



wwPDB EM Validation Summary Report ⓘ

Sep 23, 2026 – 06:41 pm BST

PDB ID : 9T6I / pdb_00009t6i
EMDB ID : EMD-55616
Title : In vitro reconstituted METAP1-NAA40-NAC bound 80S - State 2
Authors : Guan, D.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-11-07
Resolution : 3.44 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev133
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) : 2.50

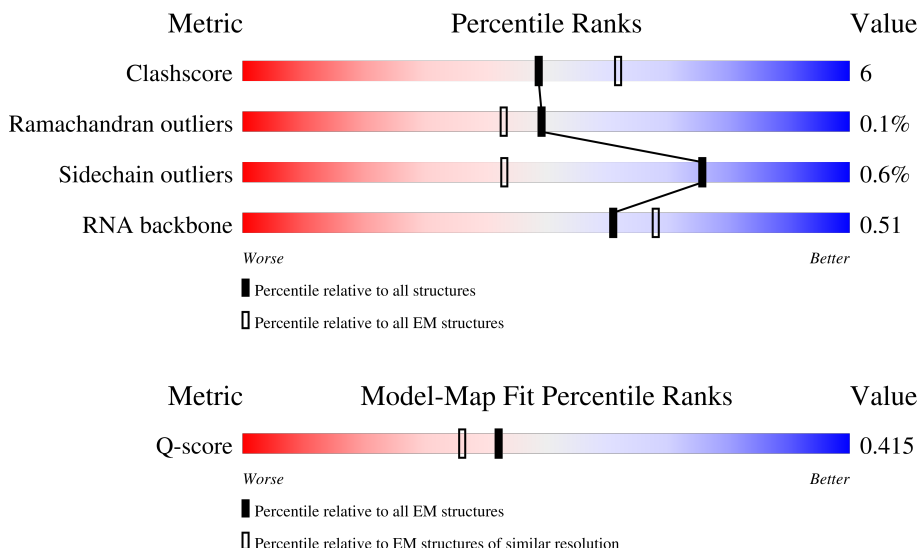
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.44 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.



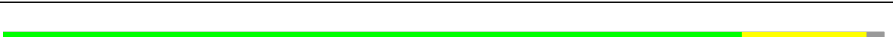
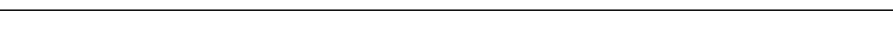
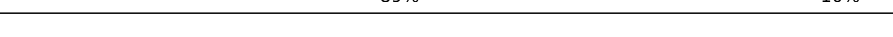
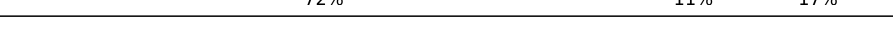
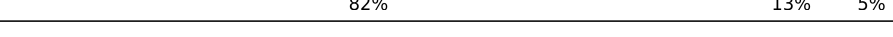
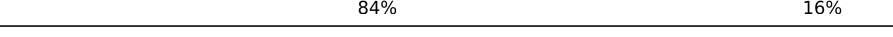
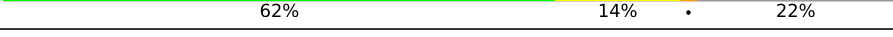
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13877 (2.94 - 3.94)

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	L5	5070	
2	L7	121	
3	L8	157	

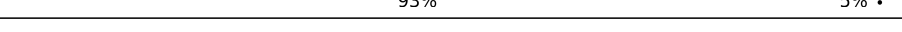
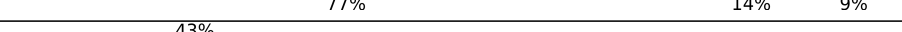
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

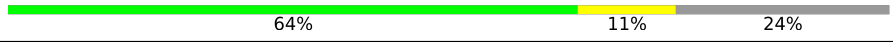
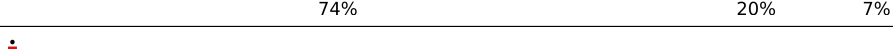
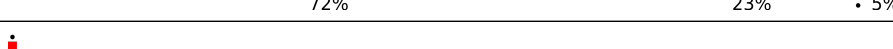
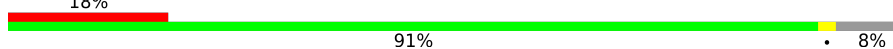
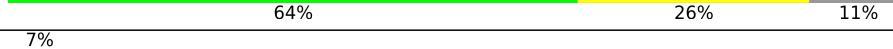
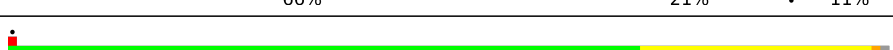
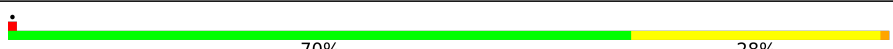
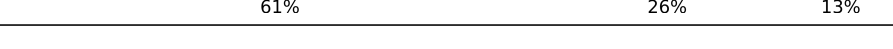
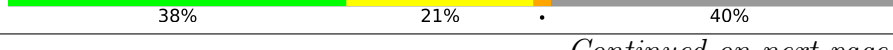
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Ls	317	
47	Lt	165	
48	MA	386	
49	N4	237	
50	NA	215	
51	NB	162	
52	S2	1869	
53	SA	295	

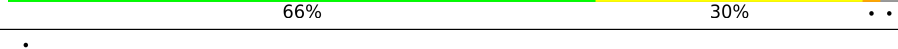
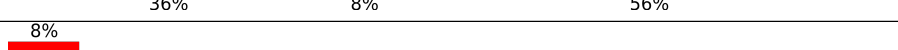
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	SB	264	
55	SC	293	
56	SD	243	
57	SE	263	
58	SF	204	
59	SG	249	
60	SH	194	
61	SI	208	
62	SJ	194	
63	SK	165	
64	SL	158	
65	SM	132	
66	SN	151	
67	SO	151	
68	SP	145	
69	SQ	146	
70	SR	135	
71	SS	152	
72	ST	145	
73	SU	119	
74	SV	83	
75	SW	130	
76	SX	143	
77	SY	133	
78	SZ	125	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	Sa	115	
80	Sb	84	
81	Sc	69	
82	Sd	56	
83	Se	133	
84	Sf	156	
85	Sg	317	

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 221549 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 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3670	Total	C	N	O	P	0	0
			78678	35036	14400	25573	3669		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	2113	C	G	conflict	GB 86475748

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called 60S ribosomal protein L8.

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

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	365	Total	C	N	O	S	0	0
			2908	1829	580	486	13		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	221	Total	C	N	O	S	0	0
			1774	1142	336	292	4		

- Molecule 9 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	202	Total	C	N	O	S	0	0
			1639	1041	316	269	13		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	171	Total	C	N	O	S	0	0
			1371	867	256	242	6		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	207	Total	C	N	O	S	0	0
			1673	1046	346	277	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

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

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

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

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

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	100	Total	C	N	O	S	0	0
			816	524	142	148	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	133	Total	C	N	O	S	0	0
			1106	694	224	185	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	109	Total	C	N	O	S	0	0
			882	549	192	137	4		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 32 is a protein called 60S ribosomal protein L31.

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

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called 60S ribosomal protein L34.

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

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

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

- Molecule 45 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 47 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 48 is a protein called Methionine aminopeptidase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	MA	315	Total	C	N	O	S	0	0
			2485	1562	443	462	18		

- Molecule 49 is a protein called N-alpha-acetyltransferase 40.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	N4	223	Total	C	N	O	S	0	0
			1809	1136	317	341	15		

- Molecule 50 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	NA	108	Total	C	N	O	S	0	0
			841	524	153	160	4		

- Molecule 51 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	NB	106	Total	C	N	O	S	0	0
			821	514	153	151	3		

- Molecule 52 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S2	1719	Total	C	N	O	P	0	0
			36456	16264	6516	11958	1718		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S2	582	C	U	conflict	GB 36162
S2	583	C	A	conflict	GB 36162
S2	584	G	A	conflict	GB 36162
S2	798	A	G	conflict	GB 36162
S2	1095	U	C	conflict	GB 36162

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 54 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SB	221	Total	C	N	O	S	0	0
			1791	1135	323	319	14		

- Molecule 55 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 56 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 57 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 58 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SF	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 59 is a protein called 40S ribosomal protein S6.

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

- Molecule 60 is a protein called 40S ribosomal protein S7.

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

- Molecule 61 is a protein called 40S ribosomal protein S8.

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

- Molecule 62 is a protein called 40S ribosomal protein S9.

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

- Molecule 63 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SK	95	Total	C	N	O	S	0	0
			799	524	139	130	6		

- Molecule 64 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SL	144	Total	C	N	O	S	0	0
			1182	752	224	200	6		

- Molecule 65 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	SM	122	Total	C	N	O	0	0
			604	359	122	123		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P25398
SM	69	LEU	CYS	conflict	UNP P25398
SM	99	ASN	LYS	conflict	UNP P25398

- Molecule 66 is a protein called 40S ribosomal protein S13.

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

- Molecule 67 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SO	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 68 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SP	129	Total	C	N	O	S	0	0
			1061	672	202	180	7		

- Molecule 69 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 70 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 71 is a protein called 40S ribosomal protein S18.

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

- Molecule 72 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 73 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 74 is a protein called 40S ribosomal protein S21.

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

- Molecule 75 is a protein called 40S ribosomal protein S15a.

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

- Molecule 76 is a protein called 40S ribosomal protein S23.

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

- Molecule 77 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SY	126	Total	C	N	O	S	0	0
			1027	648	201	173	5		

- Molecule 78 is a protein called 40S ribosomal protein S25.

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

- Molecule 79 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 80 is a protein called 40S ribosomal protein S27.

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

- Molecule 81 is a protein called 40S ribosomal protein S28.

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

- Molecule 82 is a protein called 40S ribosomal protein S29.

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

- Molecule 83 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 84 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 85 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	L5	213	Total	Mg	0
			213	213	
86	L7	3	Total	Mg	0
			3	3	
86	L8	4	Total	Mg	0
			4	4	
86	LA	1	Total	Mg	0
			1	1	
86	LI	1	Total	Mg	0
			1	1	
86	LP	1	Total	Mg	0
			1	1	

Continued on next page...

Continued from previous page...

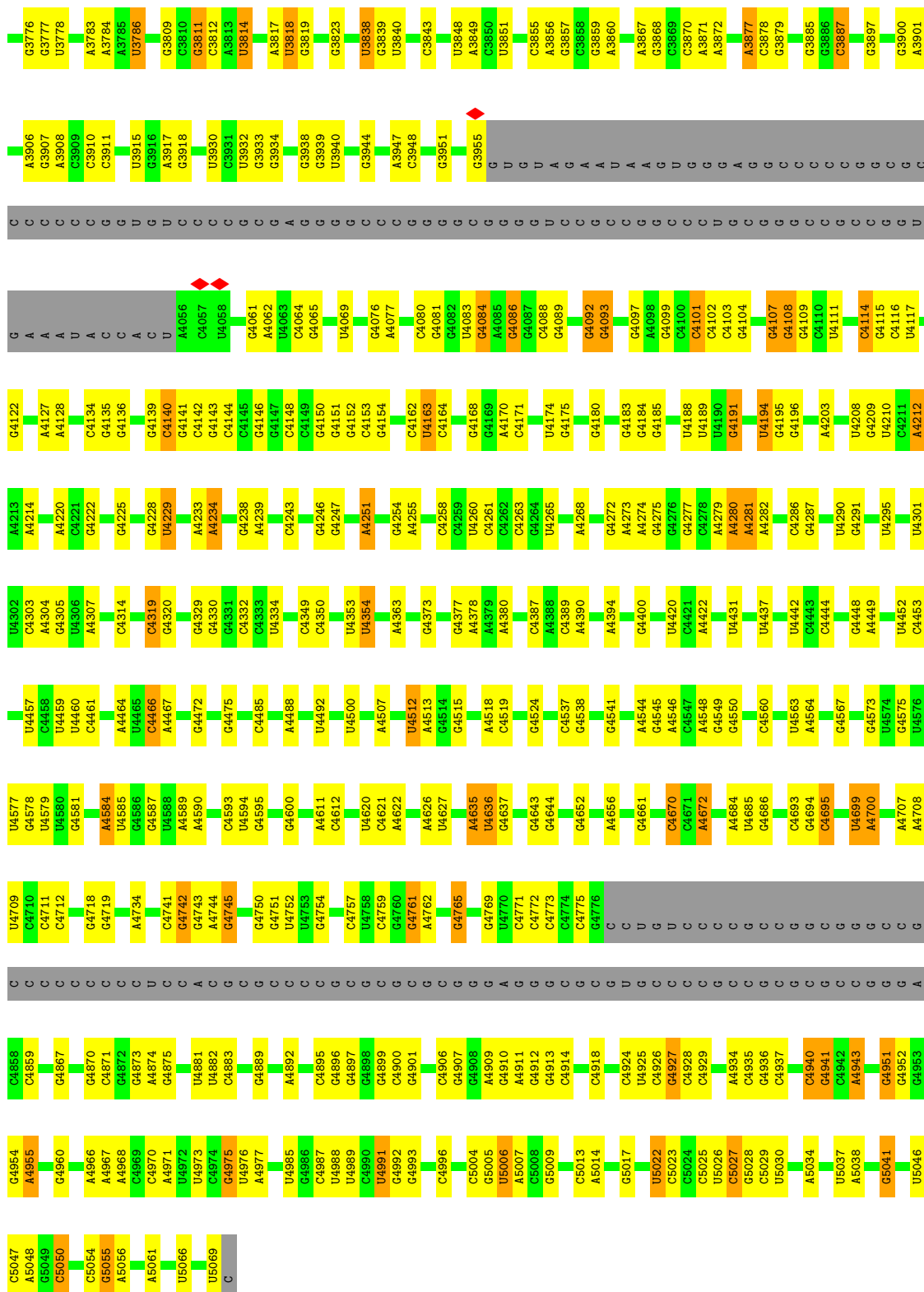
Mol	Chain	Residues	Atoms		AltConf
86	LV	1	Total 1	Mg 1	0
86	Le	1	Total 1	Mg 1	0
86	Lj	1	Total 1	Mg 1	0
86	S2	31	Total 31	Mg 31	0

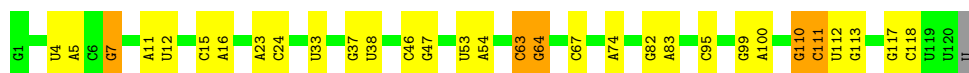
- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	Lg	1	Total 1	Zn 1	0
87	Lj	1	Total 1	Zn 1	0
87	Lm	1	Total 1	Zn 1	0
87	Lo	1	Total 1	Zn 1	0
87	Lp	1	Total 1	Zn 1	0
87	Sa	1	Total 1	Zn 1	0
87	Sd	1	Total 1	Zn 1	0
87	Sf	1	Total 1	Zn 1	0

G2099	G1995	G1910	C1768	U1683	A1558	C1447	C1340	U	G1098	G	A956
G2102	C1996	C1914	G1769	A1684	G1559	G1448	U1341	C	C1099	G	G959
G2103	A1997	U1770	A1771	G1685	A1563	G1449	C1344	U	U1100	G	A960
G2112	A1999	U1918	C1778	U1687	A1565	G1457	C1345	G	C	G	G961
G2113	G2000	G1919	A1787	G1688	C1566	C1460	G1347	G1234	C	U	G962
G	A2001	C1920	A1788	C1694	G1573	C1461	A1364	G	C	U	G963
G	G2002	C1921	A1789	C1695	G1574	C1462	A1365	G	C	U	A964
G	U2004	G1922	C1789	A1699	G1577	C1463	G1368	C1239	C	U	G965
G	A2017	G1925	A1802	A1700	G1578	C1472	G1369	G1245	C	U	A966
G	C2018	C1931	G1803	A1701	U1578	C1473	G1359	G1246	C	U	C967
G	G2019	A1932	A1804	C1702	U1591	C1478	U1364	C1252	C	U	C968
G	U2020	G1933	C1814	C1703	U1596	G1479	C1365	G1253	C	U	C969
G	G2021	A1934	G1815	G1704	U1596	C1480	G1366	A1254	C	U	U971
G	G2024	G1935	G1818	A1706	U1597	C1481	C1367	A1255	C	U	C972
G	A2025	C1936	G1819	C1707	G1604	G1482	A1368	G1262	C	U	G973
G	G2026	U1942	G1820	A1708	G1605	C1483	C1379	G1263	C	U	C974
G	A2033	A1943	G1821	C	G1612	G1487	G1383	G1266	C	U	C975
G	G2034	U1947	U1822	C	A1613	C1497	C1384	C1267	C	U	G976
G	A2040	G1948	G1823	C	G1617	G1495	G1385	G1271	C	U	C977
G	U2044	U1949	A1825	C	G1618	G1496	A1387	G1272	C	U	U982
G	G2045	U1950	G1834	G1715	G1619	G1497	G1388	G1273	C	U	C988
G	G2046	G1951	G1835	G1716	G1620	G1498	G1389	G1274	C	U	U989
G	A2047	G1952	G1836	A1719	G1624	G1499	A1391	C1280	C	U	C990
G	U2048	U1959	A1837	G1724	G1625	A1500	A1392	G1284	C	U	C991
G	G2052	A1960	G1842	U1725	G1629	G1501	G1393	G1287	C	U	G992
G	G2055	U1962	C1847	U1726	A1630	G1502	G1394	G1288	C	U	G993
G	G2056	G1969	C1848	G1731	A1631	G1503	A1397	G1290	C	U	G994
G	G2065	G1972	U1849	G1732	A1632	G1504	A1398	G1291	C	U	C995
G	A2069	U1973	A1850	G1733	A1634	G1509	G1405	G1292	C	U	C
G	G2076	G1975	G1855	G1734	A1637	G1510	G1406	G1293	C	U	C
G	G2077	G1976	G1856	A1742	C1640	U1511	C1407	A1294	C	U	C
G	C1978	C1977	U1866	A1743	G1641	U1512	G1408	G1296	C	U	A
G	U1979	U1980	G1869	A1749	C1645	U1513	U1409	G1301	C	U	C
G	U1980	G1981	U1876	G1750	A1646	U1514	U1410	U1302	C	U	C
G	G1982	G1983	G1877	U1754	G1647	G1515	G1414	C1306	C	U	G
G	A1983	A1984	U1882	C1755	A1650	G1516	G1415	A1307	C	U	C
G	G1984	G1985	A1888	U1756	G1654	A1517	G1416	C1308	C	U	C
G	U1985	U1986	A1889	U1757	C1655	A1518	C1417	C1309	C	U	G
G	G1987	C1987	A1891	G1758	C1661	A1523	A1420	A1326	C	U	A
G	G1988	G1989	A1896	G1759	C1662	G1534	C1431	C1327	C	U	A
G	A1989	A1990	C1762	G1760	C1663	C1541	A1432	G1328	C	U	U
G	U1990	U1991	G1764	G1761	C1664	U1542	A1433	G1220	C	U	C
G	A1992	C1992	C1765	C1762	A1669	G1543	G1434	G1221	C	U	C
G	G2095	G2096	G1766	A1767	C1676	A1547	U1438	A1332	C	U	C
G	U2097	C1993	A1766	A1767	U1677	G1548	C1442	A1337	C	U	C
G	G2098	C1994	A1767	A1767	C1678	G1549	A1443	U1339	C	U	A

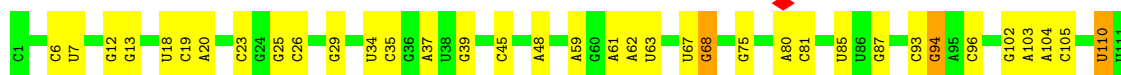
G3654	G	U2788	A2696	U2545	G2450	G2321	G
G3661	C	A2789	C2699	G2546	G2456	G2326	C
A3662	G	U2790	G2700	G2547	G2457	G2326	C
G3663	C	G2793	U2701	U2554	C2458	A	C
G3664	G	C2794	C2702	G2555	G2459	U2329	C
G3665	C	A2806	G2703	G2556	C2462	G2330	G
C3666	C	G2809	U2707	C2557	G2462	G2331	C
C3673	C	G2809	U2708	C2558	G2471	A2332	C
G3674	C	A2812	G2709	G2559	C2471	G2333	C
U3680	U	G2813	C2710	C2560	G2475	C2335	G
U3684	U	C2814	G2711	A2665	C2478	G2336	C
U3685	G	C2713	G2712	C2568	C2479	U	C
U3689	G	G2714	G2713	G2569	G2483	C	C
U3690	G	A2825	G2715	U2570	A2484	C	C
G3691	C	U2826	C2719	A2573	U2485	A2349	C
A3692	G	G2827	G2720	G2578	G2486	U2350	G
U3693	C	A2835	G2721	G2579	C2488	C2351	C
U3697	U	U2837	G2724	A2582	C2489	U2352	C
G3698	C	G2842	A2725	C2583	U2490	A2360	C
U3707	C	A2845	G2726	A2587	U2495	G2361	C
C3708	C	G2846	U2730	C2588	G2496	A2382	C
G3710	C	G2847	C2731	C2589	C2503	U2385	C
A3711	C	G2848	C2739	A2598	G2504	U2386	C
A3712	C	G2855	G2742	A2601	C2505	G2387	C
U3713	G	C2856	A2743	A2611	A2507	C2258	C
G3714	C	G2863	A2744	A2611	U2508	G2259	C
A3717	U	G2877	A2745	A2623	C2509	G2262	C
A3719	C	G2884	G2746	C2627	G2510	A2268	C
G3720	C	A2885	G2749	A2627	A2511	G2405	C
U3721	C	G2890	G2750	G2627	A2512	G2406	C
G3722	C	U2891	G2751	A2641	G2513	G2407	C
A3723	C	G2899	G2752	G2640	G2514	C2410	C
A3726	C	U2899	G2766	G2653	G2515	G2411	C
A3727	C	A2894	G2760	C2653	A2517	A2412	C
A3733	G	A2895	U2761	G2662	U2519	A2417	C
U3734	G	G2896	G2762	A2675	C2520	G2296	C
A3736	C	G2897	U2763	A2676	G2521	G2297	C
A3737	C	C2898	G2769	C2670	A2529	A2300	C
U3748	C	U2900	C2770	C2671	C2532	G2301	C
C3749	C	G2901	G2771	G2672	A2537	A2308	C
G3750	C	G2902	C2772	A2676	U2538	G2309	C
U3644	U	U2904	G2773	G2675	C2539	A2313	C
G3753	C	C2905	C2780	U2687	C2540	G2314	C
A3759	C	U2907	G2781	G2688	G2541	G2315	C
A3760	C	U2908	C2786	G2694	A2542	G2316	C
G3761	C	C2909	A2787	A2695	G2544	G2318	C





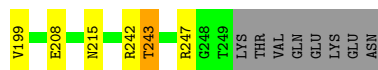
- Molecule 3: 5.8S rRNA

Chain L8: 66% 31%



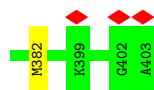
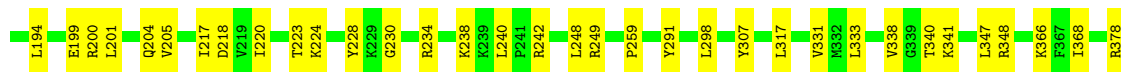
- Molecule 4: 60S ribosomal protein L8

Chain LA: 81% 15%



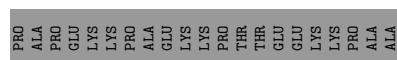
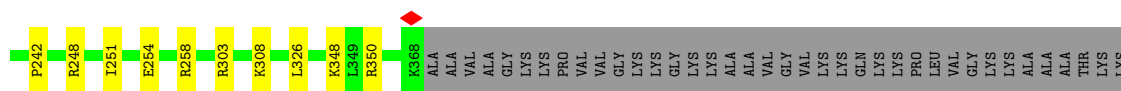
- Molecule 5: 60S ribosomal protein L3

Chain LB: 83% 16%



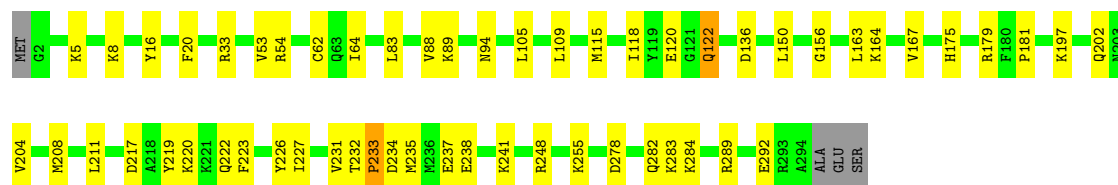
- Molecule 6: 60S ribosomal protein L4

Chain LC: 76% 10% 15%



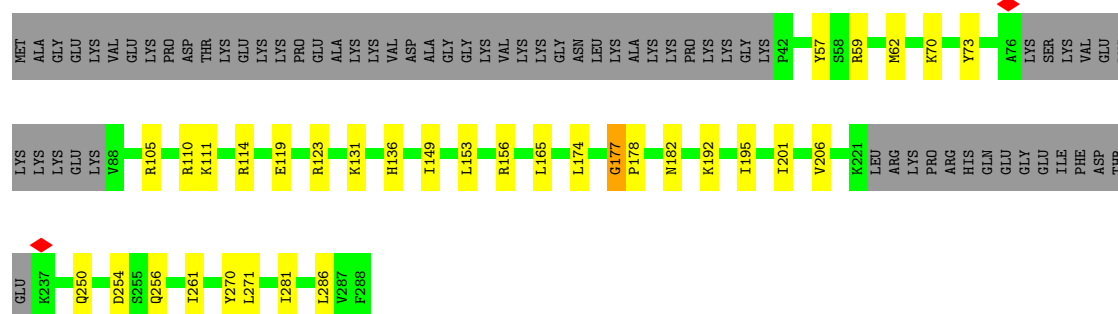
- Molecule 7: 60S ribosomal protein L5

Chain LD:  80% 18% ..



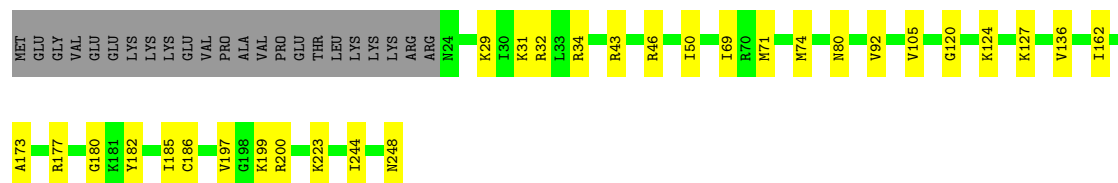
- Molecule 8: Large ribosomal subunit protein eL6

Chain LE:  65% 11% 23%



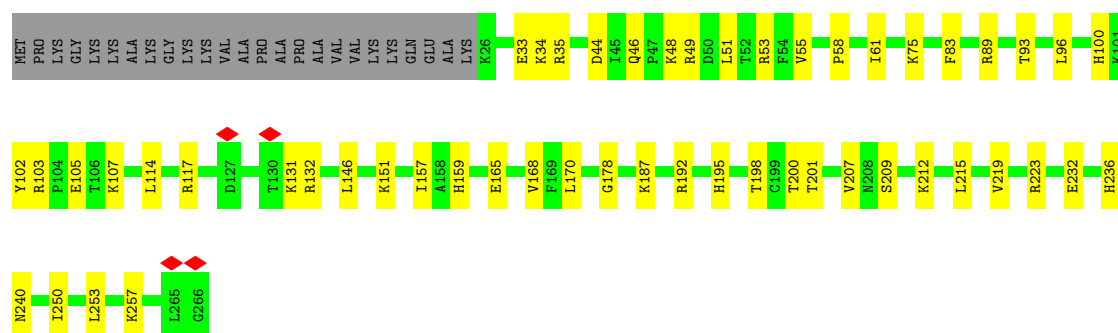
- Molecule 9: Large ribosomal subunit protein uL30

Chain LF:  79% 12% 9%



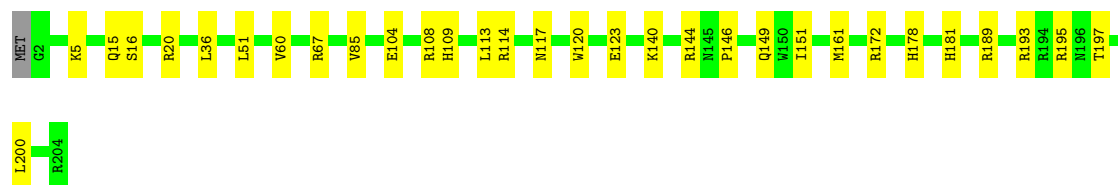
- Molecule 10: 60S ribosomal protein L7a

Chain LG:  71% 20% 9%



- Molecule 11: 60S ribosomal protein L9

Chain LN: 



- Molecule 17: 60S ribosomal protein L13a

Chain LO: 89% 10% .



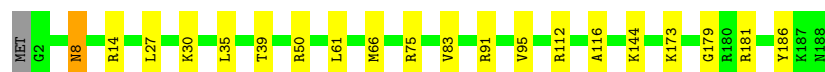
- Molecule 18: 60S ribosomal protein L17

Chain LP: 72% 11% 17%



- Molecule 19: 60S ribosomal protein L18

Chain LQ: 89% 10% ..



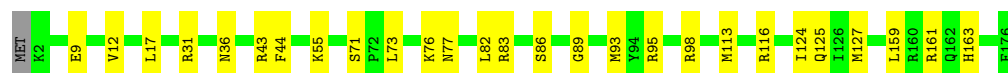
- Molecule 20: 60S ribosomal protein L19

Chain LR: 82% 13% 5%



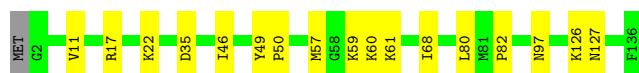
- Molecule 21: 60S ribosomal protein L18a

Chain LS: 84% 15% .



- Molecule 22: 60S ribosomal protein L21

Chain LT: 84% 16% .



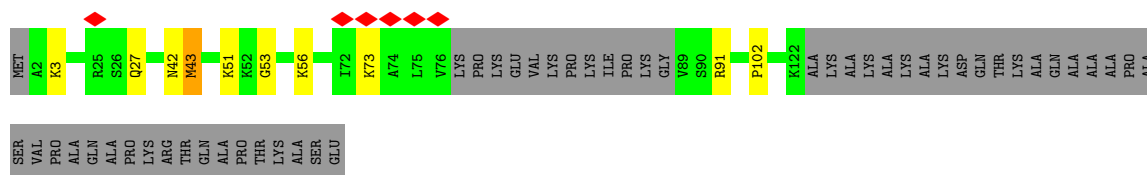
- Molecule 29: 60S ribosomal protein L27a

Chain La: 86% 14% .



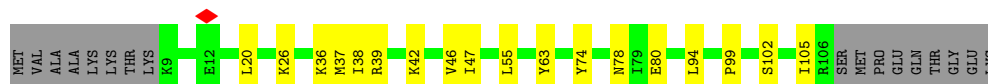
- Molecule 30: 60S ribosomal protein L29

Chain Lb: 62% 6% 31%



- Molecule 31: 60S ribosomal protein L30

Chain Lc: 70% 16% 15%



- Molecule 32: 60S ribosomal protein L31

Chain Ld: 70% 16% 14%



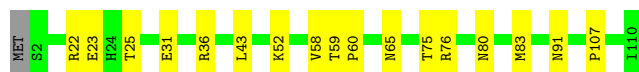
- Molecule 33: 60S ribosomal protein L32

Chain Le: 79% 16% 5%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 84% 15% .



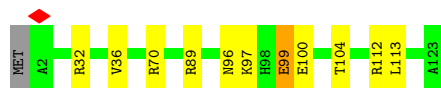
- Molecule 35: 60S ribosomal protein L34

Chain Lg:  83% 15% .



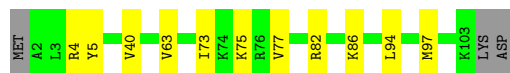
- Molecule 36: 60S ribosomal protein L35

Chain Lh:  90% 8% ..



- Molecule 37: 60S ribosomal protein L36

Chain Li:  87% 10% .



- Molecule 38: Large ribosomal subunit protein eL37

Chain Lj:  73% 15% 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk:  76% 23% .



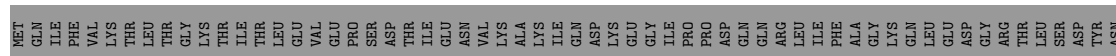
- Molecule 40: 60S ribosomal protein L39

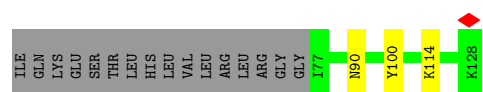
Chain Ll:  78% 20% .



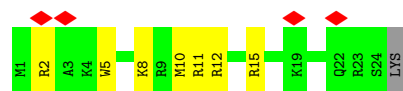
- Molecule 41: Large ribosomal subunit protein eL40

Chain Lm:  38% 59%

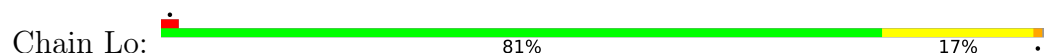




- Molecule 42: 60S ribosomal protein L41



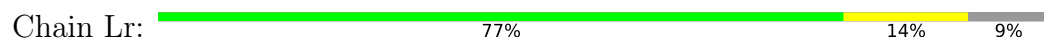
- Molecule 43: 60S ribosomal protein L36a



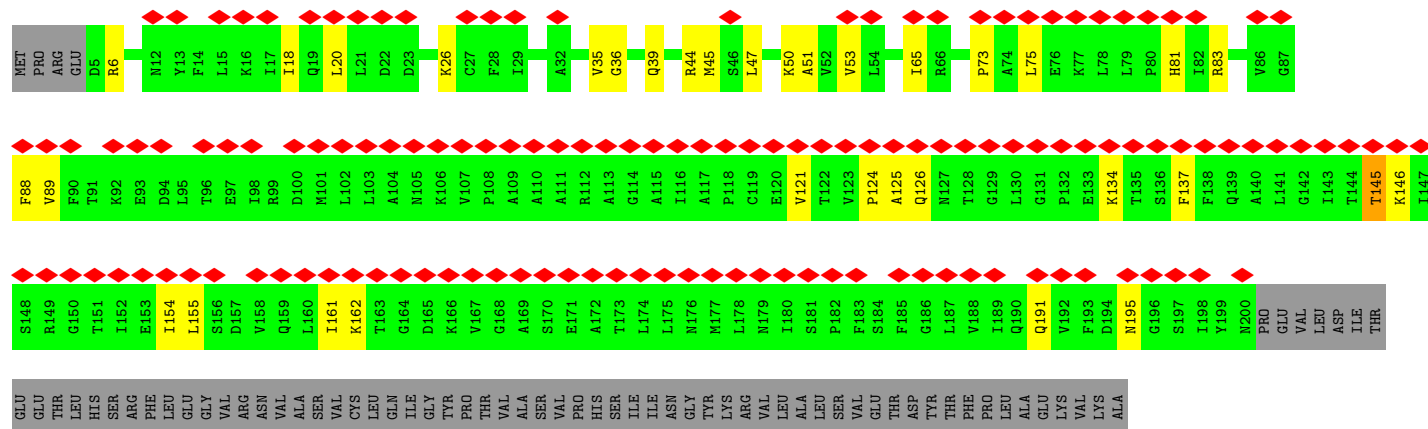
- Molecule 44: 60S ribosomal protein L37a



- Molecule 45: 60S ribosomal protein L28



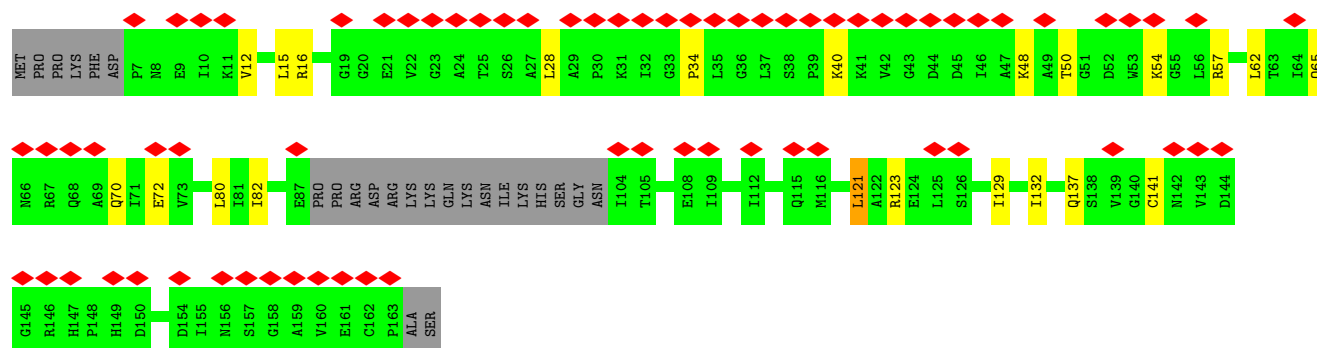
- Molecule 46: 60S acidic ribosomal protein P0



PHE LEU ALA ASP PRO PHE SER SER PHE VAL ALA ALA ALA PRO VAL ALA ALA THR THR ALA ALA ALA ALA ALA ALA ALA ALA LYS LYS VAL VAL GLU ALA LYS GLU GLU SER SER GLU SER SER GLU ASP ASP MET GLY PHE GLY LEU PHE ASP

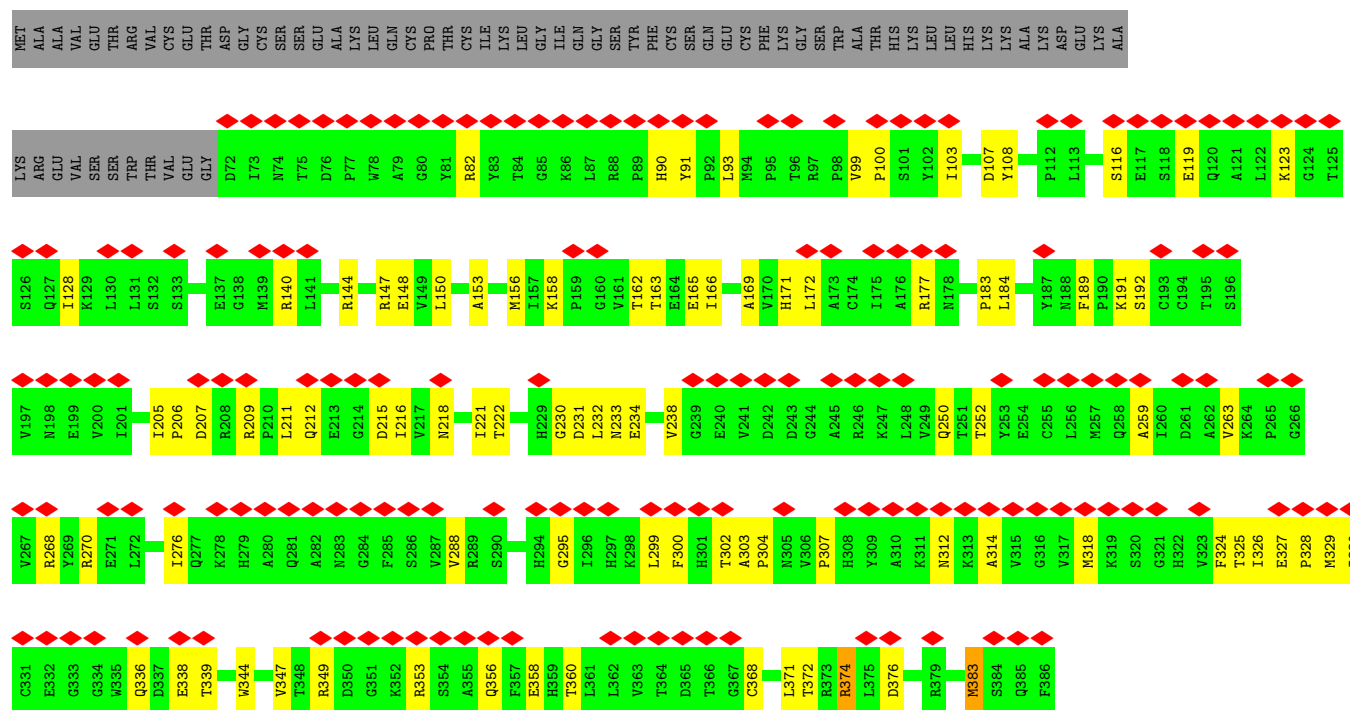
• Molecule 47: Large ribosomal subunit protein uL11

Chain Lt: 43% 72% 13% 15%



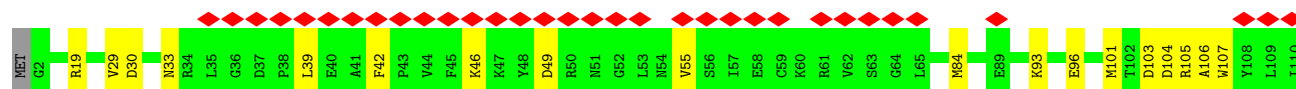
• Molecule 48: Methionine aminopeptidase 1

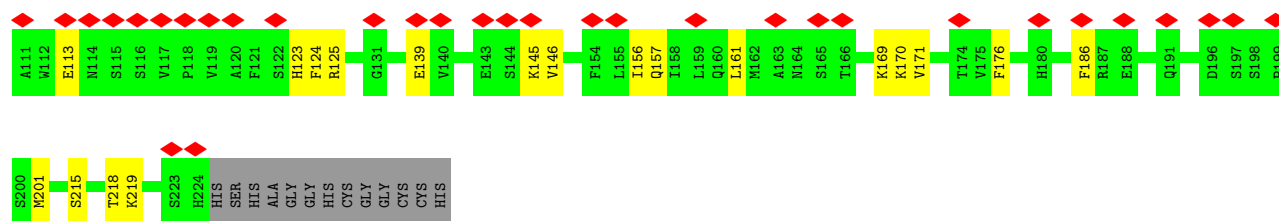
Chain MA: 43% 58% 23% 18%



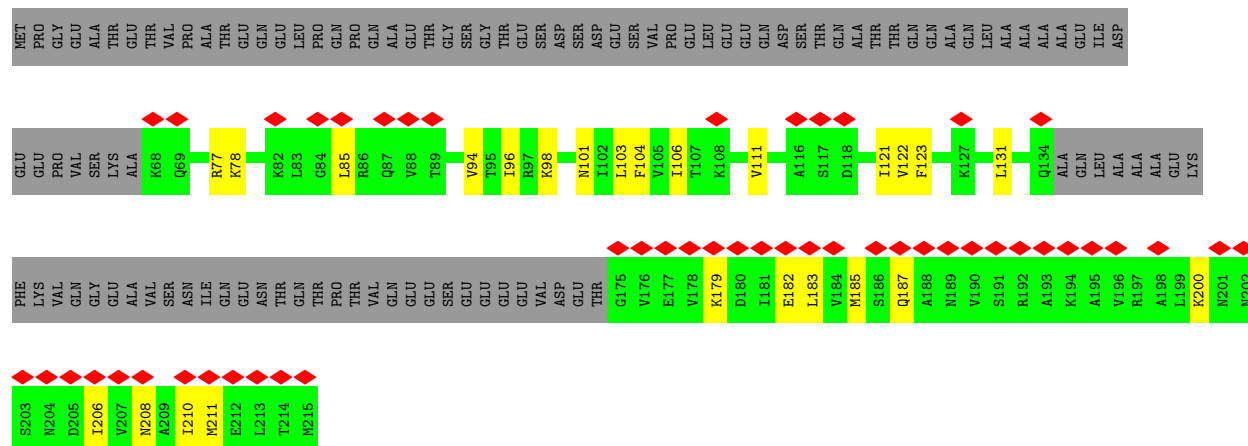
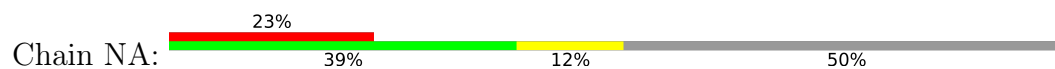
• Molecule 49: N-alpha-acetyltransferase 40

Chain N4: 27% 78% 16% 6%

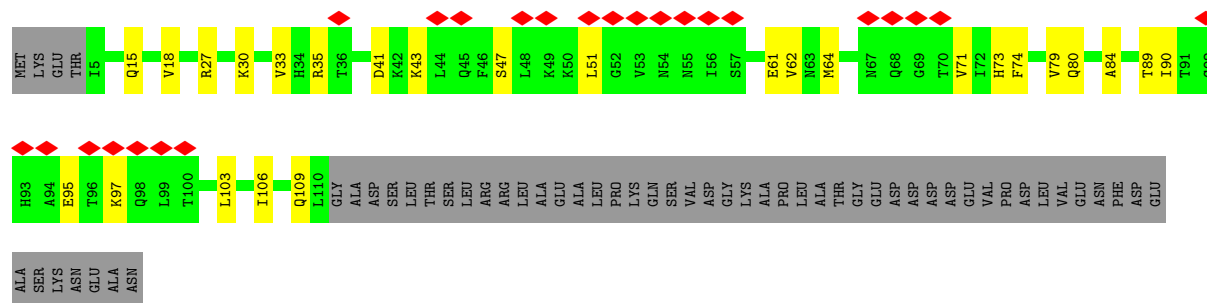




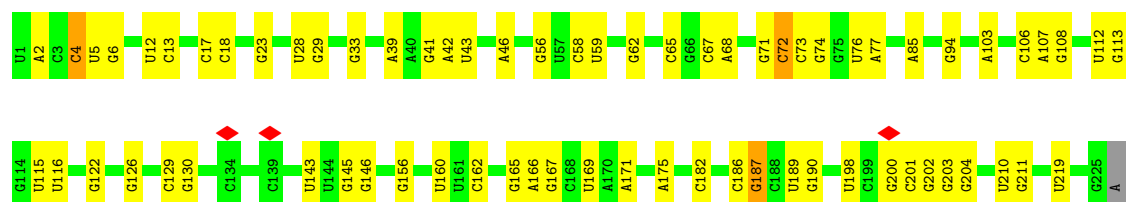
- Molecule 50: Nascent polypeptide-associated complex subunit alpha



- Molecule 51: Isoform 2 of Transcription factor BTF3



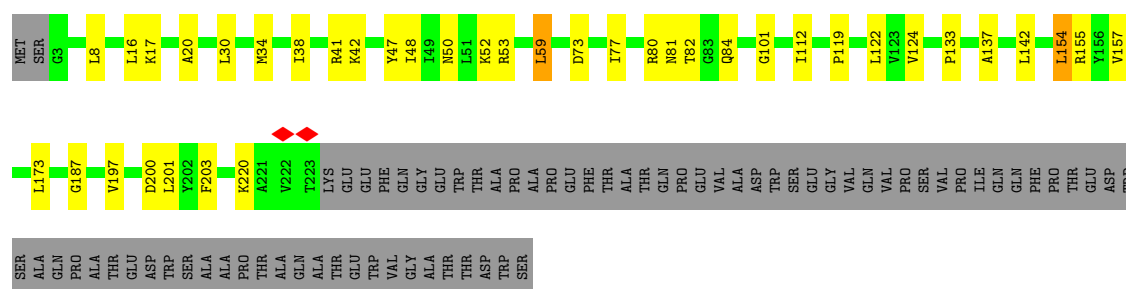
- Molecule 52: 18S rRNA



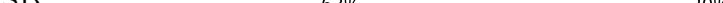


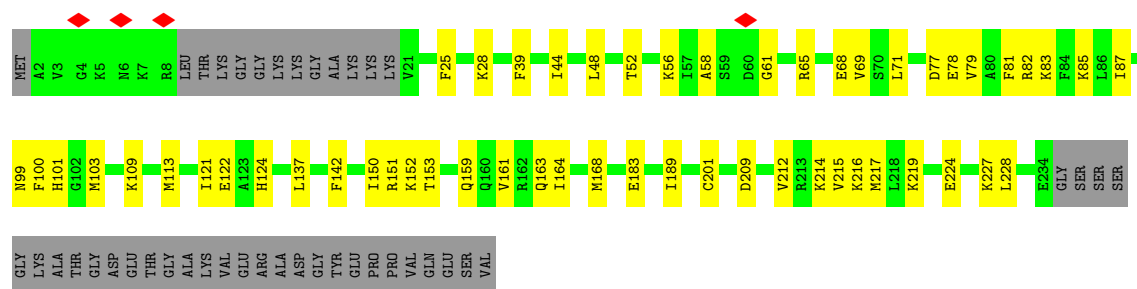
- Molecule 53: 40S ribosomal protein SA

Chain SA:



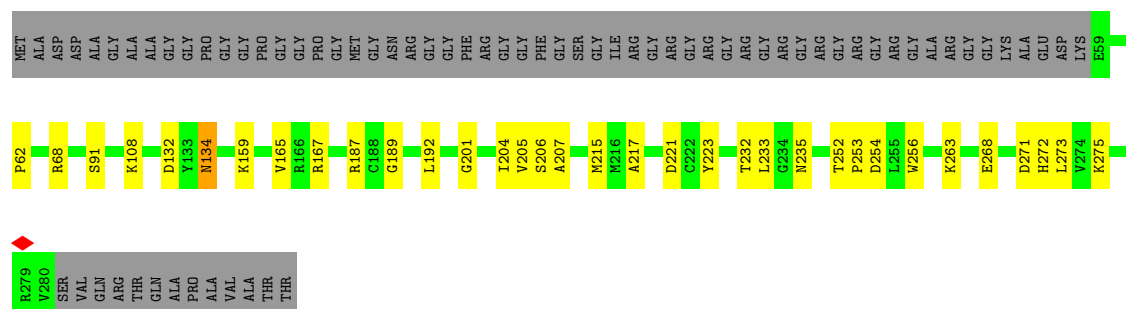
- Molecule 54: 40S ribosomal protein S3a

Chain SB:  63% 20% 16%

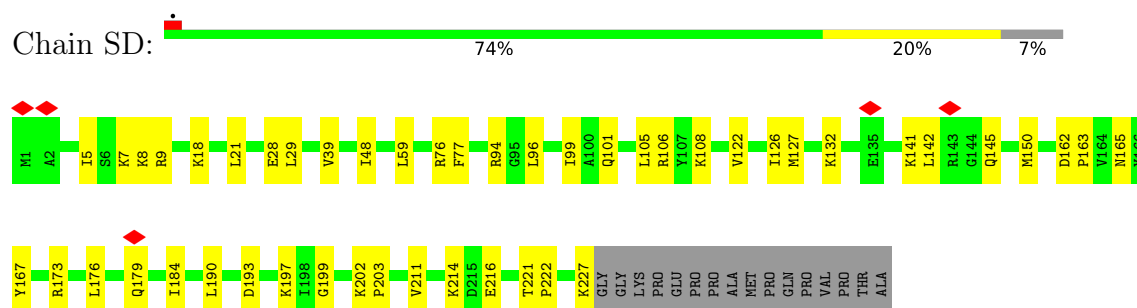


- Molecule 55: 40S ribosomal protein S2

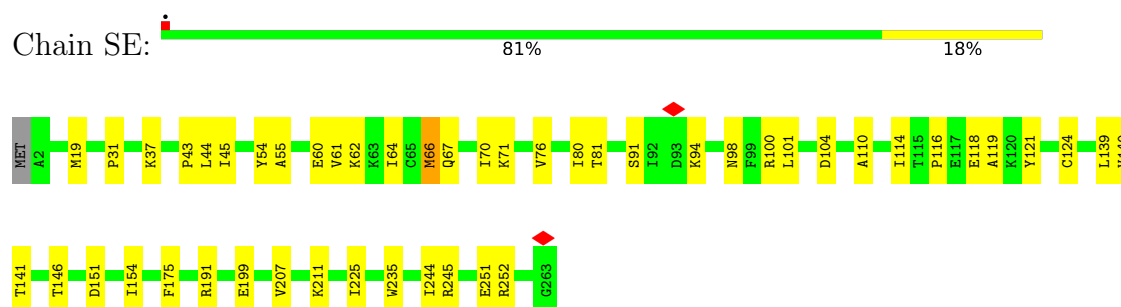
Chain SC:



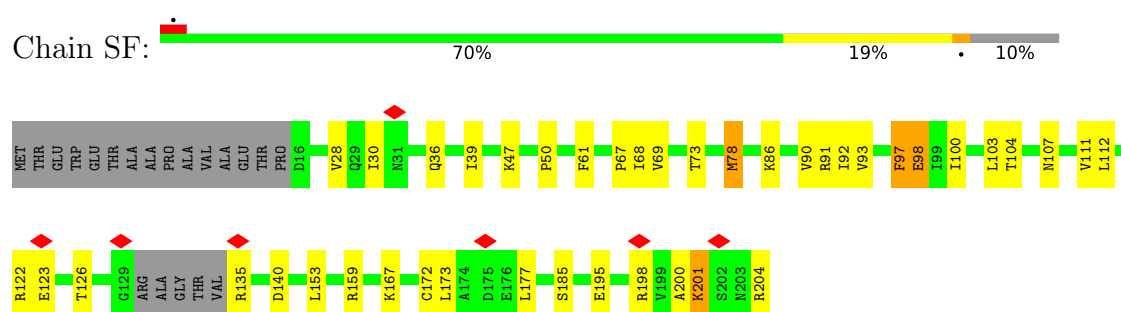
- Molecule 56: 40S ribosomal protein S3



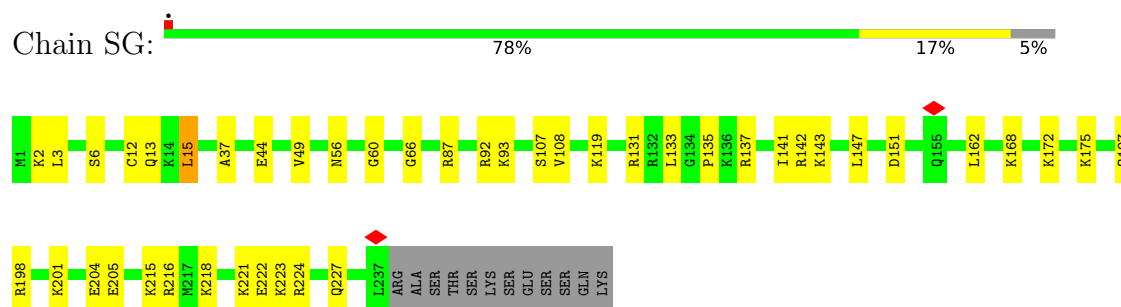
- Molecule 57: Small ribosomal subunit protein eS4, X isoform



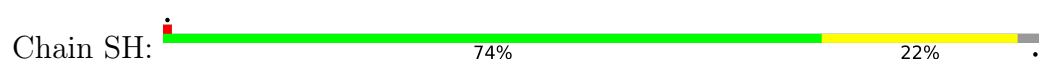
- Molecule 58: 40S ribosomal protein S5



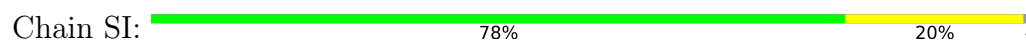
- Molecule 59: 40S ribosomal protein S6



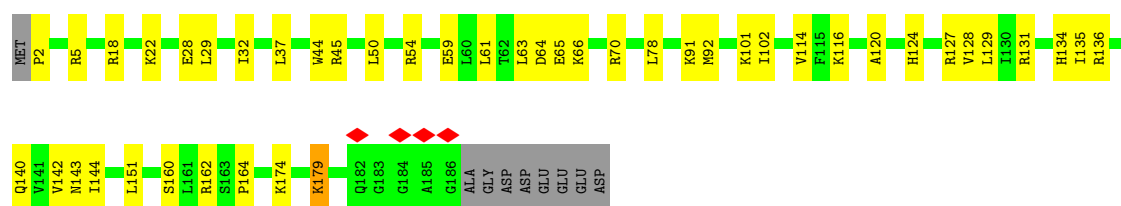
- Molecule 60: 40S ribosomal protein S7



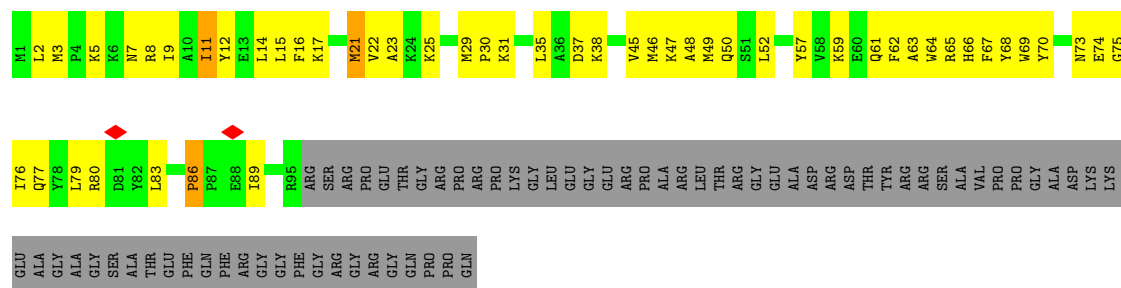
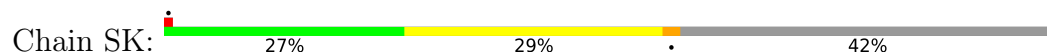
- Molecule 61: 40S ribosomal protein S8



- Molecule 62: 40S ribosomal protein S9

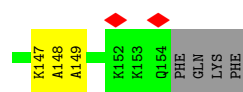


- Molecule 63: 40S ribosomal protein S10

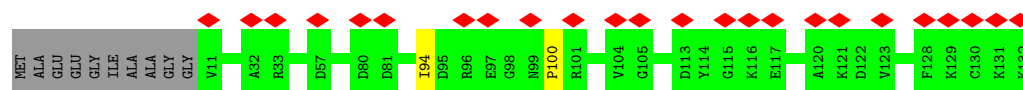
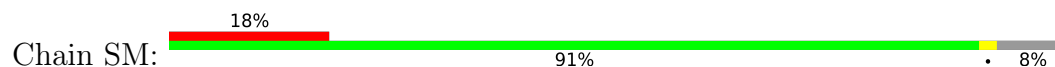


- Molecule 64: 40S ribosomal protein S11

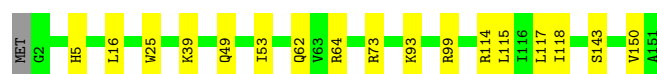




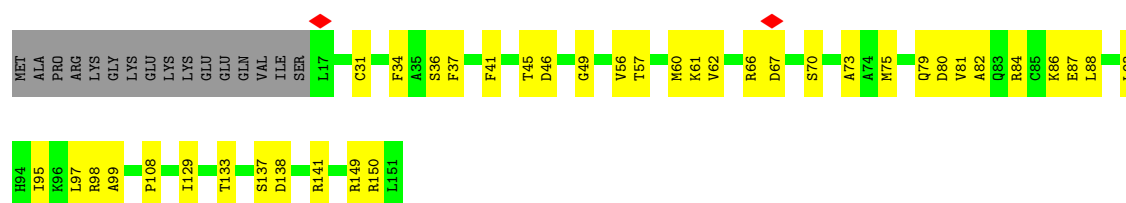
- Molecule 65: 40S ribosomal protein S12



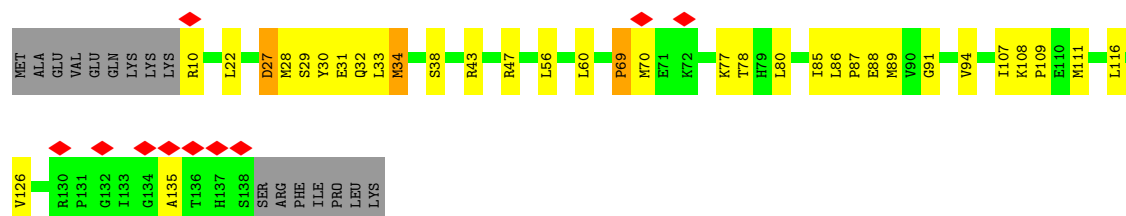
- Molecule 66: 40S ribosomal protein S13



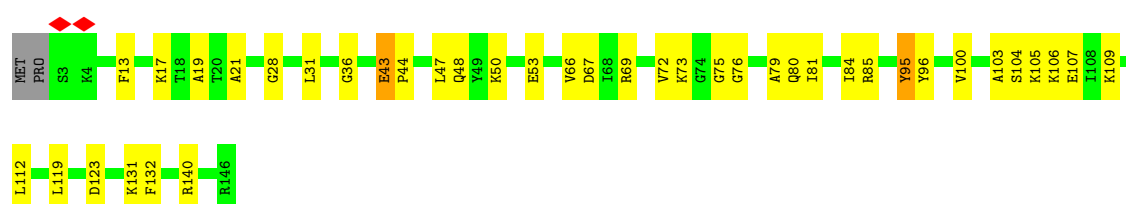
- Molecule 67: 40S ribosomal protein S14



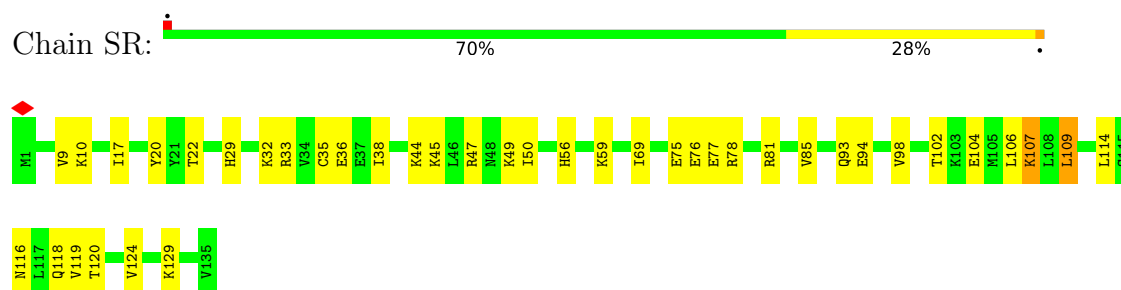
- Molecule 68: 40S ribosomal protein S15



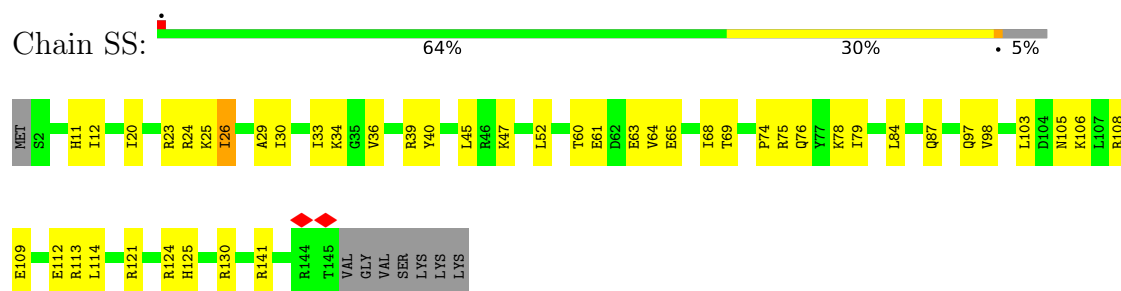
- Molecule 69: 40S ribosomal protein S16



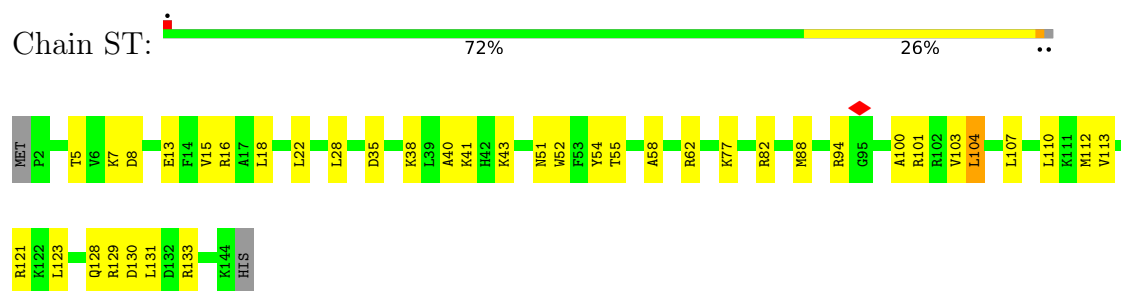
- Molecule 70: 40S ribosomal protein S17



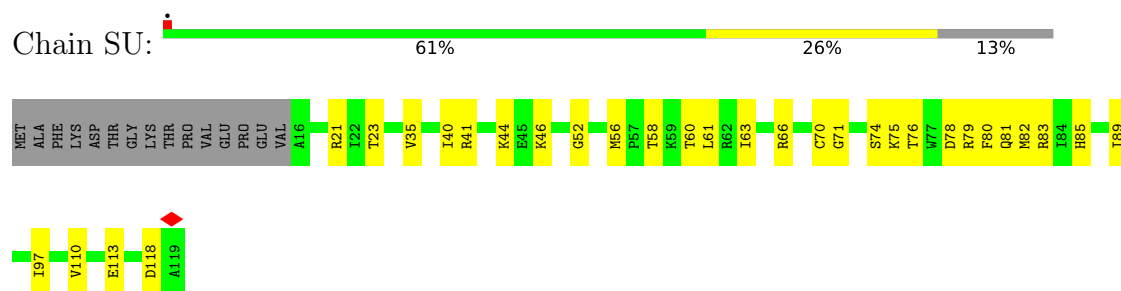
- Molecule 71: 40S ribosomal protein S18



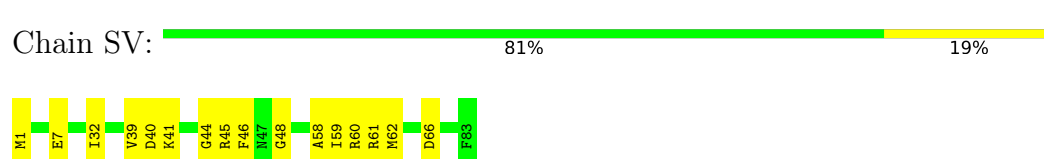
- Molecule 72: 40S ribosomal protein S19



- Molecule 73: 40S ribosomal protein S20

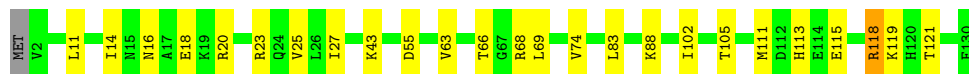


- Molecule 74: 40S ribosomal protein S21



- Molecule 75: 40S ribosomal protein S15a

Chain SW:  80% 18% ..



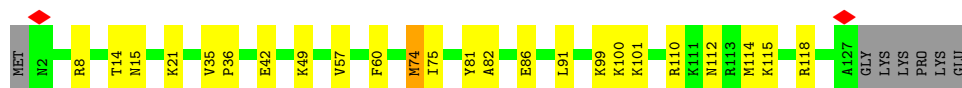
- Molecule 76: 40S ribosomal protein S23

Chain SX:  87% 12% .

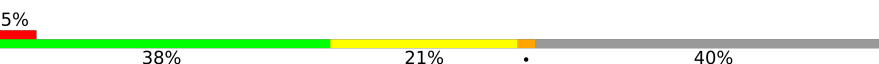


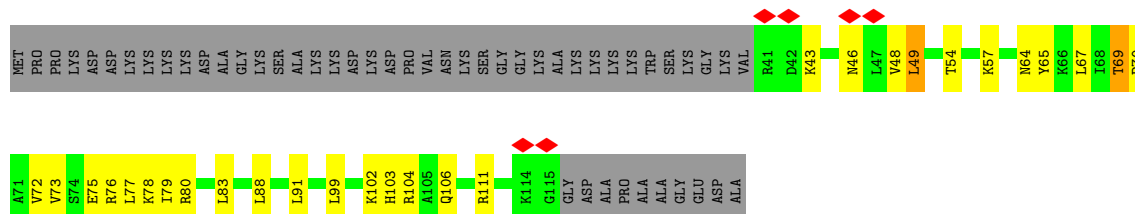
- Molecule 77: 40S ribosomal protein S24

Chain SY:  77% 17% . 5%



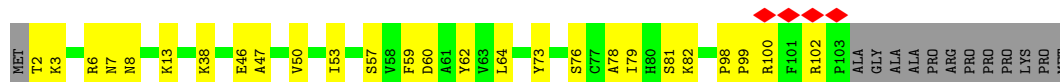
- Molecule 78: 40S ribosomal protein S25

Chain SZ:  5% 38% 21% . 40%



- Molecule 79: 40S ribosomal protein S26

Chain Sa:  66% 23% 11%

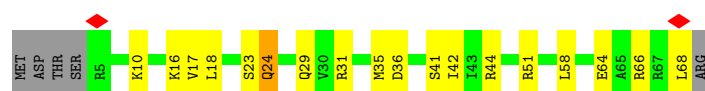


- Molecule 80: 40S ribosomal protein S27

Chain Sb:  83% 14% ..



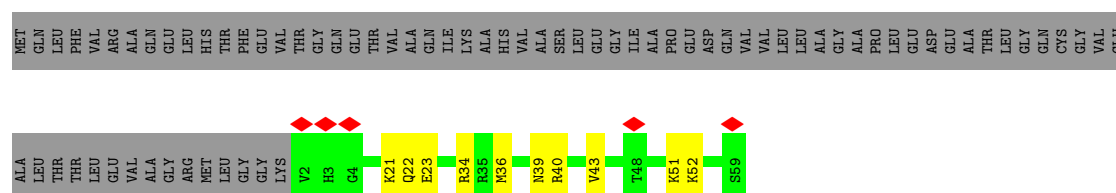
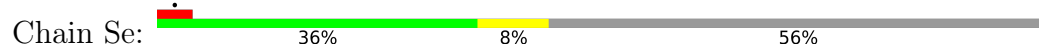
- Molecule 81: 40S ribosomal protein S28



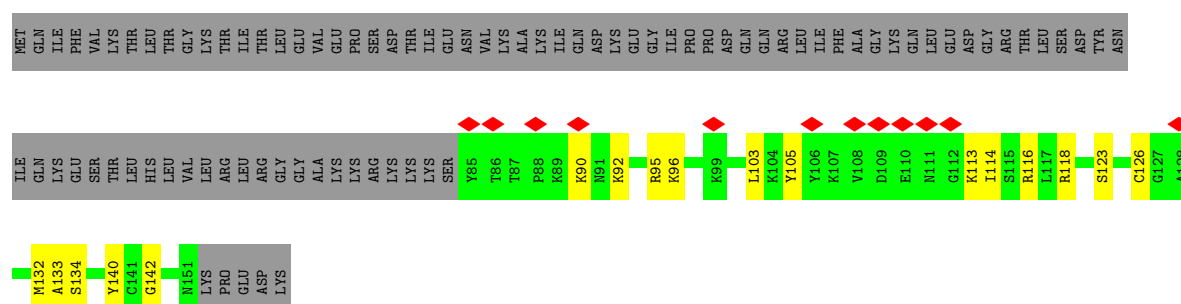
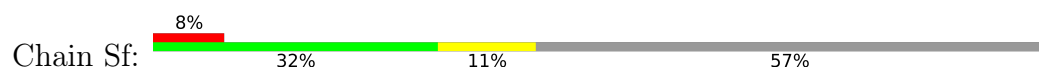
- Molecule 82: 40S ribosomal protein S29



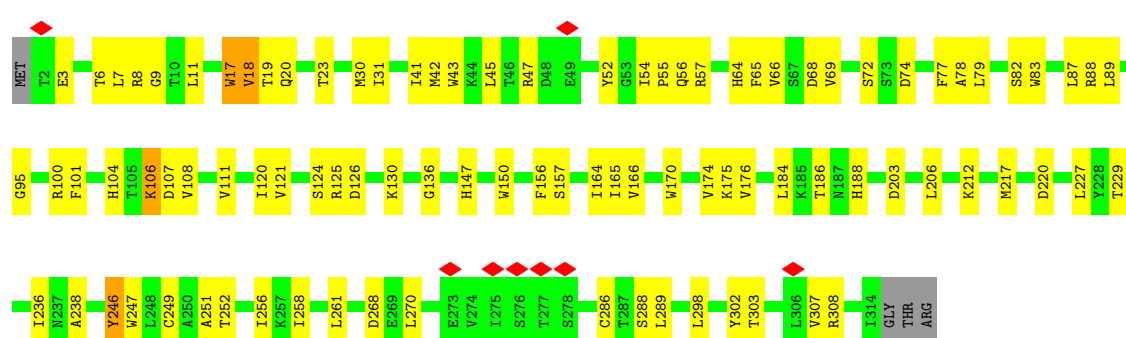
- Molecule 83: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein



- Molecule 84: Ubiquitin



- Molecule 85: Receptor of activated protein C kinase 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15772	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.471	Depositor
Minimum map value	-1.464	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.076	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	465.28, 465.28, 465.28	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	Depositor

5 Model quality

5.1 Standard geometry

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

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	L5	0.15	0/88012	0.32	0/137296
2	L7	0.14	0/2861	0.29	0/4459
3	L8	0.14	0/3701	0.30	0/5766
4	LA	0.20	0/1936	0.46	0/2596
5	LB	0.19	0/3306	0.47	1/4424 (0.0%)
6	LC	0.19	0/2962	0.41	0/3977
7	LD	0.22	0/2428	0.59	4/3252 (0.1%)
8	LE	0.21	0/1808	0.70	2/2425 (0.1%)
9	LF	0.19	0/1905	0.45	0/2539
10	LG	0.24	0/1960	0.56	0/2637
11	LH	0.22	0/1537	0.48	1/2066 (0.0%)
12	LI	0.20	0/1677	0.51	1/2237 (0.0%)
13	LJ	0.22	0/1394	0.53	0/1863
14	LL	0.20	0/1704	0.49	0/2282
15	LM	0.21	0/1161	0.55	0/1554
16	LN	0.17	0/1746	0.40	0/2338
17	LO	0.20	0/1682	0.47	0/2250
18	LP	0.15	0/1268	0.36	0/1701
19	LQ	0.18	0/1537	0.44	0/2052
20	LR	0.20	0/1582	0.46	0/2091
21	LS	0.18	0/1493	0.39	0/2003
22	LT	0.20	0/1326	0.50	0/1770
23	LU	0.23	0/830	0.63	1/1114 (0.1%)
24	LV	0.16	0/993	0.38	0/1332
25	LW	0.21	0/1030	0.57	2/1364 (0.1%)
26	LX	0.17	0/1002	0.45	0/1345
27	LY	0.20	0/1123	0.49	1/1493 (0.1%)
28	LZ	0.20	0/1130	0.46	0/1507
29	La	0.16	0/1191	0.38	0/1591
30	Lb	0.21	0/895	0.63	0/1182
31	Lc	0.18	0/774	0.43	0/1038
32	Ld	0.21	0/903	0.54	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.19	0/1071	0.45	0/1429
34	Lf	0.20	0/895	0.49	3/1198 (0.3%)
35	Lg	0.17	0/916	0.38	0/1220
36	Lh	0.17	0/1023	0.43	0/1351
37	Li	0.19	0/843	0.55	0/1115
38	Lj	0.17	0/720	0.41	0/952
39	Lk	0.23	0/575	0.60	0/761
40	Ll	0.16	0/454	0.38	0/599
41	Lm	0.13	0/425	0.36	0/561
42	Ln	0.34	0/231	0.80	1/294 (0.3%)
43	Lo	0.16	0/876	0.46	0/1156
44	Lp	0.15	0/718	0.38	0/953
45	Lr	0.18	0/1017	0.43	0/1364
46	Ls	0.24	0/1519	0.64	2/2052 (0.1%)
47	Lt	0.22	0/1058	0.65	0/1430
48	MA	0.18	0/2549	0.49	0/3462
49	N4	0.18	0/1846	0.52	0/2476
50	NA	0.24	0/845	0.63	0/1128
51	NB	0.25	0/829	0.63	0/1112
52	S2	0.13	0/40751	0.31	0/63496
53	SA	0.24	0/1778	0.64	3/2416 (0.1%)
54	SB	0.22	0/1817	0.61	1/2428 (0.0%)
55	SC	0.25	0/1762	0.61	1/2381 (0.0%)
56	SD	0.22	0/1793	0.57	2/2414 (0.1%)
57	SE	0.21	0/2118	0.60	4/2849 (0.1%)
58	SF	0.28	0/1481	0.78	6/1988 (0.3%)
59	SG	0.22	0/1946	0.63	3/2590 (0.1%)
60	SH	0.25	0/1519	0.65	2/2033 (0.1%)
61	SI	0.21	0/1715	0.55	1/2287 (0.0%)
62	SJ	0.24	0/1550	0.65	3/2069 (0.1%)
63	SK	0.36	0/823	1.03	7/1111 (0.6%)
64	SL	0.20	0/1202	0.53	1/1606 (0.1%)
65	SM	0.09	0/603	0.25	0/837
66	SN	0.16	0/1232	0.39	0/1656
67	SO	0.23	0/1023	0.70	2/1372 (0.1%)
68	SP	0.29	0/1082	0.82	4/1446 (0.3%)
69	SQ	0.28	0/1160	0.75	0/1553
70	SR	0.27	0/1105	0.73	2/1484 (0.1%)
71	SS	0.26	0/1208	0.70	1/1618 (0.1%)
72	ST	0.28	0/1131	0.73	1/1515 (0.1%)
73	SU	0.31	0/831	0.77	2/1115 (0.2%)
74	SV	0.22	0/643	0.57	1/860 (0.1%)
75	SW	0.27	0/1051	0.56	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SX	0.19	0/1116	0.45	0/1490
77	SY	0.24	0/1044	0.65	2/1388 (0.1%)
78	SZ	0.40	0/604	1.06	3/810 (0.4%)
79	Sa	0.21	0/836	0.52	0/1121
80	Sb	0.20	0/665	0.51	0/891
81	Sc	0.21	0/508	0.61	0/680
82	Sd	0.30	0/470	0.68	0/623
83	Se	0.22	0/465	0.56	0/612
84	Sf	0.22	0/560	0.66	1/745 (0.1%)
85	Sg	0.22	0/2493	0.62	2/3394 (0.1%)
All	All	0.18	0/237352	0.43	74/347657 (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
8	LE	0	1
48	MA	0	2
68	SP	0	1
75	SW	0	1
85	Sg	0	2
All	All	0	7

There are no bond length outliers.

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	LE	111	LYS	CA-C-N	18.39	145.95	120.39
8	LE	111	LYS	C-N-CA	18.39	145.95	120.39
53	SA	197	VAL	CA-C-N	9.94	133.99	120.67
53	SA	197	VAL	C-N-CA	9.94	133.99	120.67
46	Ls	73	PRO	CA-N-CD	-8.69	99.83	112.00

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	LE	177	GLY	Peptide
48	MA	303	ALA	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
48	MA	91	TYR	Peptide
68	SP	27	ASP	Peptide
75	SW	118	ARG	Sidechain

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	L5	78678	0	39756	588	0
2	L7	2561	0	1295	16	0
3	L8	3314	0	1683	26	0
4	LA	1898	0	1993	29	0
5	LB	3238	0	3376	47	0
6	LC	2908	0	3082	32	0
7	LD	2382	0	2410	38	0
8	LE	1774	0	1929	23	0
9	LF	1870	0	1996	21	0
10	LG	1927	0	2074	36	0
11	LH	1518	0	1601	17	0
12	LI	1639	0	1687	21	0
13	LJ	1371	0	1412	13	0
14	LL	1673	0	1779	24	0
15	LM	1138	0	1204	19	0
16	LN	1701	0	1749	23	0
17	LO	1650	0	1794	18	0
18	LP	1242	0	1269	14	0
19	LQ	1513	0	1628	16	0
20	LR	1566	0	1729	18	0
21	LS	1453	0	1490	19	0
22	LT	1298	0	1366	19	0
23	LU	816	0	842	11	0
24	LV	979	0	1039	9	0
25	LW	1015	0	1079	20	0
26	LX	985	0	1066	8	0
27	LY	1106	0	1192	25	0
28	LZ	1107	0	1182	13	0
29	La	1162	0	1213	16	0
30	Lb	882	0	959	9	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	Lc	764	0	804	13	0
32	Ld	888	0	930	13	0
33	Le	1053	0	1147	15	0
34	Lf	876	0	912	11	0
35	Lg	906	0	998	11	0
36	Lh	1015	0	1148	10	0
37	Li	832	0	917	8	0
38	Lj	705	0	737	12	0
39	Lk	569	0	637	10	0
40	Ll	444	0	483	8	0
41	Lm	430	0	465	3	0
42	Ln	230	0	276	7	0
43	Lo	862	0	929	13	0
44	Lp	708	0	756	4	0
45	Lr	1002	0	1068	13	0
46	Ls	1496	0	1540	22	0
47	Lt	1046	0	1076	15	0
48	MA	2485	0	2414	65	0
49	N4	1809	0	1764	24	0
50	NA	841	0	898	19	0
51	NB	821	0	867	17	0
52	S2	36456	0	18381	333	0
53	SA	1741	0	1746	27	0
54	SB	1791	0	1870	33	0
55	SC	1725	0	1813	22	0
56	SD	1765	0	1865	36	0
57	SE	2076	0	2177	30	0
58	SF	1461	0	1511	29	0
59	SG	1923	0	2089	34	0
60	SH	1497	0	1590	23	0
61	SI	1686	0	1772	27	0
62	SJ	1525	0	1640	29	0
63	SK	799	0	823	40	0
64	SL	1182	0	1253	18	0
65	SM	604	0	281	1	0
66	SN	1208	0	1294	13	0
67	SO	1010	0	1034	28	0
68	SP	1061	0	1107	24	0
69	SQ	1142	0	1212	30	0
70	SR	1090	0	1149	26	0
71	SS	1190	0	1249	36	0
72	ST	1112	0	1146	31	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
73	SU	821	0	883	26	0
74	SV	636	0	637	12	0
75	SW	1034	0	1080	24	0
76	SX	1098	0	1167	12	0
77	SY	1027	0	1093	17	0
78	SZ	598	0	656	21	0
79	Sa	821	0	870	19	0
80	Sb	651	0	672	10	0
81	Sc	506	0	536	13	0
82	Sd	459	0	448	23	0
83	Se	459	0	503	7	0
84	Sf	548	0	551	10	0
85	Sg	2436	0	2393	59	0
86	L5	213	0	0	0	0
86	L7	3	0	0	0	0
86	L8	4	0	0	0	0
86	LA	1	0	0	0	0
86	LI	1	0	0	0	0
86	LP	1	0	0	0	0
86	LV	1	0	0	0	0
86	Le	1	0	0	0	0
86	Lj	1	0	0	0	0
86	S2	31	0	0	0	0
87	Lg	1	0	0	0	0
87	Lj	1	0	0	0	0
87	Lm	1	0	0	0	0
87	Lo	1	0	0	0	0
87	Lp	1	0	0	0	0
87	Sa	1	0	0	0	0
87	Sd	1	0	0	0	0
87	Sf	1	0	0	0	0
All	All	221549	0	166131	2199	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 6.

The worst 5 of 2199 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)
52:S2:1756:C:H42	52:S2:1776:G:N2	1.51	1.07
52:S2:1756:C:N4	52:S2:1776:G:H22	1.51	1.07

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:N4:107:TRP:HB2	49:N4:124:PHE:O	1.54	1.06
1:L5:1762:C:N4	1:L5:1770:A:C2	2.33	0.95
52:S2:677:G:H21	52:S2:1028:A:H62	1.01	0.94

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	
4	LA	246/257 (96%)	228 (93%)	18 (7%)	0	100	100
5	LB	400/403 (99%)	384 (96%)	16 (4%)	0	100	100
6	LC	363/427 (85%)	353 (97%)	9 (2%)	1 (0%)	36	66
7	LD	291/297 (98%)	284 (98%)	7 (2%)	0	100	100
8	LE	215/288 (75%)	205 (95%)	10 (5%)	0	100	100
9	LF	223/248 (90%)	218 (98%)	4 (2%)	1 (0%)	30	61
10	LG	239/266 (90%)	229 (96%)	10 (4%)	0	100	100
11	LH	188/192 (98%)	178 (95%)	10 (5%)	0	100	100
12	LI	198/214 (92%)	190 (96%)	8 (4%)	0	100	100
13	LJ	169/178 (95%)	166 (98%)	3 (2%)	0	100	100
14	LL	205/211 (97%)	196 (96%)	8 (4%)	1 (0%)	24	56
15	LM	137/215 (64%)	131 (96%)	6 (4%)	0	100	100
16	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
17	LO	199/203 (98%)	197 (99%)	2 (1%)	0	100	100
18	LP	151/184 (82%)	145 (96%)	6 (4%)	0	100	100
19	LQ	185/188 (98%)	179 (97%)	6 (3%)	0	100	100
20	LR	185/196 (94%)	183 (99%)	2 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	LS	173/176 (98%)	168 (97%)	5 (3%)	0	100	100
22	LT	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
23	LU	98/128 (77%)	97 (99%)	1 (1%)	0	100	100
24	LV	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
25	LW	122/157 (78%)	115 (94%)	7 (6%)	0	100	100
26	LX	118/156 (76%)	116 (98%)	2 (2%)	0	100	100
27	LY	131/145 (90%)	125 (95%)	6 (5%)	0	100	100
28	LZ	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
29	La	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
30	Lb	105/159 (66%)	100 (95%)	5 (5%)	0	100	100
31	Lc	96/115 (84%)	96 (100%)	0	0	100	100
32	Ld	105/125 (84%)	103 (98%)	2 (2%)	0	100	100
33	Le	126/135 (93%)	121 (96%)	5 (4%)	0	100	100
34	Lf	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
35	Lg	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
36	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
38	Lj	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
39	Lk	67/70 (96%)	67 (100%)	0	0	100	100
40	Ll	48/51 (94%)	48 (100%)	0	0	100	100
41	Lm	49/128 (38%)	49 (100%)	0	0	100	100
42	Ln	22/25 (88%)	21 (96%)	1 (4%)	0	100	100
43	Lo	103/106 (97%)	97 (94%)	6 (6%)	0	100	100
44	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
45	Lr	123/137 (90%)	121 (98%)	2 (2%)	0	100	100
46	Ls	194/317 (61%)	182 (94%)	12 (6%)	0	100	100
47	Lt	137/165 (83%)	109 (80%)	26 (19%)	2 (2%)	8	34
48	MA	313/386 (81%)	302 (96%)	11 (4%)	0	100	100
49	N4	221/237 (93%)	214 (97%)	7 (3%)	0	100	100
50	NA	104/215 (48%)	96 (92%)	8 (8%)	0	100	100
51	NB	104/162 (64%)	96 (92%)	8 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	SA	219/295 (74%)	210 (96%)	9 (4%)	0	100	100
54	SB	217/264 (82%)	210 (97%)	7 (3%)	0	100	100
55	SC	220/293 (75%)	213 (97%)	7 (3%)	0	100	100
56	SD	225/243 (93%)	215 (96%)	10 (4%)	0	100	100
57	SE	260/263 (99%)	248 (95%)	12 (5%)	0	100	100
58	SF	180/204 (88%)	168 (93%)	12 (7%)	0	100	100
59	SG	235/249 (94%)	229 (97%)	5 (2%)	1 (0%)	30	61
60	SH	182/194 (94%)	179 (98%)	3 (2%)	0	100	100
61	SI	204/208 (98%)	196 (96%)	8 (4%)	0	100	100
62	SJ	183/194 (94%)	181 (99%)	2 (1%)	0	100	100
63	SK	93/165 (56%)	88 (95%)	5 (5%)	0	100	100
64	SL	140/158 (89%)	131 (94%)	9 (6%)	0	100	100
65	SM	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
66	SN	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
67	SO	133/151 (88%)	119 (90%)	13 (10%)	1 (1%)	16	47
68	SP	127/145 (88%)	117 (92%)	10 (8%)	0	100	100
69	SQ	142/146 (97%)	130 (92%)	12 (8%)	0	100	100
70	SR	133/135 (98%)	127 (96%)	5 (4%)	1 (1%)	16	47
71	SS	142/152 (93%)	131 (92%)	10 (7%)	1 (1%)	18	50
72	ST	141/145 (97%)	134 (95%)	7 (5%)	0	100	100
73	SU	102/119 (86%)	96 (94%)	6 (6%)	0	100	100
74	SV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
75	SW	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
76	SX	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
77	SY	124/133 (93%)	119 (96%)	5 (4%)	0	100	100
78	SZ	73/125 (58%)	56 (77%)	17 (23%)	0	100	100
79	Sa	100/115 (87%)	95 (95%)	4 (4%)	1 (1%)	12	42
80	Sb	81/84 (96%)	77 (95%)	4 (5%)	0	100	100
81	Sc	62/69 (90%)	61 (98%)	1 (2%)	0	100	100
82	Sd	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
83	Se	56/133 (42%)	56 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
84	Sf	65/156 (42%)	57 (88%)	8 (12%)	0	100	100
85	Sg	311/317 (98%)	274 (88%)	37 (12%)	0	100	100
All	All	12348/14244 (87%)	11816 (96%)	522 (4%)	10 (0%)	49	78

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
67	SO	138	ASP
79	Sa	46	GLU
6	LC	149	GLU
14	LL	97	SER
47	Lt	141	CYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LA	190/199 (96%)	188 (99%)	2 (1%)	65	74
5	LB	348/349 (100%)	348 (100%)	0	100	100
6	LC	304/348 (87%)	302 (99%)	2 (1%)	76	78
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	195/252 (77%)	195 (100%)	0	100	100
9	LF	194/215 (90%)	193 (100%)	1 (0%)	81	81
10	LG	203/223 (91%)	201 (99%)	2 (1%)	68	75
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	172/181 (95%)	170 (99%)	2 (1%)	63	73
13	LJ	144/149 (97%)	143 (99%)	1 (1%)	76	78
14	LL	173/177 (98%)	172 (99%)	1 (1%)	78	80
15	LM	118/161 (73%)	118 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	173 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	LP	134/163 (82%)	133 (99%)	1 (1%)	76	78
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	80
20	LR	166/175 (95%)	164 (99%)	2 (1%)	63	73
21	LS	156/157 (99%)	156 (100%)	0	100	100
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	90/115 (78%)	88 (98%)	2 (2%)	45	65
24	LV	101/107 (94%)	101 (100%)	0	100	100
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	108/133 (81%)	107 (99%)	1 (1%)	70	76
27	LY	123/135 (91%)	123 (100%)	0	100	100
28	LZ	117/118 (99%)	116 (99%)	1 (1%)	70	76
29	La	120/121 (99%)	119 (99%)	1 (1%)	73	77
30	Lb	89/126 (71%)	88 (99%)	1 (1%)	65	74
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	97 (99%)	1 (1%)	68	75
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	74
35	Lg	98/100 (98%)	98 (100%)	0	100	100
36	Lh	109/110 (99%)	108 (99%)	1 (1%)	70	76
37	Li	86/89 (97%)	85 (99%)	1 (1%)	63	73
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	47/115 (41%)	47 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	92 (99%)	1 (1%)	65	74
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100
46	Ls	162/258 (63%)	161 (99%)	1 (1%)	78	80
47	Lt	112/137 (82%)	112 (100%)	0	100	100
48	MA	270/330 (82%)	267 (99%)	3 (1%)	65	74

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	N4	195/204 (96%)	194 (100%)	1 (0%)	81	81
50	NA	95/183 (52%)	94 (99%)	1 (1%)	65	74
51	NB	90/136 (66%)	90 (100%)	0	100	100
53	SA	183/243 (75%)	180 (98%)	3 (2%)	55	70
54	SB	200/231 (87%)	200 (100%)	0	100	100
55	SC	188/225 (84%)	186 (99%)	2 (1%)	65	74
56	SD	190/202 (94%)	190 (100%)	0	100	100
57	SE	224/225 (100%)	222 (99%)	2 (1%)	70	76
58	SF	156/170 (92%)	155 (99%)	1 (1%)	78	80
59	SG	207/218 (95%)	206 (100%)	1 (0%)	81	81
60	SH	166/174 (95%)	166 (100%)	0	100	100
61	SI	178/180 (99%)	176 (99%)	2 (1%)	65	74
62	SJ	161/168 (96%)	157 (98%)	4 (2%)	42	63
63	SK	86/136 (63%)	86 (100%)	0	100	100
64	SL	130/142 (92%)	130 (100%)	0	100	100
66	SN	130/131 (99%)	130 (100%)	0	100	100
67	SO	105/119 (88%)	105 (100%)	0	100	100
68	SP	115/130 (88%)	113 (98%)	2 (2%)	53	69
69	SQ	119/121 (98%)	117 (98%)	2 (2%)	53	69
70	SR	122/122 (100%)	120 (98%)	2 (2%)	55	70
71	SS	125/132 (95%)	124 (99%)	1 (1%)	73	77
72	ST	113/115 (98%)	113 (100%)	0	100	100
73	SU	94/107 (88%)	94 (100%)	0	100	100
74	SV	67/67 (100%)	67 (100%)	0	100	100
75	SW	112/113 (99%)	111 (99%)	1 (1%)	70	76
76	SX	113/115 (98%)	113 (100%)	0	100	100
77	SY	109/115 (95%)	108 (99%)	1 (1%)	70	76
78	SZ	66/103 (64%)	64 (97%)	2 (3%)	36	60
79	Sa	89/98 (91%)	88 (99%)	1 (1%)	65	74
80	Sb	75/76 (99%)	74 (99%)	1 (1%)	61	72
81	Sc	57/62 (92%)	56 (98%)	1 (2%)	51	68

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
82	Sd	48/49 (98%)	47 (98%)	1 (2%)	47	66
83	Se	47/104 (45%)	47 (100%)	0	100	100
84	Sf	60/140 (43%)	60 (100%)	0	100	100
85	Sg	272/275 (99%)	270 (99%)	2 (1%)	76	78
All	All	10647/11996 (89%)	10583 (99%)	64 (1%)	76	80

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
78	SZ	83	LEU
80	Sb	25	VAL
37	Li	63	VAL
36	Lh	99	GLU
81	Sc	24	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 108 such sidechains are listed below:

Mol	Chain	Res	Type
48	MA	178	ASN
55	SC	115	GLN
77	SY	124	ASN
48	MA	250	GLN
51	NB	17	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3658/5070 (72%)	729 (19%)	16 (0%)
2	L7	119/121 (98%)	13 (10%)	0
3	L8	155/157 (98%)	29 (18%)	0
52	S2	1696/1869 (90%)	350 (20%)	5 (0%)
All	All	5628/7217 (77%)	1121 (19%)	21 (0%)

5 of 1121 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	17	A
1	L5	25	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	L5	39	A
1	L5	42	A
1	L5	48	G

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	4699	U
52	S2	291	G
52	S2	1434	C
52	S2	563	G
52	S2	112	U

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

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	$\# Z > 2$
41	MLZ	Lm	98	41	8,9,10	0.77	0	4,9,11	0.62	0

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
41	MLZ	Lm	98	41	-	0/7/8/10	-

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.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 265 ligands modelled in this entry, 265 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.

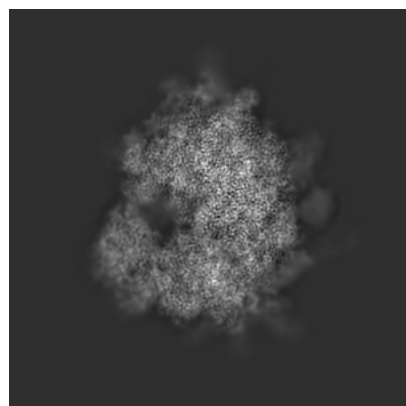
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55616. These allow visual inspection of the internal detail of the map and identification of artifacts.

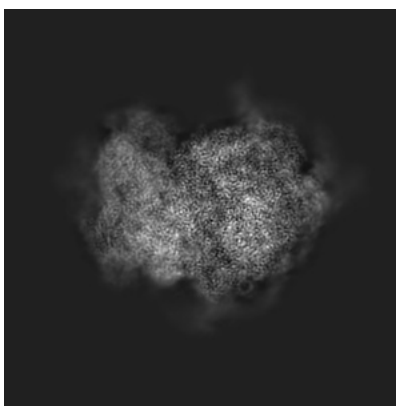
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

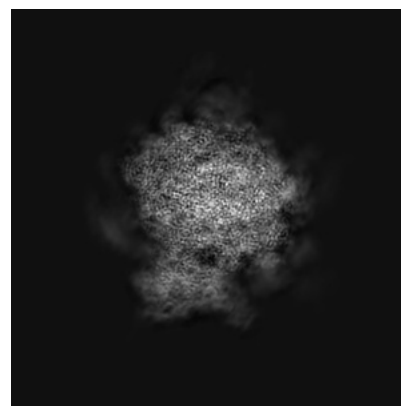
6.1.1 Primary map



X

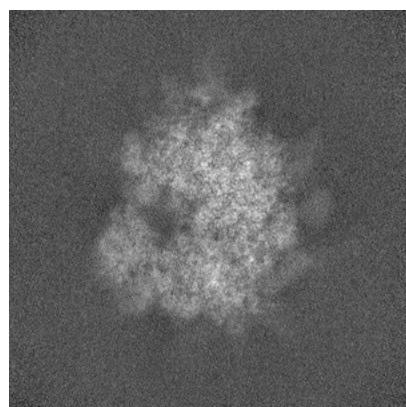


Y

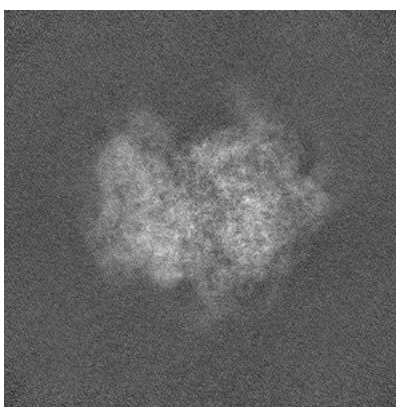


Z

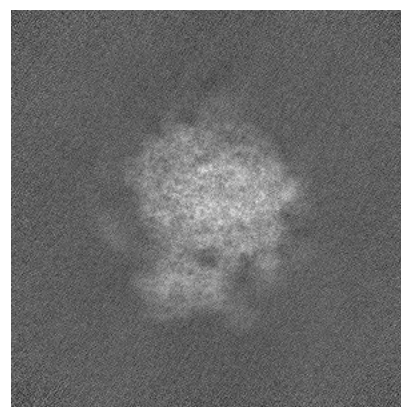
6.1.2 Raw map



X



Y

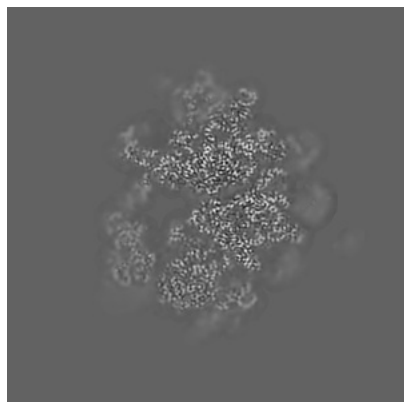


Z

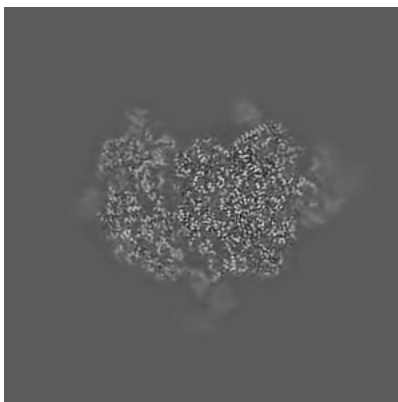
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

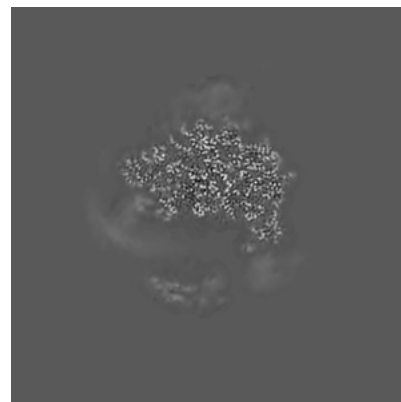
6.2.1 Primary map



X Index: 320

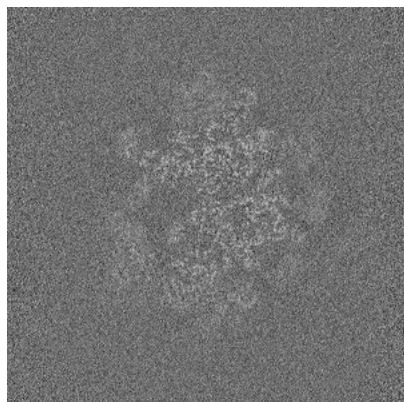


Y Index: 320

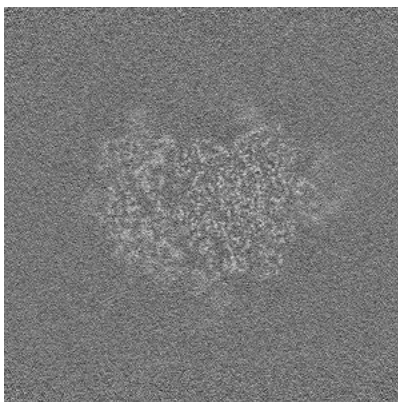


Z Index: 320

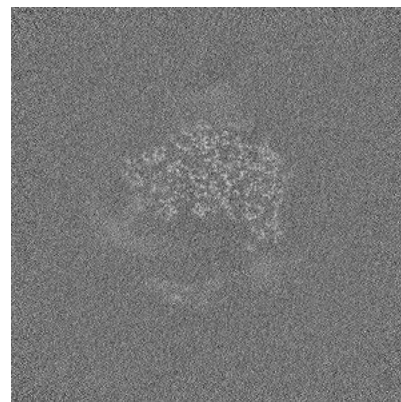
6.2.2 Raw map



X Index: 320



Y Index: 320

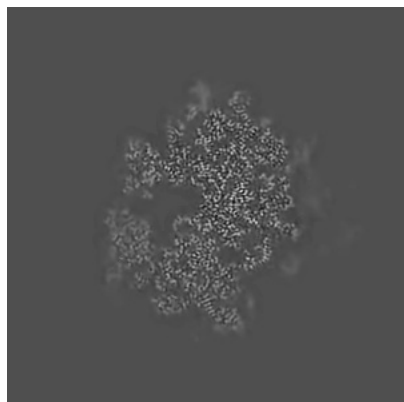


Z Index: 320

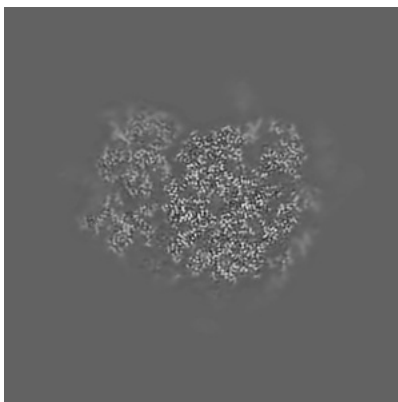
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

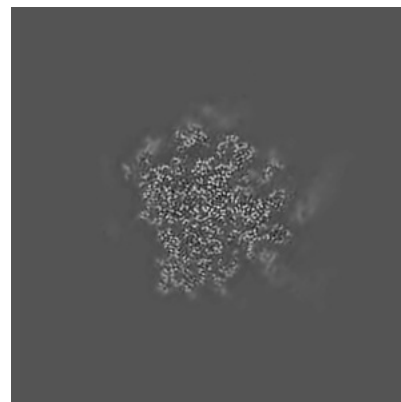
6.3.1 Primary map



X Index: 298

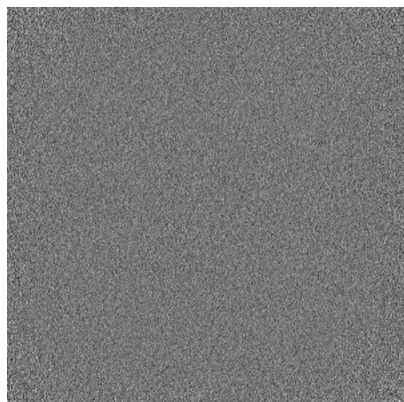


Y Index: 346

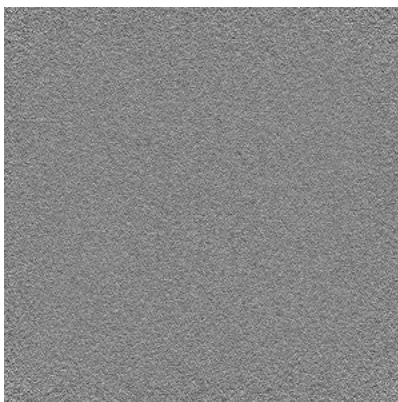


Z Index: 385

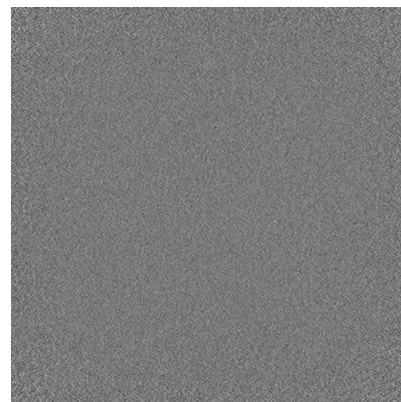
6.3.2 Raw map



X Index: 0



Y Index: 0

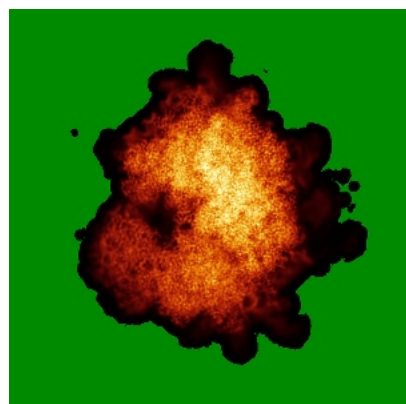


Z Index: 0

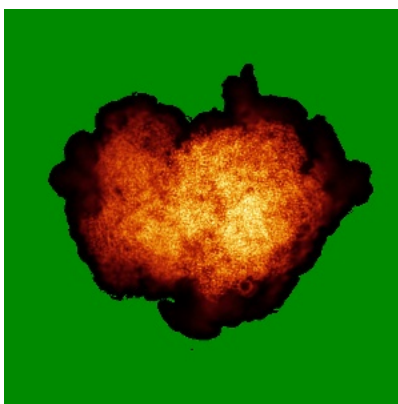
The images above show the largest variance slices of the map in three orthogonal directions.

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

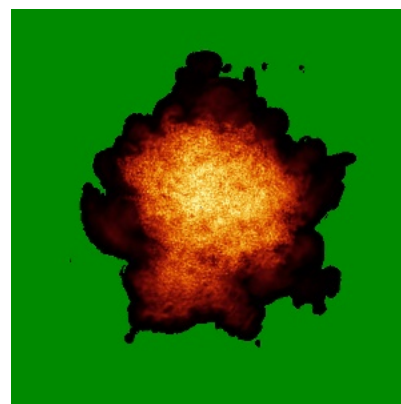
6.4.1 Primary map



X

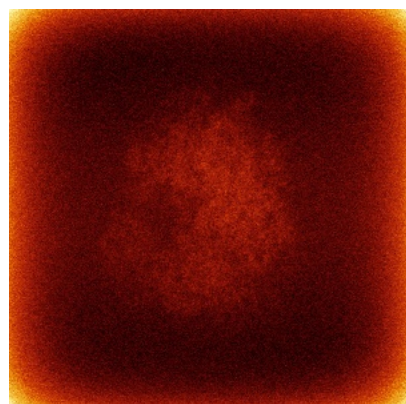


Y

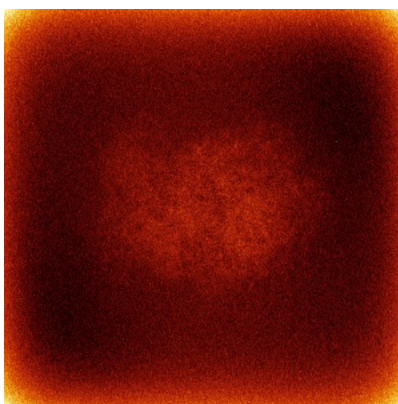


Z

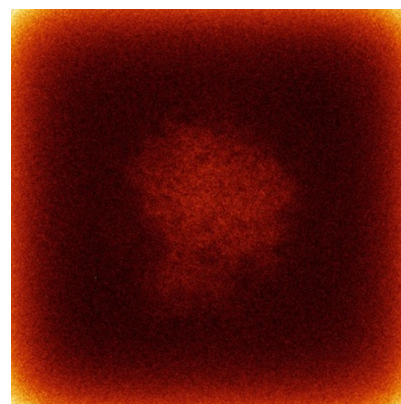
6.4.2 Raw map



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.

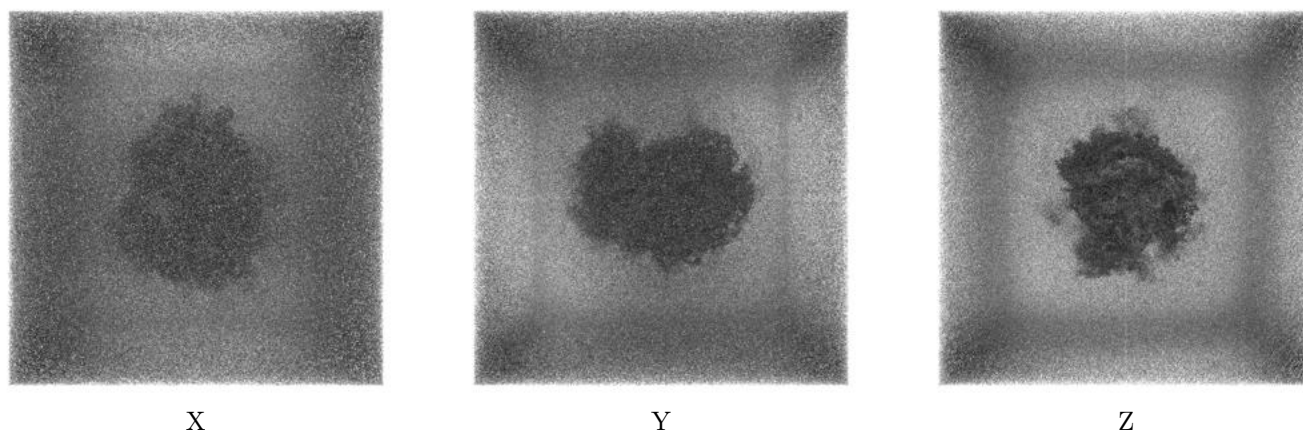
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.11. 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.

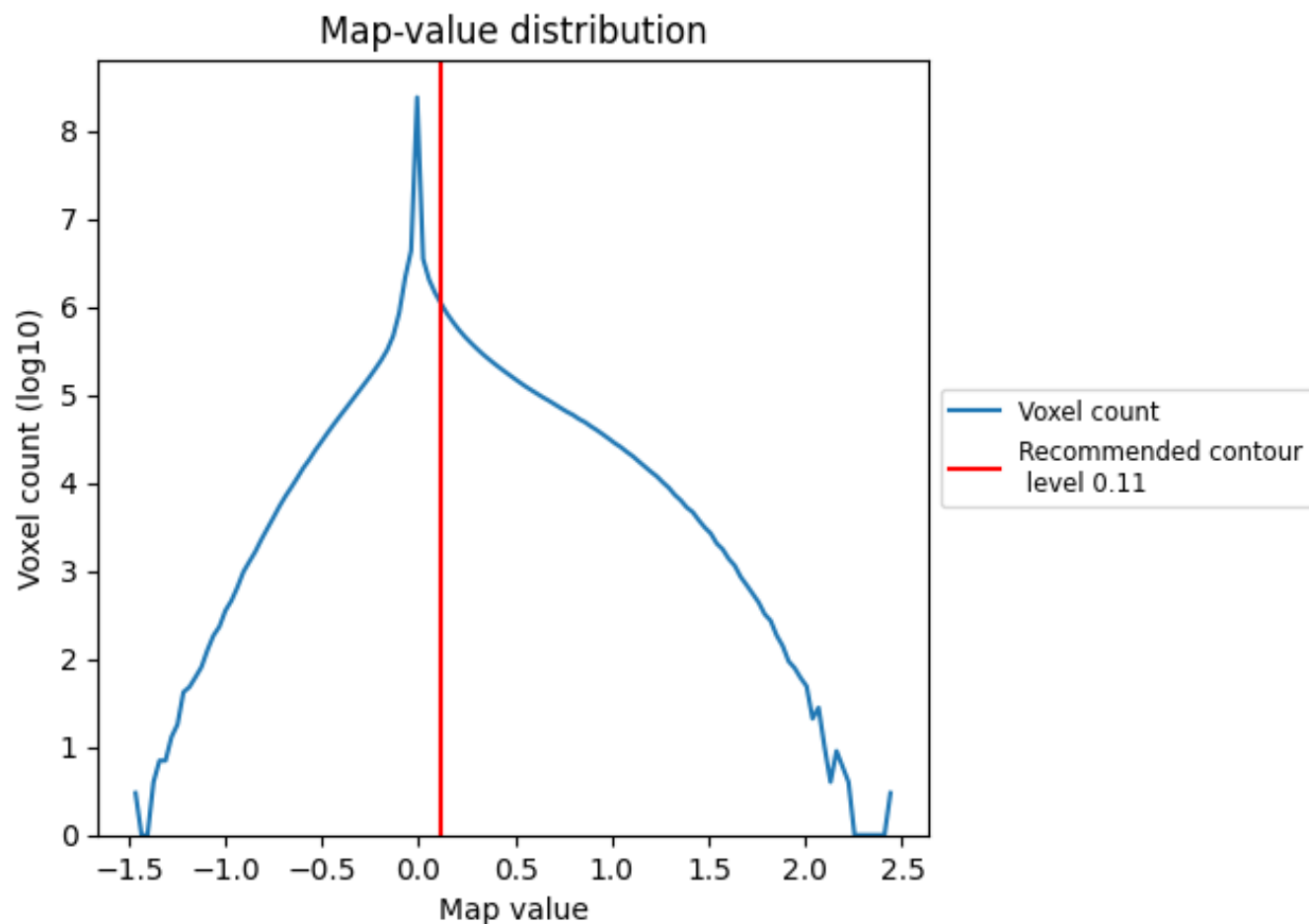
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

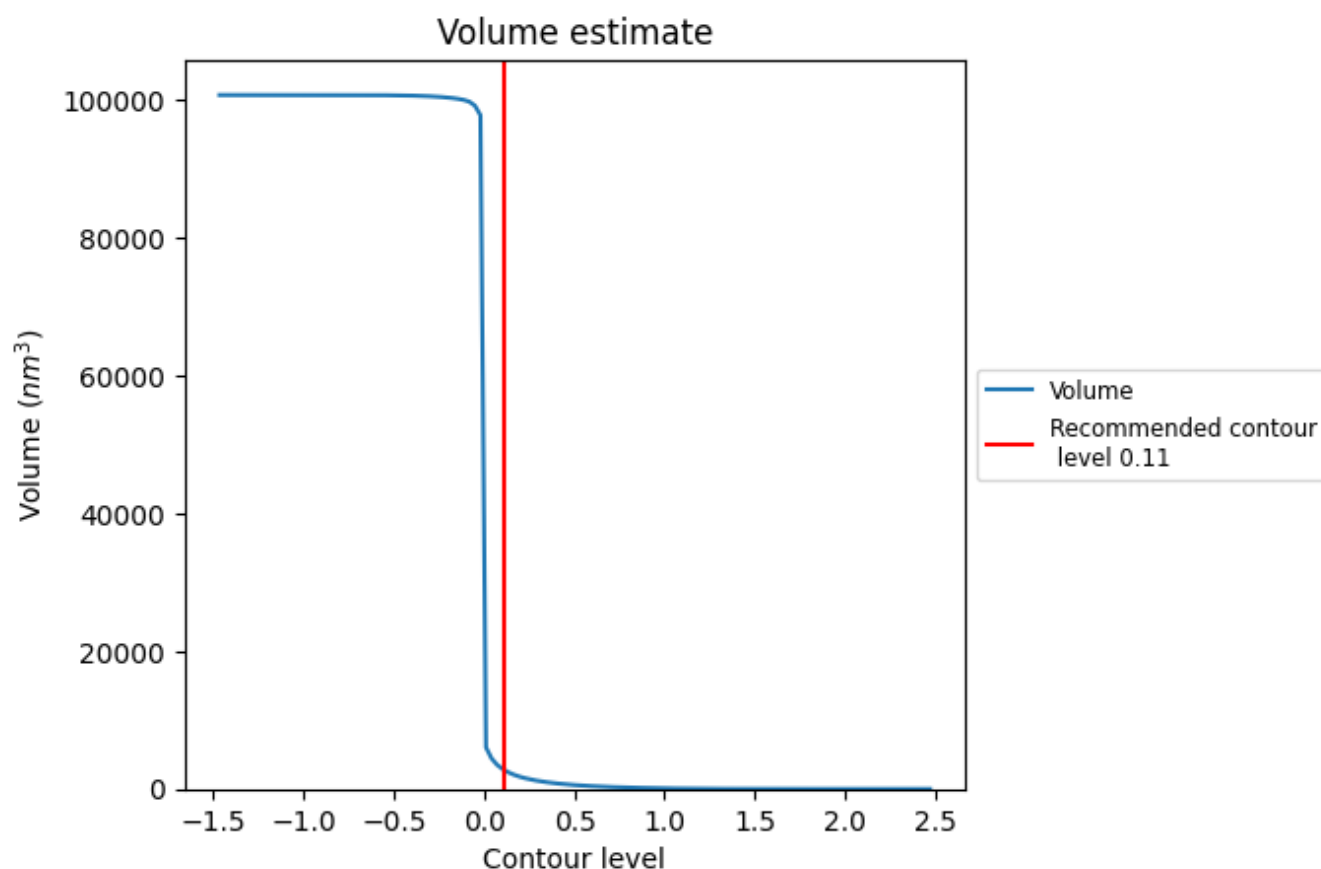
This section contains the results of statistical analysis of the map.

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.

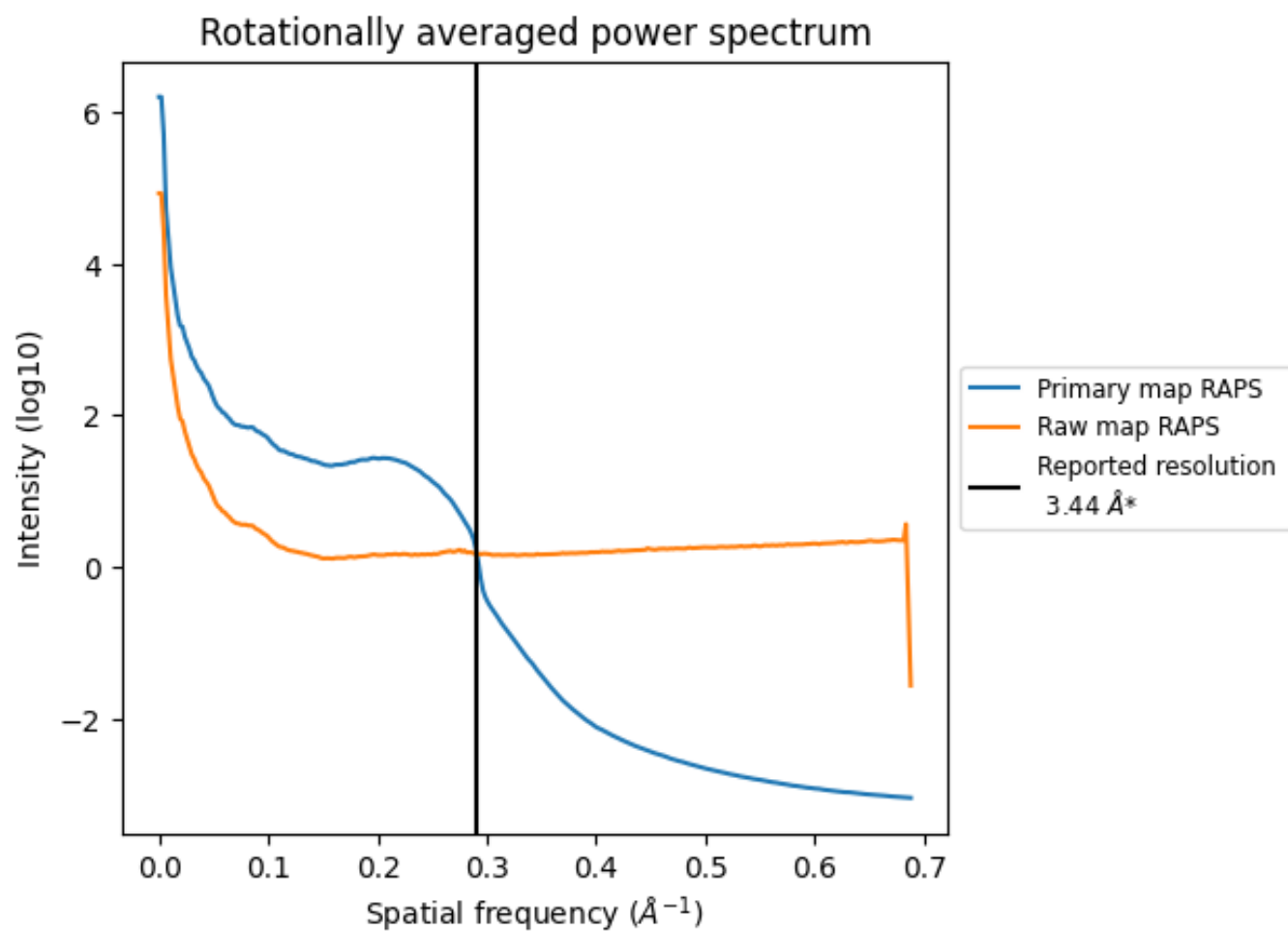
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2790 nm³; this corresponds to an approximate mass of 2521 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 ⓘ

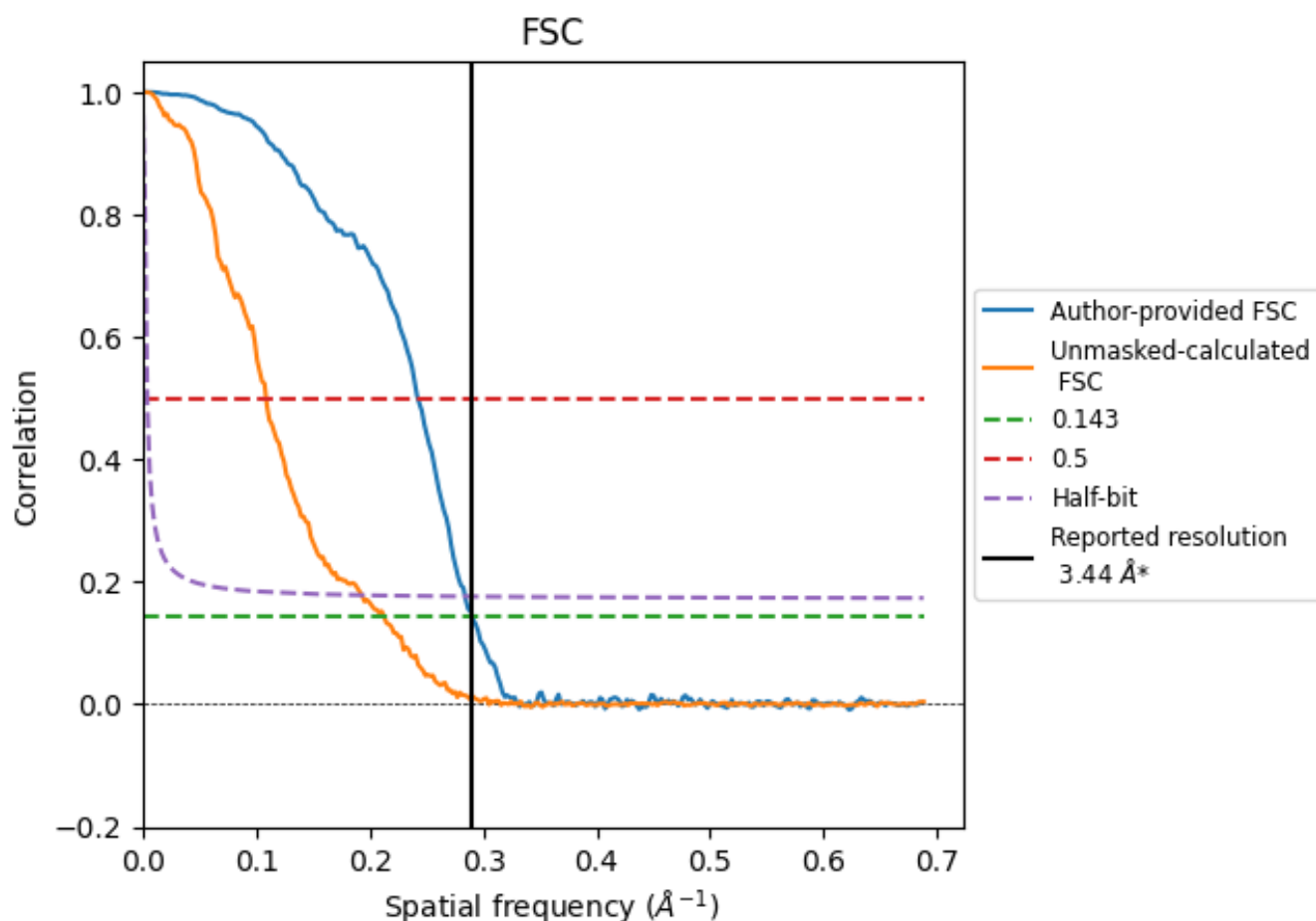


*Reported resolution corresponds to spatial frequency of 0.291 $\text{\AA}^{-1}$

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 $0.291 \text{ \AA}^{-1}$

8.2 Resolution estimates

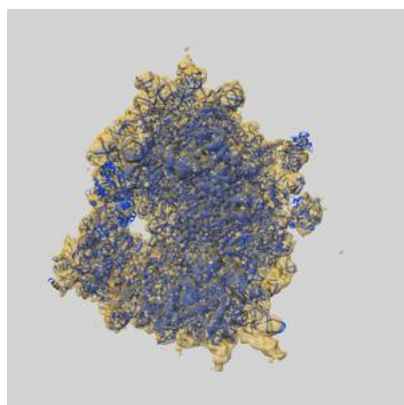
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.44	-	-
Author-provided FSC curve	3.44	4.13	3.52
Unmasked-calculated*	4.70	9.18	5.18

*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 4.70 differs from the reported value 3.44 by more than 10 %

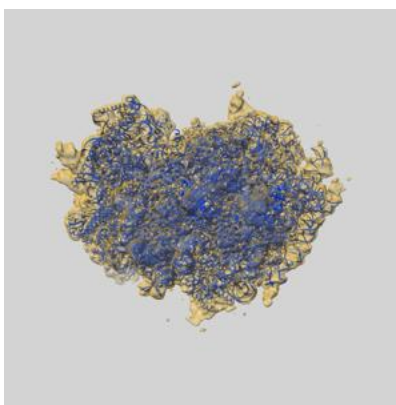
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55616 and PDB model 9T6I. Per-residue inclusion information can be found in section 3 on page 21.

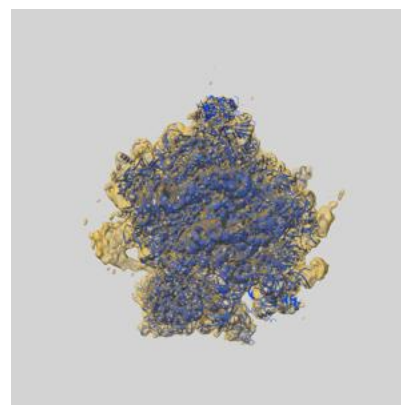
9.1 Map-model overlay [i](#)



X



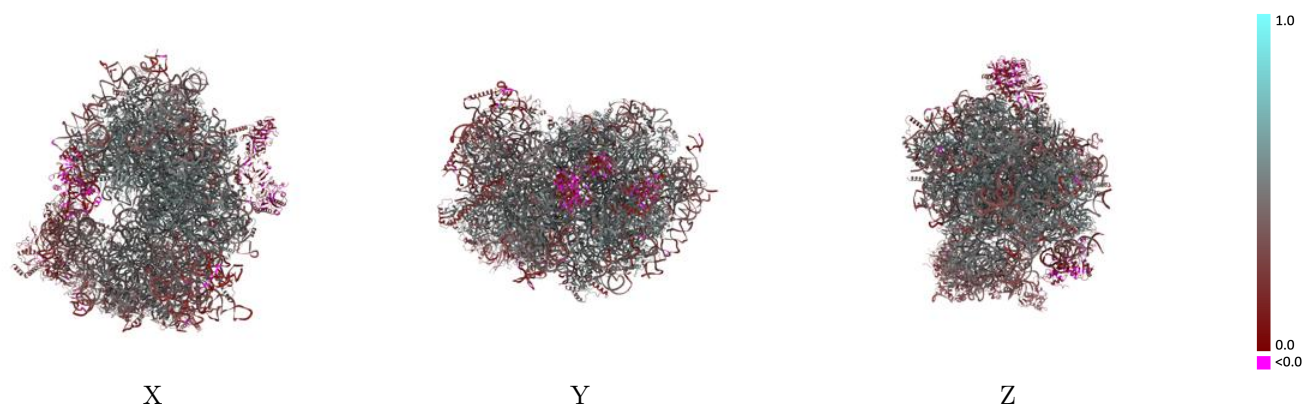
Y



Z

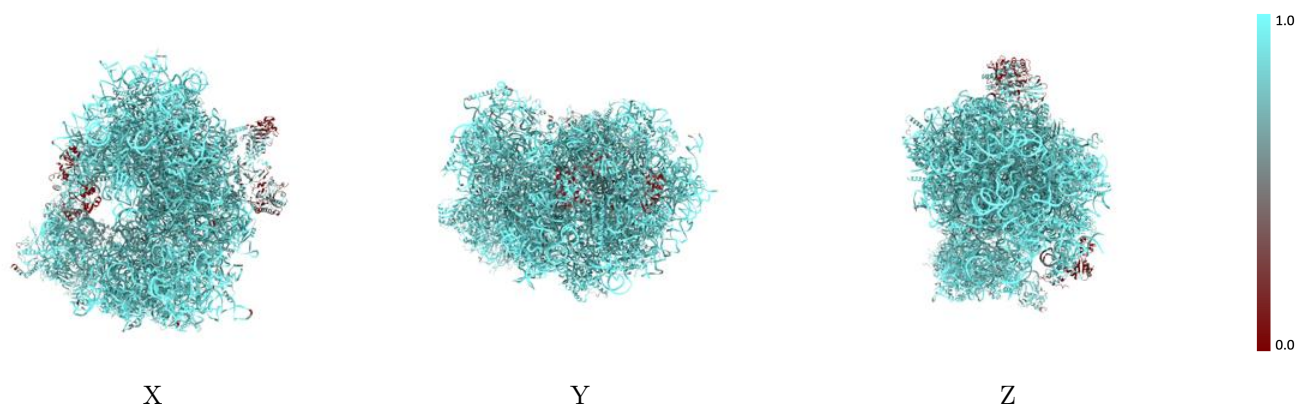
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



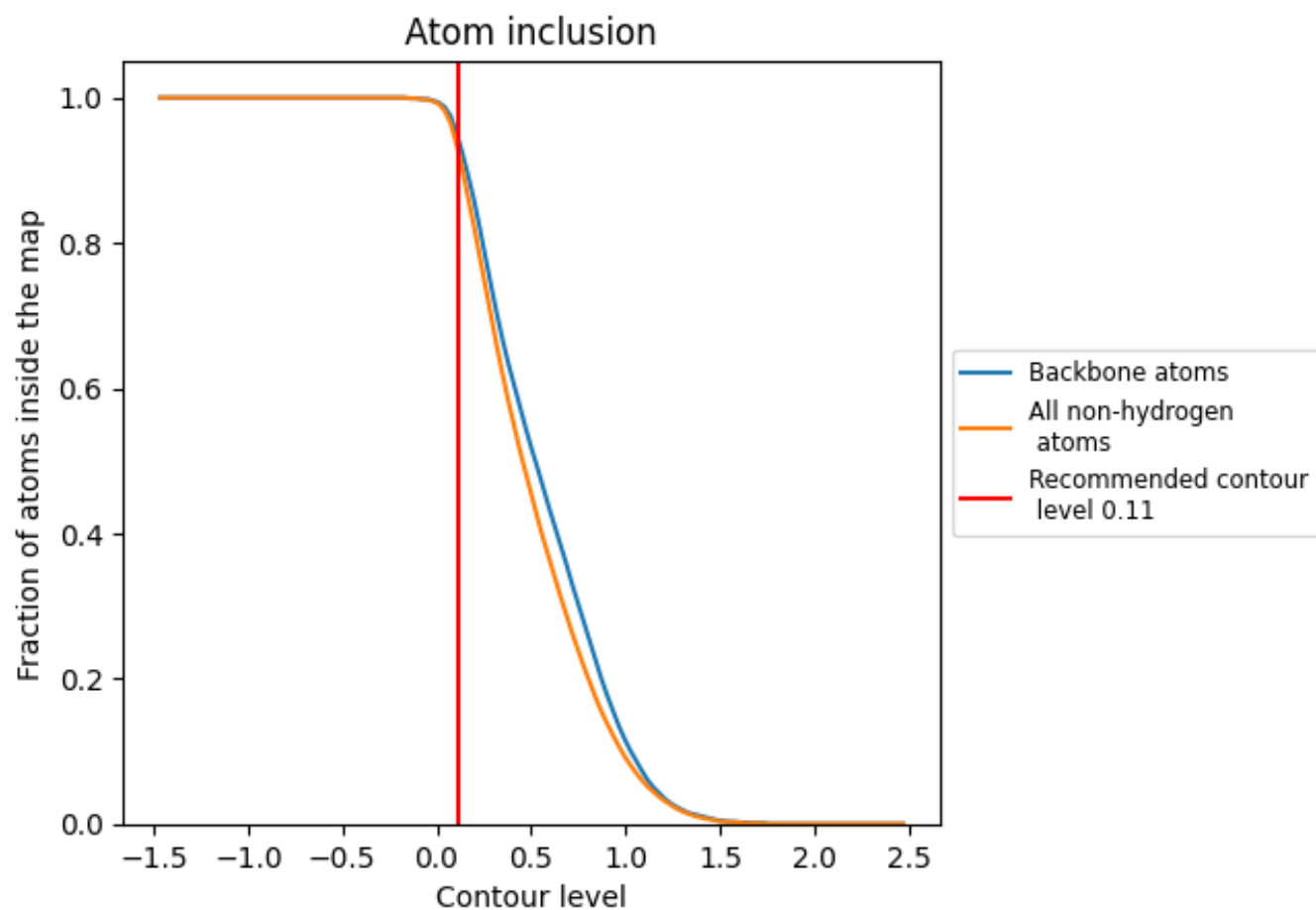
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9310	 0.4150
L5	 0.9660	 0.4380
L7	 0.9840	 0.4790
L8	 0.9620	 0.4470
LA	 0.9580	 0.5390
LB	 0.9560	 0.5150
LC	 0.9530	 0.5170
LD	 0.9560	 0.4540
LE	 0.9640	 0.4760
LF	 0.9560	 0.5170
LG	 0.9140	 0.4410
LH	 0.9590	 0.4950
LI	 0.9620	 0.5130
LJ	 0.9380	 0.4220
LL	 0.9390	 0.4890
LM	 0.9630	 0.4940
LN	 0.9560	 0.5390
LO	 0.9470	 0.5150
LP	 0.9510	 0.5290
LQ	 0.9610	 0.5310
LR	 0.9210	 0.4620
LS	 0.9690	 0.5350
LT	 0.9450	 0.4970
LU	 0.9540	 0.4450
LV	 0.9570	 0.5210
LW	 0.8490	 0.3480
LX	 0.9160	 0.4860
LY	 0.9470	 0.5010
LZ	 0.9690	 0.4920
La	 0.9630	 0.5250
Lb	 0.8990	 0.4290
Lc	 0.9370	 0.4880
Ld	 0.9310	 0.4900
Le	 0.9630	 0.5370
Lf	 0.9620	 0.5490



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Lg	 0.9450	 0.5070
Lh	 0.9380	 0.4770
Li	 0.9400	 0.4740
Lj	 0.9560	 0.5390
Lk	 0.9160	 0.4310
Ll	 0.9670	 0.5340
Lm	 0.9380	 0.5020
Ln	 0.6080	 0.3140
Lo	 0.9340	 0.5000
Lp	 0.9420	 0.5140
Lr	 0.9610	 0.5200
Ls	 0.2890	 0.0790
Lt	 0.4610	 0.0700
MA	 0.4400	 0.0790
N4	 0.6070	 0.1370
NA	 0.4820	 0.1120
NB	 0.7060	 0.1800
S2	 0.9660	 0.3790
SA	 0.9210	 0.4150
SB	 0.9080	 0.4160
SC	 0.9420	 0.4420
SD	 0.8490	 0.3060
SE	 0.9290	 0.4310
SF	 0.8680	 0.2700
SG	 0.9010	 0.3100
SH	 0.9020	 0.3600
SI	 0.9210	 0.4330
SJ	 0.9050	 0.3940
SK	 0.8690	 0.2220
SL	 0.9020	 0.4640
SM	 0.7190	 0.2150
SN	 0.9370	 0.4710
SO	 0.9080	 0.4220
SP	 0.8200	 0.2280
SQ	 0.9040	 0.3010
SR	 0.8910	 0.3350
SS	 0.8590	 0.2340
ST	 0.8890	 0.2610
SU	 0.8950	 0.3000
SV	 0.9520	 0.4310
SW	 0.9300	 0.4750
SX	 0.9390	 0.4800

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SY	 0.9300	 0.3540
SZ	 0.8410	 0.2120
Sa	 0.9160	 0.4620
Sb	 0.9470	 0.4330
Sc	 0.9280	 0.3340
Sd	 0.8980	 0.3140
Se	 0.8940	 0.3770
Sf	 0.7290	 0.1530
Sg	 0.8930	 0.2180