



wwPDB EM Validation Summary Report ⓘ

Aug 25, 2026 – 05:02 PM EDT

PDB ID : 11HG / pdb_000011hg
EMDB ID : EMD-75689
Title : Rabbit 80S with eEF2,CCDC124,and LARP1,40S-head-swiveled
Authors : Seraj, Z.; Zottig, X.; Huang, C.H.; Loveland, A.B.; Diggs, S.; Sholi, E.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2026-02-24
Resolution : 2.90 Å(reported)
Based on initial models : ., 7TOR

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.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

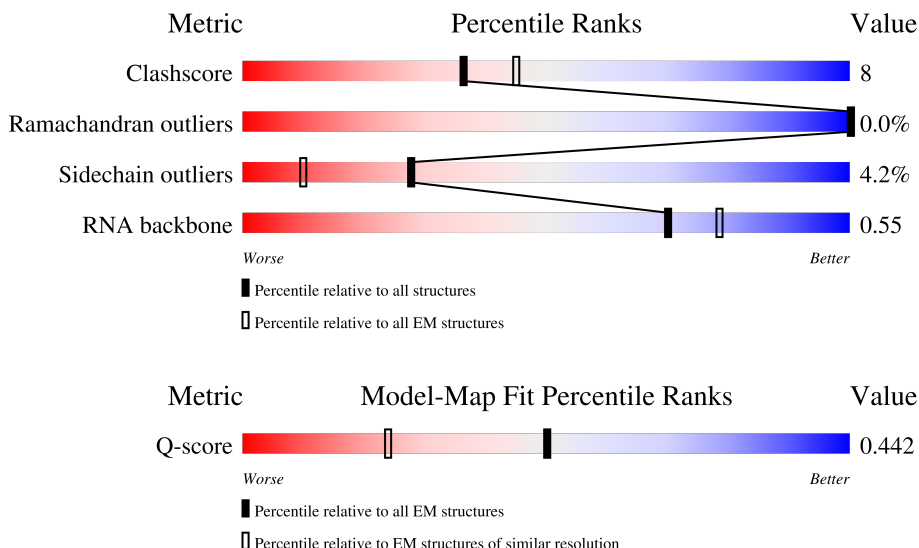
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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	BB	217	50% 76% 24%
2	S2	221	39% 79% 20%
3	PP	83	59% 84% 14%

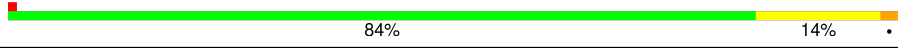
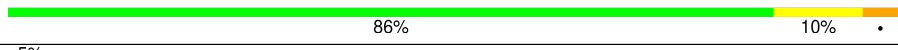
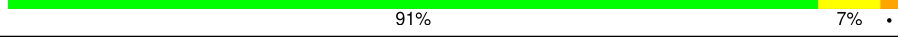
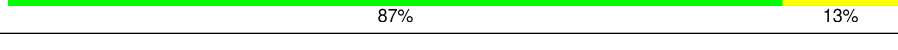
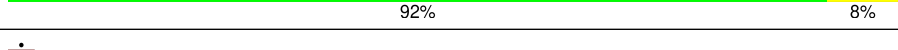
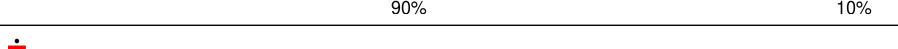
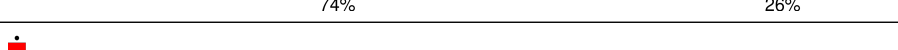
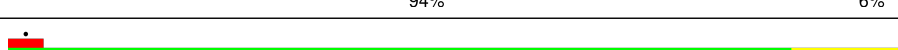
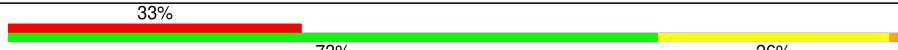
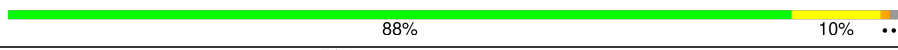
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Mol	Chain	Length	Quality of chain
4	DD	151	
5	58	156	
6	6	120	
7	L8	248	
8	L3	394	
9	L4	362	
10	L5	293	
11	L6	251	
12	L7	225	
13	aa	240	
14	10	213	
15	13	211	
16	14	138	
17	15	203	
18	bb	199	
19	17	153	
20	19	180	
21	20	176	
22	21	159	
23	22	99	
24	cc	118	
25	26	134	
26	27	135	
27	dd	147	
28	29	245	

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Mol	Chain	Length	Quality of chain
29	30	98	
30	31	107	
31	32	128	
32	ee	109	
33	34	114	
34	35	122	
35	36	102	
36	37	86	
37	38	69	
38	39	50	
39	40	52	
40	41	25	
41	42	104	
42	ff	91	
43	gg	124	
44	AS	213	
45	FF	149	
46	VV	83	
47	s	196	
48	t	153	
49	F	358	
50	Q	188	
51	ZZ	68	
52	EE	117	
53	TT	75	

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Mol	Chain	Length	Quality of chain
54	S5	191	
55	WW	62	
56	II	142	
57	CC	96	
58	AA	313	
59	OO	100	
60	MM	141	
61	LL	144	
62	XX	55	
63	RR	143	
64	SS	124	
65	S6	237	
66	S4	262	
67	S9	185	
68	S7	189	
69	YY	55	
70	S3	214	
71	RS	132	
72	WX	129	
73	S8	206	
74	W	121	
75	GG	136	
76	UU	101	
77	11	170	
78	L9	190	

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Mol	Chain	Length	Quality of chain
79	18	1688	
80	v	857	
81	LA	1096	
82	CE	223	
83	A	121	
84	ES	5070	
85	28	4808	
86	23	140	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 221973 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	BB	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 2 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	S2	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 3 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	PP	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 4 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	DD	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 6 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 7 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L8	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L3	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L4	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 10 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L5	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 11 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L6	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L7	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 13 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	aa	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 14 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	10	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	13	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	14	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 17 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 18 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	bb	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 19 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	17	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	19	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 21 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	20	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	22	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	cc	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 25 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	26	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 26 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 27 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	dd	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 28 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	30	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 30 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	31	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 31 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	32	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 32 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 33 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	34	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 34 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 35 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	36	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 36 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	37	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 37 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 38 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 39 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 40 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	41	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 41 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	42	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 42 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	ff	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 43 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	gg	124	Total	C	N	O	S	0	0
			990	615	202	167	6		

- Molecule 44 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AS	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 45 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	FF	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 46 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	VV	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 47 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 48 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 49 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	F	358	Total	C	N	O	S	0	0
			2798	1762	482	537	17		

- Molecule 50 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Q	187	Total	C	N	O	S	0	0
			1514	946	315	249	4		

- Molecule 51 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	ZZ	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 52 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	EE	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 53 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	TT	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 54 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	S5	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 55 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	WW	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 56 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	II	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 57 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	CC	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 58 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AA	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 59 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	OO	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 60 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	MM	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 61 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LL	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 62 is a protein called 40S ribosomal protein S29.

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

- Molecule 63 is a protein called uS12.

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

- Molecule 64 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SS	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 65 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	S6	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 66 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	S4	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 67 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	S9	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 68 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	S7	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 69 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	YY	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 70 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	S3	214	Total	C	N	O	S	0	0
			1662	1060	302	292	8		

- Molecule 71 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	RS	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 72 is a protein called 40S ribosomal protein S15a.

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

- Molecule 73 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	S8	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 74 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 75 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	GG	135	Total	C	N	O	S	0	0
			1007	615	198	188	6		

- Molecule 76 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	UU	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 77 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	11	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 78 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	L9	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 79 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	18	1688	Total	C	N	O	P	0	0
			36043	16088	6476	11792	1687		

- Molecule 80 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	v	829	Total	C	N	O	S	0	0
			6470	4114	1108	1205	43		

- Molecule 81 is a protein called La-related protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	LA	51	Total	C	N	O	S	0	0
			421	264	74	82	1		

- Molecule 82 is a protein called Coiled-coil domain-containing protein 124.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CE	73	Total	C	N	O	S	0	0
			613	369	122	121	1		

- Molecule 83 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	A	121	Total	C	N	O	S	0	0
			983	622	184	170	7		

- Molecule 84 is a RNA chain called ES27L.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	ES	35	Total	C	N	O	P	0	0
			756	335	142	244	35		

- Molecule 85 is a RNA chain called 28s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	28	3502	Total	C	N	O	P	0	0
			75105	33448	13761	24394	3502		

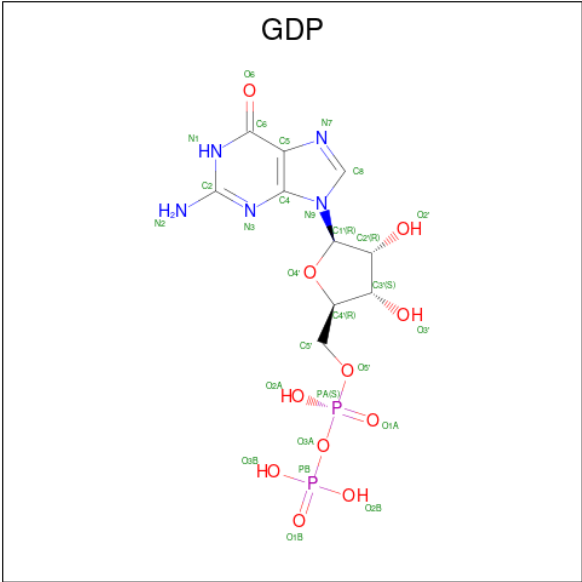
- Molecule 86 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	23	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
87	34	1	Total	Zn	0
			1	1	
87	37	1	Total	Zn	0
			1	1	
87	ff	1	Total	Zn	0
			1	1	
87	UU	1	Total	Zn	0
			1	1	

- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂) (labeled as "Ligand of Interest" by depositor).

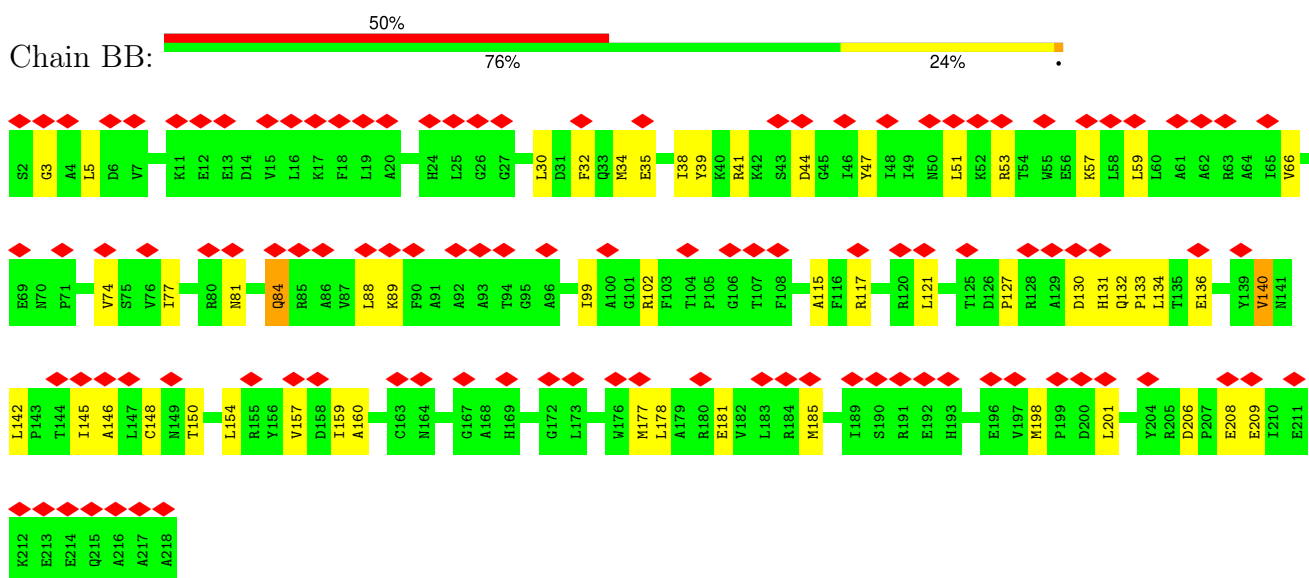


Mol	Chain	Residues	Atoms					AltConf
88	v	1	Total	C	N	O	P	0
			28	10	5	11	2	

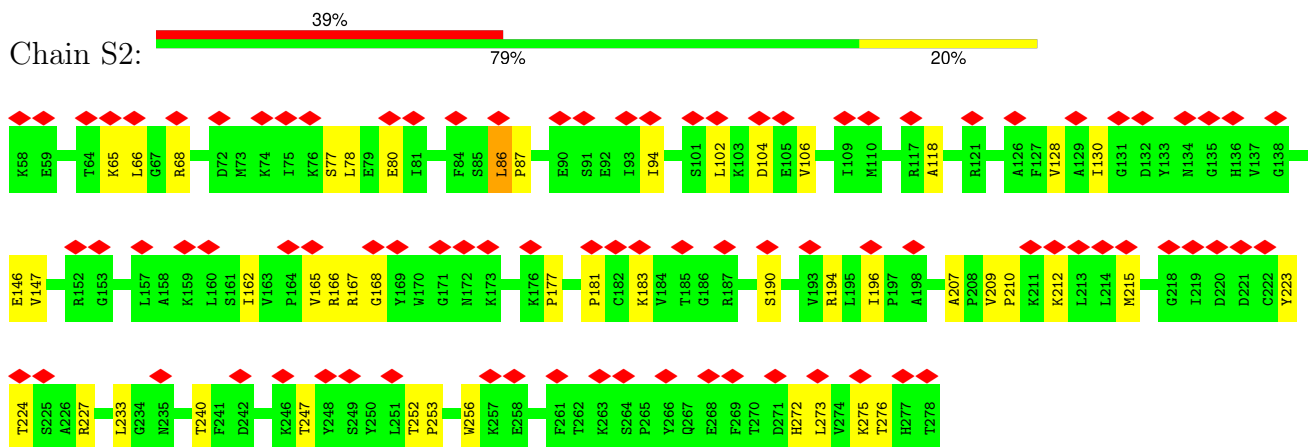
3 Residue-property plots

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.

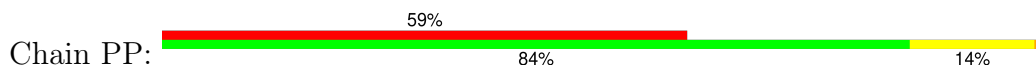
- Molecule 1: 40S_SA_C domain-containing protein

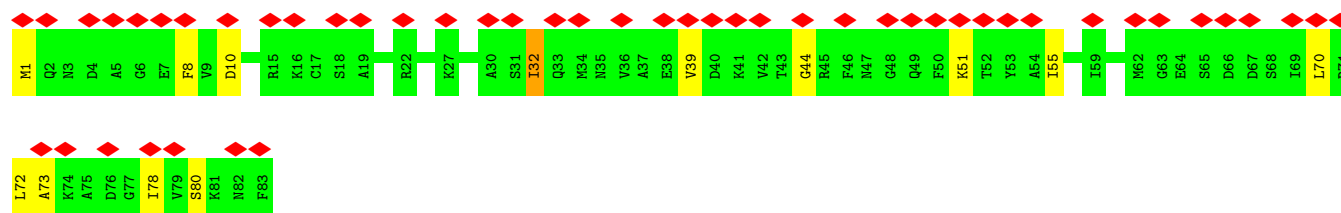


- Molecule 2: 40S ribosomal protein S2

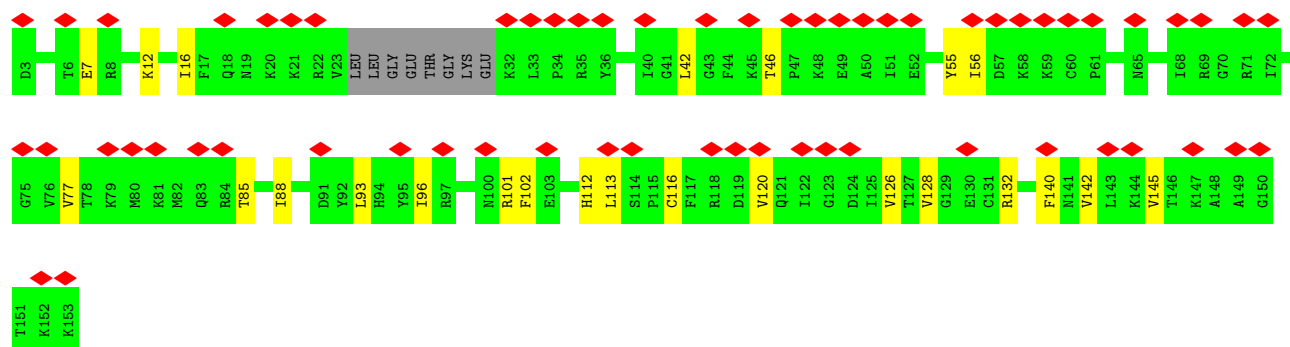
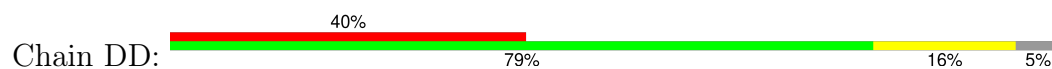


- Molecule 3: eS21

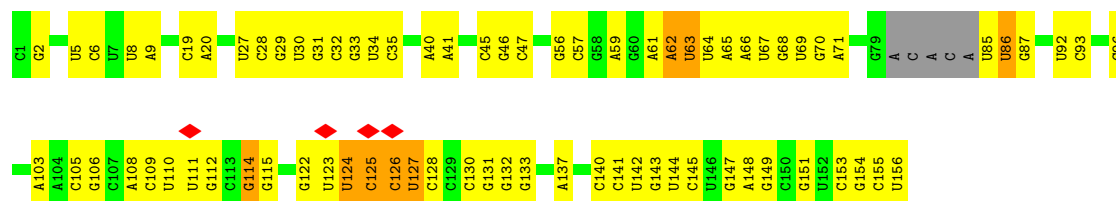




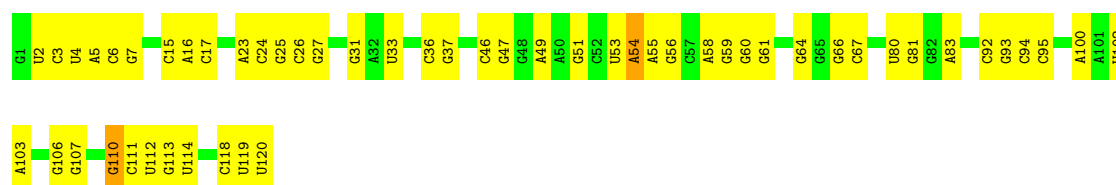
• Molecule 4: Small ribosomal subunit protein uS17



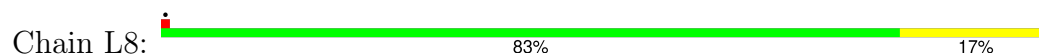
• Molecule 5: 5.8S rRNA

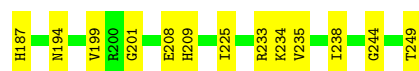


• Molecule 6: 5S rRNA



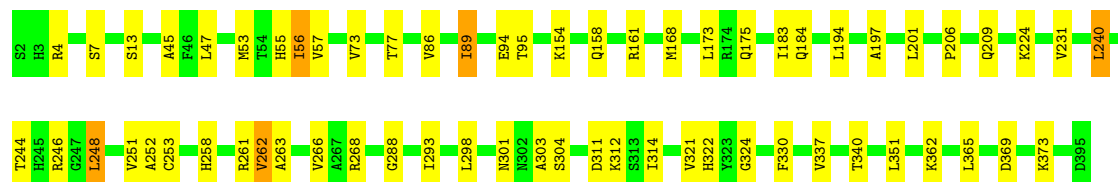
• Molecule 7: 60S ribosomal protein L8





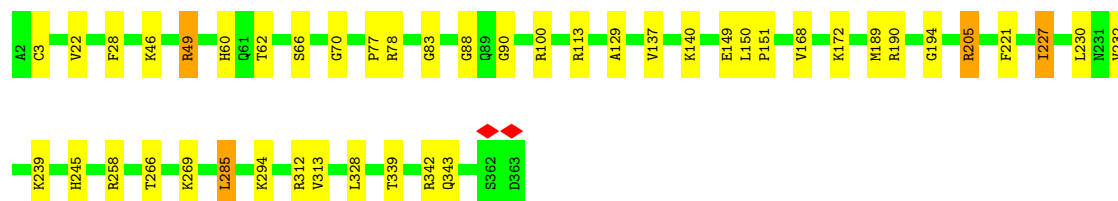
• Molecule 8: 60S ribosomal protein L3

Chain L3: 84% 15%



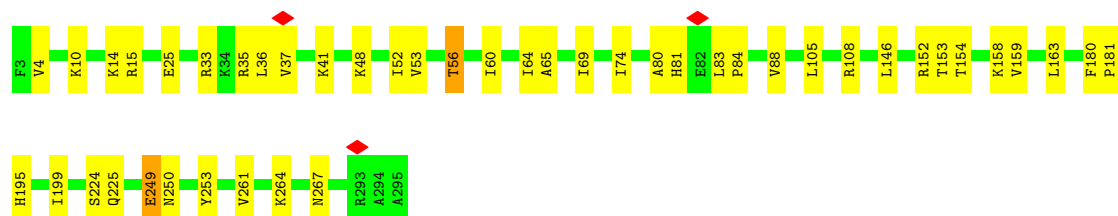
• Molecule 9: 60S ribosomal protein L4

Chain L4: 88% 11%



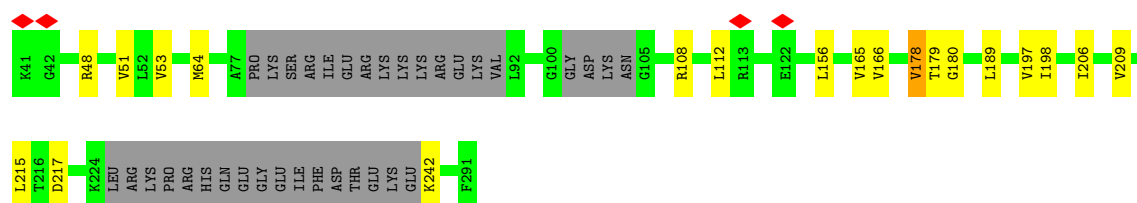
• Molecule 10: 60S ribosomal protein L5

Chain L5: 85% 15%



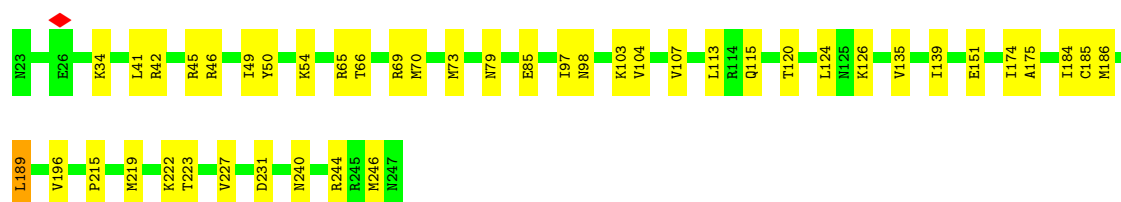
• Molecule 11: Large ribosomal subunit protein eL6

Chain L6: 78% 8% 14%

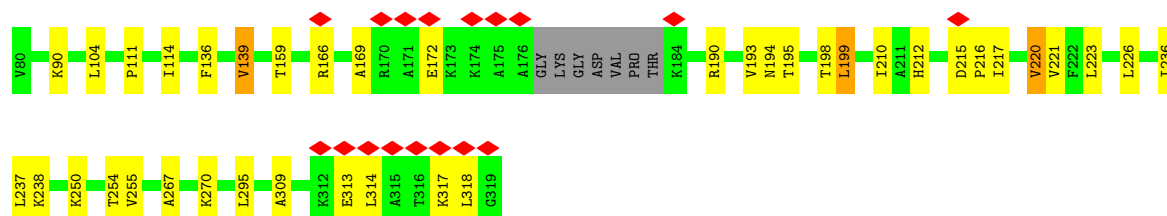
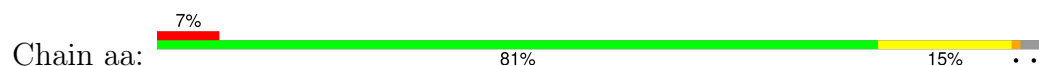


• Molecule 12: 60S ribosomal protein L7

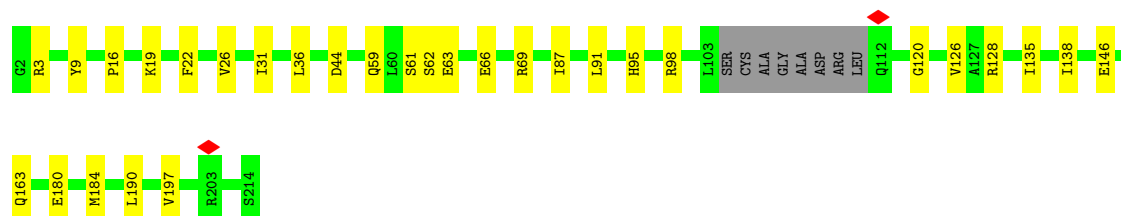
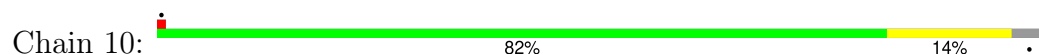
Chain L7: 80% 19%



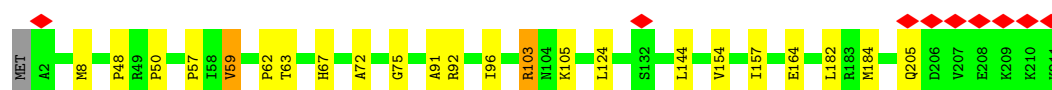
- Molecule 13: Large ribosomal subunit protein eL8



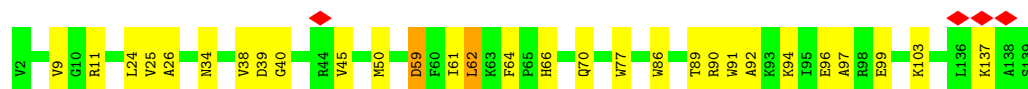
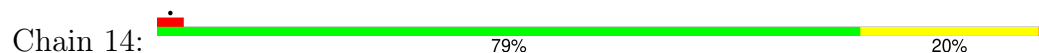
- Molecule 14: Ribosomal protein L10



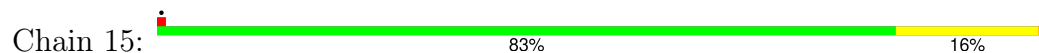
- Molecule 15: 60S ribosomal protein L13

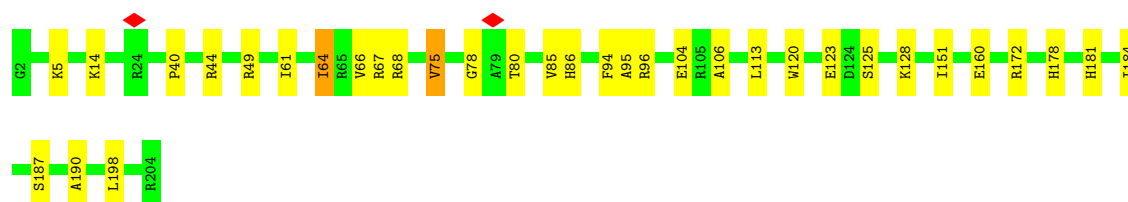


- Molecule 16: 60S ribosomal protein L14



- Molecule 17: 60S ribosomal protein L15





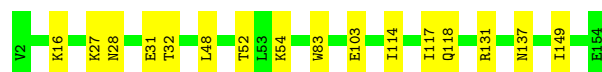
- Molecule 18: Large ribosomal subunit protein uL13

Chain bb: 79% 20% .



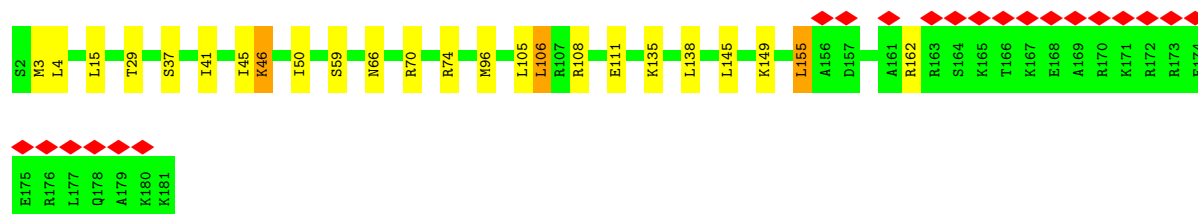
- Molecule 19: 60S ribosomal protein L17

Chain 17: 90% 10% .



- Molecule 20: 60S ribosomal protein L19

Chain 19: 12% 87% 12% .



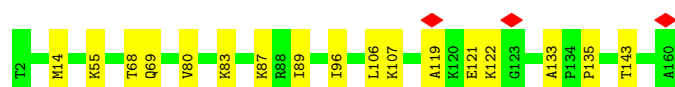
- Molecule 21: Large ribosomal subunit protein eL20

Chain 20: 85% 14% .



- Molecule 22: 60S ribosomal protein L21

Chain 21: 89% 11% .



- [illegible]

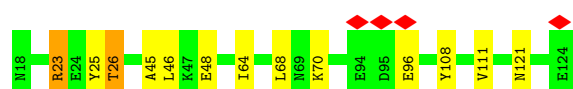
- Molecule 29: 60S ribosomal protein L30

Chain 30:  87% 12%



- Molecule 30: 60S ribosomal protein L31

Chain 31:  88% 10%



- Molecule 31: Large ribosomal subunit protein eL32

Chain 32:  84% 14%



- Molecule 32: Large ribosomal subunit protein eL33

Chain ee:  86% 10%

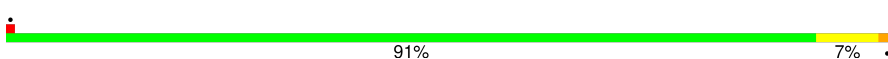


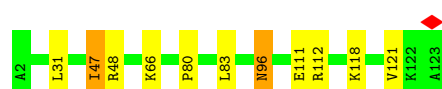
- Molecule 33: 60S ribosomal protein L34

Chain 34:  5% 90% 9%



- Molecule 34: 60S ribosomal protein L35

Chain 35:  91% 7%



- Molecule 35: 60S ribosomal protein L36

Chain 36:  87% 13%



- Molecule 36: 60S ribosomal protein L37

Chain 37: 92% 8%



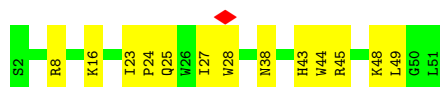
- Molecule 37: Large ribosomal subunit protein eL38

Chain 38: 90% 10%



- Molecule 38: 60S ribosomal protein L39

Chain 39: 74% 26%



- Molecule 39: Large ribosomal subunit protein eL40

Chain 40: 94% 6%



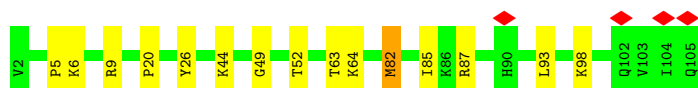
- Molecule 40: eL41

Chain 41: 88% 12%



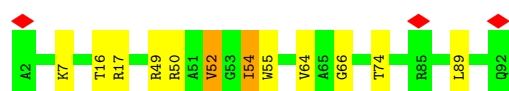
- Molecule 41: eL42

Chain 42: 86% 13%



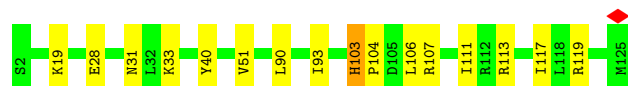
- Molecule 42: 60S ribosomal protein L37a

Chain ff:  87% 11% .



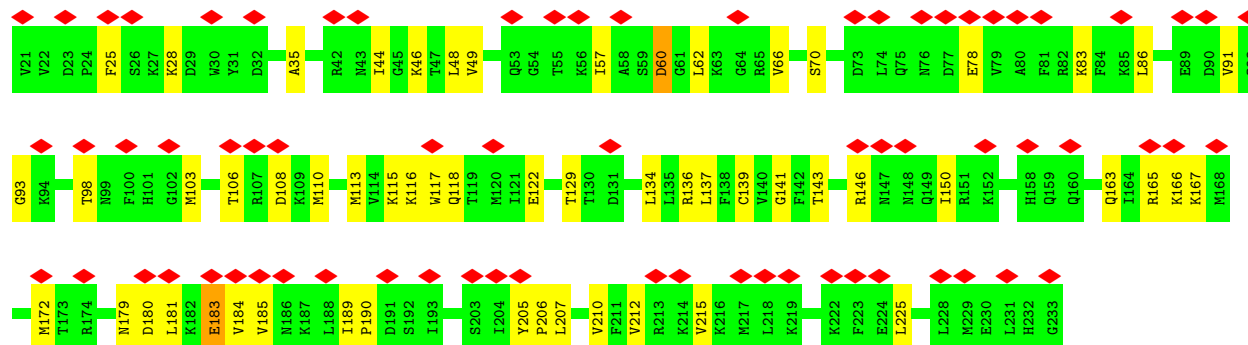
- Molecule 43: 60S ribosomal protein L28

Chain gg:  87% 12% .



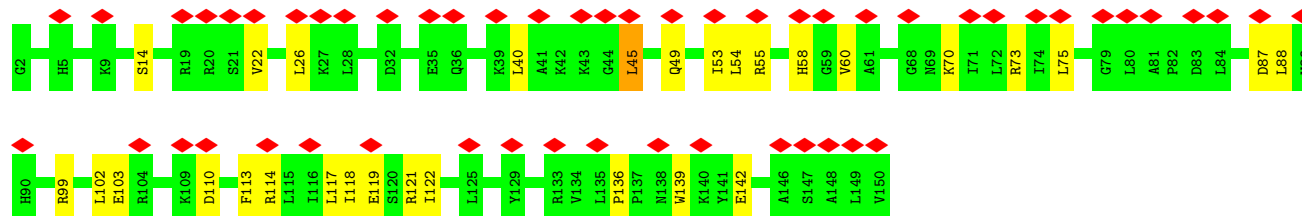
- Molecule 44: 40S ribosomal protein S3a

Chain AS:  33% 73% 26% .



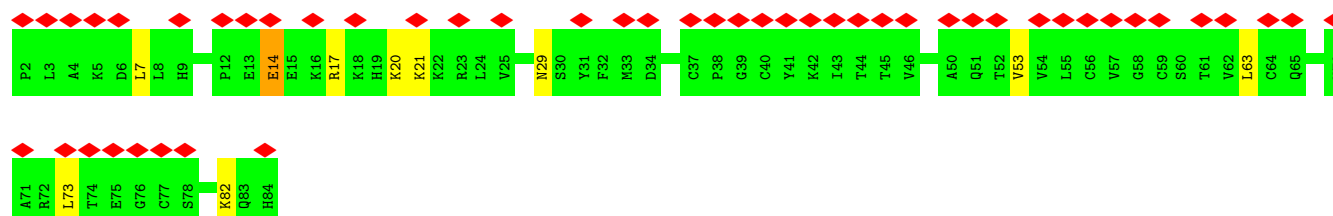
- Molecule 45: 40S ribosomal protein S13

Chain FF:  36% 80% 19% .

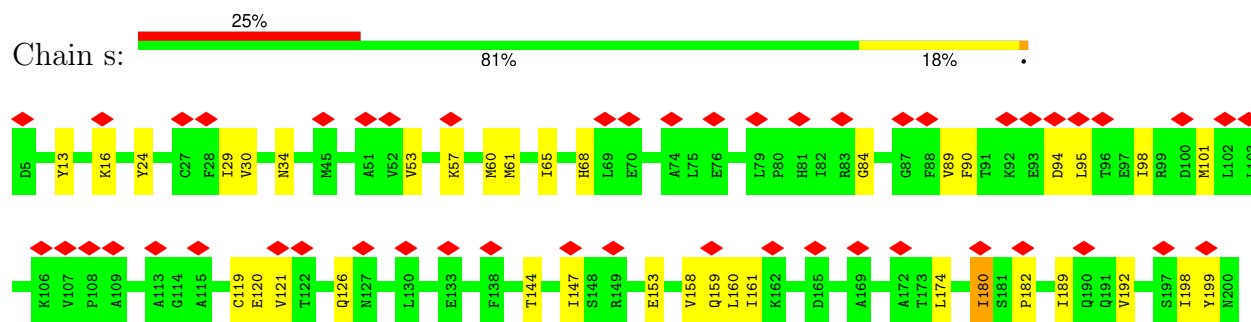


- Molecule 46: 40S ribosomal protein S27

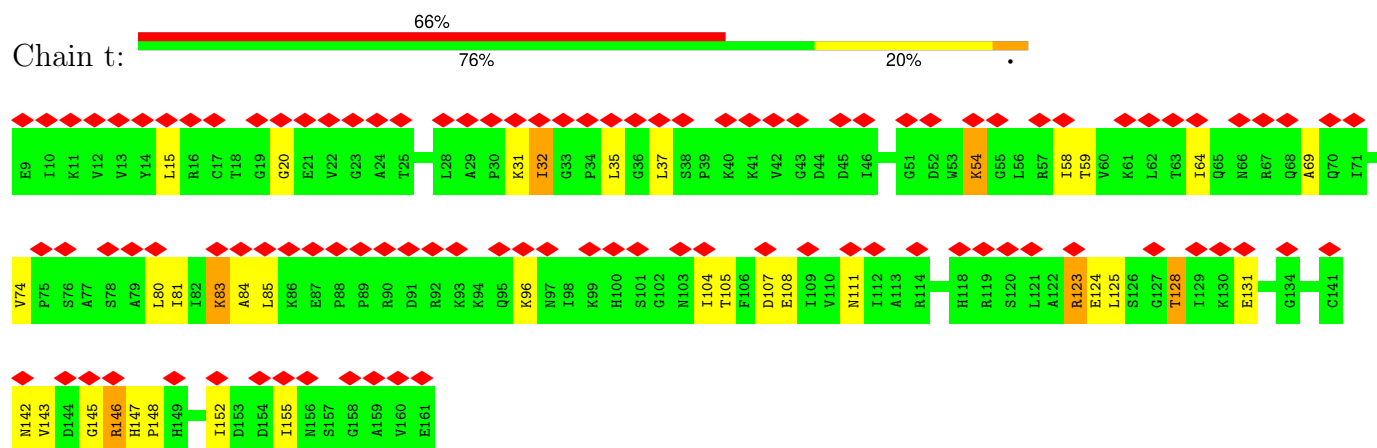
Chain VV:  59% 88% 11% .



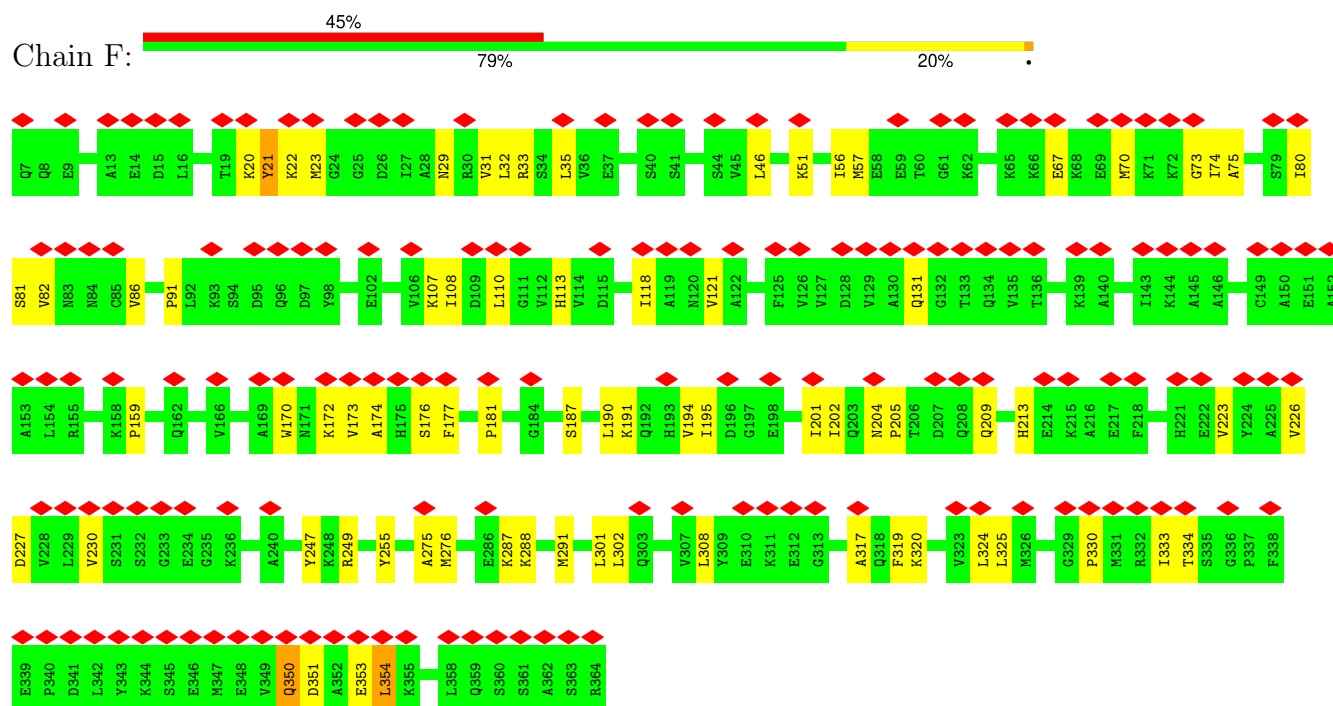
- Molecule 47: 60S acidic ribosomal protein P0



- Molecule 48: uL11



- Molecule 49: Proliferation-associated protein 2G4



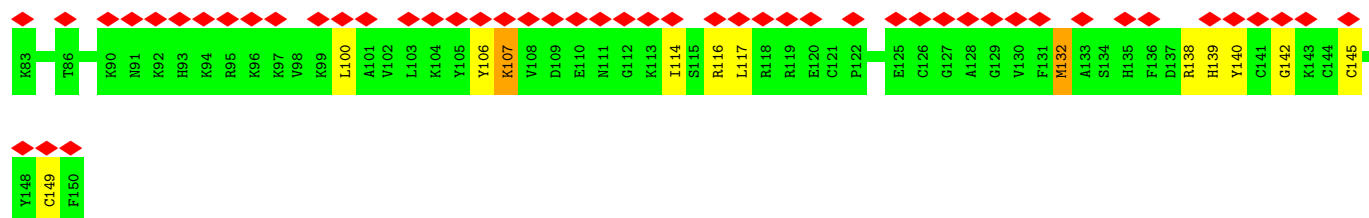
- Molecule 50: Large ribosomal subunit protein eL18

Chain Q:  88% 10% ..



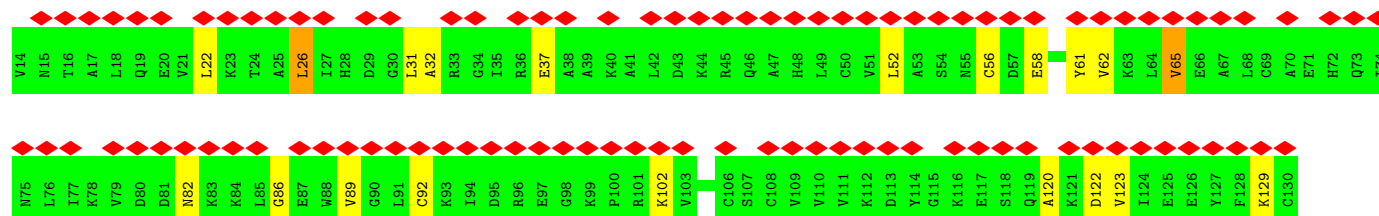
- Molecule 51: 40S ribosomal protein S27a

Chain ZZ:  74% 81% 16% .



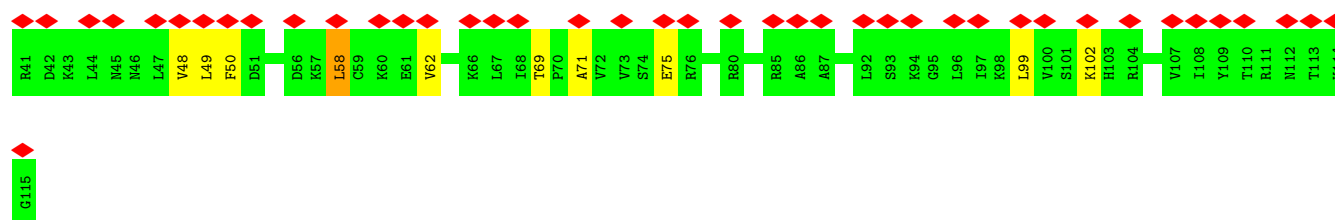
- Molecule 52: 40S ribosomal protein S12

Chain EE:  84% 83% 15% .



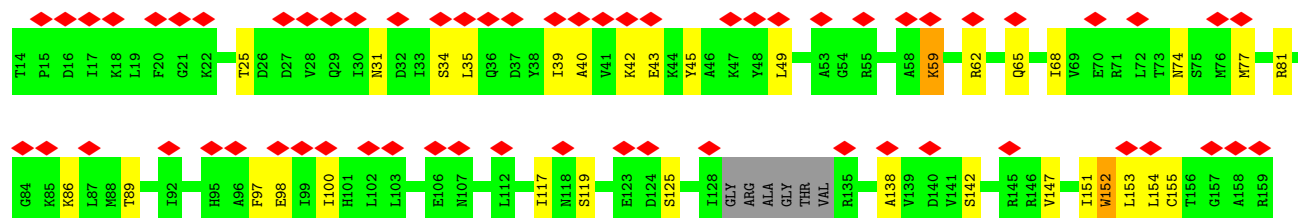
- Molecule 53: 40S ribosomal protein S25

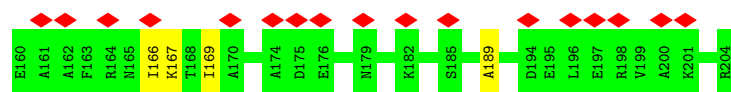
Chain TT:  56% 87% 12% .



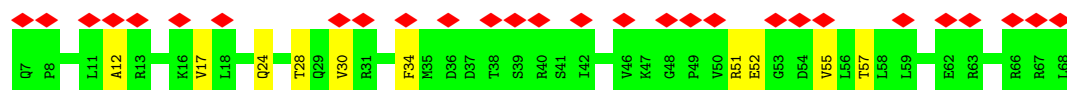
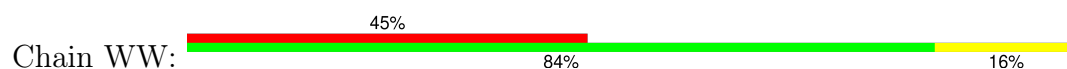
- Molecule 54: Small ribosomal subunit protein uS7

Chain S5:  41% 77% 18% ..

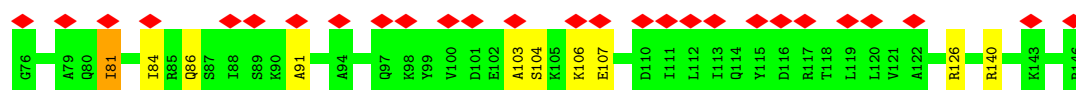
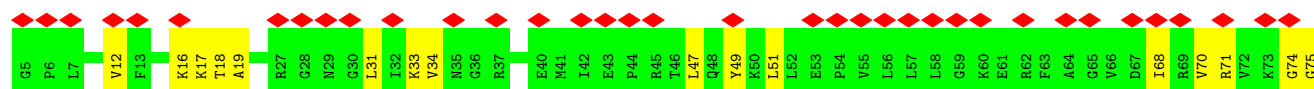
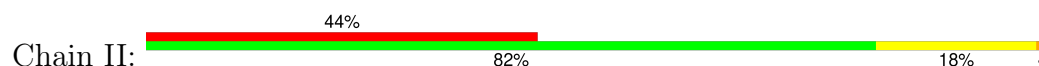




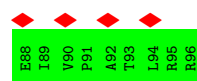
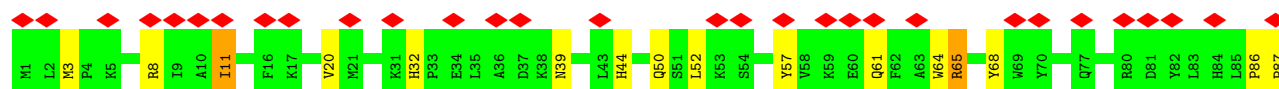
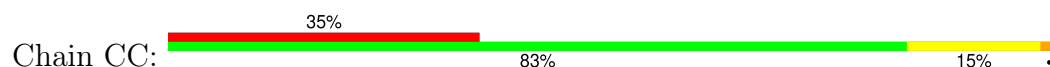
- Molecule 55: 40S ribosomal protein S28



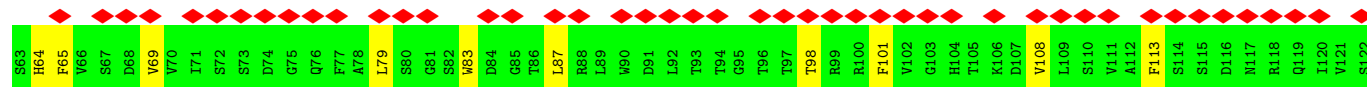
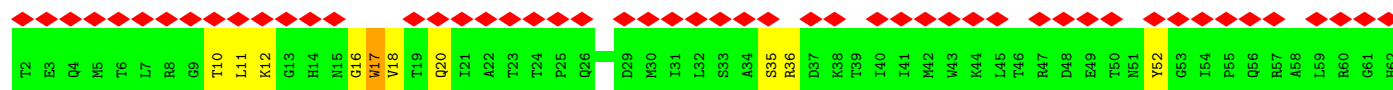
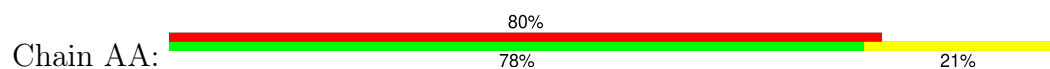
- Molecule 56: Small ribosomal subunit protein uS9

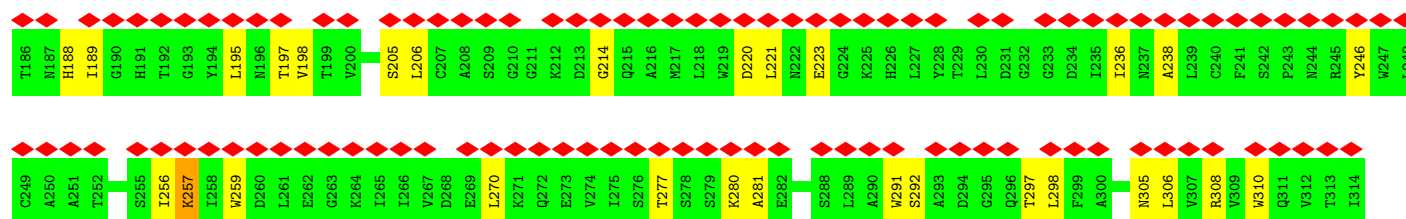


- Molecule 57: 40S ribosomal protein S10

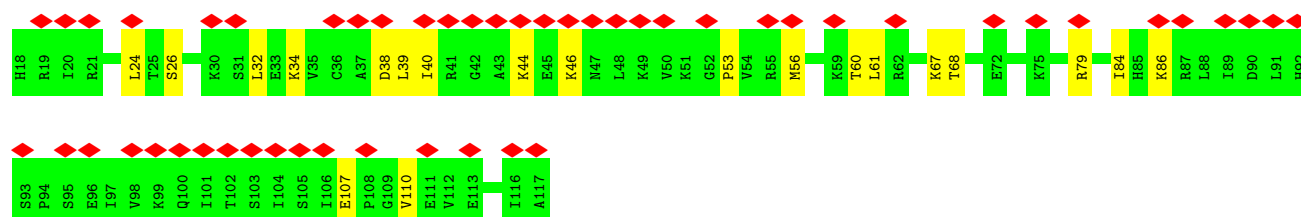
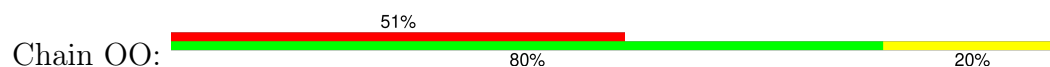


- Molecule 58: Receptor of activated protein C kinase 1

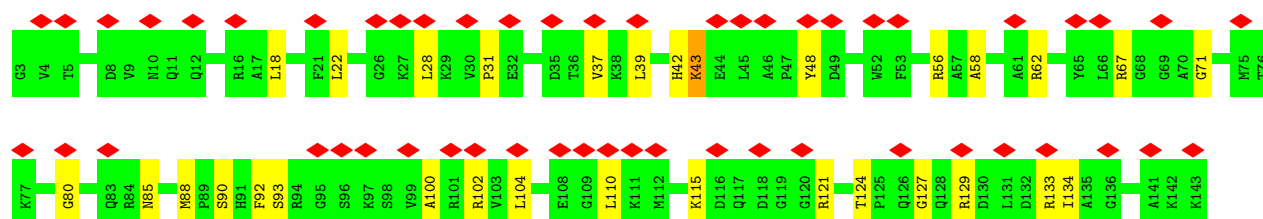
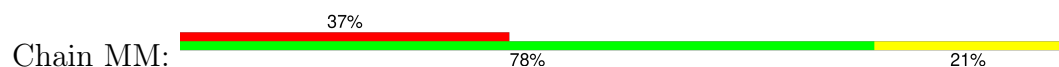




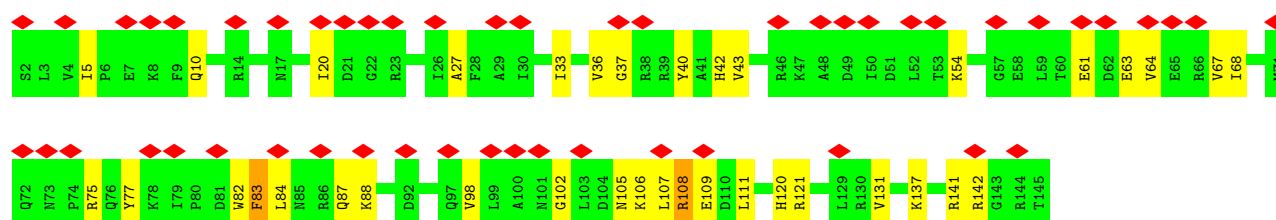
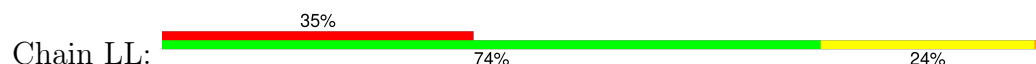
• Molecule 59: 40S ribosomal protein S20



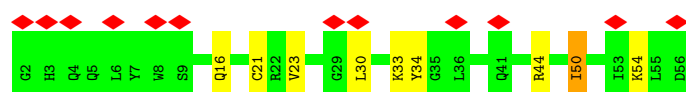
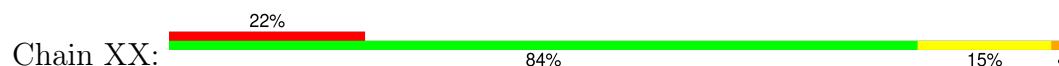
• Molecule 60: Small ribosomal subunit protein eS19



• Molecule 61: 40S ribosomal protein S18

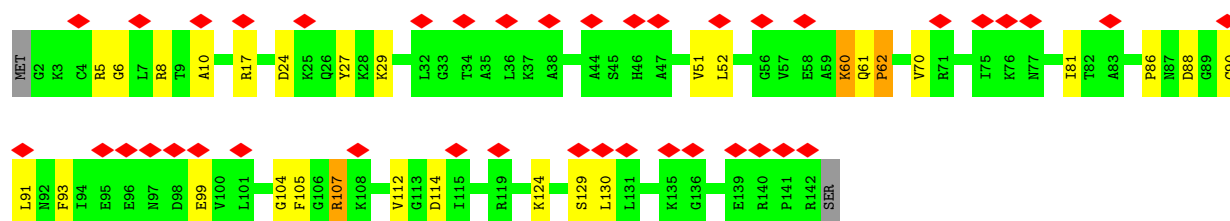


• Molecule 62: 40S ribosomal protein S29



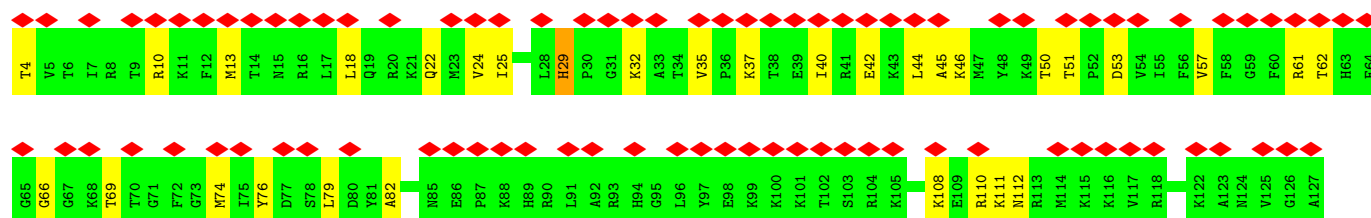
• Molecule 63: uS12

Chain RR: 



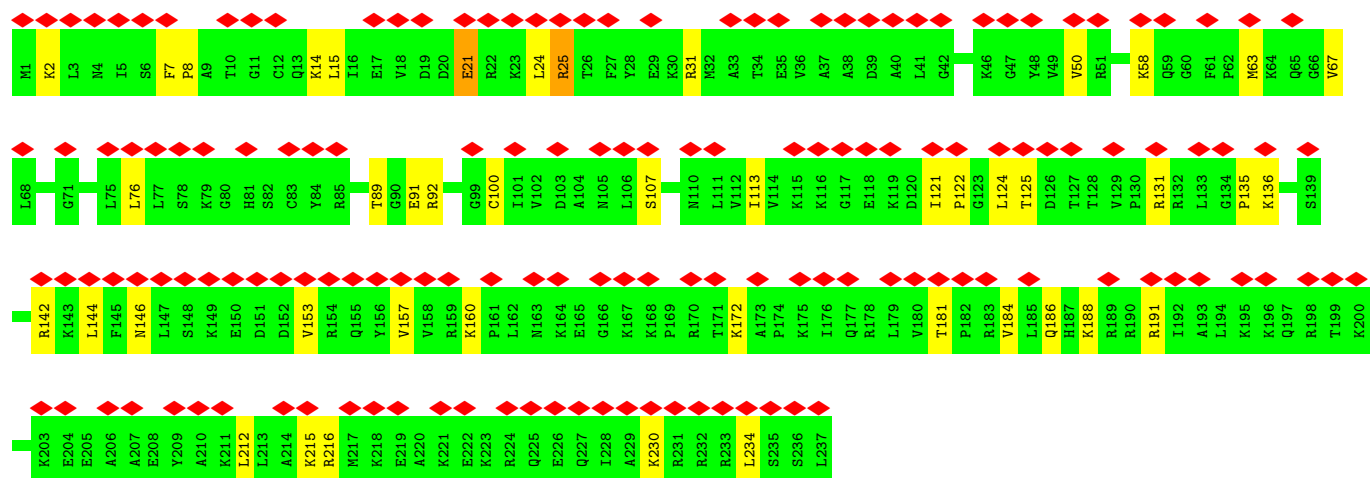
• Molecule 64: 40S ribosomal protein S24

Chain SS: 



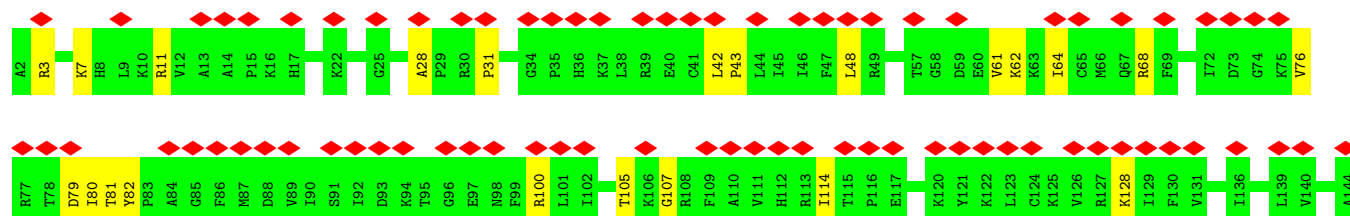
• Molecule 65: 40S ribosomal protein S6

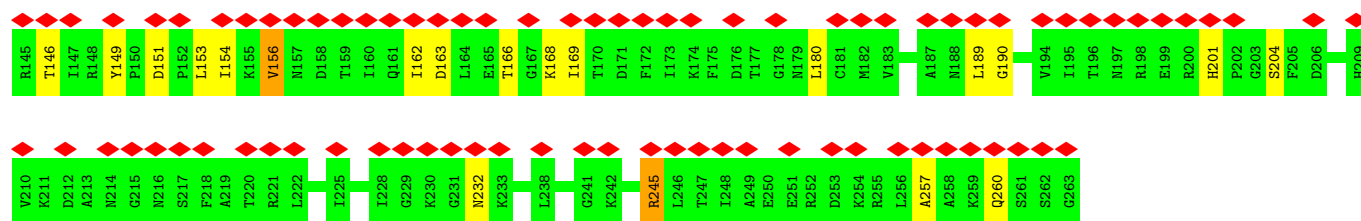
Chain S6: 



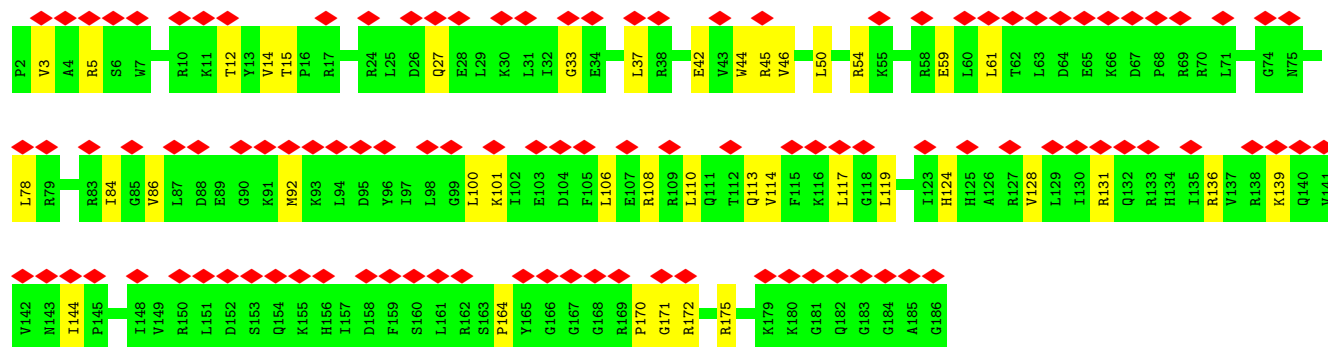
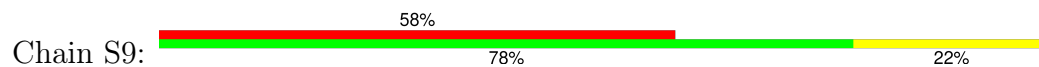
• Molecule 66: 40S ribosomal protein S4

Chain S4: 

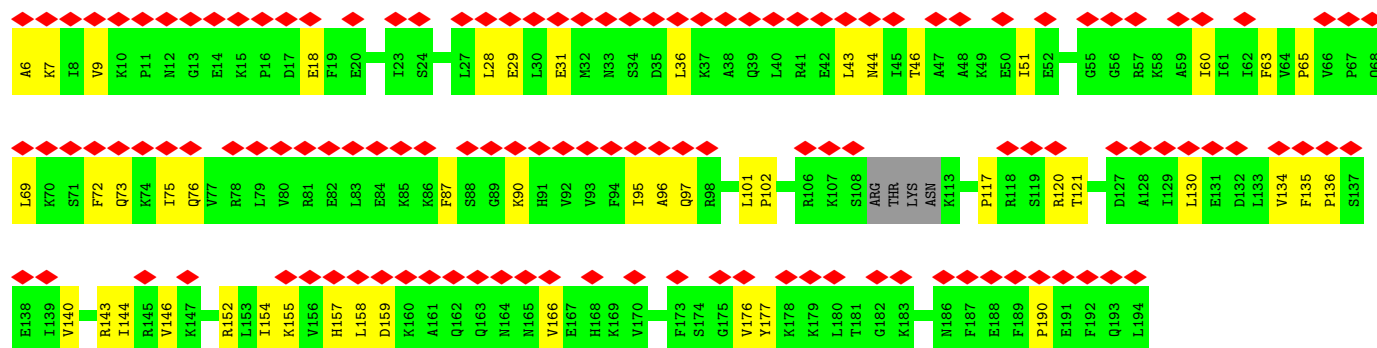
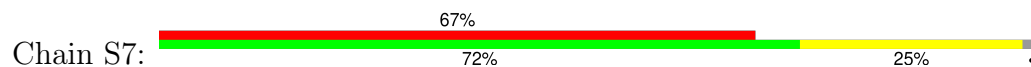




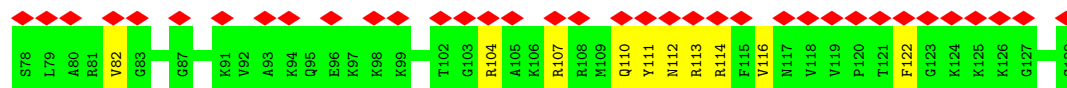
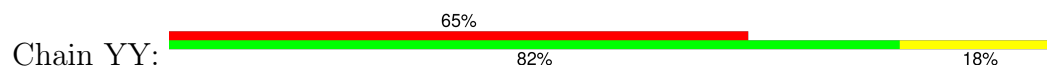
• Molecule 67: 40S ribosomal protein S9



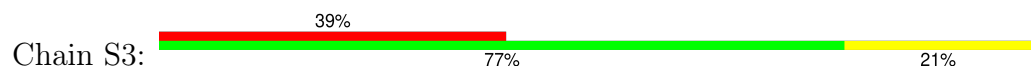
• Molecule 68: Small ribosomal subunit protein eS7

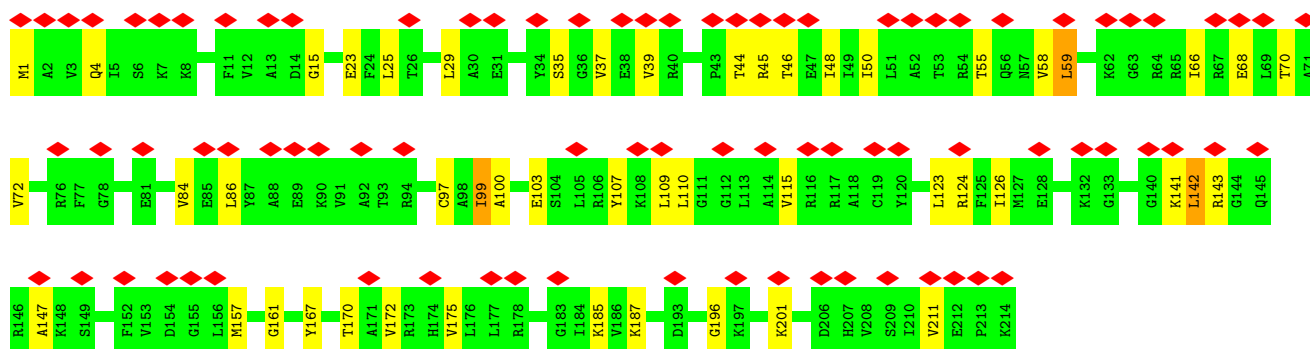


• Molecule 69: 40S ribosomal protein S30

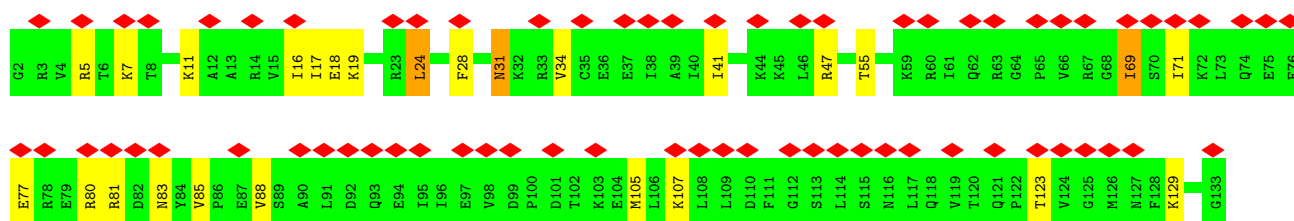
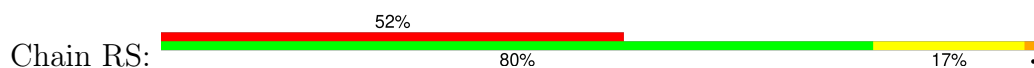


• Molecule 70: Small ribosomal subunit protein uS3

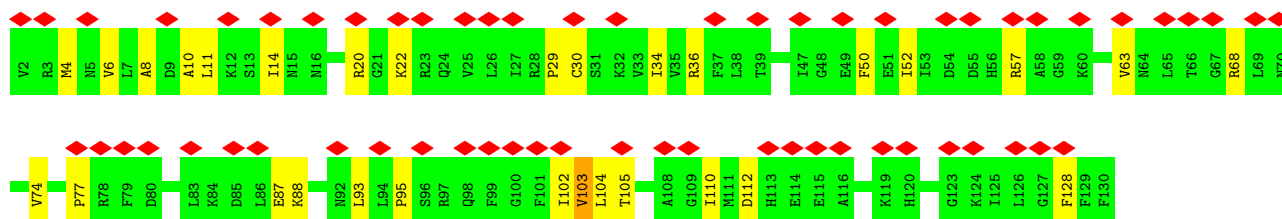
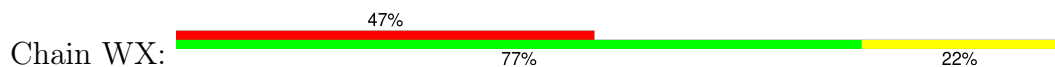




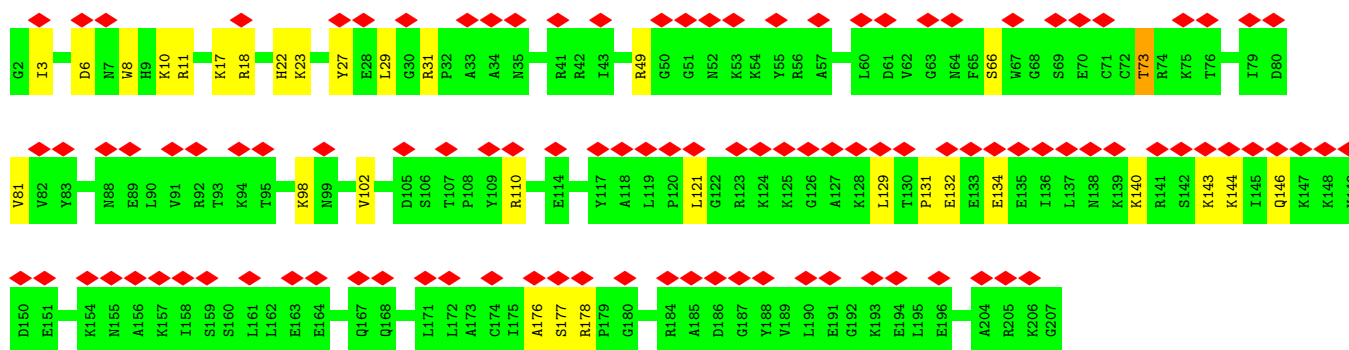
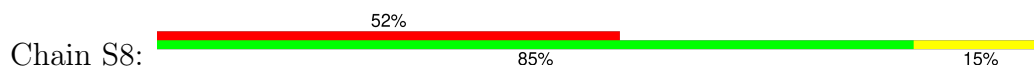
- Molecule 71: 40S ribosomal protein S17



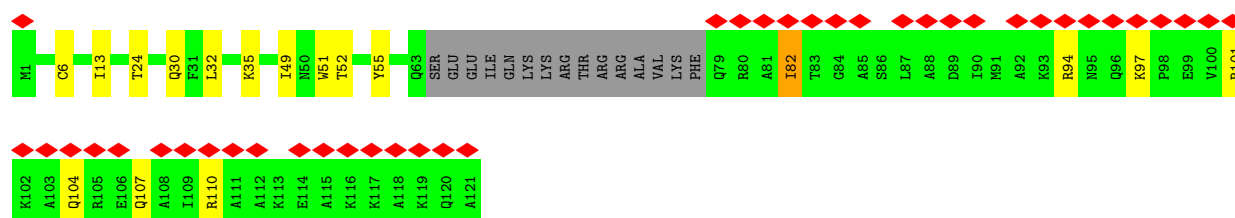
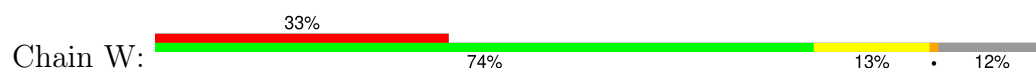
- Molecule 72: 40S ribosomal protein S15a



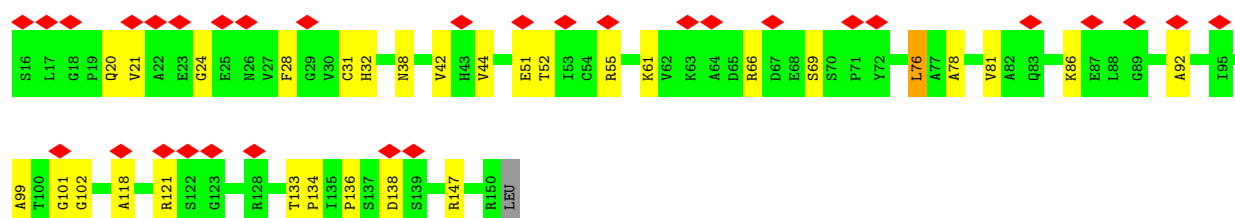
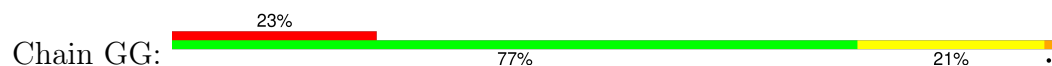
- Molecule 73: 40S ribosomal protein S8



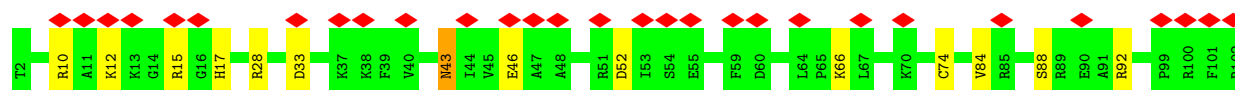
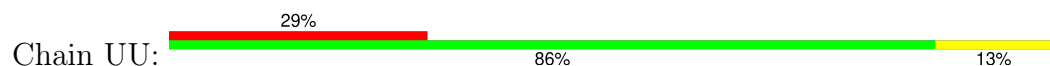
- Molecule 74: Ribosomal protein L24



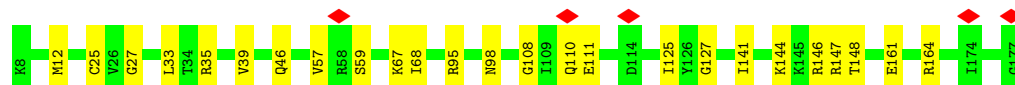
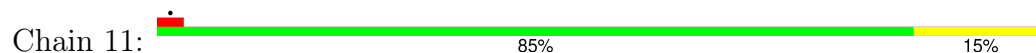
- Molecule 75: Small ribosomal subunit protein uS11



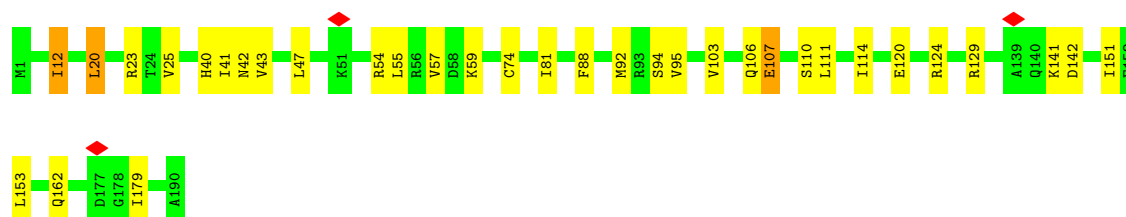
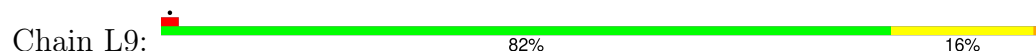
- Molecule 76: eS26



- Molecule 77: 60S ribosomal protein L11



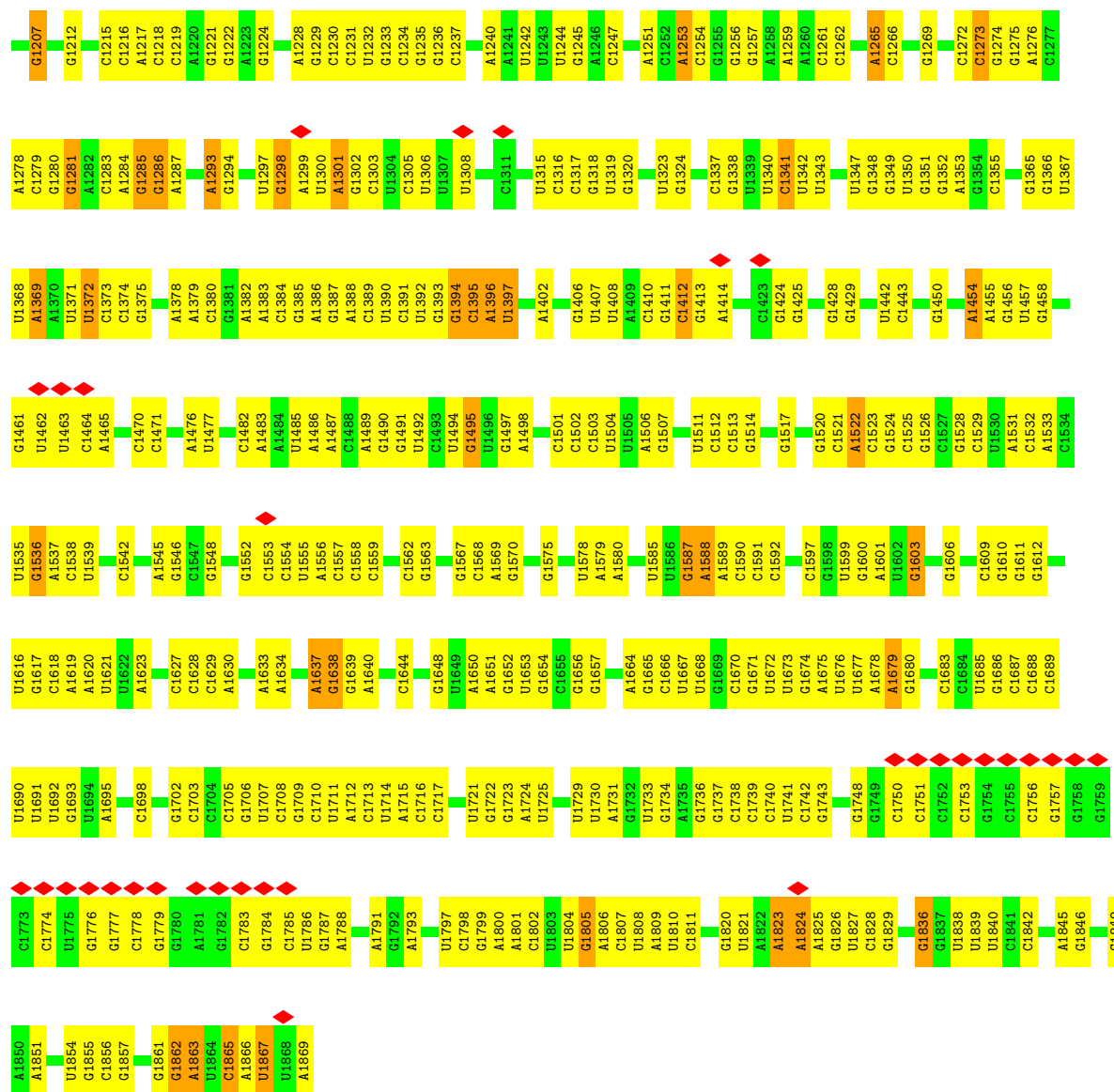
- Molecule 78: 60S ribosomal protein L9



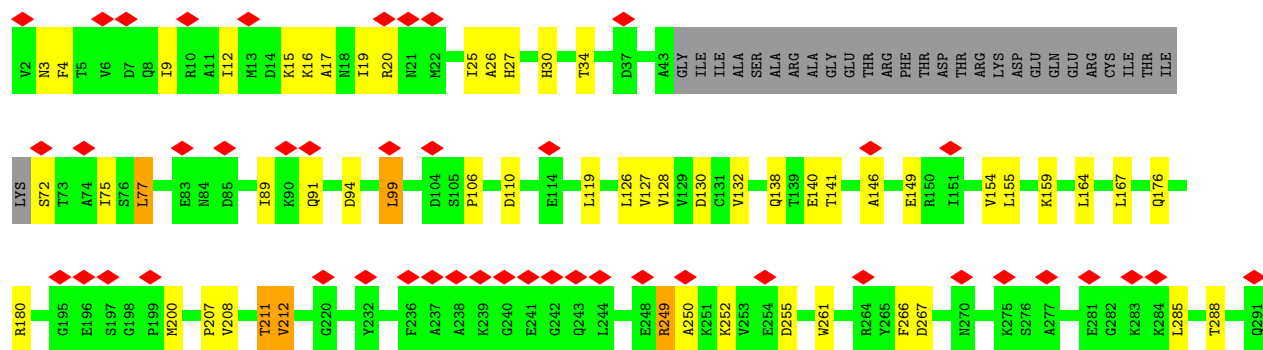
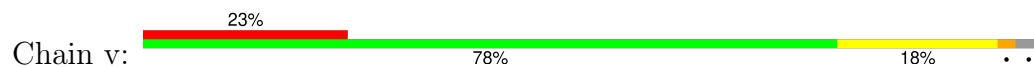
- Molecule 79: 18S rRNA

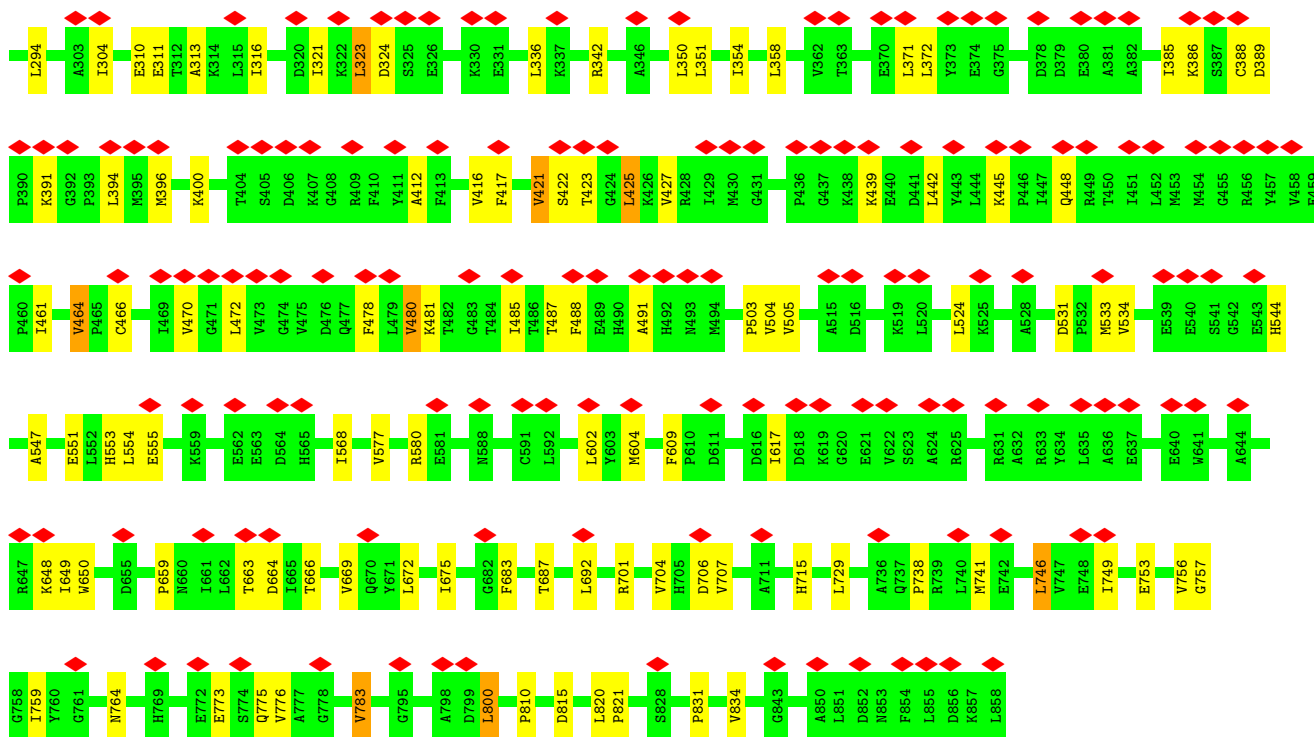






• Molecule 80: Elongation factor 2





- Molecule 81: La-related protein 1

Chain LA: 

95%

[illegible]



[illegible]

3

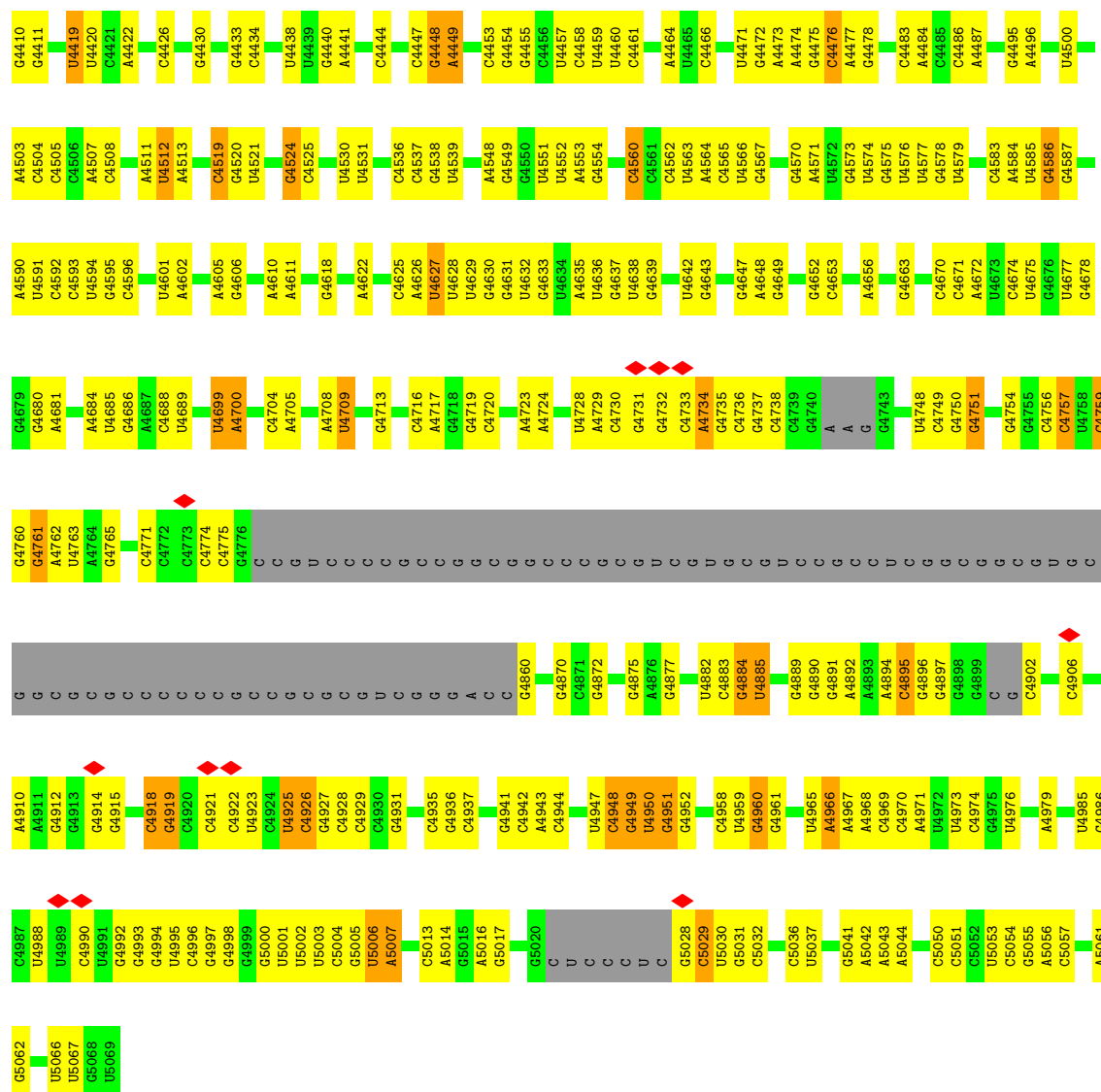




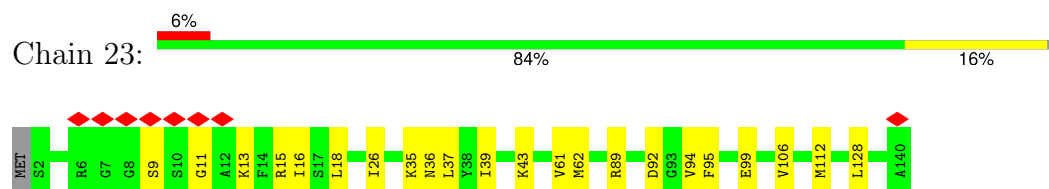


G2896	A2787	C2704	G2624	G2522	C2441	G2348	G	A2103	C2011	A1941	A1825	A1742	G1654
G2897	U2788	G2705	G2625	G2523	C2446	G2349	C	A2104	A2012	A1942	C1828	A1743	G1655
C2898	U2789	U2706	U2626	A2524	U2447	C2351	G2261	G2105	U2015	A1943	C1829	U1744	C1661
U2900	U2790	U2707	C2627	U2530	U2448	G2357	A2263	G2106	C2016	G1948	G1830	A1746	C1662
G	G2796	U2708	U2630	C2533	A2449	G2358	C2264	G2107	A2017	U1949	G1831	U1675	C1663
G	G2710	U2709	G	G	A2450	U2359	C2265	G2108	G	U1950	C1832	U1749	U1664
G	G2711	U2710	U2633	A2537	U2454	A2360	U2266	G2109	U2020	G1951	G1836	U1750	C1665
G	G2712	U2711	U2634	U2538	U2455	A2361	A2267	G	G2021	G1955	A1837	U1751	G
G	C2713	C2712	U2635	U2539	G2456	C2373	A2268	G	A2025	A1956	G	U1752	A1669
G	G2714	G2713	U2636	U2540	U2457	A2374	G2273	A	A2026	U1957	G1842	U1672	U1673
G	G2715	G2714	U2637	G2541	C2458	A2375	C2274	G	G	A1958	G	U1674	U1675
C	C2716	C2715	U2638	G2542	C2459	A2376	G2275	C	A2033	U1959	G1846	C1674	C1675
C	G	G	U2639	G2543	C2460	C2377	A2276	G	C2034	U1960	C1847	U1757	C1676
C	G	G	U2640	A2544	G2466	G	G2277	C	C2035	G1961	G	U1677	G
C	G	G	A2641	U2545	G2467	G2380	G2278	C	G2046	A1962	G1855	U1758	G
C	G	G	G	U2546	C2470	G	G2279	C	A2047	C1963	C1856	U1759	G
C	G	G	A2647	G2547	G2471	U2385	U2280	C	U2048	A1964	C1857	U1760	G
C	G	G	G	C2548	G	U2386	A2282	C	G	G1965	A1858	U1761	A1682
C	G	G	G	A2553	G2475	G2387	G2289	G	C2051	U1966	G	U1762	A1683
C	G	G	C2653	U2554	A2476	A2388	G	G	G2052	G1967	U1866	U1763	C1686
C	G	G	G	G2555	G2477	A2389	G2290	G	G	U1968	U1867	U1764	G1687
C	G	G	G	G2556	G2478	G	G2291	A	G2055	A1970	A1867	U1765	G1688
C	G	G	G	G2557	G2479	A2396	C2292	C	G2056	U1971	A1868	U1766	G1689
C	G	G	G	C2558	G2480	G2397	U2293	U	A2057	U1972	G1869	U1767	C1690
C	G	G	G	G2559	G2481	U2398	G2294	C	C2058	G1973	A1874	U1768	G1691
C	G	G	G	G2560	G2482	U2399	C2295	C	G2059	U1974	C1875	U1769	C1692
C	G	G	G	G2561	G2483	G2400	G2296	C	C2060	G1975	U1876	U1770	U1693
C	G	G	G	C2562	A2484	A2401	G2297	C	U2061	U1976	G	U1771	C1694
C	G	G	G	C2563	U2485	G2402	U2298	C	A2069	A1979	G1883	U1772	U1695
C	G	G	G	G2566	G2486	G	G2299	C	U2070	U1980	C1884	U1773	C1696
C	G	G	G	G2567	G2487	A2404	A2300	C	G	G	G1885	G	G
C	G	G	G	G2568	C2488	G	G2301	C	G	A1984	C1893	A	A
C	G	G	G	G2569	U2489	U2409	C2302	G	G2075	G1985	G1894	A	C
C	G	G	G	U2575	C2491	C2411	U2304	G	G2076	U1986	G1895	C	C
C	G	G	G	C2583	C2492	A2412	U2305	G	C2078	C1987	G1896	C	C
C	G	G	G	G	G2493	U2413	G2306	U	G2079	G1988	A1897	U1778	C
C	G	G	G	A2587	U2494	G2414	A2307	C	U2080	G1989	G	U1779	C
C	G	G	G	G2588	U2495	U2415	A2308	C	C2081	A1990	A1907	U1780	C
C	G	G	G	C2589	G2496	G2416	G2309	C	G2082	U1991	G	U1781	G1720
C	G	G	G	G2590	C2497	A2417	C2310	C	G	U1992	G	G	G1721
C	G	G	G	A2591	U2500	A2418	C2311	C	U1993	C1993	G	U1787	U1726
C	G	G	G	U2592	U2501	G	U2312	G	C1994	G	G1912	U1788	U1727
C	G	G	G	G2602	A2502	G2424	G2314	C	U1997	C1996	U1918	U1728	U1729
C	G	G	G	C2603	G2503	U2425	G2315	C	G	G	G1919	U1792	A1729
C	G	G	G	G2607	C2504	U2426	G2318	C	G2090	C1997	C1920	U1793	U1730
C	G	G	G	G2608	C2505	G2427	U2329	C	G2093	G	C1921	G1797	C1732
C	G	G	G	G2609	C2506	A2428	G2330	C	C2094	G2000	G1922	U1798	G1733
C	G	G	G	G2610	G2507	A2429	G2333	C	A2095	A2002	C1931	A1802	U1735
C	G	G	G	A2611	A2513	G	C2334	C	G2098	G1932	G1734	G1803	U1736
C	G	G	G	G2612	G2518	G2433	C2335	C	C2099	A1933	A1934	A1804	A1737
C	G	G	G	A2623	U2519	G2434	G2336	C	G2100	G2007	C1937	A1738	A1739
C	G	G	G	G	U2520	U2436	C2337	C	A2101	A2009	G	G1806	G1739
C	G	G	G	G	G2521	G	G	C	G2102	A2010	G1940	C1807	C1740
C	G	G	G	G	G	G	G	C	G	G	G	C1808	G1741
C	G	G	G	G	G	G	G	C	G	G	G	G1821	G1822
C	G	G	G	G	G	G	G	C	G	G	G	U1823	G1824





• Molecule 86: Ribosomal protein L23



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8501	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 ($e^-/\text{\AA}^2$)	39	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	OTHER	Depositor
Maximum map value	26.920	Depositor
Minimum map value	-14.119	Depositor
Average map value	0.004	Depositor
Map value standard deviation	1.115	Depositor
Recommended contour level	3.3	Depositor
Map size ($\text{\AA}$)	664.0, 664.0, 664.0	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DDE, GDP, 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	BB	0.13	0/1747	0.34	0/2374
2	S2	0.13	0/1753	0.31	0/2369
3	PP	0.12	0/643	0.28	0/860
4	DD	0.12	0/1195	0.32	0/1597
5	58	0.13	0/3581	0.29	0/5577
6	6	0.13	0/2858	0.26	0/4455
7	L8	0.13	0/1936	0.32	0/2596
8	L3	0.13	0/3240	0.33	0/4339
9	L4	0.12	0/2937	0.31	0/3946
10	L5	0.13	0/2437	0.32	0/3264
11	L6	0.13	0/1762	0.32	0/2362
12	L7	0.12	0/1911	0.28	0/2549
13	aa	0.14	0/1910	0.33	0/2569
14	10	0.12	0/1702	0.29	0/2272
15	13	0.12	0/1733	0.30	0/2316
16	14	0.14	0/1158	0.33	0/1547
17	15	0.13	0/1746	0.32	0/2338
18	bb	0.13	0/1662	0.31	0/2222
19	17	0.13	0/1268	0.33	0/1700
20	19	0.13	0/1524	0.29	0/2013
21	20	0.13	0/1501	0.28	0/2012
22	21	0.11	0/1326	0.27	0/1770
23	22	0.13	0/823	0.35	0/1104
24	cc	0.12	0/984	0.30	0/1323
25	26	0.12	0/1132	0.31	0/1504
26	27	0.12	0/1130	0.30	0/1507
27	dd	0.13	0/1191	0.33	0/1590
28	29	0.12	0/861	0.29	0/1138
29	30	0.12	0/771	0.27	0/1034
30	31	0.14	0/903	0.33	0/1216
31	32	0.12	0/1071	0.32	0/1429
32	ee	0.13	0/895	0.33	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	34	0.13	0/916	0.33	0/1220
34	35	0.12	0/1021	0.31	0/1348
35	36	0.12	0/841	0.29	0/1112
36	37	0.12	0/720	0.34	0/952
37	38	0.11	0/575	0.28	0/761
38	39	0.13	0/459	0.29	0/608
39	40	0.12	0/435	0.28	0/575
40	41	0.13	0/240	0.26	0/305
41	42	0.13	0/864	0.30	0/1140
42	ff	0.12	0/718	0.34	0/953
43	gg	0.12	0/1006	0.29	0/1349
44	AS	0.14	0/1756	0.34	0/2350
45	FF	0.15	0/1226	0.36	0/1649
46	VV	0.13	0/665	0.30	0/891
47	s	0.14	0/1530	0.37	0/2064
48	t	0.16	0/1174	0.43	0/1582
49	F	0.25	1/2845 (0.0%)	0.33	0/3828
50	Q	0.12	0/1538	0.36	0/2054
51	ZZ	0.13	0/567	0.35	0/753
52	EE	0.15	0/918	0.36	0/1233
53	TT	0.29	1/604 (0.2%)	0.39	0/810
54	S5	0.14	0/1492	0.36	0/2005
55	WW	0.11	0/490	0.29	0/656
56	II	0.14	0/1146	0.35	0/1534
57	CC	0.16	0/834	0.41	0/1125
58	AA	0.13	0/2493	0.33	0/3394
59	OO	0.13	0/805	0.33	0/1081
60	MM	0.13	0/1115	0.33	0/1493
61	LL	0.14	0/1208	0.39	0/1618
62	XX	0.12	0/470	0.33	0/623
63	RR	0.13	0/1116	0.35	0/1490
64	SS	0.13	0/1028	0.31	0/1366
65	S6	0.13	0/1946	0.35	1/2590 (0.0%)
66	S4	0.27	1/2118 (0.0%)	0.35	0/2849
67	S9	0.13	0/1550	0.32	0/2069
68	S7	0.13	0/1510	0.34	0/2022
69	YY	0.13	0/447	0.34	0/587
70	S3	0.14	0/1688	0.34	0/2269
71	RS	0.13	0/1082	0.35	0/1452
72	WX	0.14	0/1051	0.34	0/1406
73	S8	0.13	0/1715	0.32	0/2287
74	W	0.13	0/873	0.31	0/1158
75	GG	0.13	0/1020	0.35	0/1369

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	UU	0.12	0/828	0.30	0/1109
77	11	0.12	0/1385	0.31	0/1852
78	L9	0.13	0/1535	0.33	0/2063
79	18	0.13	0/40302	0.31	0/62804
80	v	0.14	0/6577	0.33	0/8883
81	LA	0.12	0/426	0.31	0/568
82	CE	0.16	0/616	0.30	0/812
83	A	0.14	0/1001	0.35	0/1339
84	ES	0.16	0/844	0.40	0/1314
85	28	0.14	0/84014	0.31	0/131028
86	23	0.13	0/1048	0.32	0/1402
All	All	0.14	3/237682 (0.0%)	0.32	1/347244 (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
47	s	0	1
63	RR	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	F	204	ASN	C-O	10.96	1.29	1.23
66	S4	149	TYR	C-O	-9.98	1.19	1.23
53	TT	62	VAL	CA-CB	6.34	1.57	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	S6	67	VAL	N-CA-C	-6.02	107.99	113.71

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
63	RR	60	LYS	Peptide
47	s	119	CYS	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	BB	1710	0	1708	27	0
2	S2	1716	0	1806	29	0
3	PP	636	0	637	6	0
4	DD	1175	0	1249	13	0
5	58	3208	0	1629	60	0
6	6	2558	0	1296	38	0
7	L8	1898	0	1993	28	0
8	L3	3172	0	3310	36	0
9	L4	2883	0	3053	27	0
10	L5	2391	0	2424	31	0
11	L6	1729	0	1887	12	0
12	L7	1875	0	1995	29	0
13	aa	1879	0	2027	23	0
14	10	1664	0	1712	17	0
15	13	1702	0	1820	14	0
16	14	1137	0	1211	14	0
17	15	1701	0	1749	21	0
18	bb	1630	0	1778	23	0
19	17	1242	0	1274	10	0
20	19	1508	0	1664	14	0
21	20	1462	0	1508	15	0
22	21	1298	0	1366	11	0
23	22	809	0	833	6	0
24	cc	967	0	1040	12	0
25	26	1115	0	1205	10	0
26	27	1107	0	1182	13	0
27	dd	1162	0	1209	16	0
28	29	848	0	920	6	0
29	30	761	0	794	8	0
30	31	888	0	930	7	0
31	32	1053	0	1147	13	0
32	ee	876	0	912	11	0
33	34	906	0	1000	8	0
34	35	1013	0	1147	8	0
35	36	830	0	916	6	0
36	37	705	0	738	4	0
37	38	569	0	637	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	39	447	0	480	11	0
39	40	429	0	469	3	0
40	41	239	0	289	3	0
41	42	851	0	924	9	0
42	ff	708	0	758	8	0
43	gg	990	0	1044	9	0
44	AS	1729	0	1803	35	0
45	FF	1202	0	1289	16	0
46	VV	651	0	672	3	0
47	s	1507	0	1564	15	0
48	t	1160	0	1218	24	0
49	F	2798	0	2809	41	0
50	Q	1514	0	1634	15	0
51	ZZ	555	0	567	8	0
52	EE	908	0	939	11	0
53	TT	598	0	656	5	0
54	S5	1471	0	1522	21	0
55	WW	488	0	514	4	0
56	II	1128	0	1195	16	0
57	CC	810	0	836	12	0
58	AA	2436	0	2393	36	0
59	OO	795	0	862	11	0
60	MM	1097	0	1132	18	0
61	LL	1190	0	1249	23	0
62	XX	459	0	452	9	0
63	RR	1098	0	1167	19	0
64	SS	1011	0	1083	18	0
65	S6	1923	0	2089	27	0
66	S4	2076	0	2177	23	0
67	S9	1525	0	1640	23	0
68	S7	1488	0	1582	24	0
69	YY	443	0	492	6	0
70	S3	1662	0	1760	27	0
71	RS	1068	0	1121	15	0
72	WX	1034	0	1080	20	0
73	S8	1686	0	1772	20	0
74	W	860	0	903	10	0
75	GG	1007	0	1028	20	0
76	UU	814	0	865	12	0
77	11	1362	0	1399	14	0
78	L9	1516	0	1597	16	0
79	18	36043	0	18202	676	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	v	6470	0	6548	75	0
81	LA	421	0	405	2	0
82	CE	613	0	625	2	0
83	A	983	0	1030	11	0
84	ES	756	0	384	21	0
85	28	75105	0	37942	1216	0
86	23	1034	0	1097	12	0
87	34	1	0	0	0	0
87	37	1	0	0	0	0
87	UU	1	0	0	0	0
87	ff	1	0	0	0	0
88	v	28	0	12	1	0
All	All	221973	0	168976	3002	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 8.

The worst 5 of 3002 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)
79:18:639:C:H2'	79:18:640:A:H8	1.33	0.91
85:28:2492:C:H2'	85:28:2493:G:H8	1.36	0.91
79:18:730:C:H2'	79:18:731:G:C8	2.07	0.88
79:18:677:G:H21	79:18:1028:A:H62	1.21	0.87
85:28:2478:C:H2'	85:28:2479:G:H8	1.38	0.86

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BB	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
2	S2	219/221 (99%)	217 (99%)	2 (1%)	0	100	100
3	PP	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
4	DD	139/151 (92%)	132 (95%)	7 (5%)	0	100	100
7	L8	246/248 (99%)	239 (97%)	7 (3%)	0	100	100
8	L3	392/394 (100%)	379 (97%)	13 (3%)	0	100	100
9	L4	360/362 (99%)	354 (98%)	6 (2%)	0	100	100
10	L5	291/293 (99%)	285 (98%)	6 (2%)	0	100	100
11	L6	208/251 (83%)	199 (96%)	9 (4%)	0	100	100
12	L7	223/225 (99%)	214 (96%)	8 (4%)	1 (0%)	30	59
13	aa	229/240 (95%)	224 (98%)	5 (2%)	0	100	100
14	10	201/213 (94%)	200 (100%)	1 (0%)	0	100	100
15	13	208/211 (99%)	202 (97%)	6 (3%)	0	100	100
16	14	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
17	15	201/203 (99%)	193 (96%)	8 (4%)	0	100	100
18	bb	197/199 (99%)	196 (100%)	1 (0%)	0	100	100
19	17	151/153 (99%)	151 (100%)	0	0	100	100
20	19	178/180 (99%)	175 (98%)	3 (2%)	0	100	100
21	20	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
22	21	157/159 (99%)	156 (99%)	1 (1%)	0	100	100
23	22	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
24	cc	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
25	26	132/134 (98%)	132 (100%)	0	0	100	100
26	27	133/135 (98%)	129 (97%)	4 (3%)	0	100	100
27	dd	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
28	29	100/245 (41%)	98 (98%)	2 (2%)	0	100	100
29	30	96/98 (98%)	95 (99%)	1 (1%)	0	100	100
30	31	105/107 (98%)	103 (98%)	2 (2%)	0	100	100
31	32	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
32	ee	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
33	34	112/114 (98%)	112 (100%)	0	0	100	100
34	35	120/122 (98%)	118 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	36	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
36	37	84/86 (98%)	84 (100%)	0	0	100	100
37	38	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
38	39	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
39	40	50/52 (96%)	50 (100%)	0	0	100	100
40	41	23/25 (92%)	23 (100%)	0	0	100	100
41	42	102/104 (98%)	101 (99%)	1 (1%)	0	100	100
42	ff	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
43	gg	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
44	AS	211/213 (99%)	207 (98%)	4 (2%)	0	100	100
45	FF	147/149 (99%)	145 (99%)	2 (1%)	0	100	100
46	VV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
47	s	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
48	t	151/153 (99%)	143 (95%)	8 (5%)	0	100	100
49	F	356/358 (99%)	349 (98%)	7 (2%)	0	100	100
50	Q	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
51	ZZ	66/68 (97%)	65 (98%)	1 (2%)	0	100	100
52	EE	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
53	TT	73/75 (97%)	69 (94%)	4 (6%)	0	100	100
54	S5	181/191 (95%)	168 (93%)	13 (7%)	0	100	100
55	WW	60/62 (97%)	60 (100%)	0	0	100	100
56	II	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
57	CC	94/96 (98%)	86 (92%)	7 (7%)	1 (1%)	11	36
58	AA	311/313 (99%)	297 (96%)	14 (4%)	0	100	100
59	OO	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
60	MM	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
61	LL	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
62	XX	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
63	RR	139/143 (97%)	135 (97%)	3 (2%)	1 (1%)	18	48
64	SS	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
65	S6	235/237 (99%)	234 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	S4	260/262 (99%)	257 (99%)	3 (1%)	0	100	100
67	S9	183/185 (99%)	179 (98%)	4 (2%)	0	100	100
68	S7	181/189 (96%)	178 (98%)	3 (2%)	0	100	100
69	YY	53/55 (96%)	53 (100%)	0	0	100	100
70	S3	212/214 (99%)	209 (99%)	3 (1%)	0	100	100
71	RS	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
72	WX	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
73	S8	204/206 (99%)	199 (98%)	5 (2%)	0	100	100
74	W	102/121 (84%)	101 (99%)	1 (1%)	0	100	100
75	GG	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
76	UU	99/101 (98%)	98 (99%)	1 (1%)	0	100	100
77	11	168/170 (99%)	166 (99%)	2 (1%)	0	100	100
78	L9	188/190 (99%)	181 (96%)	7 (4%)	0	100	100
80	v	824/857 (96%)	809 (98%)	15 (2%)	0	100	100
81	LA	45/1096 (4%)	45 (100%)	0	0	100	100
82	CE	71/223 (32%)	71 (100%)	0	0	100	100
83	A	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
86	23	137/140 (98%)	137 (100%)	0	0	100	100
All	All	12809/14451 (89%)	12518 (98%)	288 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
63	RR	62	PRO
57	CC	65	ARG
12	L7	196	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BB	180/181 (99%)	167 (93%)	13 (7%)	13	39
2	S2	187/187 (100%)	180 (96%)	7 (4%)	30	64
3	PP	67/67 (100%)	63 (94%)	4 (6%)	17	47
4	DD	130/136 (96%)	124 (95%)	6 (5%)	24	57
7	L8	190/190 (100%)	182 (96%)	8 (4%)	26	60
8	L3	342/342 (100%)	327 (96%)	15 (4%)	25	59
9	L4	302/302 (100%)	293 (97%)	9 (3%)	36	70
10	L5	247/247 (100%)	240 (97%)	7 (3%)	38	72
11	L6	190/223 (85%)	183 (96%)	7 (4%)	30	64
12	L7	196/196 (100%)	189 (96%)	7 (4%)	31	65
13	aa	200/205 (98%)	191 (96%)	9 (4%)	24	58
14	10	175/180 (97%)	171 (98%)	4 (2%)	44	76
15	13	175/176 (99%)	166 (95%)	9 (5%)	21	53
16	14	117/117 (100%)	111 (95%)	6 (5%)	21	53
17	15	171/171 (100%)	164 (96%)	7 (4%)	27	61
18	bb	171/171 (100%)	163 (95%)	8 (5%)	23	56
19	17	134/134 (100%)	133 (99%)	1 (1%)	76	92
20	19	159/159 (100%)	151 (95%)	8 (5%)	22	53
21	20	157/157 (100%)	150 (96%)	7 (4%)	24	58
22	21	139/139 (100%)	136 (98%)	3 (2%)	45	77
23	22	89/89 (100%)	86 (97%)	3 (3%)	32	66
24	cc	106/106 (100%)	105 (99%)	1 (1%)	70	90
25	26	124/124 (100%)	117 (94%)	7 (6%)	19	50
26	27	117/117 (100%)	114 (97%)	3 (3%)	40	73
27	dd	119/119 (100%)	117 (98%)	2 (2%)	53	82
28	29	84/184 (46%)	82 (98%)	2 (2%)	43	75
29	30	84/84 (100%)	82 (98%)	2 (2%)	43	75
30	31	98/98 (100%)	92 (94%)	6 (6%)	17	46
31	32	114/114 (100%)	108 (95%)	6 (5%)	20	52
32	ee	88/88 (100%)	83 (94%)	5 (6%)	18	49
33	34	98/98 (100%)	97 (99%)	1 (1%)	68	89
34	35	109/109 (100%)	106 (97%)	3 (3%)	38	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	36	86/86 (100%)	82 (95%)	4 (5%)	23	56
36	37	73/73 (100%)	71 (97%)	2 (3%)	39	73
37	38	64/64 (100%)	62 (97%)	2 (3%)	35	69
38	39	47/47 (100%)	47 (100%)	0	100	100
39	40	48/48 (100%)	48 (100%)	0	100	100
40	41	24/24 (100%)	24 (100%)	0	100	100
41	42	92/92 (100%)	90 (98%)	2 (2%)	45	77
42	ff	74/74 (100%)	70 (95%)	4 (5%)	20	51
43	gg	107/108 (99%)	104 (97%)	3 (3%)	38	72
44	AS	194/194 (100%)	188 (97%)	6 (3%)	35	69
45	FF	130/130 (100%)	123 (95%)	7 (5%)	20	51
46	VV	75/75 (100%)	69 (92%)	6 (8%)	11	34
47	s	164/164 (100%)	151 (92%)	13 (8%)	11	34
48	t	126/126 (100%)	115 (91%)	11 (9%)	9	30
49	F	307/307 (100%)	295 (96%)	12 (4%)	28	63
50	Q	164/165 (99%)	162 (99%)	2 (1%)	63	86
51	ZZ	61/61 (100%)	58 (95%)	3 (5%)	22	54
52	EE	99/99 (100%)	96 (97%)	3 (3%)	36	70
53	TT	66/66 (100%)	63 (96%)	3 (4%)	24	58
54	S5	158/161 (98%)	150 (95%)	8 (5%)	21	53
55	WW	55/55 (100%)	52 (94%)	3 (6%)	19	50
56	II	117/117 (100%)	112 (96%)	5 (4%)	26	60
57	CC	87/87 (100%)	84 (97%)	3 (3%)	32	66
58	AA	272/272 (100%)	263 (97%)	9 (3%)	33	67
59	OO	92/92 (100%)	86 (94%)	6 (6%)	15	44
60	MM	111/111 (100%)	108 (97%)	3 (3%)	39	73
61	LL	125/125 (100%)	117 (94%)	8 (6%)	16	44
62	XX	48/48 (100%)	47 (98%)	1 (2%)	47	77
63	RR	113/115 (98%)	108 (96%)	5 (4%)	25	59
64	SS	107/107 (100%)	100 (94%)	7 (6%)	15	44
65	S6	207/207 (100%)	201 (97%)	6 (3%)	37	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	S4	224/224 (100%)	220 (98%)	4 (2%)	51	80
67	S9	161/161 (100%)	153 (95%)	8 (5%)	22	53
68	S7	165/169 (98%)	159 (96%)	6 (4%)	31	65
69	YY	46/46 (100%)	44 (96%)	2 (4%)	26	60
70	S3	177/177 (100%)	162 (92%)	15 (8%)	10	31
71	RS	119/119 (100%)	110 (92%)	9 (8%)	12	36
72	WX	112/112 (100%)	108 (96%)	4 (4%)	31	65
73	S8	178/178 (100%)	172 (97%)	6 (3%)	32	66
74	W	86/100 (86%)	82 (95%)	4 (5%)	23	56
75	GG	105/106 (99%)	101 (96%)	4 (4%)	29	64
76	UU	88/88 (100%)	86 (98%)	2 (2%)	44	76
77	11	143/143 (100%)	139 (97%)	4 (3%)	38	72
78	L9	169/169 (100%)	160 (95%)	9 (5%)	20	52
80	v	705/728 (97%)	664 (94%)	41 (6%)	18	49
81	LA	45/948 (5%)	41 (91%)	4 (9%)	9	28
82	CE	62/190 (33%)	59 (95%)	3 (5%)	23	55
83	A	107/107 (100%)	96 (90%)	11 (10%)	7	23
86	23	106/107 (99%)	103 (97%)	3 (3%)	38	72
All	All	11150/12382 (90%)	10678 (96%)	472 (4%)	28	60

5 of 472 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	s	158	VAL
80	v	675	ILE
57	CC	32	HIS
80	v	480	VAL
77	11	67	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 141 such sidechains are listed below:

Mol	Chain	Res	Type
67	S9	113	GLN
68	S7	193	GLN
78	L9	140	GLN

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Mol	Chain	Res	Type
22	21	98	HIS
21	20	156	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	58	149/156 (95%)	20 (13%)	1 (0%)
6	6	119/120 (99%)	9 (7%)	0
79	18	1675/1688 (99%)	300 (17%)	14 (0%)
84	ES	34/5070 (0%)	7 (20%)	1 (2%)
85	28	3479/4808 (72%)	581 (16%)	48 (1%)
All	All	5456/11842 (46%)	917 (16%)	64 (1%)

5 of 917 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	58	2	G
5	58	34	U
5	58	35	C
5	58	59	A
5	58	62	A

5 of 64 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	28	4232	U
85	28	4699	U
85	28	275	C
85	28	265	C
85	28	4884	G

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

1 non-standard protein/DNA/RNA residue is 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
80	DDE	v	715	80	18,20,21	1.03	1 (5%)	17,28,30	0.85	1 (5%)

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
80	DDE	v	715	80	-	9/20/21/23	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
80	v	715	DDE	CD2-CG	2.57	1.41	1.36

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	v	715	DDE	CAU-CBW-CBI	-2.29	106.75	111.22

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
80	v	715	DDE	C-CA-CB-CG
80	v	715	DDE	NAD-CBI-CBW-CAU
80	v	715	DDE	CAT-CAU-CBW-CBI
80	v	715	DDE	CAT-CAU-CBW-NCB
80	v	715	DDE	OAG-CBI-CBW-CAU

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	GDP	v	900	-	29,30,30	3.49	12 (41%)	45,47,47	1.89	12 (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
88	GDP	v	900	-	-	0/16/32/32	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	v	900	GDP	O6-C6	9.57	1.41	1.23
88	v	900	GDP	C2'-C3'	-8.18	1.31	1.53
88	v	900	GDP	O4'-C4'	-6.89	1.29	1.45
88	v	900	GDP	O4'-C1'	5.72	1.55	1.42
88	v	900	GDP	C2-N2	4.69	1.45	1.34

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	v	900	GDP	C5-C4-N3	-6.03	118.79	128.39
88	v	900	GDP	C2-N3-C4	5.04	120.98	112.30
88	v	900	GDP	N9-C4-N3	4.17	134.29	125.95
88	v	900	GDP	C8-N7-C5	2.92	109.46	104.26
88	v	900	GDP	C4-C5-N7	-2.91	106.06	110.67

There are no chirality outliers.

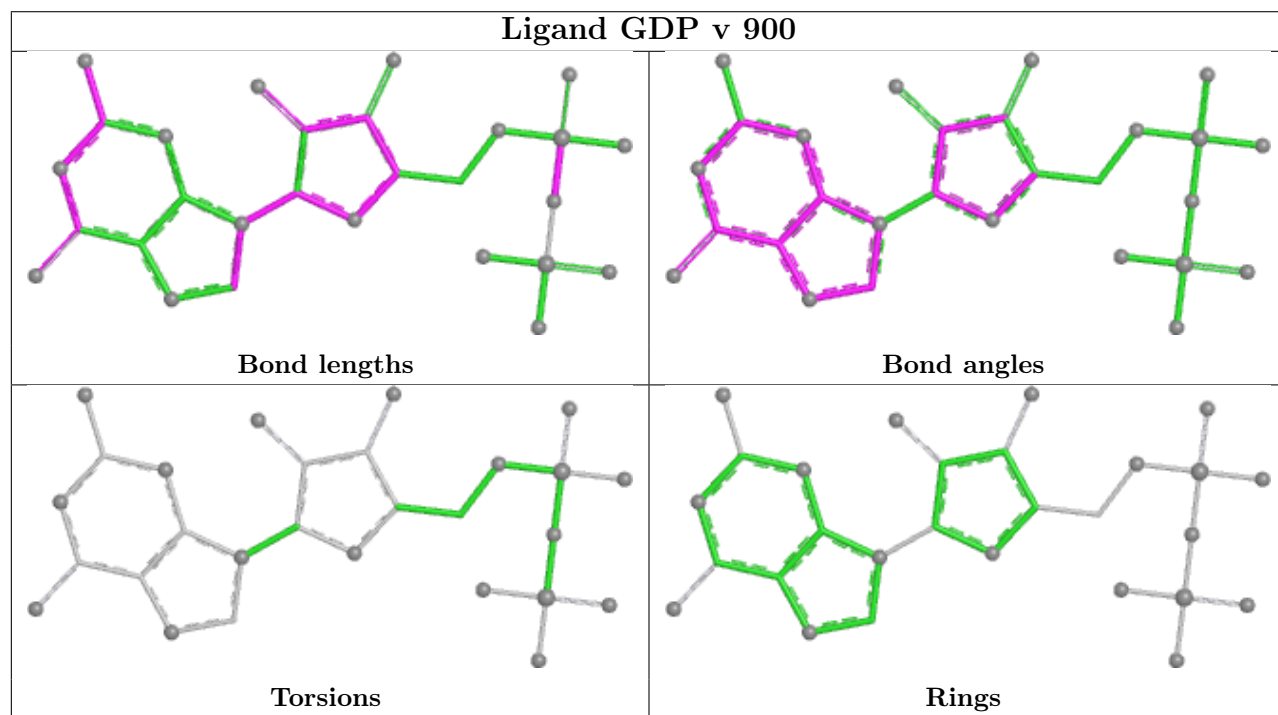
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	v	900	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
79	18	12

The worst 5 of 12 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	18	756:C	O3'	788:G	P	20.22
1	18	697:G	O3'	729:C	P	19.25
1	18	1417:C	O3'	1423:C	P	17.97
1	18	321:C	O3'	329:G	P	16.66
1	18	1759:G	O3'	1773:C	P	16.39

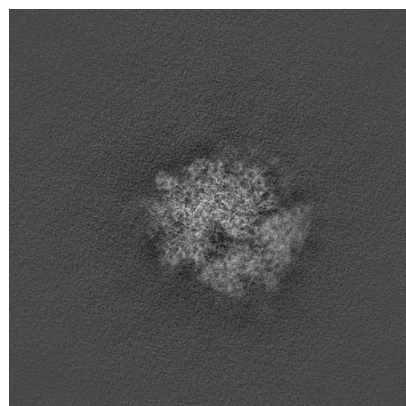
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75689. These allow visual inspection of the internal detail of the map and identification of artifacts.

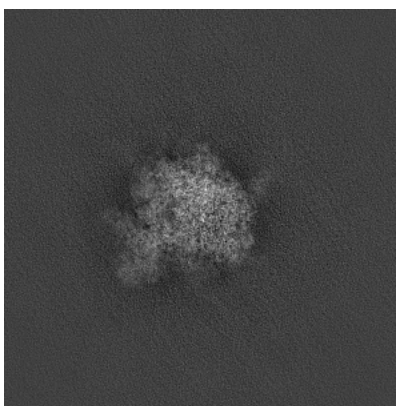
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

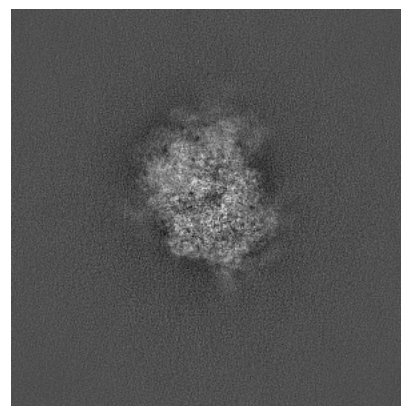
6.1.1 Primary map



X

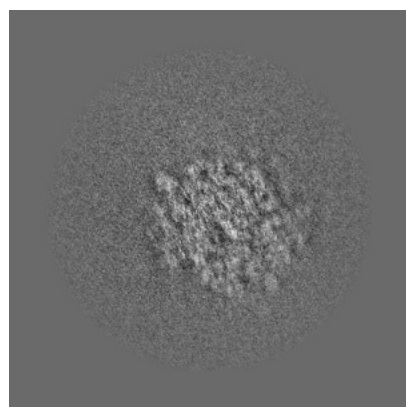


Y

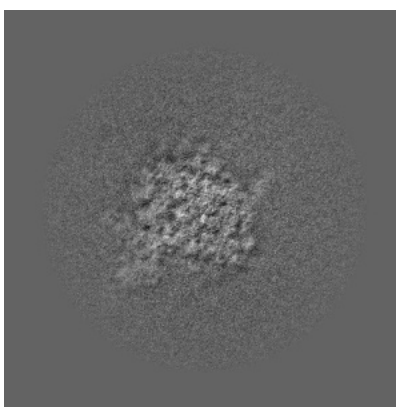


Z

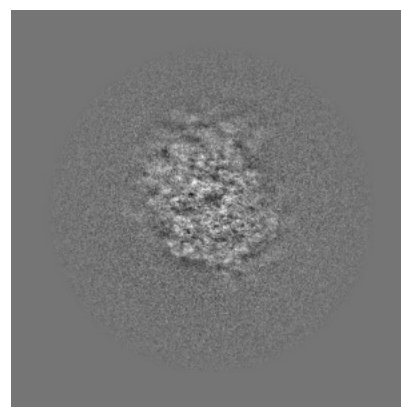
6.1.2 Raw map



X



Y

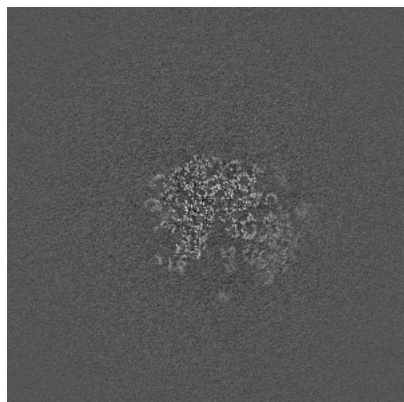


Z

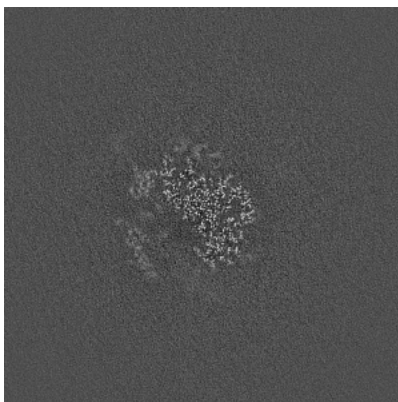
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

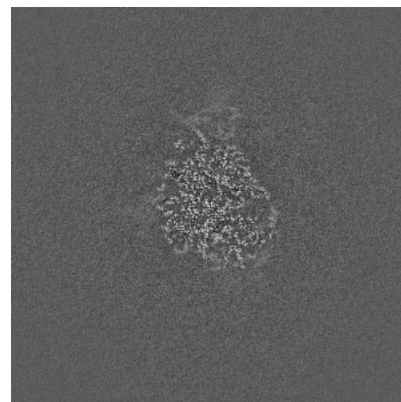
6.2.1 Primary map



X Index: 400

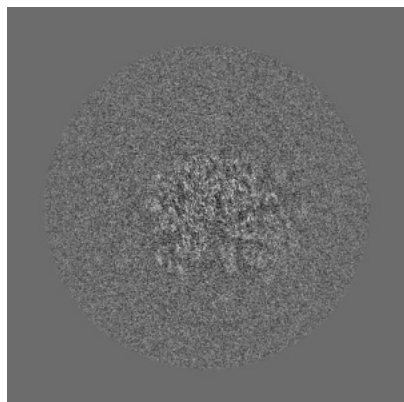


Y Index: 400

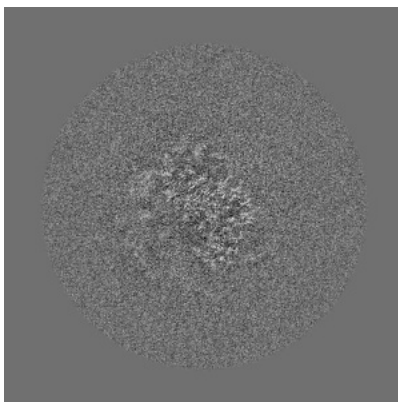


Z Index: 400

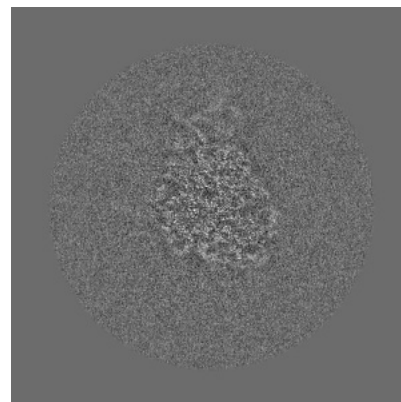
6.2.2 Raw map



X Index: 400



Y Index: 400

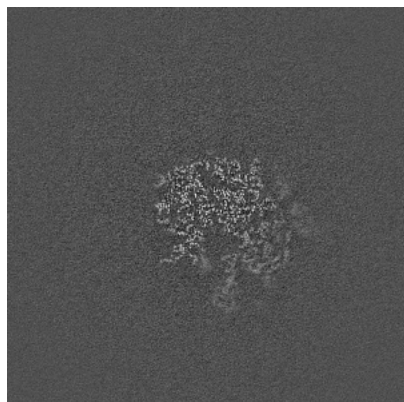


Z Index: 400

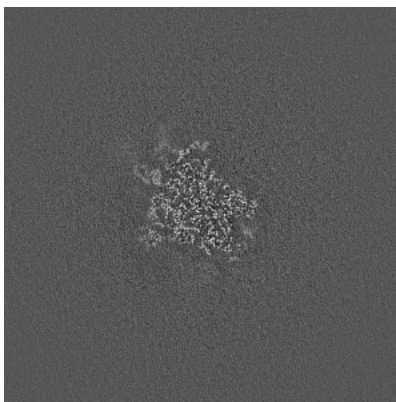
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

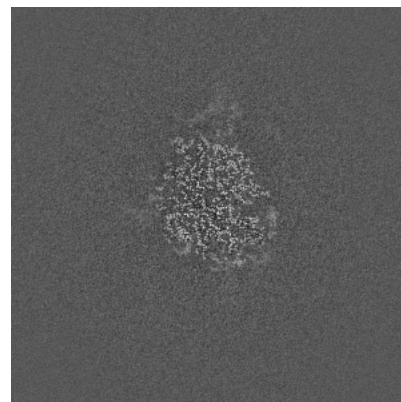
6.3.1 Primary map



X Index: 385

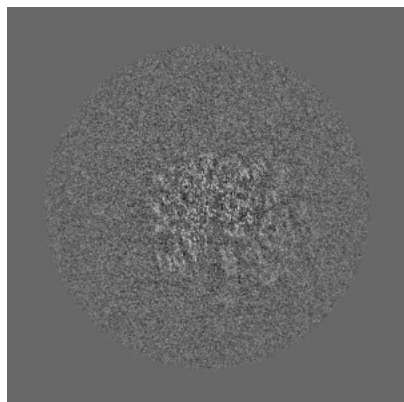


Y Index: 376

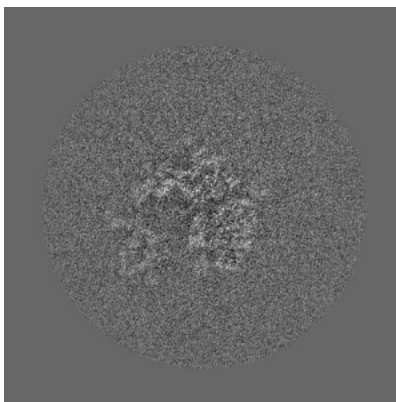


Z Index: 403

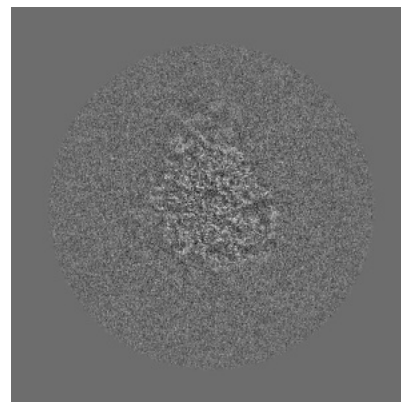
6.3.2 Raw map



X Index: 396



Y Index: 420

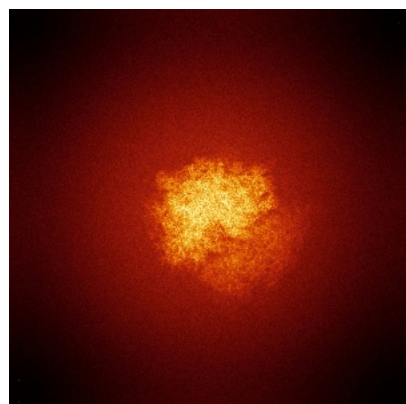


Z Index: 402

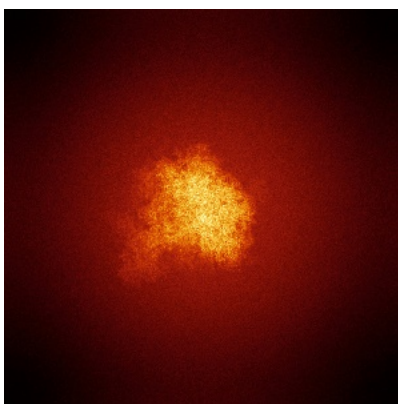
The images above show the largest variance slices of the map in three orthogonal directions.

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

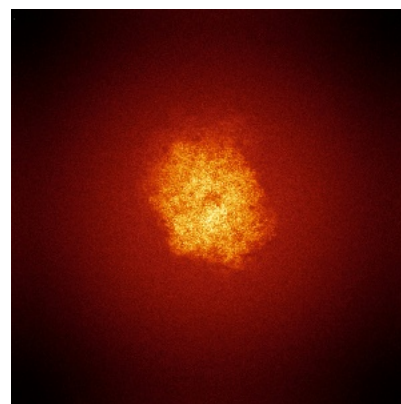
6.4.1 Primary map



X

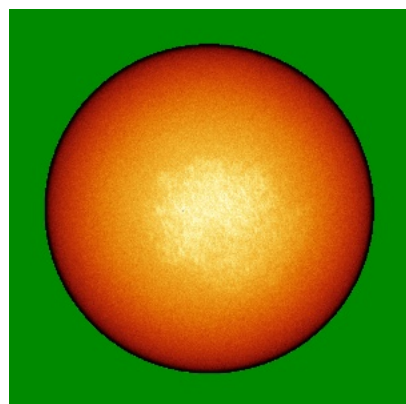


Y

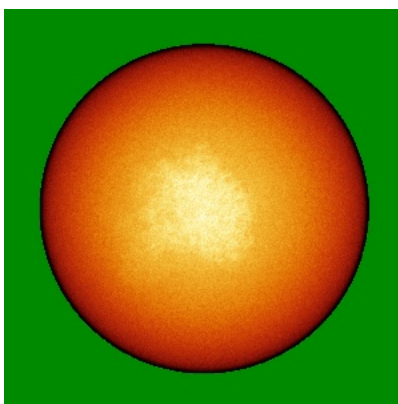


Z

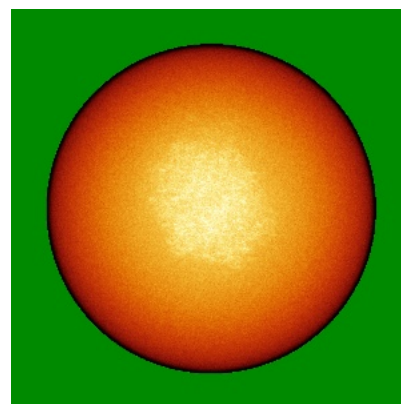
6.4.2 Raw map



X



Y

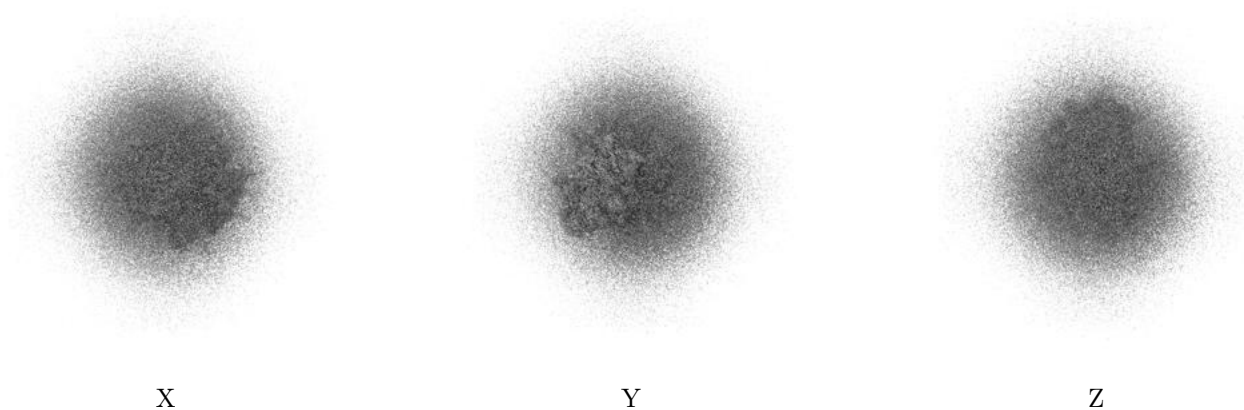


Z

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.

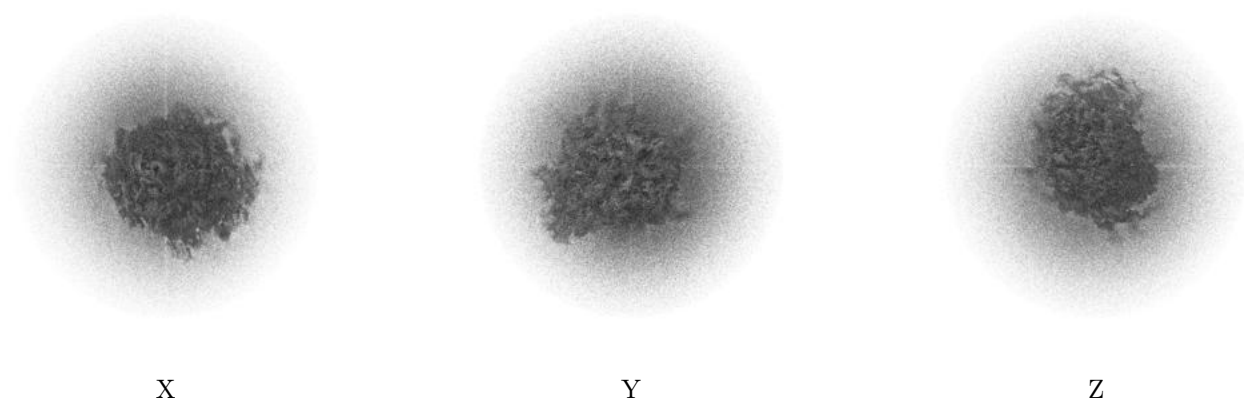
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

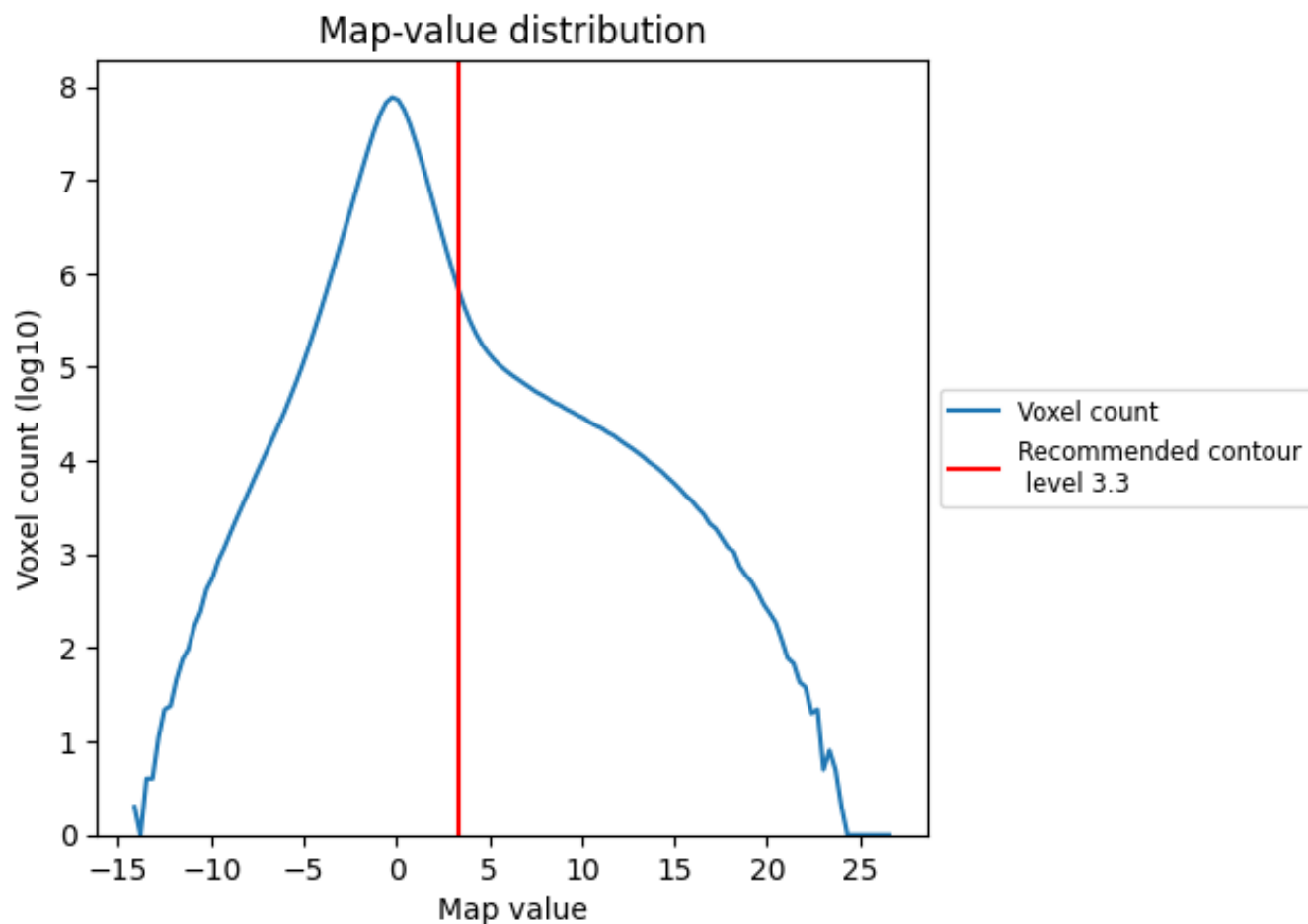
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

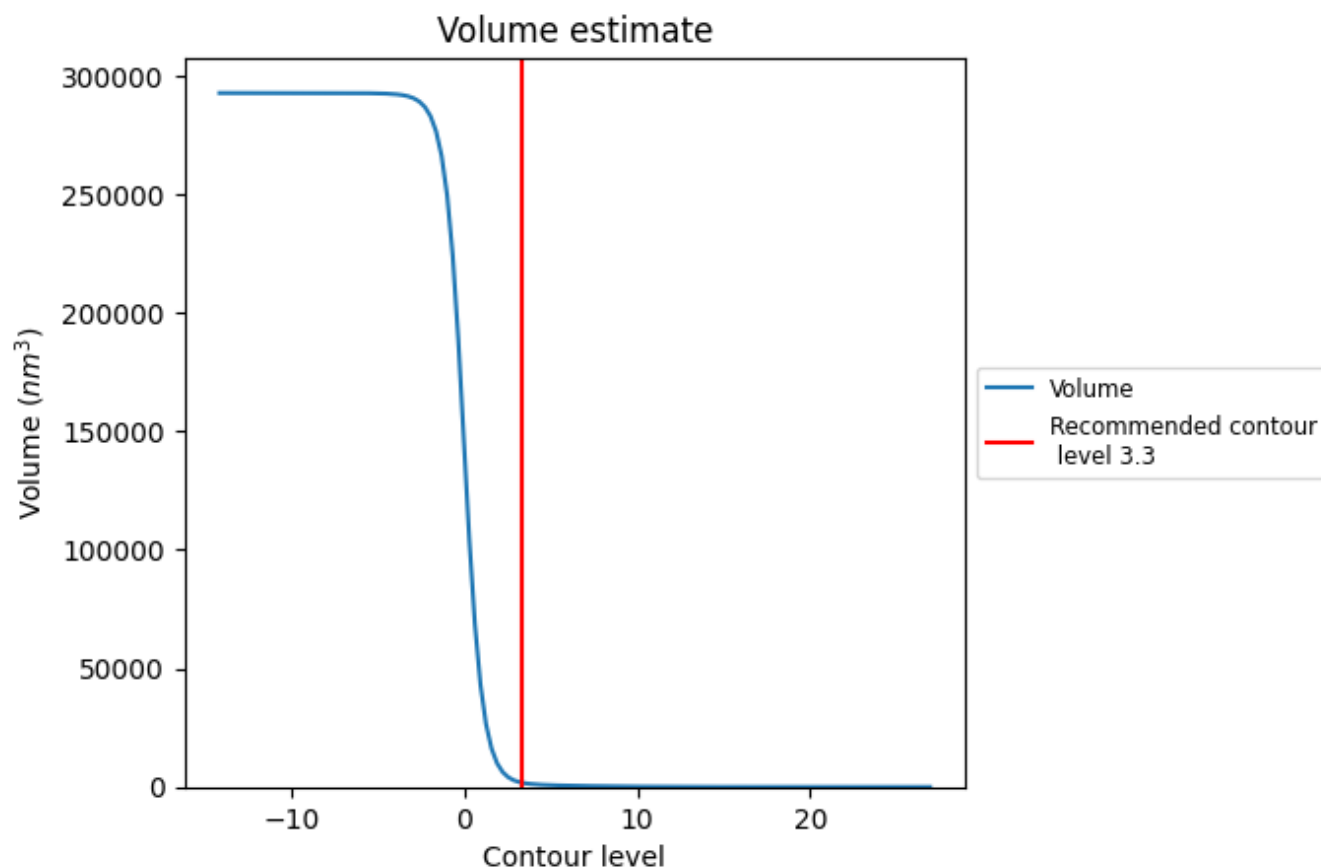
This section contains the results of statistical analysis of the map.

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.

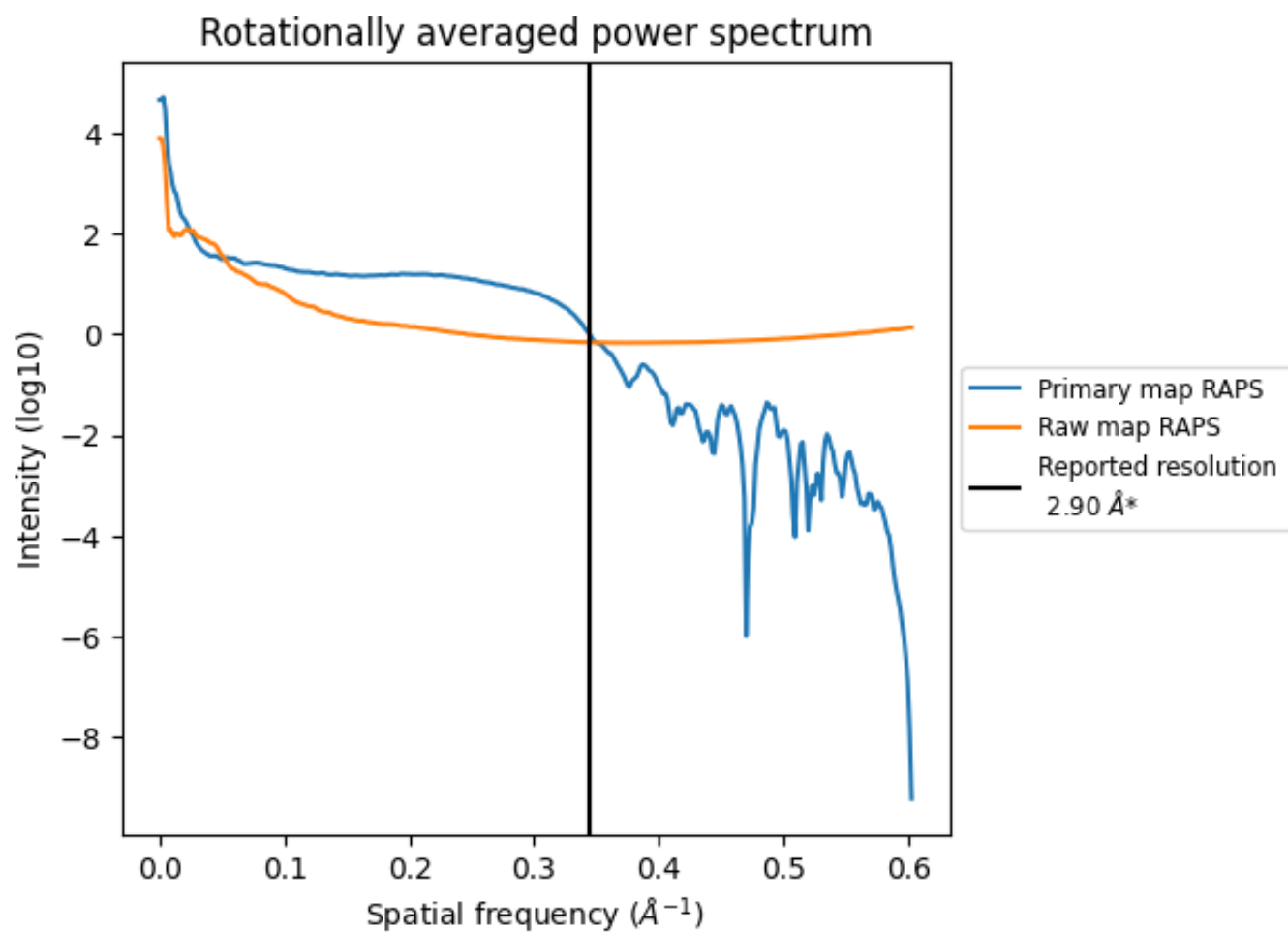
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1898 nm³; this corresponds to an approximate mass of 1715 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 ⓘ

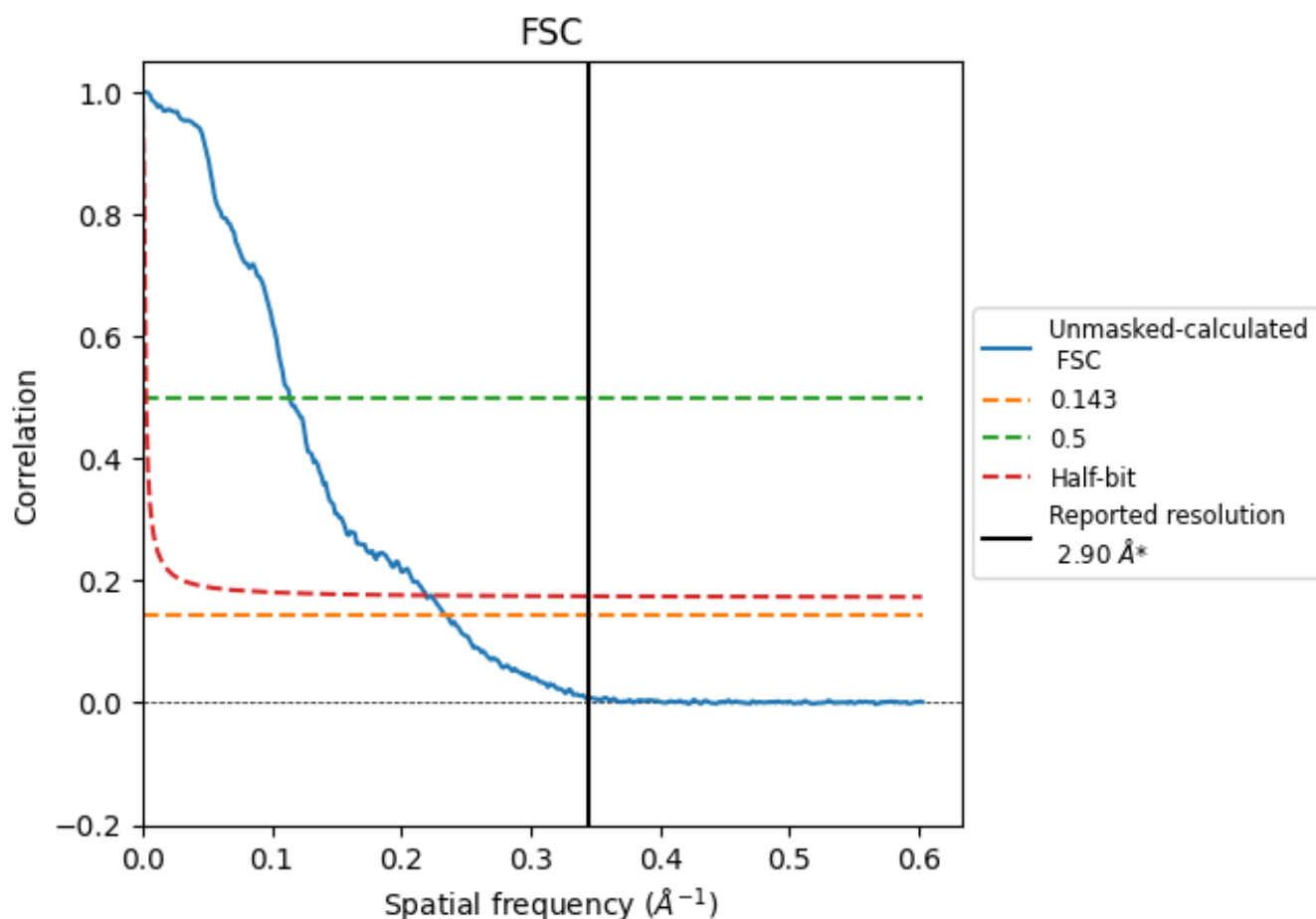


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

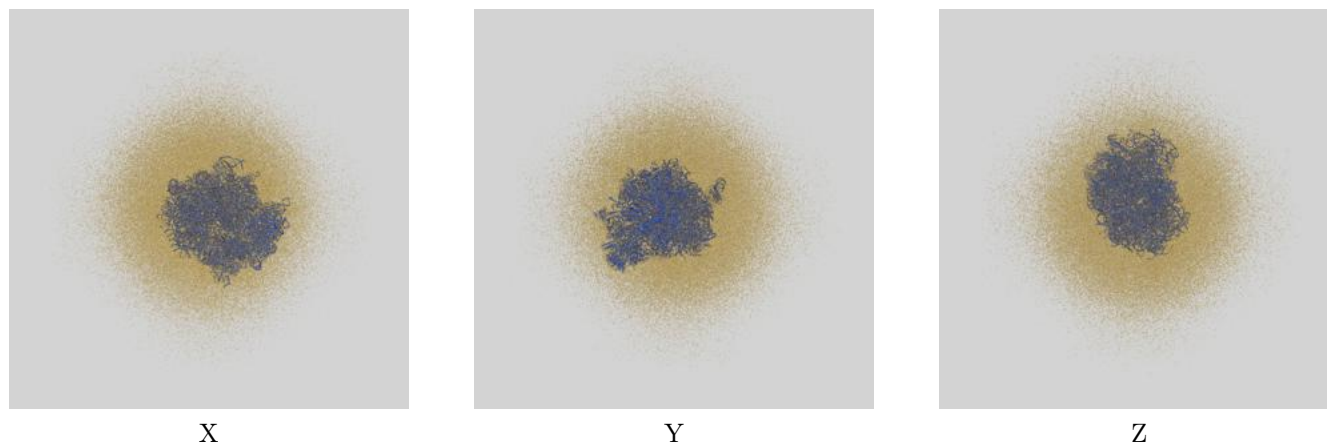
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.25	8.78	4.56

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.25 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

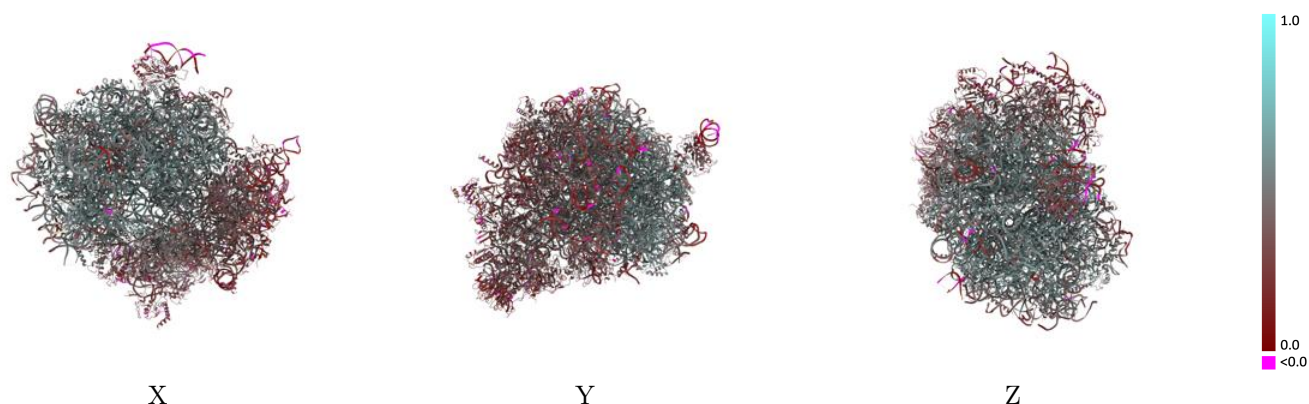
This section contains information regarding the fit between EMDB map EMD-75689 and PDB model 11HG. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



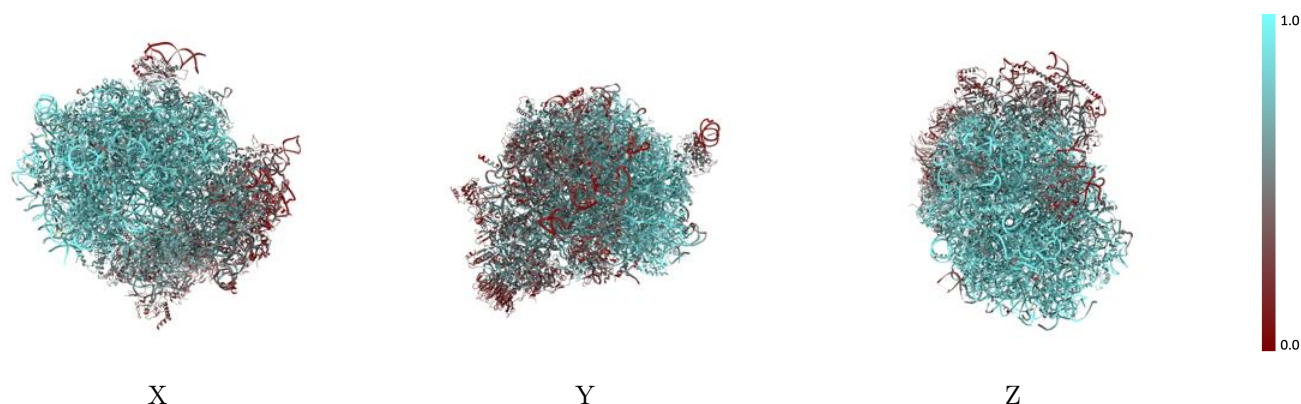
The images above show the 3D surface view of the map at the recommended contour level 3.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



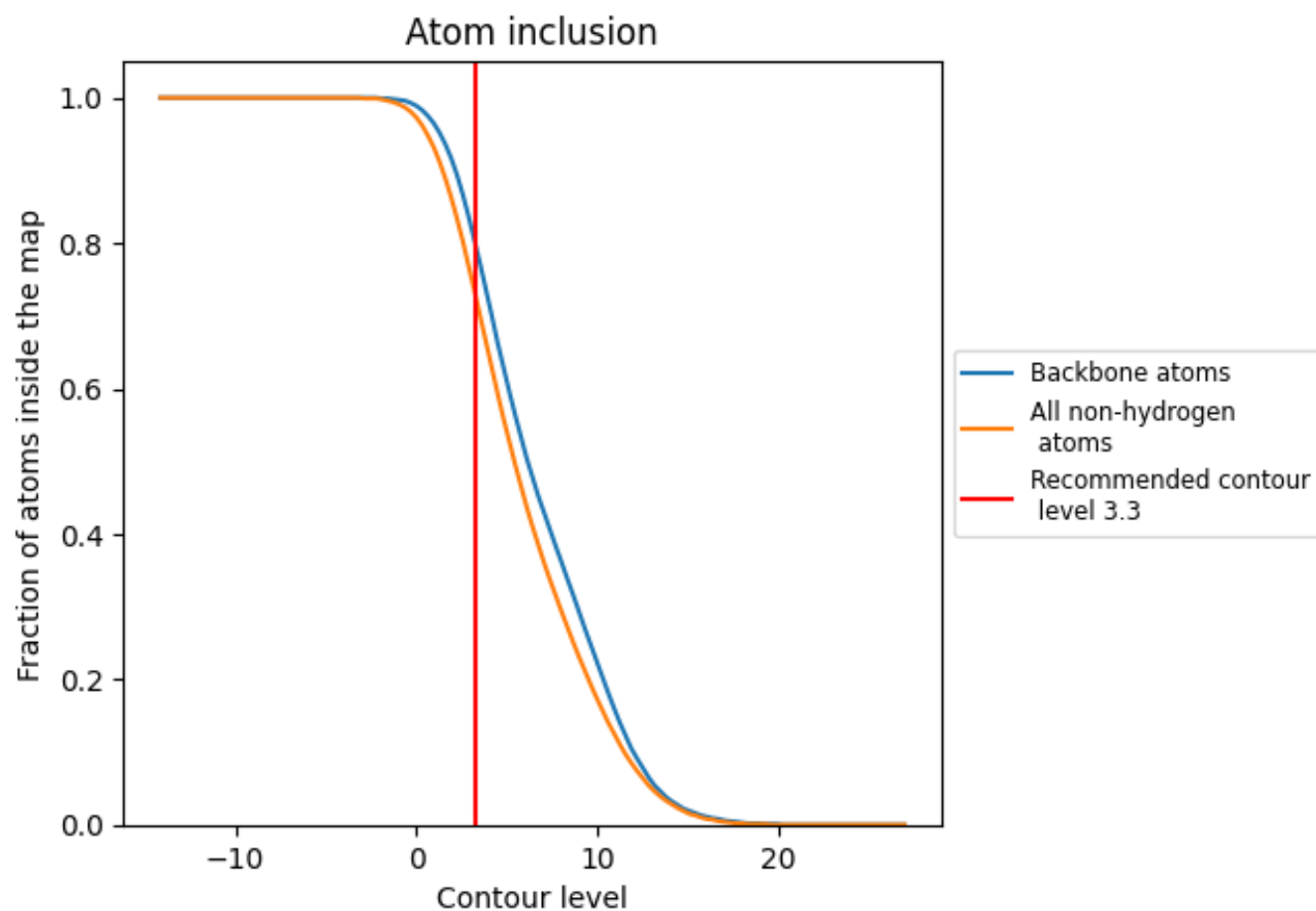
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 72% 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 (3.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7230	 0.4420
10	 0.8140	 0.5240
11	 0.7250	 0.4540
13	 0.8000	 0.5120
14	 0.8250	 0.5140
15	 0.8640	 0.5650
17	 0.8380	 0.5420
18	 0.6610	 0.3730
19	 0.7440	 0.4780
20	 0.8520	 0.5420
21	 0.8160	 0.5180
22	 0.6880	 0.4230
23	 0.7780	 0.5200
26	 0.8120	 0.5180
27	 0.8040	 0.5130
28	 0.8810	 0.5040
29	 0.7470	 0.4800
30	 0.7750	 0.5000
31	 0.7880	 0.4920
32	 0.8610	 0.5550
34	 0.7950	 0.5160
35	 0.7850	 0.5110
36	 0.8140	 0.5100
37	 0.8650	 0.5570
38	 0.7200	 0.4570
39	 0.8240	 0.5260
40	 0.7850	 0.5060
41	 0.7250	 0.4510
42	 0.7880	 0.5150
58	 0.8940	 0.5170
6	 0.9330	 0.5430
A	 0.5330	 0.3280
AA	 0.2430	 0.2290
AS	 0.4930	 0.3670
BB	 0.4030	 0.3340



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Chain	Atom inclusion	Q-score
CC	0.4730	0.3120
CE	0.3390	0.2980
DD	0.4610	0.3730
EE	0.2460	0.2150
ES	0.1350	0.0620
F	0.4420	0.3130
FF	0.4890	0.3710
GG	0.5780	0.3760
II	0.4330	0.3240
L3	0.8210	0.5340
L4	0.8560	0.5420
L5	0.8010	0.4940
L6	0.8140	0.5000
L7	0.8310	0.5440
L8	0.8390	0.5540
L9	0.7890	0.5050
LA	0.3300	0.2710
LL	0.4910	0.3030
MM	0.4490	0.3120
OO	0.4160	0.3240
PP	0.3760	0.2930
Q	0.8580	0.5540
RR	0.5270	0.3710
RS	0.3830	0.3070
S2	0.4600	0.3460
S3	0.4530	0.3200
S4	0.3340	0.2970
S5	0.4600	0.3230
S6	0.3410	0.2710
S7	0.3210	0.2960
S8	0.4190	0.3440
S9	0.3690	0.3000
SS	0.3050	0.2670
TT	0.3840	0.2960
UU	0.5430	0.3760
VV	0.3870	0.3380
W	0.5580	0.3860
WW	0.4210	0.3170
WX	0.4450	0.3590
XX	0.5740	0.3960
YY	0.3500	0.2870
ZZ	0.2830	0.2210

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Chain	Atom inclusion	Q-score
aa	 0.7630	 0.4810
bb	 0.8520	 0.5370
cc	 0.7960	 0.5150
dd	 0.8530	 0.5580
ee	 0.8400	 0.5460
ff	 0.7950	 0.5120
gg	 0.8340	 0.5330
s	 0.5250	 0.3450
t	 0.3210	 0.2140
v	 0.5600	 0.3700