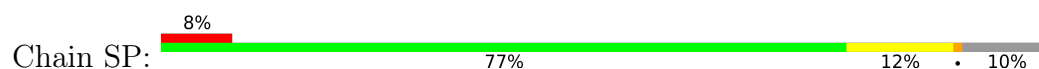
• Molecule 9: 40S ribosomal protein S10



• Molecule 10: 40S ribosomal protein S11

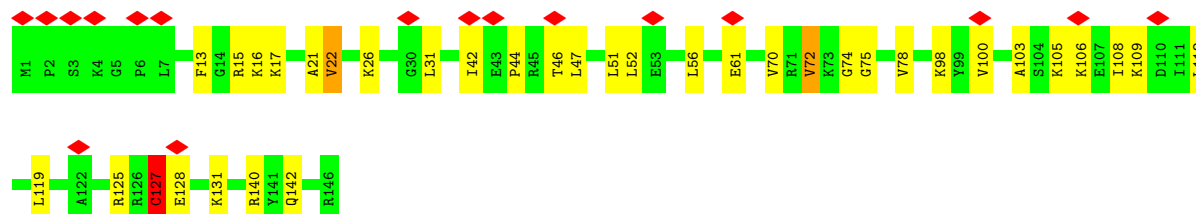
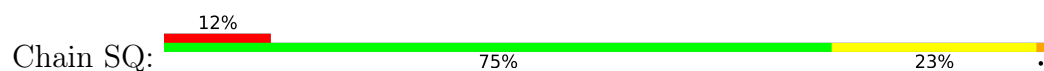


• Molecule 11: 40S ribosomal protein S15

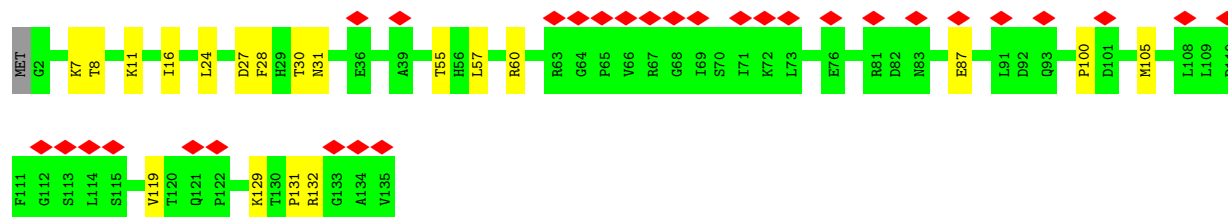
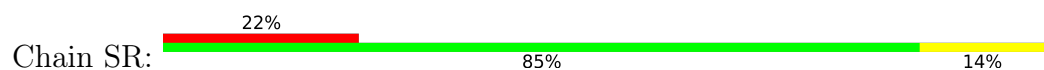




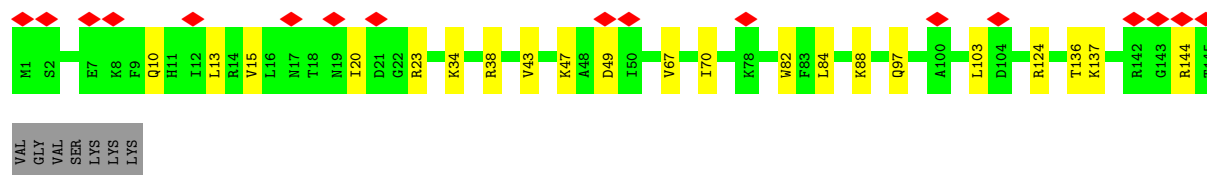
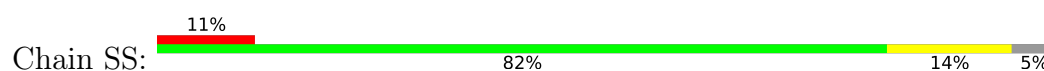
- Molecule 12: Rps16 protein



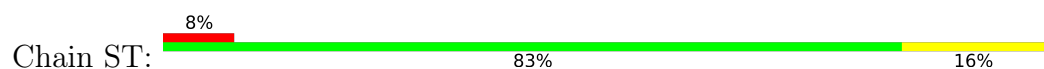
- Molecule 13: 40S ribosomal protein S17



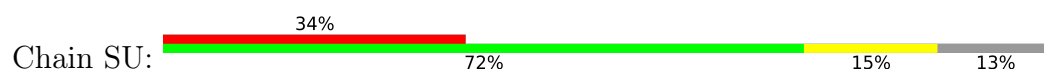
- Molecule 14: 40S ribosomal protein S18

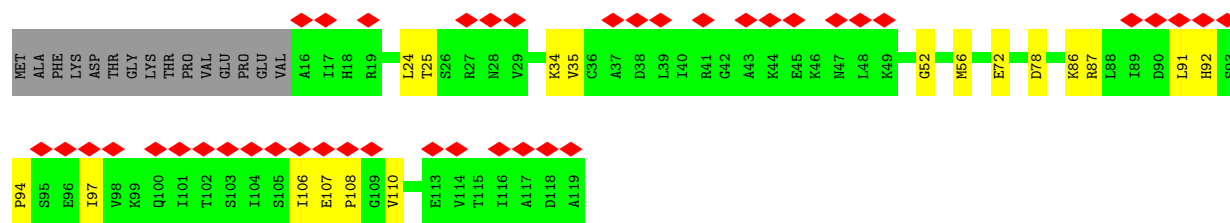


- Molecule 15: 40S ribosomal protein S19

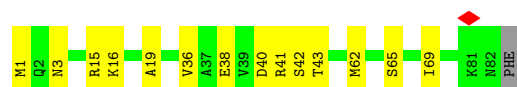
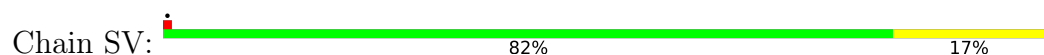


- Molecule 16: 40S ribosomal protein S20





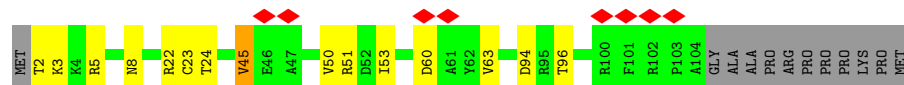
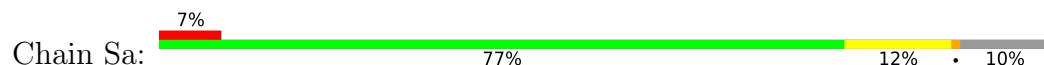
- Molecule 17: 40S ribosomal protein S21



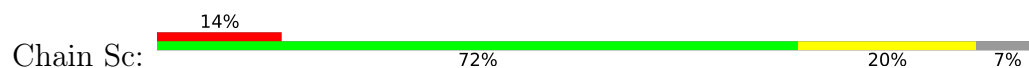
- Molecule 18: 40S ribosomal protein S23



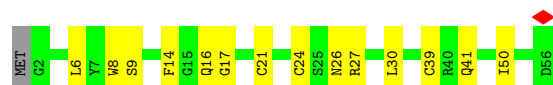
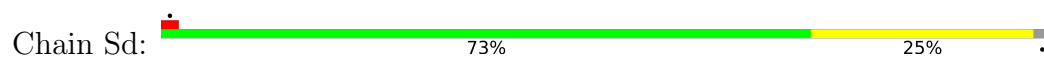
- Molecule 19: 40S ribosomal protein S26



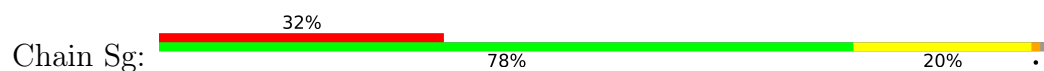
- Molecule 20: 40S ribosomal protein S28

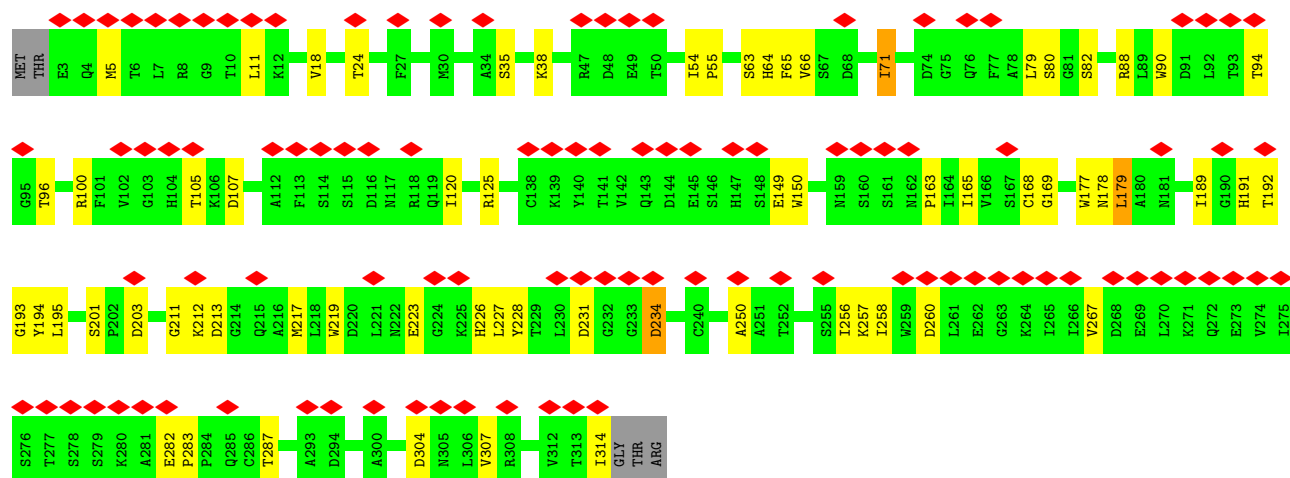


- Molecule 21: 40S ribosomal protein S29

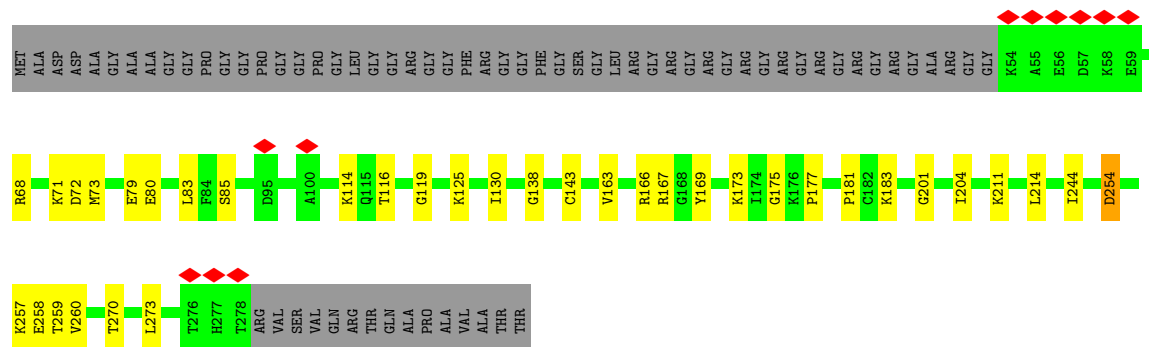


- Molecule 22: Receptor of activated protein C kinase 1

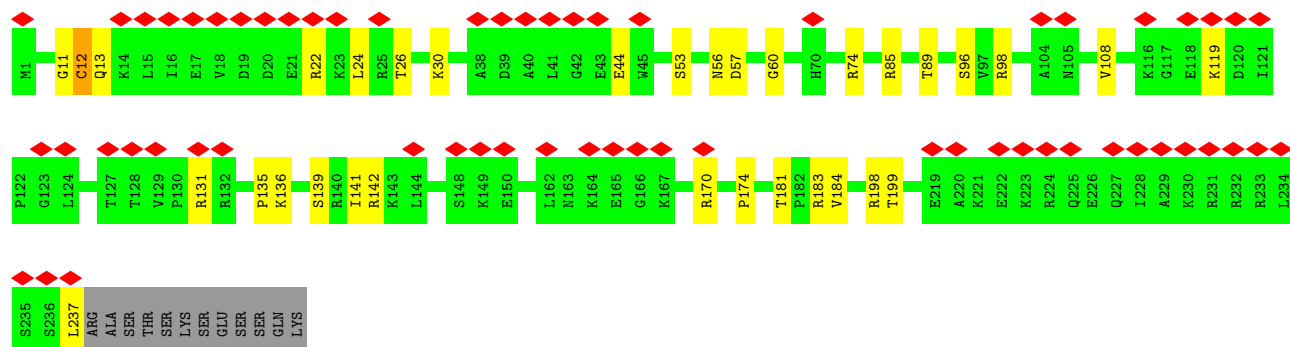
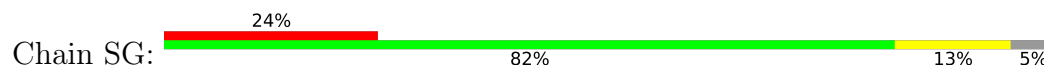




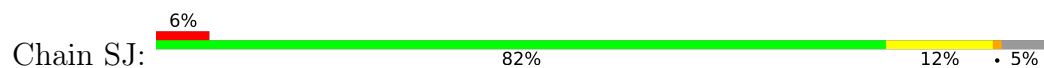
• Molecule 23: 40S ribosomal protein S2

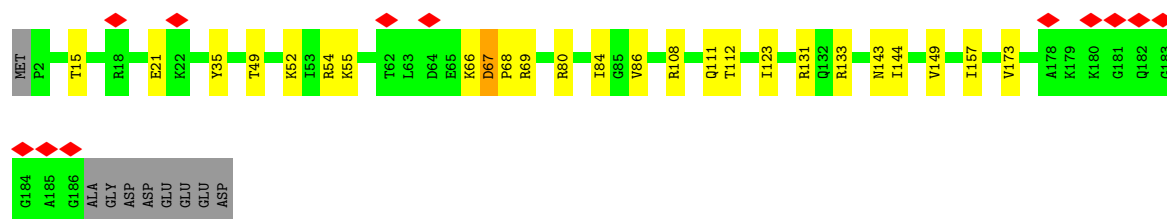


• Molecule 24: 40S ribosomal protein S6

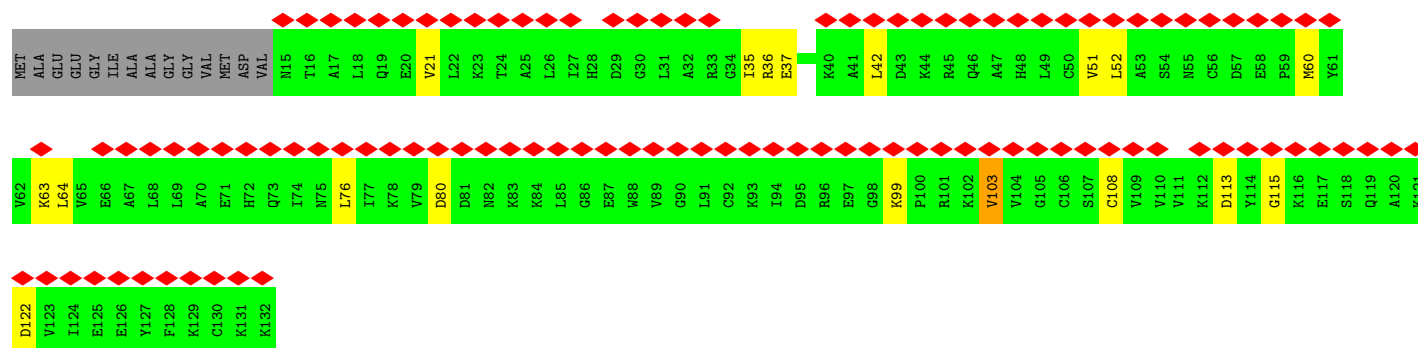
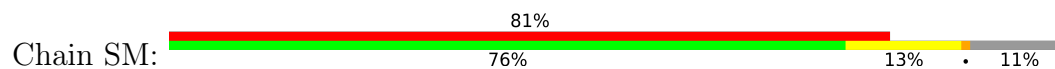


• Molecule 25: 40S ribosomal protein S9

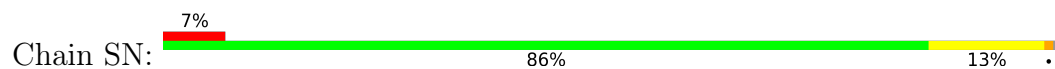




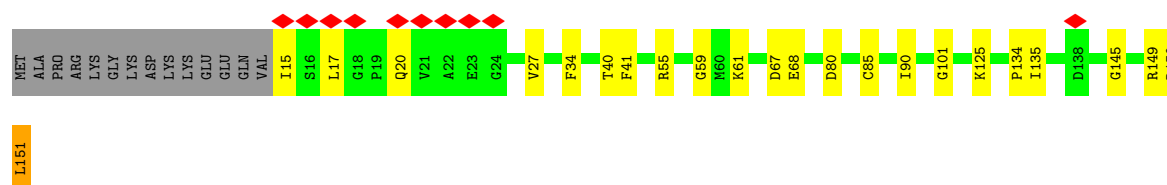
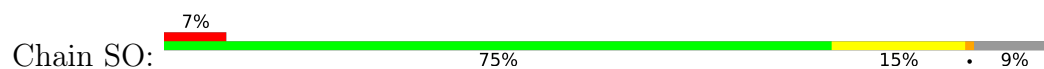
- Molecule 26: 40S ribosomal protein S12



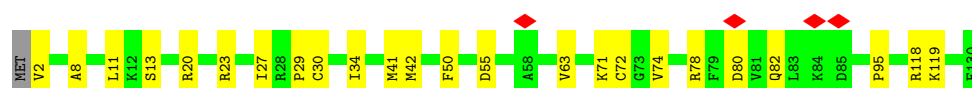
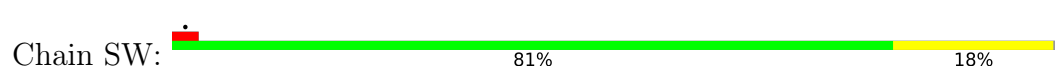
- Molecule 27: 40S ribosomal protein S13



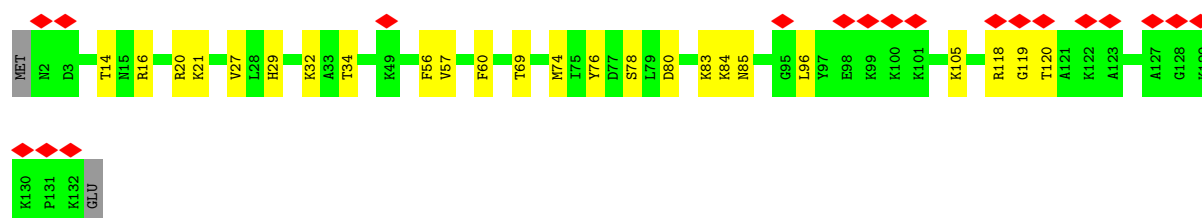
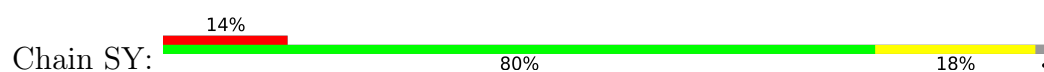
- Molecule 28: 40S ribosomal protein S14



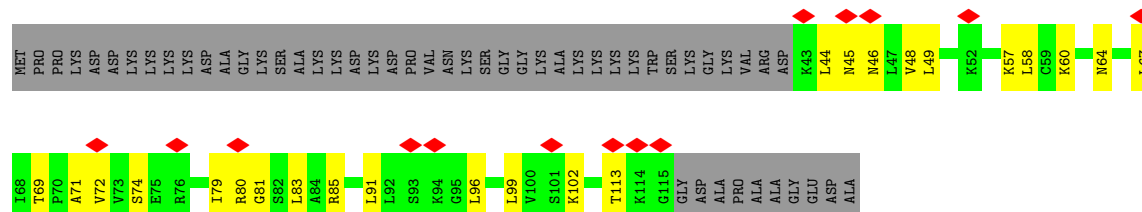
- Molecule 29: 40S ribosomal protein S15a



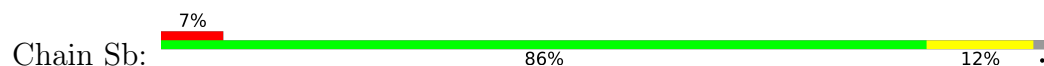
- Molecule 30: 40S ribosomal protein S24



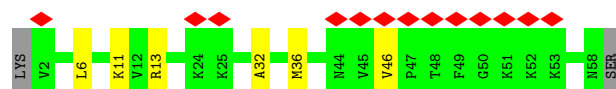
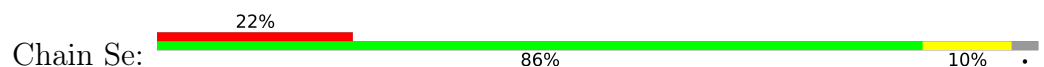
- Molecule 31: 40S ribosomal protein S25



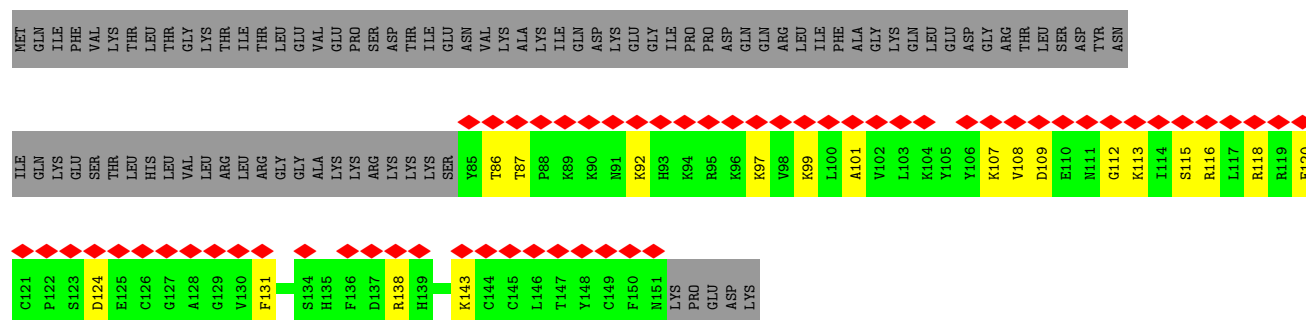
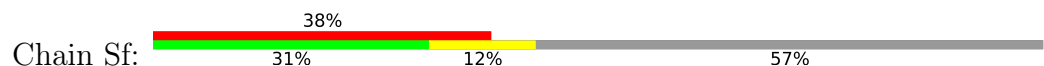
- Molecule 32: 40S ribosomal protein S27



- Molecule 33: Ubiquitin-like domain-containing protein



- Molecule 34: Ubiquitin-40S ribosomal protein S27a

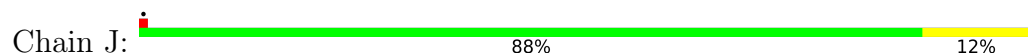


- Molecule 35: 60S ribosomal protein L8

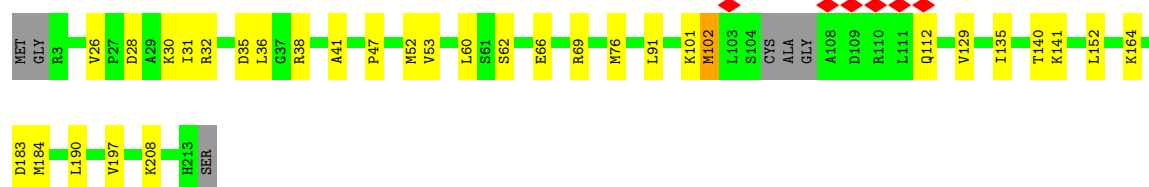
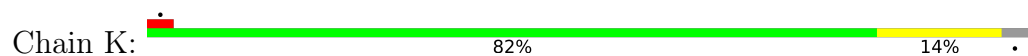




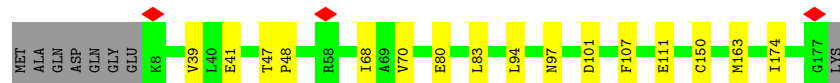
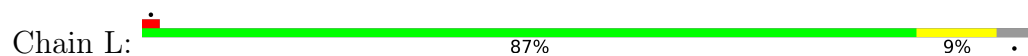
- Molecule 44: 60S ribosomal protein L9



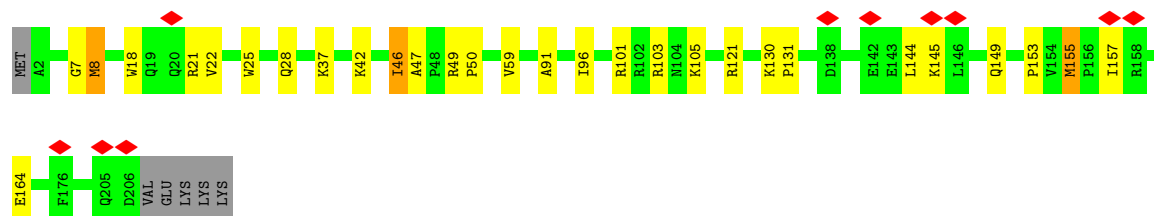
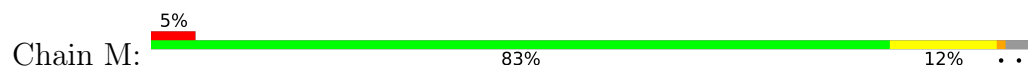
- Molecule 45: 60S ribosomal protein L10



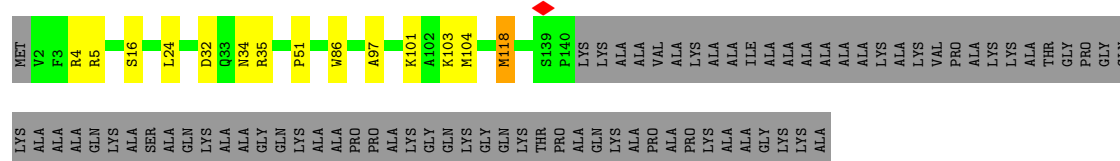
- Molecule 46: 60S ribosomal protein L11



- Molecule 47: 60S ribosomal protein L13



- Molecule 48: 60S ribosomal protein L14



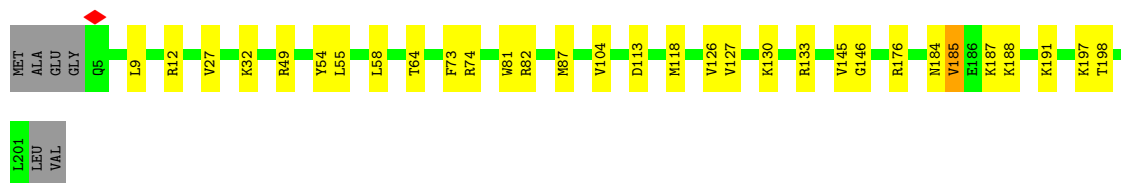
- Molecule 49: Ribosomal protein L15

Chain O:  87% 12%



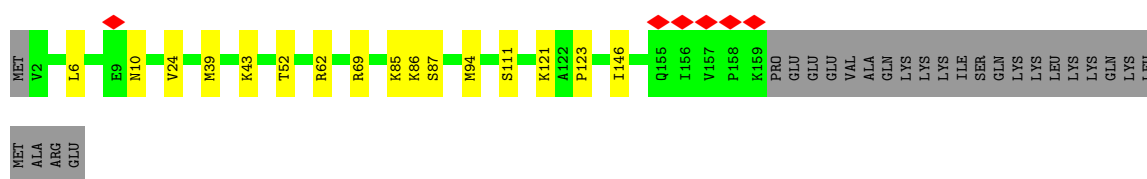
- Molecule 50: 60S ribosomal protein L13a

Chain P:  82% 15%



- Molecule 51: 60S ribosomal protein L17

Chain Q:  77% 9% 14%



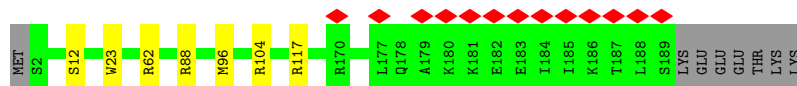
- Molecule 52: 60S ribosomal protein L18

Chain R:  87% 12%



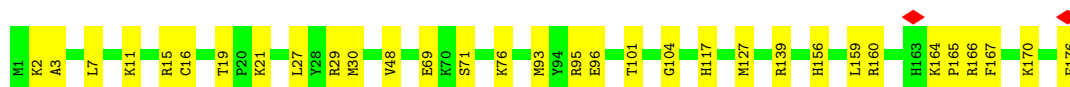
- Molecule 53: Ribosomal protein L19

Chain S:  7% 92%



- Molecule 54: 60S ribosomal protein L18a

Chain T:  82% 18%

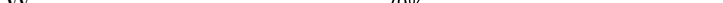


- Molecule 55: 60S ribosomal protein L21

ME1	T2	N3	T4	K7	P18	K21	R32	D41	I42	V48	T68	V80	K100	S101	R102	R108	K116	W125	V126	K129	P132	A133	P148	L151	E152	P153	P159	A174
-----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

- Chain V:  63% 14% 23%

ASP	MET
GLU	ALA
ASP	PRO
	VAL
	LYS
	LYS
	LEU
	VAL
	ALA
	LYS
	GLY
	GLY
	LYS
	LYS
	LYS
	GLN
	V18
	C25
	P28
	E45
	R46
	T62
	T63
	R64
	R65
	S66
	K67
	T73
	V76
	S79
	L86
	D98
	N99
	L100
	S106
	K107
	L112
	Q116
	T1E
	ASN
	GLN
	ASP
	GLU
	GLU
	GLU
	GLU

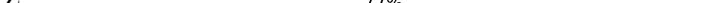
- Chain W:  79% 16% ..

MET
SER
LYS
ARG
GLY
ARG
G7
S9
S10
K13
F14
R15
C28
A29
D30
G33
N50
R51
V57
K69
I82
R83
K91
L96
E99
V104
M107
E111
M112
K113
I117
T118
G119
P120
V121
A136
V140

- Chain X: 34% 5% 61%

GLN	ARG	GLU	GLN	ILE	ARG	ALA	LYS	GLU	ALA	LYS	LYS	THR	GLU	ILE	GLN	LYS	ARG	THR	ARG	ALA	VAL	LYS	PHE	GLN	ARG	ALA	ILE	ILE	THR	GLY	ALA	SER	LEU	ASP	ILE	MET	ALA	LYS	ARG	ASN	GLN	LYS	PRO	GLU	VAL	ARG	LYS
MET	K2	R20	Y21	F29	L32	M45	Q48	T52	N53	L54	G62	GLN	SER	GLU	GLU	ILE	GLN	LYS	ARG	ALA	VAL	LYS	PHE	GLN	ARG	ALA	ILE	ILE	THR	GLY	ALA	SER	LEU	ASP	ILE	MET	ALA	LYS	ARG	ASN	GLN	LYS	PRO	GLU	VAL	ARG	LYS

- Chain Y: 67% 9% 23%

- Chain Z:  77% 15% 8%

M1 T8 S9 D10 R11 H18 S31 S32 E37 R45 P48 D52 V55 Y74 E83 R84 R87 V95 P101 K110 R126 Q127 K130 E131 K132 G133 K134 TYR LYS GLU GLU THR ILE GLU LYS MET GLN CII

(Note: Red diamonds are positioned above positions E131, K132, and G133.)

- Molecule 61: 60S ribosomal protein L27

Chain a:  85% 14%



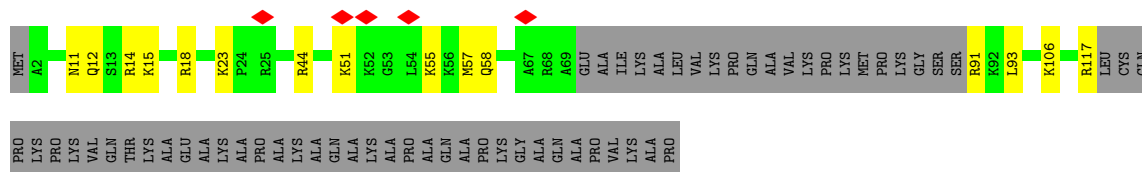
- Molecule 62: 60S ribosomal protein L27a

Chain b:  86% 13%



- Molecule 63: 60S ribosomal protein L29

Chain c:  51% 10% 39%



- Molecule 64: 60S ribosomal protein L30

Chain d:  5% 75% 11% 12%



- Molecule 65: 60S ribosomal protein L31

Chain e:  74% 10% 15%



- Molecule 66: 60S ribosomal protein L32

Chain f:  82% 13%

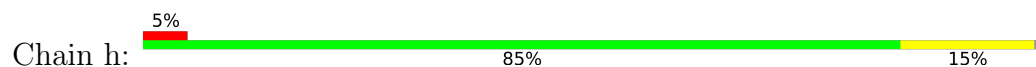


- Molecule 67: 60S ribosomal protein L35a

Chain g:  89% 10%



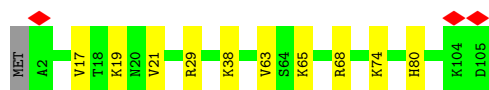
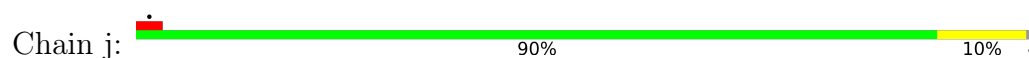
- Molecule 68: 60S ribosomal protein L34



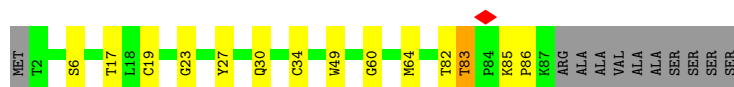
- Molecule 69: 60S ribosomal protein L35



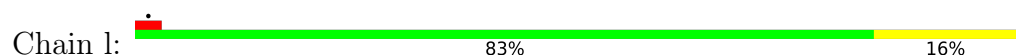
- Molecule 70: 60S ribosomal protein L36



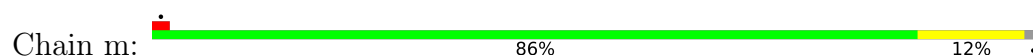
- Molecule 71: Ribosomal protein L37



- Molecule 72: 60S ribosomal protein L38

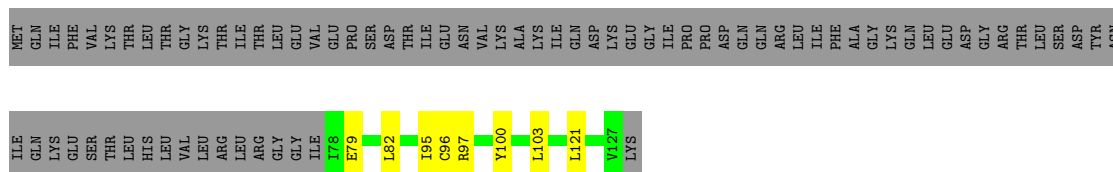


- Molecule 73: 60S ribosomal protein L39



- Molecule 74: Ubiquitin-60S ribosomal protein L40

Chain n:  33% 6% 61%



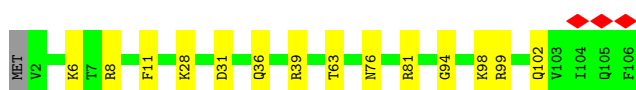
- Molecule 75: 60S ribosomal protein L41

Chain o:  80% 20%



- Molecule 76: Ribosomal protein L36a

Chain p:  86% 13% .



- Molecule 77: 60S ribosomal protein L37a

Chain q:  91% 7% ..



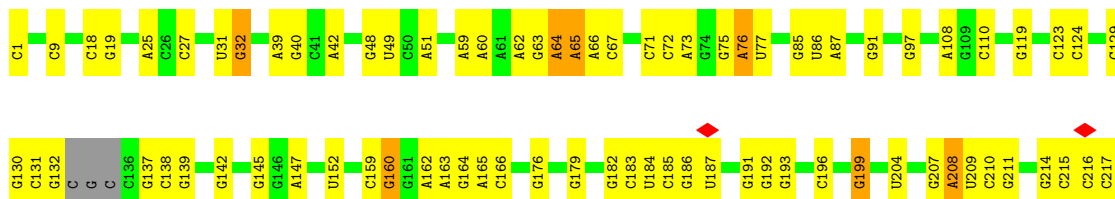
- Molecule 78: 60S ribosomal protein L28

Chain r:  7% 82% 14% .



- Molecule 79: RNA (4803-MER)

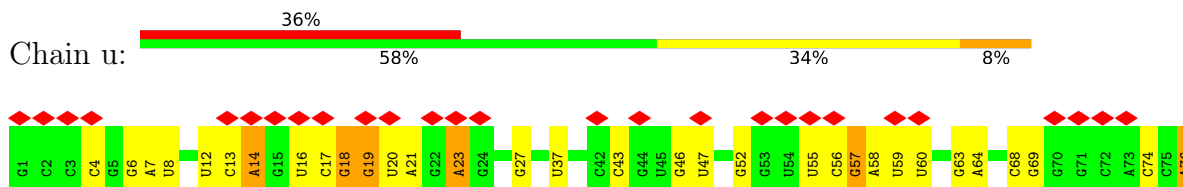
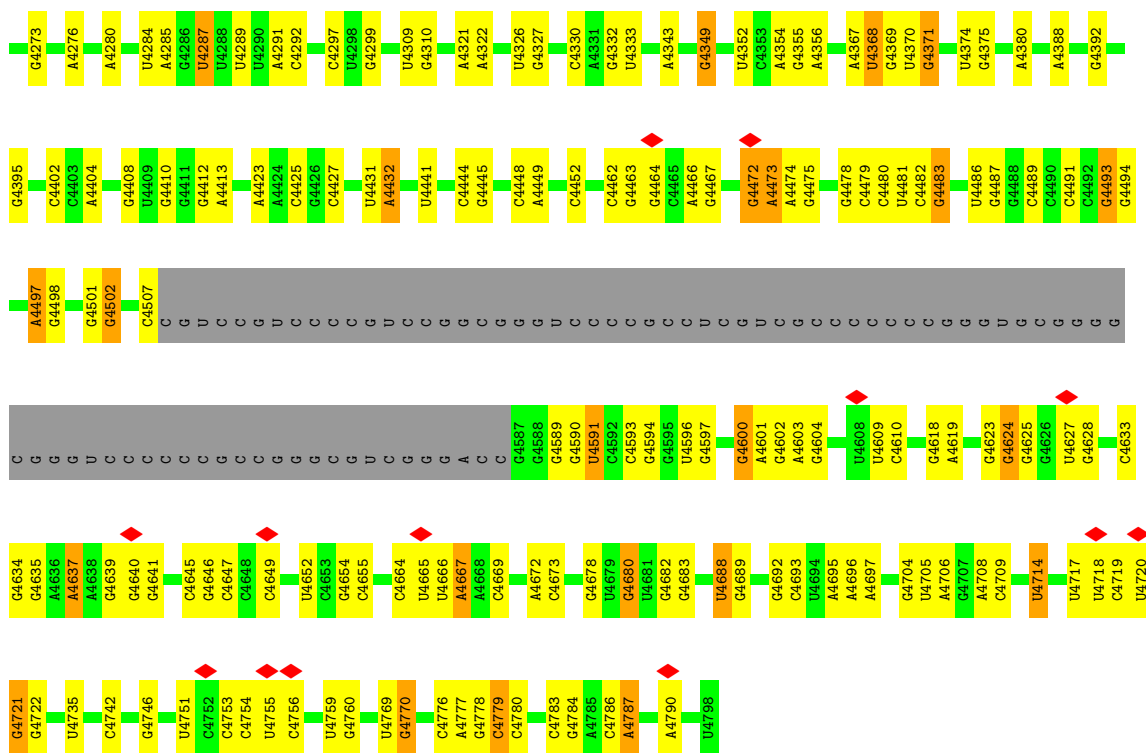
Chain t:  49% 24% 23%



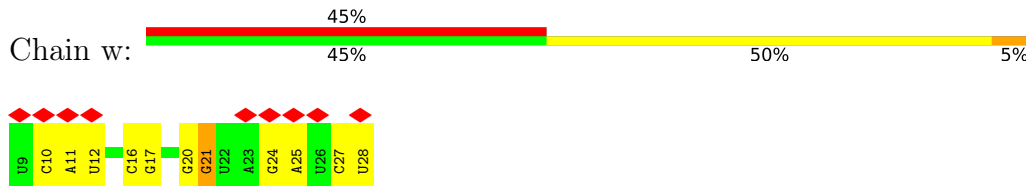






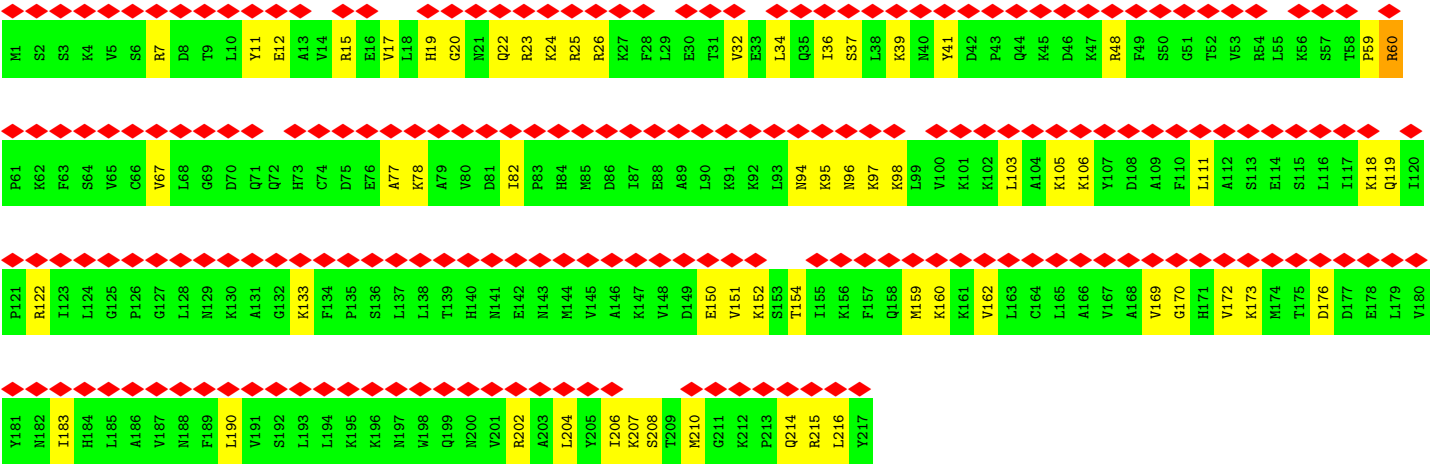


• Molecule 82: RNA (5'-D(P*()P*()P*()P*())-R(P*UP*UP*AP*CP*GP*GP*CP*GP*GP*UP*()P*()P*()P*()P*())-3')

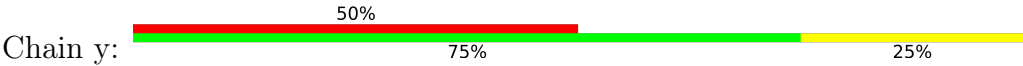


• Molecule 83: 60S ribosomal protein L10a





● Molecule 84: ALA-ALA-LYS-ALA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	62369	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.703	Depositor
Minimum map value	-0.357	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.0475	Depositor
Map size ($\text{\AA}$)	420.18, 420.18, 420.18	wwPDB
Map dimensions	298, 298, 298	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.41, 1.41, 1.41	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, A2M, MG, M7A, OMU, 5MC, PSU, MA6, ZN, B8N, 5MU, 6MZ, OMG, 4AC, MMX, UR3

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	S2	0.16	2/39984 (0.0%)	0.30	4/62292 (0.0%)
2	SA	0.21	0/1730	0.49	0/2350
3	SB	0.28	0/1765	0.52	1/2362 (0.0%)
4	SD	0.60	5/1784 (0.3%)	0.66	3/2402 (0.1%)
5	SE	0.36	2/2101 (0.1%)	0.52	1/2828 (0.0%)
6	SF	0.27	0/1516	0.51	1/2037 (0.0%)
7	SH	0.30	0/1519	0.52	0/2033
8	SI	0.27	0/1702	0.43	0/2271
9	SK	0.17	0/851	0.45	0/1147
10	SL	0.27	0/1241	0.50	0/1662
11	SP	0.37	0/1094	0.66	2/1460 (0.1%)
12	SQ	0.41	0/1177	0.68	0/1575
13	SR	0.39	0/1093	0.73	0/1469
14	SS	0.32	0/1216	0.58	1/1628 (0.1%)
15	ST	0.16	0/1134	0.42	0/1519
16	SU	0.24	0/832	0.50	0/1117
17	SV	0.20	0/632	0.53	0/845
18	SX	0.27	0/1116	0.56	0/1490
19	Sa	0.16	0/841	0.44	0/1128
20	Sc	0.20	0/508	0.59	0/680
21	Sd	0.14	0/470	0.40	0/623
22	Sg	0.19	0/2486	0.51	0/3384
23	SC	0.19	0/1795	0.48	0/2424
24	SG	0.16	0/1946	0.45	0/2590
25	SJ	0.17	0/1561	0.49	0/2083
26	SM	0.11	0/922	0.32	0/1237
27	SN	0.11	0/1232	0.29	0/1656
28	SO	0.12	0/1037	0.36	0/1391
29	SW	0.16	0/1051	0.40	0/1406
30	SY	0.14	0/1094	0.39	0/1452
31	SZ	0.30	0/585	0.68	0/785
32	Sb	0.17	0/653	0.42	0/876

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Se	0.19	0/458	0.49	0/604
34	Sf	0.15	0/559	0.42	0/743
35	A	0.20	0/1968	0.37	0/2639
36	B	0.15	0/3272	0.40	1/4380 (0.0%)
37	C	0.31	0/2943	0.52	3/3951 (0.1%)
38	D	0.13	0/3726	0.29	0/5804
39	E	0.12	0/2839	0.28	0/4425
40	F	0.13	0/2444	0.36	0/3272
41	G	0.15	0/1998	0.40	0/2676
42	H	0.14	0/1900	0.33	0/2534
43	I	0.16	0/1968	0.42	1/2649 (0.0%)
44	J	0.28	0/1547	0.55	2/2080 (0.1%)
45	K	0.13	0/1730	0.35	0/2311
46	L	0.18	0/1385	0.48	0/1852
47	M	0.17	0/1690	0.46	1/2261 (0.0%)
48	N	0.25	0/1164	0.54	2/1556 (0.1%)
49	O	0.12	0/1746	0.33	0/2338
50	P	0.23	0/1641	0.45	0/2195
51	Q	0.12	0/1309	0.31	0/1756
52	R	0.13	0/1540	0.37	0/2054
53	S	0.17	0/1588	0.47	0/2099
54	T	0.15	0/1498	0.42	1/2010 (0.0%)
55	U	0.23	0/1321	0.46	0/1764
56	V	0.22	0/822	0.54	0/1103
57	W	0.15	0/1007	0.40	0/1350
58	X	0.17	0/524	0.43	0/698
59	Y	0.13	0/1001	0.36	0/1345
60	Z	0.16	0/1132	0.40	0/1503
61	a	0.19	0/1126	0.47	0/1502
62	b	0.11	0/1194	0.33	0/1594
63	c	0.12	0/794	0.32	0/1045
64	d	0.13	0/796	0.37	0/1068
65	e	0.14	0/894	0.37	0/1204
66	f	0.13	0/1082	0.39	0/1443
67	g	0.14	0/895	0.34	0/1198
68	h	0.13	0/930	0.35	0/1238
69	i	0.13	0/1023	0.38	0/1350
70	j	0.15	0/860	0.44	0/1137
71	k	0.13	0/720	0.36	0/952
72	l	0.17	0/575	0.45	0/761
73	m	0.13	0/454	0.36	0/599
74	n	0.16	0/417	0.41	0/553
75	o	0.19	0/241	0.41	0/305

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	p	0.20	0/877	0.51	0/1156
77	q	0.15	0/718	0.45	0/954
78	r	0.18	0/1074	0.47	0/1437
79	t	0.18	7/88201 (0.0%)	0.34	28/137564 (0.0%)
80	u	0.14	0/1800	0.33	0/2804
81	v	0.16	0/1806	0.37	0/2813
82	w	0.13	0/471	0.36	0/731
83	Cz	0.20	0/1769	0.48	0/2371
84	y	0.15	0/23	0.45	0/29
All	All	0.19	16/234128 (0.0%)	0.38	52/343962 (0.0%)

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
12	SQ	0	1

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	SD	163	PRO	C-N	17.61	1.55	1.34
5	SE	101	LEU	C-N	-9.69	1.20	1.33
79	t	479	G	O3'-P	-9.28	1.47	1.61
1	S2	1833	UR3	O3'-P	-7.71	1.48	1.56
79	t	1990	G	O5'-C5'	-7.11	1.32	1.42

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	4473	A	O5'-P-OP1	-22.77	39.70	108.00
79	t	479	G	C1'-C2'-O2'	-19.39	79.32	108.40
79	t	3797	G	O5'-P-OP2	-17.37	55.89	108.00
79	t	480	C	C1'-C2'-O2'	-12.82	89.17	108.40
79	t	3797	G	O5'-P-OP1	-12.71	69.89	108.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	SQ	75	GLY	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	S2	36502	0	18416	301	0
2	SA	1693	0	1694	26	0
3	SB	1738	0	1809	23	0
4	SD	1756	0	1851	20	0
5	SE	2059	0	2164	26	0
6	SF	1495	0	1549	13	0
7	SH	1497	0	1590	16	0
8	SI	1673	0	1756	35	0
9	SK	827	0	854	12	0
10	SL	1220	0	1289	11	0
11	SP	1073	0	1128	11	0
12	SQ	1158	0	1232	23	0
13	SR	1079	0	1128	12	0
14	SS	1198	0	1261	15	0
15	ST	1115	0	1150	16	0
16	SU	822	0	887	12	0
17	SV	626	0	624	15	0
18	SX	1098	0	1167	12	0
19	Sa	826	0	875	9	0
20	Sc	506	0	536	8	0
21	Sd	459	0	449	9	0
22	Sg	2429	0	2386	34	0
23	SC	1755	0	1847	22	0
24	SG	1923	0	2089	25	0
25	SJ	1533	0	1653	15	0
26	SM	912	0	940	19	0
27	SN	1208	0	1294	14	0
28	SO	1024	0	1050	16	0
29	SW	1034	0	1080	16	0
30	SY	1073	0	1155	17	0
31	SZ	579	0	639	13	0
32	Sb	640	0	665	6	0
33	Se	452	0	498	5	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	Sf	547	0	549	15	0
35	A	1930	0	2030	23	0
36	B	3204	0	3349	41	0
37	C	2889	0	3064	33	0
38	D	3337	0	1692	25	0
39	E	2541	0	1285	10	0
40	F	2399	0	2425	23	0
41	G	1960	0	2112	23	0
42	H	1865	0	1991	14	0
43	I	1935	0	2081	13	0
44	J	1528	0	1607	14	0
45	K	1692	0	1744	19	0
46	L	1362	0	1399	7	0
47	M	1659	0	1758	22	0
48	N	1142	0	1219	11	0
49	O	1701	0	1749	16	0
50	P	1611	0	1765	21	0
51	Q	1282	0	1322	9	0
52	R	1516	0	1641	20	0
53	S	1572	0	1734	5	0
54	T	1458	0	1500	22	0
55	U	1293	0	1363	17	0
56	V	808	0	831	9	0
57	W	993	0	1050	13	0
58	X	511	0	521	6	0
59	Y	984	0	1066	11	0
60	Z	1116	0	1211	13	0
61	a	1103	0	1179	13	0
62	b	1165	0	1212	16	0
63	c	781	0	846	12	0
64	d	785	0	825	9	0
65	e	879	0	924	7	0
66	f	1064	0	1160	13	0
67	g	876	0	912	5	0
68	h	920	0	1020	12	0
69	i	1015	0	1156	10	0
70	j	849	0	934	6	0
71	k	705	0	737	7	0
72	l	569	0	637	6	0
73	m	444	0	483	5	0
74	n	411	0	443	7	0
75	o	240	0	289	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
76	p	863	0	929	10	0
77	q	708	0	750	4	0
78	r	1059	0	1138	12	0
79	t	78855	0	39846	599	0
80	u	1613	0	821	13	0
81	v	1618	0	822	8	0
82	w	423	0	215	3	0
83	Cz	1741	0	1854	42	0
84	y	24	0	27	1	0
85	B	1	0	0	0	0
85	D	6	0	0	0	0
85	E	9	0	0	0	0
85	S2	3	0	0	0	0
85	Z	1	0	0	0	0
85	t	13	0	0	0	0
86	S2	1	0	0	0	0
86	Sa	1	0	0	0	0
86	Sf	1	0	0	0	0
86	k	1	0	0	0	0
86	p	1	0	0	0	0
86	q	1	0	0	0	0
87	S2	5	0	0	1	0
87	SS	1	0	0	0	0
87	Sf	1	0	0	0	0
87	u	1	0	0	0	0
All	All	218574	0	161922	1743	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 5.

The worst 5 of 1743 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:S2:1835:6MZ:C3'	1:S2:1835:6MZ:O3'	1.71	1.37
79:t:1708:G:H1	79:t:1734:C:N4	1.26	1.32
26:SM:52:LEU:CD2	26:SM:108:CYS:HB2	1.75	1.16
79:t:1708:G:N1	79:t:1734:C:N4	1.88	1.12
79:t:1708:G:C6	79:t:1734:C:N4	2.22	1.07

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	SA	212/295 (72%)	196 (92%)	16 (8%)	0	100	100
3	SB	212/264 (80%)	201 (95%)	9 (4%)	2 (1%)	14	28
4	SD	224/243 (92%)	197 (88%)	23 (10%)	4 (2%)	6	15
5	SE	257/263 (98%)	238 (93%)	16 (6%)	3 (1%)	10	22
6	SF	187/204 (92%)	172 (92%)	15 (8%)	0	100	100
7	SH	182/194 (94%)	169 (93%)	12 (7%)	1 (0%)	24	42
8	SI	202/208 (97%)	183 (91%)	17 (8%)	2 (1%)	12	25
9	SK	96/165 (58%)	87 (91%)	9 (9%)	0	100	100
10	SL	148/158 (94%)	140 (95%)	6 (4%)	2 (1%)	9	19
11	SP	128/145 (88%)	121 (94%)	7 (6%)	0	100	100
12	SQ	144/146 (99%)	133 (92%)	9 (6%)	2 (1%)	9	19
13	SR	132/135 (98%)	115 (87%)	16 (12%)	1 (1%)	16	31
14	SS	143/152 (94%)	127 (89%)	15 (10%)	1 (1%)	18	35
15	ST	141/145 (97%)	134 (95%)	7 (5%)	0	100	100
16	SU	102/119 (86%)	95 (93%)	6 (6%)	1 (1%)	12	25
17	SV	80/83 (96%)	75 (94%)	5 (6%)	0	100	100
18	SX	139/143 (97%)	123 (88%)	16 (12%)	0	100	100
19	Sa	101/115 (88%)	95 (94%)	6 (6%)	0	100	100
20	Sc	62/69 (90%)	51 (82%)	11 (18%)	0	100	100
21	Sd	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
22	Sg	310/317 (98%)	273 (88%)	37 (12%)	0	100	100
23	SC	224/293 (76%)	208 (93%)	16 (7%)	0	100	100
24	SG	235/249 (94%)	217 (92%)	18 (8%)	0	100	100
25	SJ	184/194 (95%)	169 (92%)	14 (8%)	1 (0%)	24	42
26	SM	116/132 (88%)	101 (87%)	15 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	SN	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
28	SO	135/151 (89%)	120 (89%)	15 (11%)	0	100	100
29	SW	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
30	SY	130/133 (98%)	118 (91%)	12 (9%)	0	100	100
31	SZ	71/125 (57%)	62 (87%)	9 (13%)	0	100	100
32	Sb	80/84 (95%)	75 (94%)	5 (6%)	0	100	100
33	Se	55/59 (93%)	48 (87%)	7 (13%)	0	100	100
34	Sf	65/156 (42%)	51 (78%)	14 (22%)	0	100	100
35	A	250/257 (97%)	231 (92%)	19 (8%)	0	100	100
36	B	395/403 (98%)	367 (93%)	28 (7%)	0	100	100
37	C	361/421 (86%)	333 (92%)	21 (6%)	7 (2%)	6	14
40	F	292/297 (98%)	275 (94%)	15 (5%)	2 (1%)	18	35
41	G	239/298 (80%)	209 (87%)	28 (12%)	2 (1%)	16	31
42	H	223/260 (86%)	210 (94%)	13 (6%)	0	100	100
43	I	239/266 (90%)	222 (93%)	17 (7%)	0	100	100
44	J	189/192 (98%)	176 (93%)	12 (6%)	1 (0%)	24	42
45	K	204/214 (95%)	193 (95%)	11 (5%)	0	100	100
46	L	168/178 (94%)	159 (95%)	8 (5%)	1 (1%)	21	38
47	M	203/211 (96%)	175 (86%)	25 (12%)	3 (2%)	8	18
48	N	137/214 (64%)	132 (96%)	5 (4%)	0	100	100
49	O	201/204 (98%)	191 (95%)	9 (4%)	1 (0%)	24	42
50	P	195/203 (96%)	189 (97%)	5 (3%)	1 (0%)	24	42
51	Q	156/184 (85%)	151 (97%)	5 (3%)	0	100	100
52	R	185/188 (98%)	172 (93%)	13 (7%)	0	100	100
53	S	186/196 (95%)	180 (97%)	6 (3%)	0	100	100
54	T	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
55	U	156/160 (98%)	149 (96%)	6 (4%)	1 (1%)	21	38
56	V	97/128 (76%)	94 (97%)	3 (3%)	0	100	100
57	W	132/140 (94%)	126 (96%)	6 (4%)	0	100	100
58	X	59/157 (38%)	56 (95%)	3 (5%)	0	100	100
59	Y	118/156 (76%)	114 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	Z	132/145 (91%)	124 (94%)	8 (6%)	0	100	100
61	a	132/136 (97%)	122 (92%)	10 (8%)	0	100	100
62	b	145/148 (98%)	133 (92%)	12 (8%)	0	100	100
63	c	91/156 (58%)	86 (94%)	5 (6%)	0	100	100
64	d	99/115 (86%)	93 (94%)	6 (6%)	0	100	100
65	e	104/125 (83%)	99 (95%)	5 (5%)	0	100	100
66	f	127/135 (94%)	118 (93%)	8 (6%)	1 (1%)	16	31
67	g	107/110 (97%)	102 (95%)	5 (5%)	0	100	100
68	h	114/117 (97%)	106 (93%)	8 (7%)	0	100	100
69	i	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
70	j	102/105 (97%)	95 (93%)	7 (7%)	0	100	100
71	k	84/97 (87%)	79 (94%)	3 (4%)	2 (2%)	4	10
72	l	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
73	m	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
74	n	48/128 (38%)	46 (96%)	2 (4%)	0	100	100
75	o	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
76	p	103/106 (97%)	93 (90%)	9 (9%)	1 (1%)	12	25
77	q	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
78	r	129/137 (94%)	114 (88%)	15 (12%)	0	100	100
83	Cz	215/217 (99%)	183 (85%)	31 (14%)	1 (0%)	24	42
84	y	2/4 (50%)	2 (100%)	0	0	100	100
All	All	11465/12921 (89%)	10600 (92%)	821 (7%)	44 (0%)	31	48

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	SB	191	ASP
5	SE	165	GLU
10	SL	82	MET
37	C	55	SER
37	C	58	ALA

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	
2	SA	179/242 (74%)	176 (98%)	3 (2%)	53	75
3	SB	195/231 (84%)	194 (100%)	1 (0%)	81	90
4	SD	189/202 (94%)	188 (100%)	1 (0%)	81	90
5	SE	222/225 (99%)	220 (99%)	2 (1%)	70	84
6	SF	159/171 (93%)	157 (99%)	2 (1%)	61	79
7	SH	166/174 (95%)	163 (98%)	3 (2%)	51	73
8	SI	177/180 (98%)	176 (99%)	1 (1%)	78	89
9	SK	89/136 (65%)	88 (99%)	1 (1%)	65	81
10	SL	134/142 (94%)	132 (98%)	2 (2%)	57	77
11	SP	116/130 (89%)	114 (98%)	2 (2%)	53	75
12	SQ	121/121 (100%)	116 (96%)	5 (4%)	27	52
13	SR	120/121 (99%)	119 (99%)	1 (1%)	73	86
14	SS	126/132 (96%)	126 (100%)	0	100	100
15	ST	113/115 (98%)	112 (99%)	1 (1%)	70	84
16	SU	94/107 (88%)	94 (100%)	0	100	100
17	SV	66/67 (98%)	66 (100%)	0	100	100
18	SX	113/115 (98%)	112 (99%)	1 (1%)	70	84
19	Sa	89/98 (91%)	85 (96%)	4 (4%)	24	48
20	Sc	57/62 (92%)	55 (96%)	2 (4%)	32	57
21	Sd	48/49 (98%)	45 (94%)	3 (6%)	16	34
22	Sg	271/275 (98%)	259 (96%)	12 (4%)	25	49
23	SC	191/224 (85%)	185 (97%)	6 (3%)	35	60
24	SG	207/218 (95%)	204 (99%)	3 (1%)	59	78
25	SJ	162/168 (96%)	158 (98%)	4 (2%)	42	66
26	SM	98/108 (91%)	94 (96%)	4 (4%)	27	52
27	SN	130/131 (99%)	128 (98%)	2 (2%)	57	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	SO	107/119 (90%)	104 (97%)	3 (3%)	38	62
29	SW	112/113 (99%)	110 (98%)	2 (2%)	51	73
30	SY	114/115 (99%)	113 (99%)	1 (1%)	70	84
31	SZ	64/103 (62%)	61 (95%)	3 (5%)	23	47
32	Sb	74/76 (97%)	74 (100%)	0	100	100
33	Se	46/48 (96%)	45 (98%)	1 (2%)	45	69
34	Sf	60/140 (43%)	60 (100%)	0	100	100
35	A	194/199 (98%)	187 (96%)	7 (4%)	31	56
36	B	345/349 (99%)	332 (96%)	13 (4%)	29	54
37	C	304/349 (87%)	290 (95%)	14 (5%)	24	48
40	F	248/250 (99%)	242 (98%)	6 (2%)	43	67
41	G	216/256 (84%)	212 (98%)	4 (2%)	50	72
42	H	195/224 (87%)	193 (99%)	2 (1%)	68	83
43	I	205/223 (92%)	197 (96%)	8 (4%)	28	54
44	J	171/172 (99%)	167 (98%)	4 (2%)	44	68
45	K	178/181 (98%)	172 (97%)	6 (3%)	32	58
46	L	143/149 (96%)	138 (96%)	5 (4%)	32	57
47	M	171/177 (97%)	165 (96%)	6 (4%)	32	57
48	N	118/157 (75%)	116 (98%)	2 (2%)	53	75
49	O	171/172 (99%)	166 (97%)	5 (3%)	37	61
50	P	169/173 (98%)	165 (98%)	4 (2%)	43	67
51	Q	139/163 (85%)	135 (97%)	4 (3%)	37	61
52	R	164/165 (99%)	163 (99%)	1 (1%)	78	89
53	S	167/175 (95%)	165 (99%)	2 (1%)	63	80
54	T	156/156 (100%)	152 (97%)	4 (3%)	40	65
55	U	139/140 (99%)	131 (94%)	8 (6%)	18	38
56	V	89/114 (78%)	83 (93%)	6 (7%)	15	31
57	W	102/107 (95%)	98 (96%)	4 (4%)	28	54
58	X	53/126 (42%)	53 (100%)	0	100	100
59	Y	108/133 (81%)	106 (98%)	2 (2%)	50	72
60	Z	124/135 (92%)	122 (98%)	2 (2%)	55	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	a	117/118 (99%)	115 (98%)	2 (2%)	53	75
62	b	120/121 (99%)	119 (99%)	1 (1%)	73	86
63	c	80/124 (64%)	78 (98%)	2 (2%)	42	66
64	d	86/97 (89%)	84 (98%)	2 (2%)	44	68
65	e	97/110 (88%)	94 (97%)	3 (3%)	35	60
66	f	115/121 (95%)	114 (99%)	1 (1%)	70	84
67	g	88/89 (99%)	86 (98%)	2 (2%)	44	68
68	h	99/100 (99%)	97 (98%)	2 (2%)	48	71
69	i	109/110 (99%)	107 (98%)	2 (2%)	51	73
70	j	88/89 (99%)	87 (99%)	1 (1%)	65	81
71	k	73/80 (91%)	71 (97%)	2 (3%)	39	63
72	l	64/65 (98%)	63 (98%)	1 (2%)	55	76
73	m	47/48 (98%)	47 (100%)	0	100	100
74	n	46/116 (40%)	46 (100%)	0	100	100
75	o	24/24 (100%)	22 (92%)	2 (8%)	10	22
76	p	93/94 (99%)	93 (100%)	0	100	100
77	q	74/75 (99%)	70 (95%)	4 (5%)	20	42
78	r	115/121 (95%)	112 (97%)	3 (3%)	40	65
83	Cz	195/196 (100%)	192 (98%)	3 (2%)	57	77
84	y	1/1 (100%)	1 (100%)	0	100	100
All	All	10009/11002 (91%)	9781 (98%)	228 (2%)	44	68

5 of 228 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	F	172	SER
77	q	91	ASP
46	L	83	LEU
77	q	74	THR
63	c	55	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 156 such sidechains are listed below:

Mol	Chain	Res	Type
59	Y	73	HIS
78	r	23	GLN
61	a	78	ASN
66	f	24	GLN
83	Cz	22	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S2	1697/1872 (90%)	392 (23%)	19 (1%)
38	D	156/157 (99%)	32 (20%)	1 (0%)
39	E	118/121 (97%)	11 (9%)	0
79	t	3660/4803 (76%)	691 (18%)	0
80	u	75/76 (98%)	20 (26%)	0
81	v	75/76 (98%)	26 (34%)	0
82	w	19/20 (95%)	8 (42%)	0
All	All	5800/7125 (81%)	1180 (20%)	20 (0%)

5 of 1180 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S2	2	A
1	S2	9	U
1	S2	25	A
1	S2	33	G
1	S2	41	G

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	S2	1575	C
1	S2	1818	A
38	D	86	U
1	S2	1827	A
1	S2	561	G

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

33 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	S2	826	1	18,21,22	1.08	1 (5%)	22,30,33	1.66	5 (22%)
1	PSU	S2	1084	1	18,21,22	1.06	1 (5%)	22,30,33	1.71	4 (18%)
1	5MU	S2	817	1	19,22,23	0.40	0	28,32,35	0.91	2 (7%)
1	OMG	S2	686	1	23,26,27	0.48	0	33,38,41	0.53	0
1	UR3	S2	1833	1	19,22,23	3.00	7 (36%)	26,32,35	1.65	4 (15%)
1	B8N	S2	1251	1	24,29,30	3.06	5 (20%)	29,42,45	1.74	5 (17%)
1	OMG	S2	647	1	23,26,27	0.47	0	33,38,41	0.46	0
1	A2M	S2	1034	1	22,25,26	3.18	9 (40%)	31,36,39	2.97	10 (32%)
1	OMC	S2	1706	1	19,22,23	0.50	0	26,31,34	0.66	0
1	A2M	S2	487	1	22,25,26	3.19	9 (40%)	31,36,39	2.95	10 (32%)
1	PSU	S2	615	1	18,21,22	1.02	1 (5%)	22,30,33	1.66	4 (18%)
1	A2M	S2	1681	1	22,25,26	3.16	9 (40%)	31,36,39	2.98	11 (35%)
1	6MZ	S2	1835	1	22,25,26	4.96	15 (68%)	30,36,39	4.58	23 (76%)
1	4AC	S2	1845	1	21,24,25	3.56	10 (47%)	29,34,37	1.13	3 (10%)
1	OMU	S2	116	1	19,22,23	3.10	8 (42%)	26,31,34	1.69	5 (19%)
1	PSU	S2	1246	1	18,21,22	1.08	1 (5%)	22,30,33	1.72	4 (18%)
1	OMG	S2	512	1	23,26,27	0.47	0	33,38,41	0.48	0
1	A2M	S2	166	1	22,25,26	3.18	9 (40%)	31,36,39	3.00	11 (35%)
1	5MC	S2	1377	1	18,22,23	0.53	0	26,32,35	0.75	0
1	MA6	S2	1854	1	23,26,27	1.31	3 (13%)	34,38,41	3.28	12 (35%)
1	PSU	S2	825	1	18,21,22	1.10	1 (5%)	22,30,33	1.70	4 (18%)
1	A2M	S2	159	1	22,25,26	3.19	9 (40%)	31,36,39	3.01	11 (35%)
1	PSU	S2	119	1	18,21,22	1.10	1 (5%)	22,30,33	1.71	4 (18%)
1	MA6	S2	1853	1	23,26,27	1.33	4 (17%)	34,38,41	3.25	11 (32%)
1	A2M	S2	671	1	22,25,26	3.18	9 (40%)	31,36,39	3.00	13 (41%)
1	MMX	S2	571	1	19,23,24	4.00	4 (21%)	22,33,36	2.83	6 (27%)
1	OMC	S2	1713	1	19,22,23	0.51	0	26,31,34	0.67	0
1	OMC	S2	174	1	19,22,23	0.51	0	26,31,34	0.67	0
1	OMC	S2	520	1	19,22,23	0.52	0	26,31,34	0.77	0
1	4AC	S2	1340	1	21,24,25	3.56	10 (47%)	29,34,37	1.12	3 (10%)
1	A2M	S2	27	1	22,25,26	3.19	9 (40%)	31,36,39	2.94	11 (35%)
1	M7A	S2	1809	1	20,25,26	2.07	3 (15%)	28,37,40	4.10	8 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMU	S2	121	1	19,22,23	1.39	3 (15%)	26,31,34	1.96	7 (26%)

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
1	PSU	S2	826	1	-	2/7/25/26	0/2/2/2
1	PSU	S2	1084	1	-	0/7/25/26	0/2/2/2
1	5MU	S2	817	1	-	0/7/25/26	0/2/2/2
1	OMG	S2	686	1	-	2/9/27/28	0/3/3/3
1	UR3	S2	1833	1	-	2/7/25/26	0/2/2/2
1	B8N	S2	1251	1	-	2/16/34/35	0/2/2/2
1	OMG	S2	647	1	-	2/9/27/28	0/3/3/3
1	A2M	S2	1034	1	-	0/9/27/28	0/3/3/3
1	OMC	S2	1706	1	-	0/9/27/28	0/2/2/2
1	A2M	S2	487	1	-	0/9/27/28	0/3/3/3
1	PSU	S2	615	1	-	0/7/25/26	0/2/2/2
1	A2M	S2	1681	1	-	2/9/27/28	0/3/3/3
1	6MZ	S2	1835	1	-	1/9/27/28	0/3/3/3
1	4AC	S2	1845	1	-	0/11/29/30	0/2/2/2
1	OMU	S2	116	1	-	2/9/27/28	0/2/2/2
1	PSU	S2	1246	1	-	2/7/25/26	0/2/2/2
1	OMG	S2	512	1	-	0/9/27/28	0/3/3/3
1	A2M	S2	166	1	-	0/9/27/28	0/3/3/3
1	5MC	S2	1377	1	-	0/7/25/26	0/2/2/2
1	MA6	S2	1854	1	-	6/11/29/30	0/3/3/3
1	PSU	S2	825	1	-	0/7/25/26	0/2/2/2
1	A2M	S2	159	1	-	1/9/27/28	0/3/3/3
1	PSU	S2	119	1	-	0/7/25/26	0/2/2/2
1	MA6	S2	1853	1	-	5/11/29/30	0/3/3/3
1	A2M	S2	671	1	-	2/9/27/28	0/3/3/3
1	MMX	S2	571	1	-	4/9/44/45	0/2/2/2
1	OMC	S2	1713	1	-	0/9/27/28	0/2/2/2
1	OMC	S2	174	1	-	0/9/27/28	0/2/2/2
1	OMC	S2	520	1	-	2/9/27/28	0/2/2/2
1	4AC	S2	1340	1	-	0/11/29/30	0/2/2/2
1	A2M	S2	27	1	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	M7A	S2	1809	1	-	1/7/37/38	0/3/3/3
1	OMU	S2	121	1	-	1/9/27/28	0/2/2/2

The worst 5 of 141 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S2	1835	6MZ	O3'-C3'	11.94	1.71	1.43
1	S2	571	MMX	C2-N1	10.18	1.50	1.37
1	S2	571	MMX	C4-N3	9.93	1.53	1.45
1	S2	1835	6MZ	C3'-C4'	-8.85	1.30	1.53
1	S2	166	A2M	C3'-C4'	-8.82	1.30	1.53

The worst 5 of 191 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S2	1809	M7A	C5-C6-N6	13.86	147.41	123.74
1	S2	1854	MA6	N1-C6-N6	-12.80	103.09	117.08
1	S2	1853	MA6	N1-C6-N6	-12.69	103.21	117.08
1	S2	1809	M7A	N6-C6-N1	-11.78	92.55	118.35
1	S2	1835	6MZ	O2'-C2'-C1'	-9.14	79.48	110.02

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	S2	27	A2M	C3'-C4'-C5'-O5'
1	S2	116	OMU	C3'-C4'-C5'-O5'
1	S2	116	OMU	O4'-C4'-C5'-O5'
1	S2	121	OMU	C1'-C2'-O2'-CM2
1	S2	520	OMC	O4'-C4'-C5'-O5'

There are no ring outliers.

14 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	S2	826	PSU	1	0
1	S2	1833	UR3	2	0
1	S2	647	OMG	1	0
1	S2	1034	A2M	1	0
1	S2	615	PSU	1	0
1	S2	1681	A2M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	S2	1835	6MZ	5	0
1	S2	1845	4AC	1	0
1	S2	116	OMU	1	0
1	S2	512	OMG	2	0
1	S2	166	A2M	1	0
1	S2	1853	MA6	2	0
1	S2	27	A2M	1	0
1	S2	121	OMU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 39 ligands modelled in this entry, 39 are 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 [i](#)

There are no chain breaks in this entry.

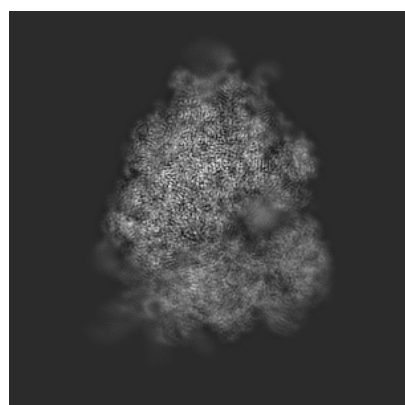
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13954. These allow visual inspection of the internal detail of the map and identification of artifacts.

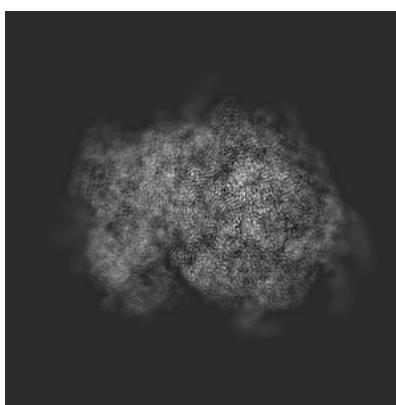
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

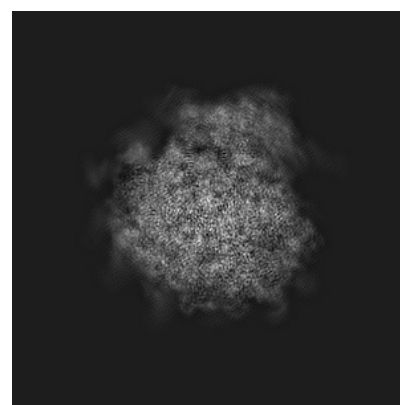
6.1.1 Primary map



X



Y

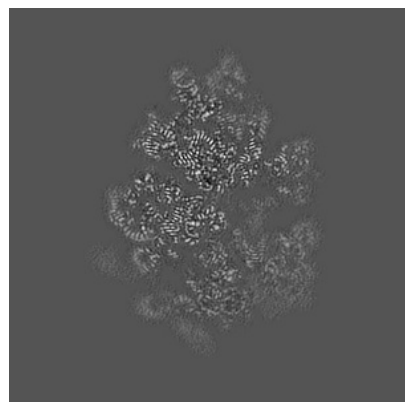


Z

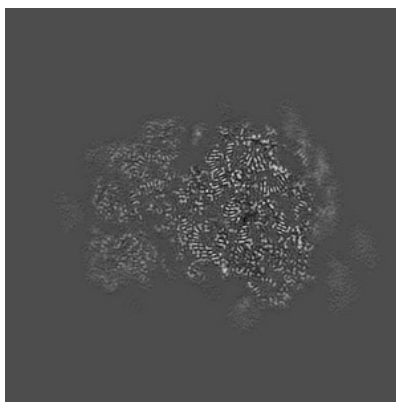
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

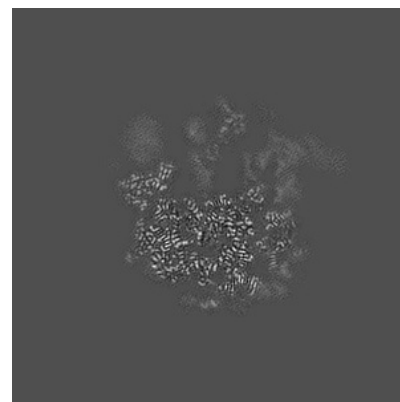
6.2.1 Primary map



X Index: 149



Y Index: 149

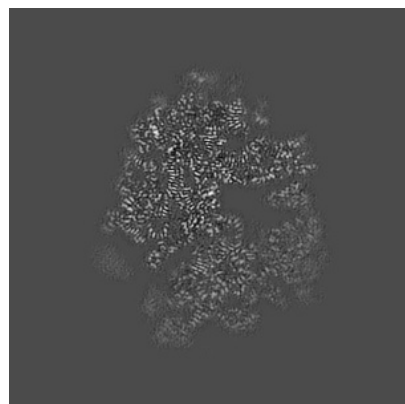


Z Index: 149

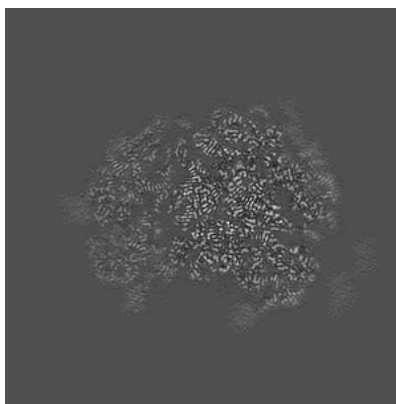
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

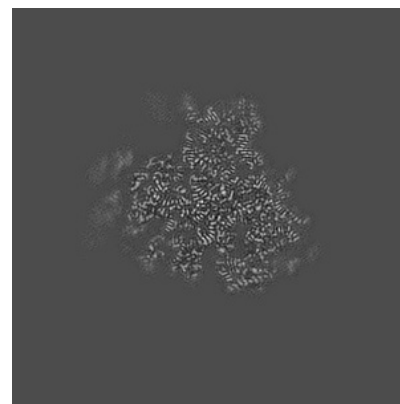
6.3.1 Primary map



X Index: 162



Y Index: 141

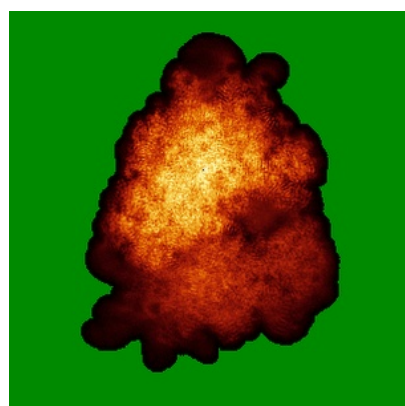


Z Index: 183

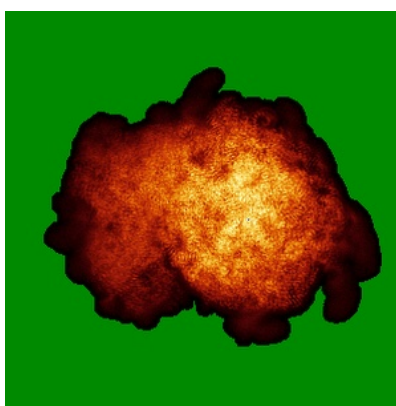
The images above show the largest variance slices of the map in three orthogonal directions.

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

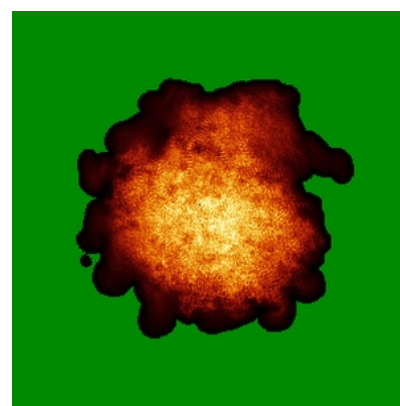
6.4.1 Primary map



X



Y

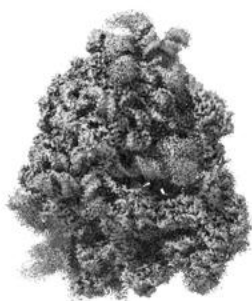


Z

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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0475. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

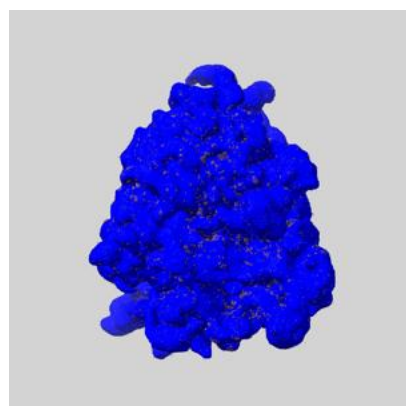
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

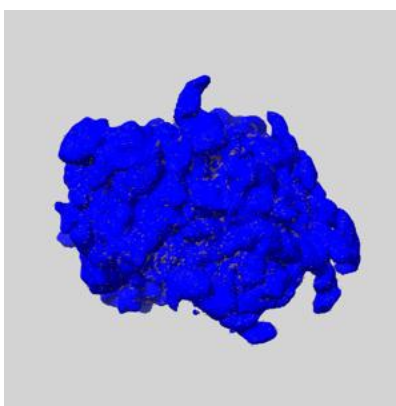
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

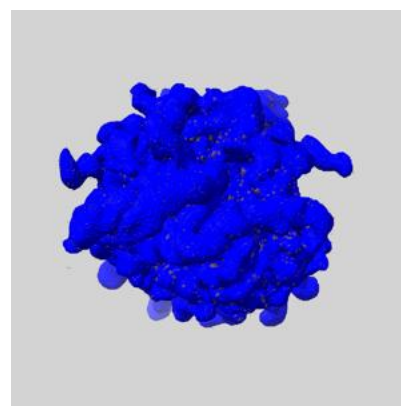
6.6.1 emd_13954_msk_1.map [i](#)



X



Y

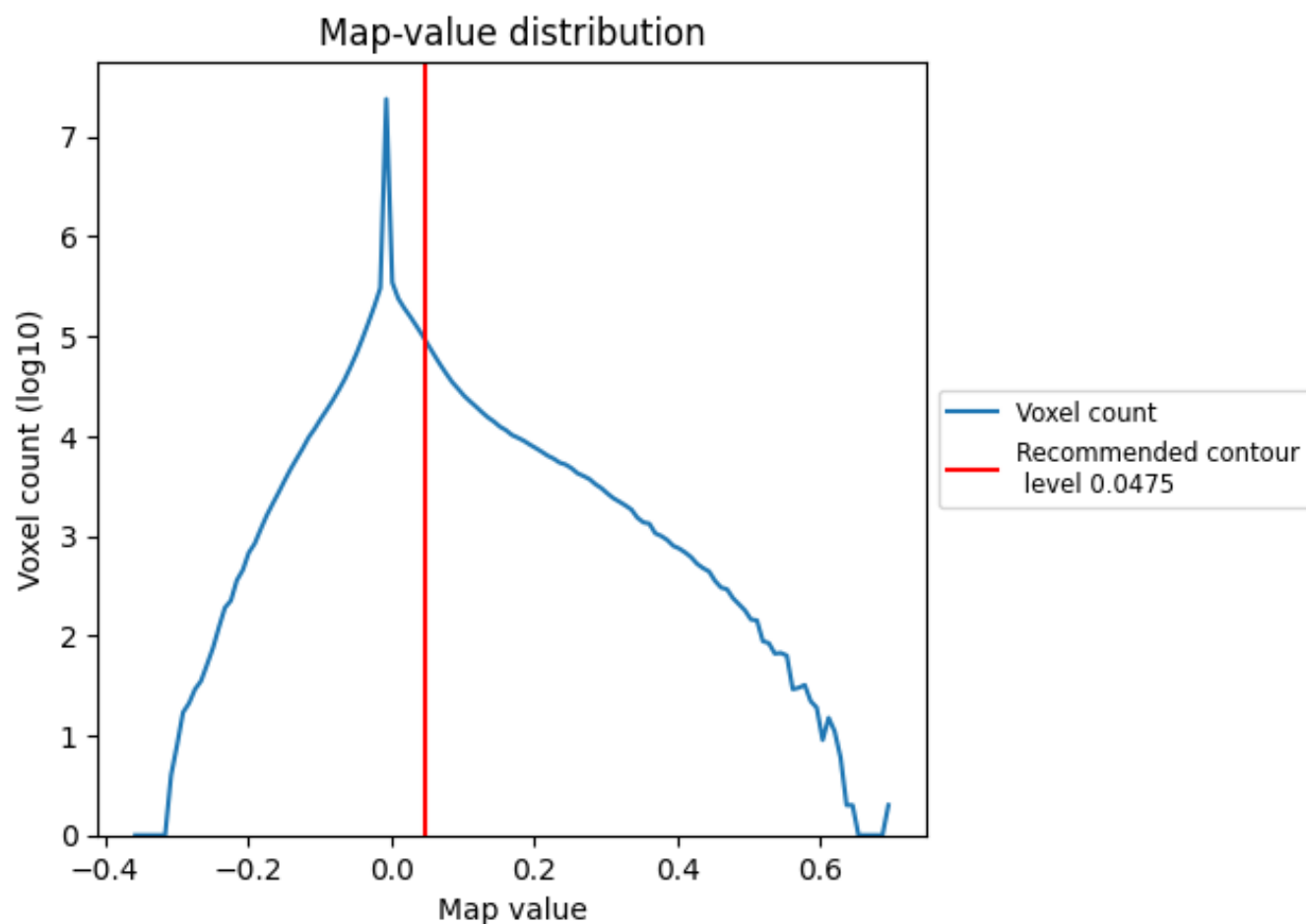


Z

7 Map analysis [i](#)

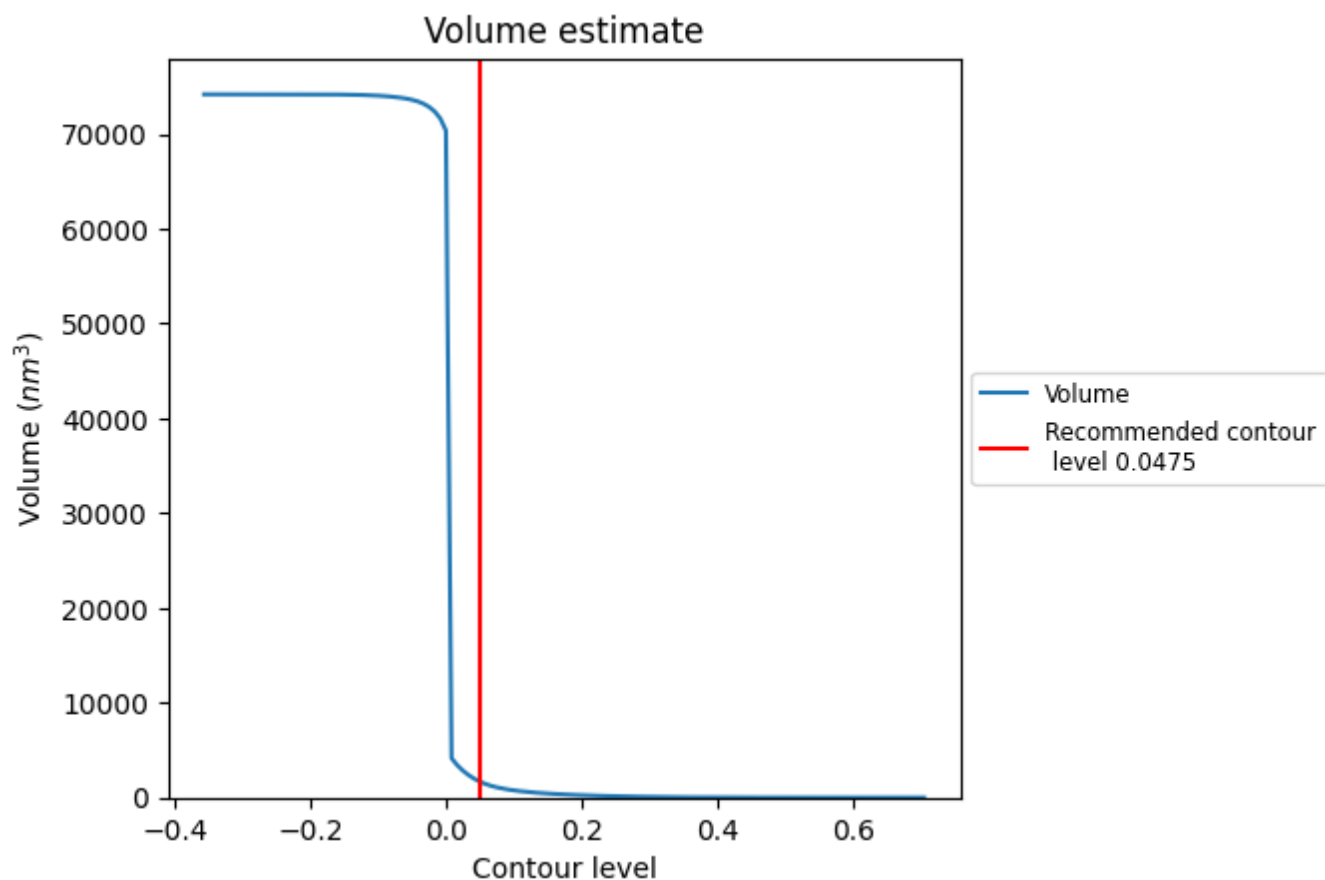
This section contains the results of statistical analysis of the map.

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.

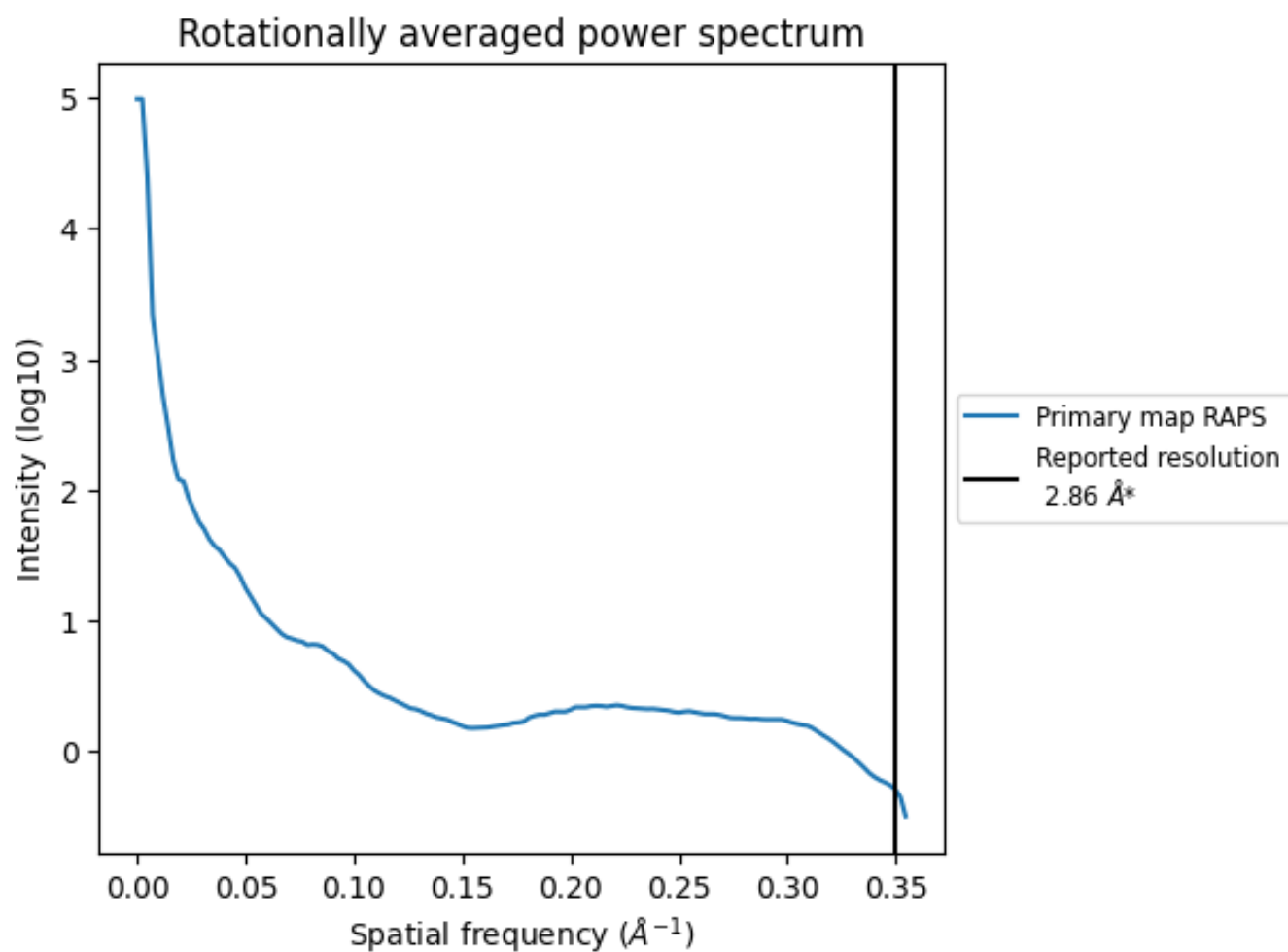
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1728 nm³; this corresponds to an approximate mass of 1561 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 ⓘ

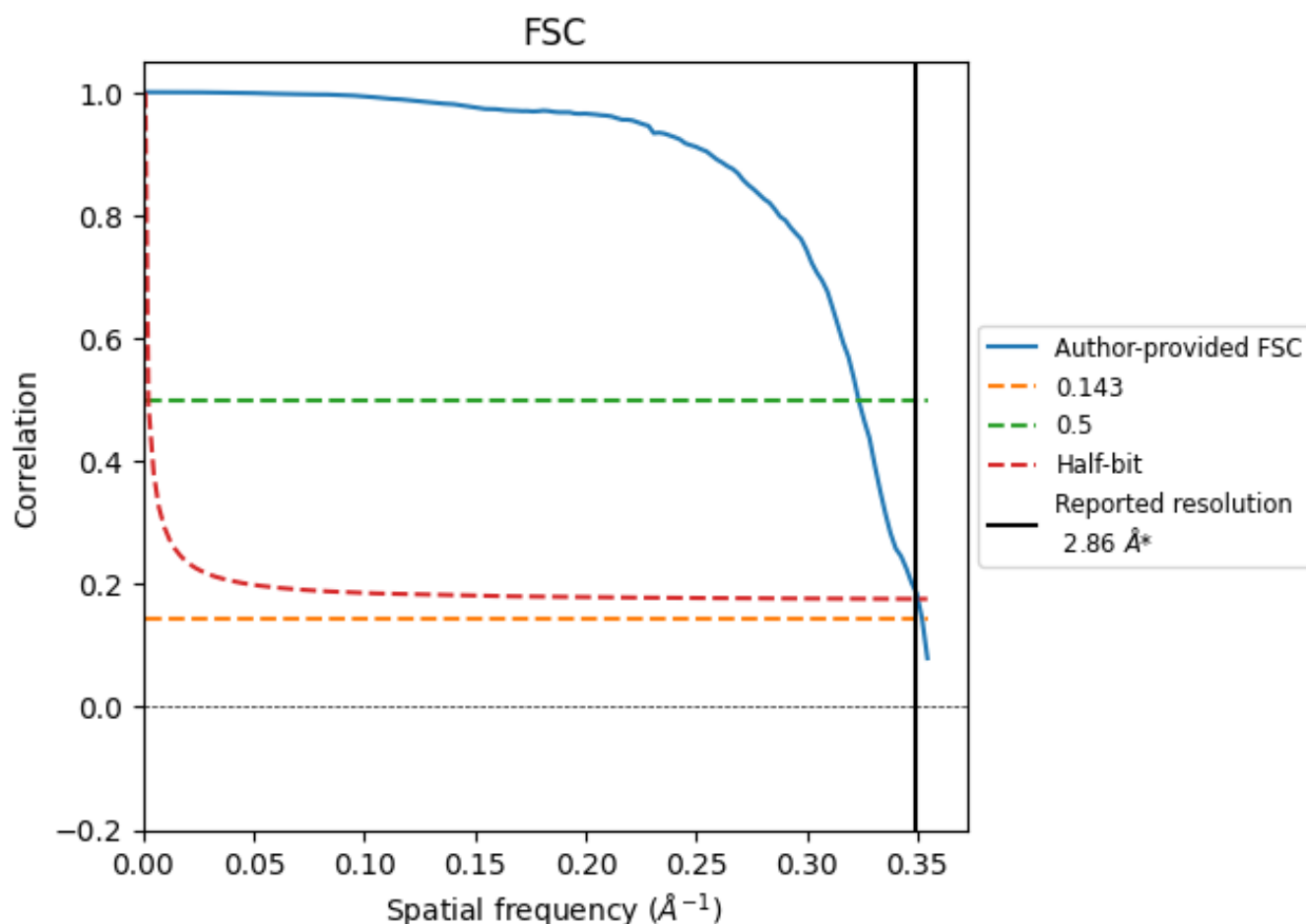


*Reported resolution corresponds to spatial frequency of 0.350 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.350 Å⁻¹

8.2 Resolution estimates [i](#)

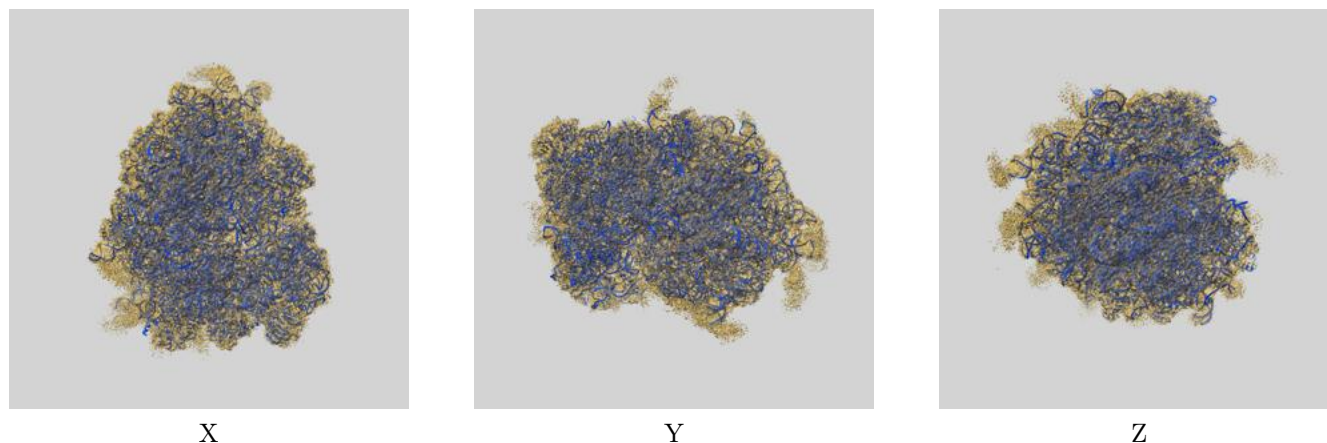
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	2.84	3.09	2.85
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

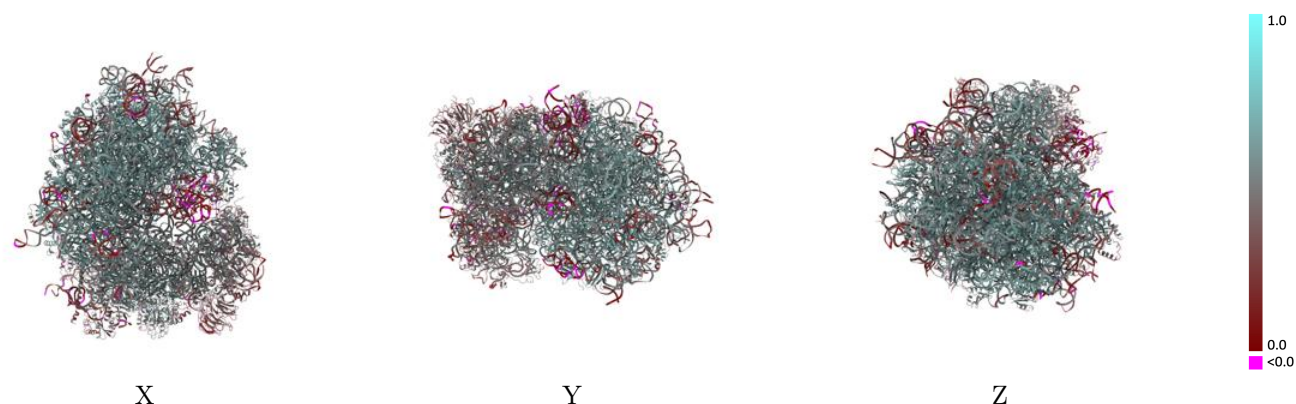
This section contains information regarding the fit between EMDB map EMD-13954 and PDB model 7QGG. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



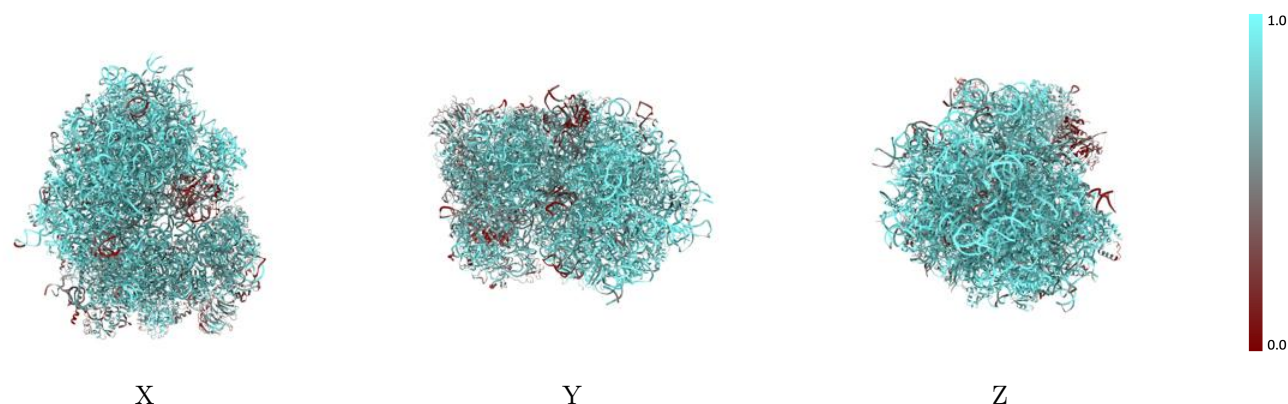
The images above show the 3D surface view of the map at the recommended contour level 0.0475 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



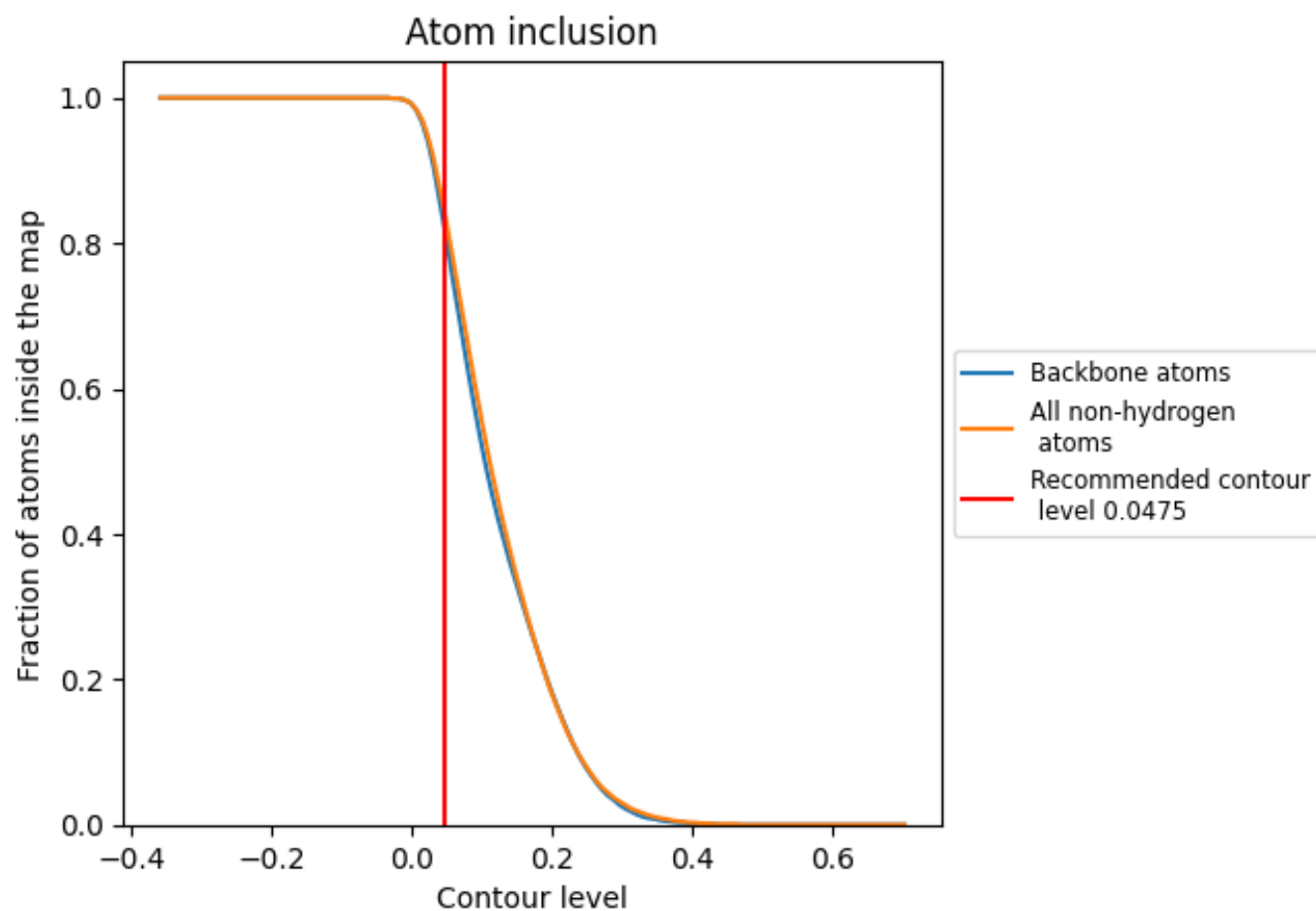
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0475).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 84% 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 (0.0475) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8420	 0.5000
A	 0.9150	 0.6060
B	 0.9330	 0.5960
C	 0.9360	 0.5990
Cz	 0.1280	 0.1170
D	 0.9130	 0.5300
E	 0.9860	 0.5870
F	 0.9260	 0.5610
G	 0.8330	 0.5180
H	 0.9470	 0.6150
I	 0.8110	 0.5150
J	 0.9190	 0.5800
K	 0.8980	 0.5820
L	 0.8630	 0.5240
M	 0.8610	 0.5390
N	 0.9340	 0.5880
O	 0.9640	 0.6240
P	 0.9300	 0.5940
Q	 0.9250	 0.5960
R	 0.9300	 0.6150
S	 0.8290	 0.5400
S2	 0.8380	 0.4570
SA	 0.7690	 0.4890
SB	 0.7510	 0.4850
SC	 0.7840	 0.5210
SD	 0.6230	 0.4060
SE	 0.7740	 0.4790
SF	 0.6770	 0.4500
SG	 0.6170	 0.3890
SH	 0.6220	 0.3970
SI	 0.7000	 0.4390
SJ	 0.7850	 0.4560
SK	 0.6840	 0.3910
SL	 0.7170	 0.4950
SM	 0.1180	 0.1860



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Chain	Atom inclusion	Q-score
SN	 0.7680	 0.5080
SO	 0.7890	 0.5040
SP	 0.7560	 0.4500
SQ	 0.7110	 0.4330
SR	 0.6250	 0.4020
SS	 0.7270	 0.4630
ST	 0.7430	 0.4590
SU	 0.5020	 0.3760
SV	 0.7870	 0.4980
SW	 0.8580	 0.5550
SX	 0.8030	 0.5330
SY	 0.7040	 0.4200
SZ	 0.5950	 0.3790
Sa	 0.8220	 0.5210
Sb	 0.7370	 0.4730
Sc	 0.6280	 0.4060
Sd	 0.8120	 0.4640
Se	 0.6220	 0.4270
Sf	 0.1460	 0.2010
Sg	 0.5340	 0.3160
T	 0.9330	 0.5910
U	 0.9170	 0.5790
V	 0.8730	 0.5120
W	 0.8990	 0.5960
X	 0.9230	 0.5950
Y	 0.9100	 0.5880
Z	 0.9230	 0.5890
a	 0.9200	 0.5730
b	 0.9520	 0.6140
c	 0.8700	 0.5450
d	 0.8700	 0.5460
e	 0.9200	 0.5860
f	 0.9280	 0.6010
g	 0.9550	 0.6230
h	 0.8750	 0.5660
i	 0.9090	 0.5820
j	 0.8920	 0.5700
k	 0.9390	 0.5960
l	 0.8280	 0.5250
m	 0.9170	 0.6110
n	 0.9600	 0.5870
o	 0.8080	 0.5540

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Chain	Atom inclusion	Q-score
p	 0.8900	 0.5700
q	 0.8870	 0.5890
r	 0.8950	 0.5690
t	 0.9050	 0.5110
u	 0.5060	 0.3080
v	 0.6020	 0.3140
w	 0.5650	 0.3760
y	 0.4580	 0.3900