



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:12 AM UTC

PDB ID : 6ZME / pdb_00006zme
EMDB ID : EMD-11289
Title : SARS-CoV-2 Nsp1 bound to the human CCDC124-80S-eERF1 ribosome complex
Authors : Thoms, M.; Buschauer, R.; Ameismeier, M.; Denk, T.; Kratzat, H.; Mackens-Kiani, T.; Cheng, J.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2020-07-02
Resolution : 3.00 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:

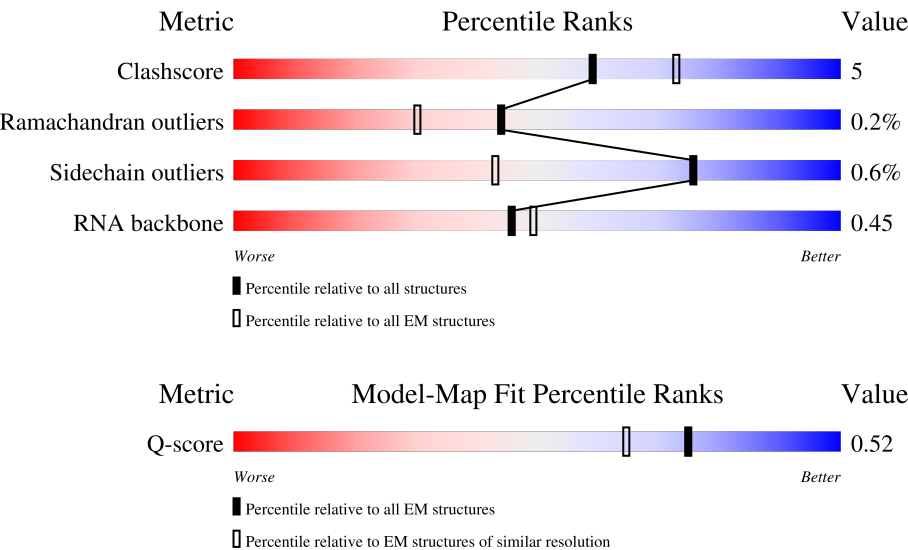
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.00 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.



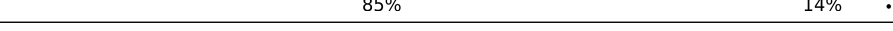
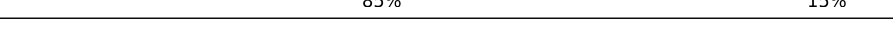
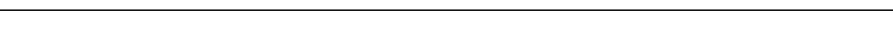
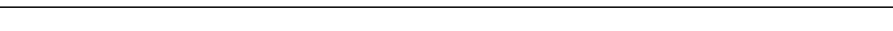
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	5066	
2	L7	121	
3	L8	157	

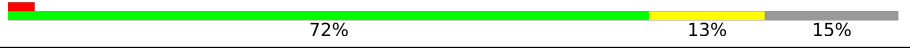
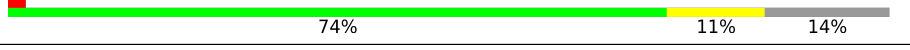
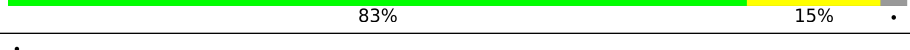
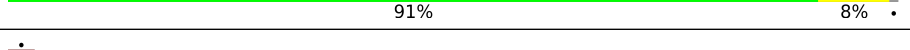
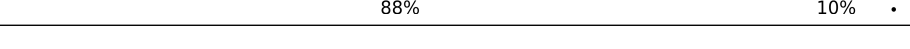
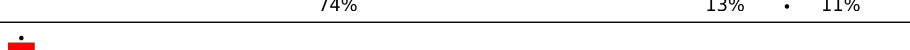
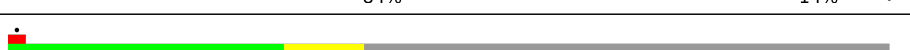
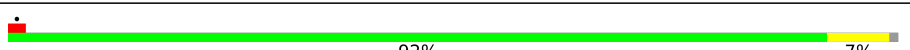
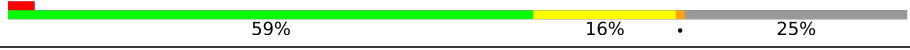
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	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

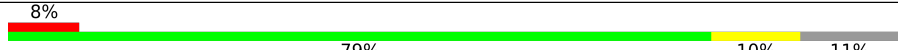
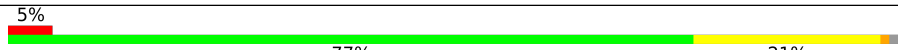
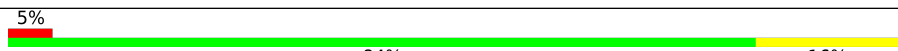
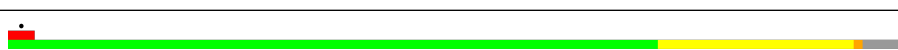
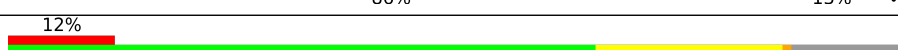
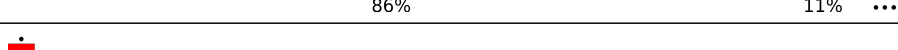
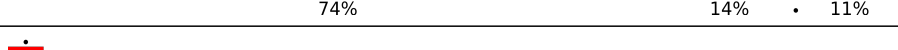
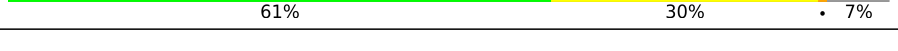
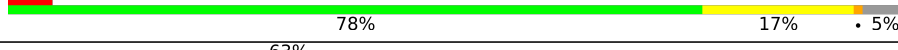
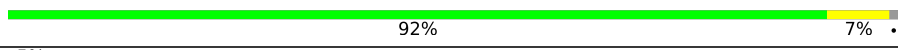
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Ls	317	
47	Lt	165	
48	Lz	217	
49	S2	1869	
50	SA	295	
51	SB	264	
52	SD	243	
53	SE	263	

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Mol	Chain	Length	Quality of chain
54	SF	204	
55	SH	194	
56	SI	208	
57	SK	165	
58	SL	158	
59	SP	145	
60	SQ	146	
61	SR	135	
62	SS	152	
63	ST	145	
64	SU	119	
65	SV	83	
66	SX	143	
67	Sa	115	
68	Sc	69	
69	Sd	56	
70	Sg	317	
71	SC	293	
72	SG	249	
73	SJ	194	
74	SM	132	
75	SN	151	
76	SO	151	
77	SW	130	
78	SY	133	

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Mol	Chain	Length	Quality of chain
79	SZ	125	
80	Sb	84	
81	Se	59	
82	Sf	156	
83	CA	394	
84	CC	75	
85	CE	223	
86	CF	180	
87	CI	599	
88	CH	437	

2 Entry composition

There are 92 unique types of molecules in this entry. The entry contains 233375 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3773	Total	C	N	O	P	0	0
			80138	35655	14589	26122	3772		

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

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 ribosomal RNA.

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	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- 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 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

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-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	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	101	Total	C	N	O	S	0	0
			825	529	144	150	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	134	Total	C	N	O	S	0	0
			1115	700	226	186	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
			876	546	189	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 60S ribosomal protein L37.

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 Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	52	Total	C	N	O	S	0	0
			429	266	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 60S ribosomal protein L12.

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 60S ribosomal protein L10a.

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

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	1740	Total	C	N	O	P	0	0
			36899	16459	6598	12103	1739		

- Molecule 50 is a protein called 40S ribosomal protein SA.

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

- Molecule 51 is a protein called 40S ribosomal protein S3a.

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

- Molecule 52 is a protein called 40S ribosomal protein S3.

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

- Molecule 53 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 54 is a protein called 40S ribosomal protein S5.

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

- Molecule 55 is a protein called 40S ribosomal protein S7.

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

- Molecule 56 is a protein called 40S ribosomal protein S8.

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

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

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

- Molecule 58 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 59 is a protein called 40S ribosomal protein S15.

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

- Molecule 60 is a protein called 40S ribosomal protein S16.

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

- Molecule 61 is a protein called 40S ribosomal protein S17.

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

- Molecule 62 is a protein called 40S ribosomal protein S18.

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

- Molecule 63 is a protein called 40S ribosomal protein S19.

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

- Molecule 64 is a protein called 40S ribosomal protein S20.

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

- Molecule 65 is a protein called 40S ribosomal protein S21.

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

- Molecule 66 is a protein called 40S ribosomal protein S23.

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

- Molecule 67 is a protein called 40S ribosomal protein S26.

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

- Molecule 68 is a protein called 40S ribosomal protein S28.

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

- Molecule 69 is a protein called 40S ribosomal protein S29.

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

- Molecule 70 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 71 is a protein called 40S ribosomal protein S2.

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

- Molecule 72 is a protein called 40S ribosomal protein S6.

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

- Molecule 73 is a protein called 40S ribosomal protein S9.

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

- Molecule 74 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 75 is a protein called 40S ribosomal protein S13.

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

- Molecule 76 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 77 is a protein called 40S ribosomal protein S15a.

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

- Molecule 78 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 79 is a protein called 40S ribosomal protein S25.

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

- 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 S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Se	58	Total	C	N	O	S	0	0
			439	268	97	73	1		

- Molecule 82 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 83 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	17		

- Molecule 84 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CC	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

- Molecule 85 is a protein called Coiled-coil domain-containing protein 124.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	CE	117	Total	C	N	O	S	0	0
			998	611	199	184	4		

- Molecule 86 is a protein called Non-structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	CF	29	Total	C	N	O	S	0	0
			239	145	43	50	1		

- Molecule 87 is a protein called ATP-binding cassette sub-family E member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	CI	582	Total	C	N	O	S	0	0
			4586	2931	785	839	31		

- Molecule 88 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	CH	415	Total	C	N	O	S	0	0
			3257	2073	556	617	11		

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	L5	210	Total	Mg	0
			210	210	
89	L7	3	Total	Mg	0
			3	3	
89	L8	4	Total	Mg	0
			4	4	
89	LA	1	Total	Mg	0
			1	1	
89	LB	1	Total	Mg	0
			1	1	
89	LI	1	Total	Mg	0
			1	1	

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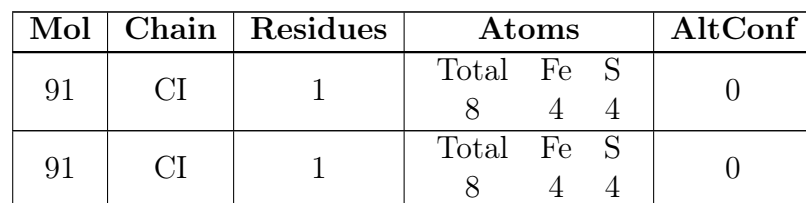
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Mol	Chain	Residues	Atoms		AltConf
89	LP	1	Total 1	Mg 1	0
89	LV	1	Total 1	Mg 1	0
89	LX	1	Total 1	Mg 1	0
89	Le	2	Total 2	Mg 2	0
89	Lg	1	Total 1	Mg 1	0
89	S2	29	Total 29	Mg 29	0
89	SG	1	Total 1	Mg 1	0

- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 91 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



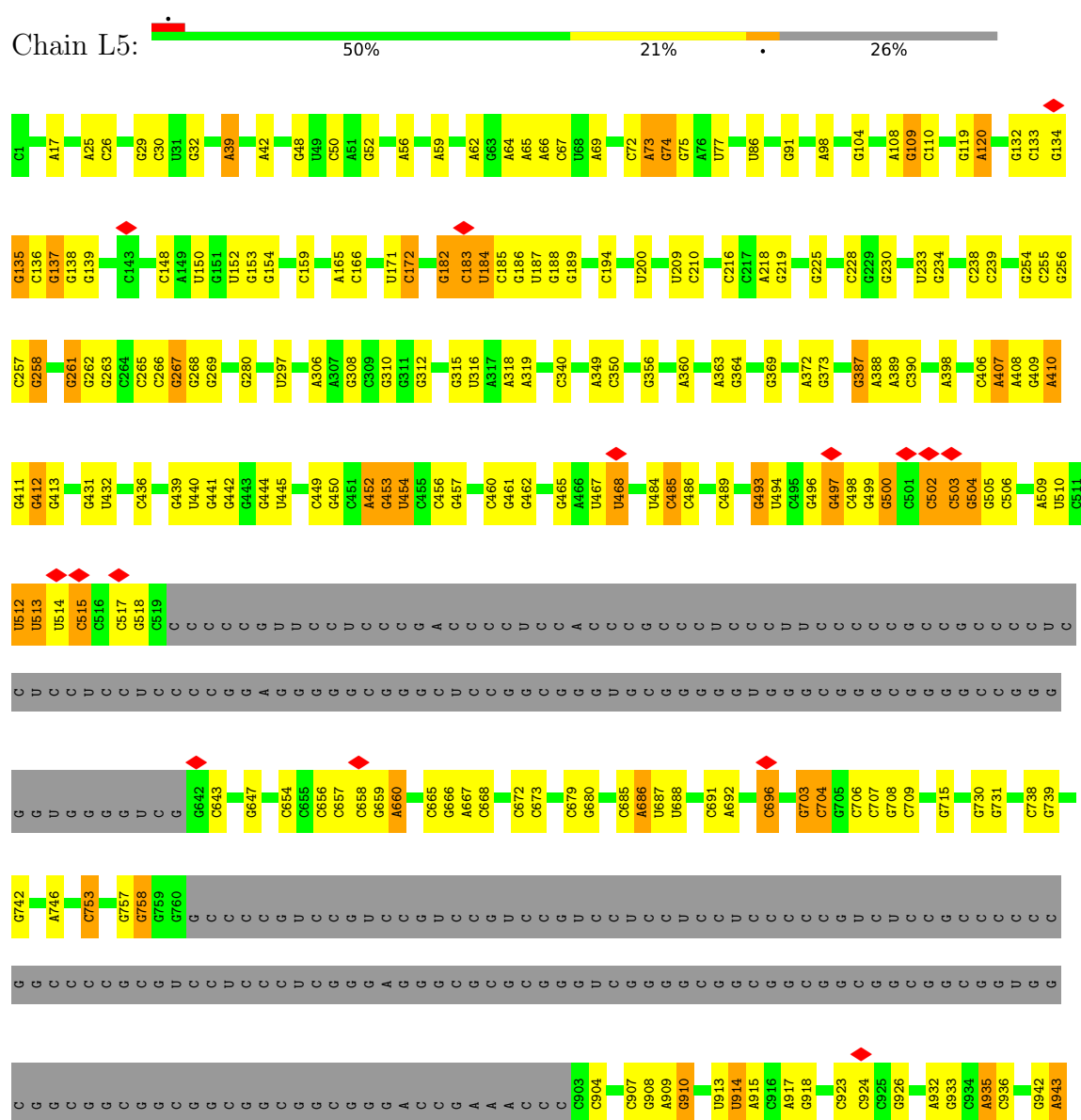
- # ADP

Mol	Chain	Residues	Atoms					AltConf
92	CI	1	Total 27	C 10	N 5	O 10	P 2	0

3 Residue-property plots [i](#)

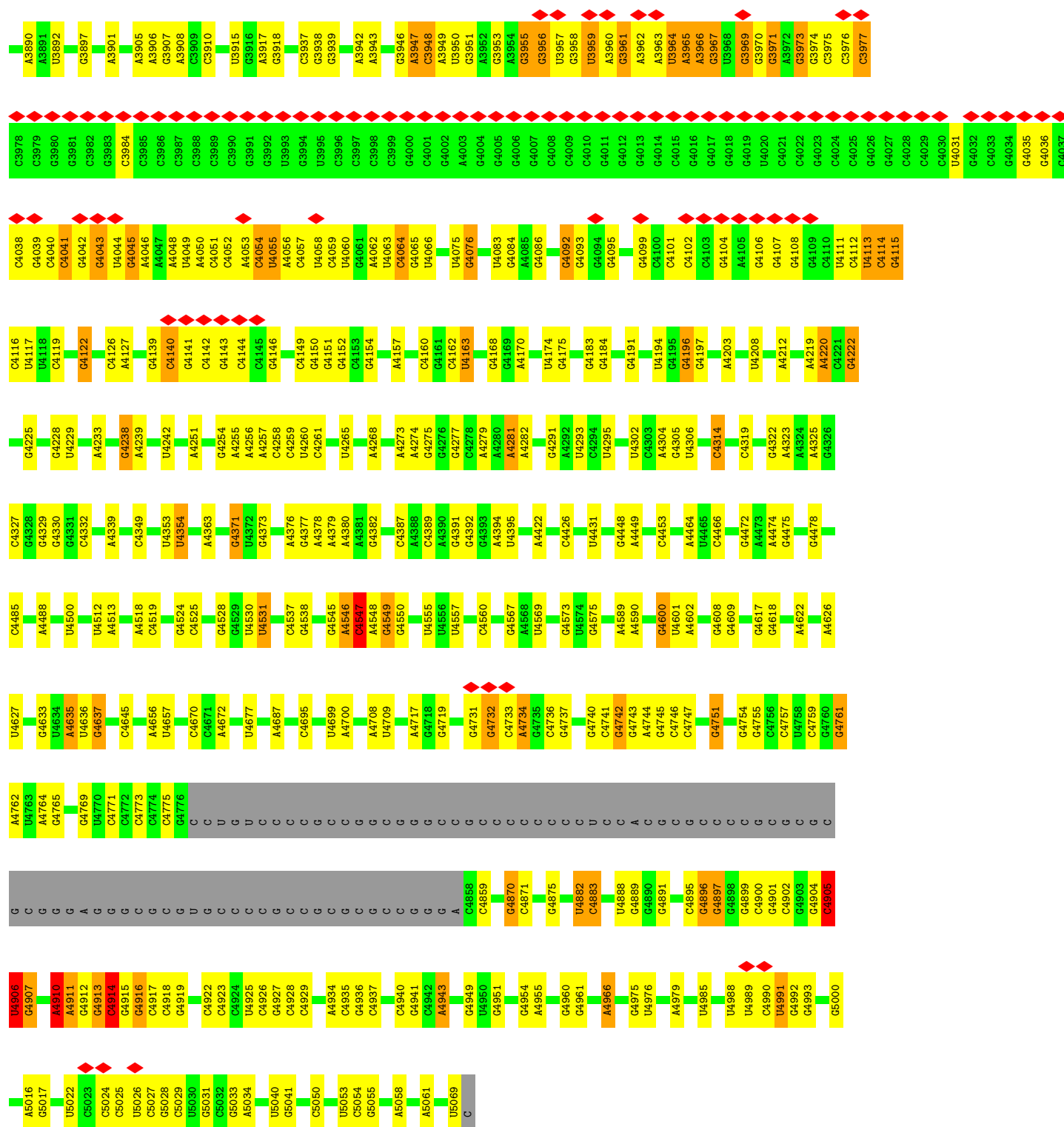
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 28S ribosomal RNA





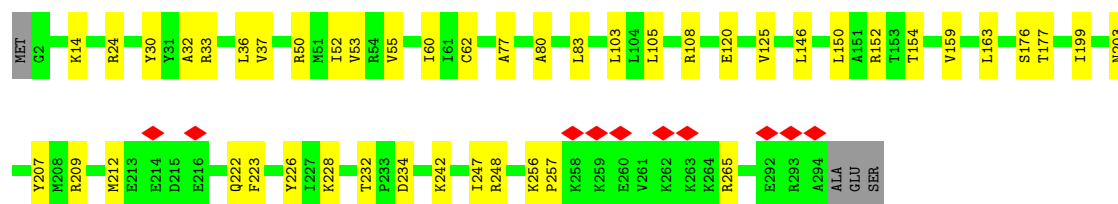




• Molecule 2: 5S ribosomal RNA

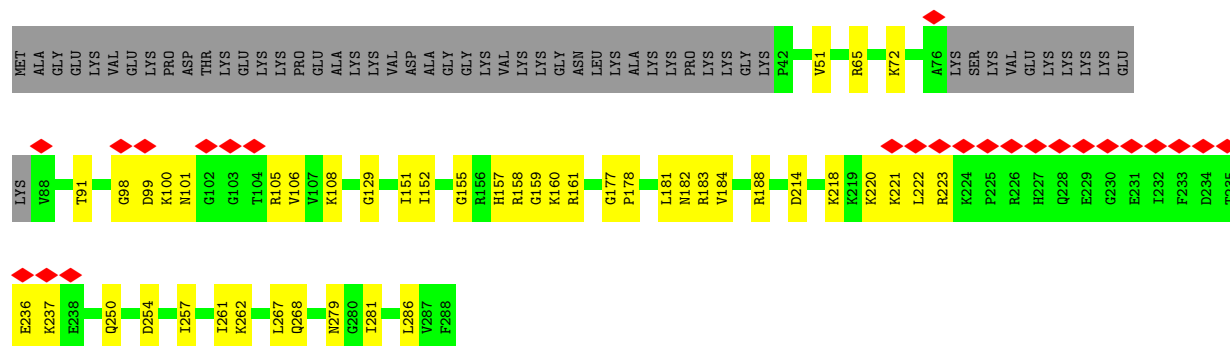
Chain L7: 81% 18%

Chain LD:  83% 15%



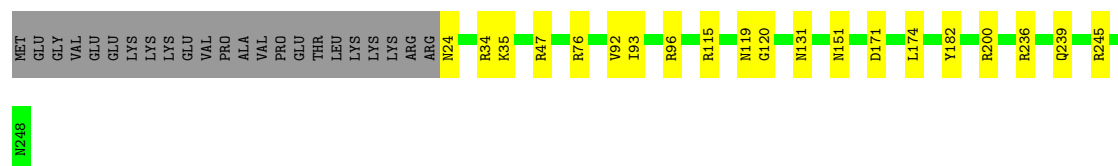
• Molecule 8: 60S ribosomal protein L6

Chain LE:  9% 66% 16% 18%



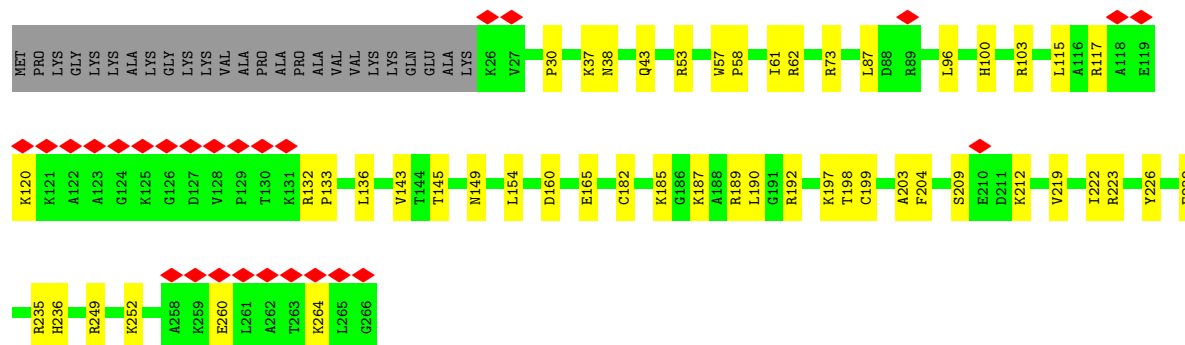
• Molecule 9: 60S ribosomal protein L7

Chain LF:  83% 8% 9%



• Molecule 10: 60S ribosomal protein L7a

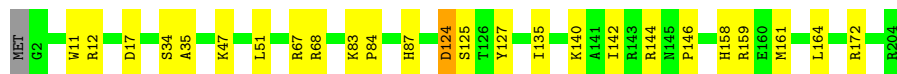
Chain LG:  10% 72% 19% 9%



• Molecule 11: 60S ribosomal protein L9

- Molecule 16: 60S ribosomal protein L15

Chain LN:  87% 12%



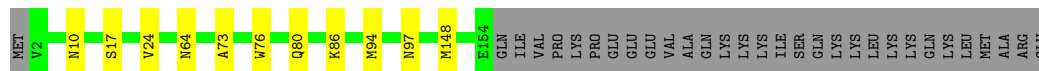
- Molecule 17: 60S ribosomal protein L13a

Chain LO:  88% 10%



- Molecule 18: 60S ribosomal protein L17

Chain LP:  77% 6% 17%



- Molecule 19: 60S ribosomal protein L18

Chain LQ:  89% 10%



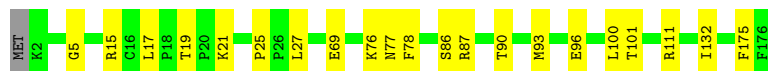
- Molecule 20: 60S ribosomal protein L19

Chain LR:  6% 84% 12% 5%



- Molecule 21: 60S ribosomal protein L18a

Chain LS:  88% 12%



- Molecule 22: 60S ribosomal protein L21

Chain LT:  86% 14%



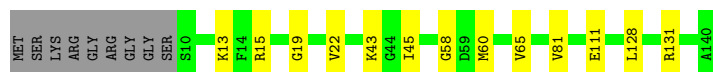
- Molecule 23: 60S ribosomal protein L22

Chain LU:  71% 8% 21%



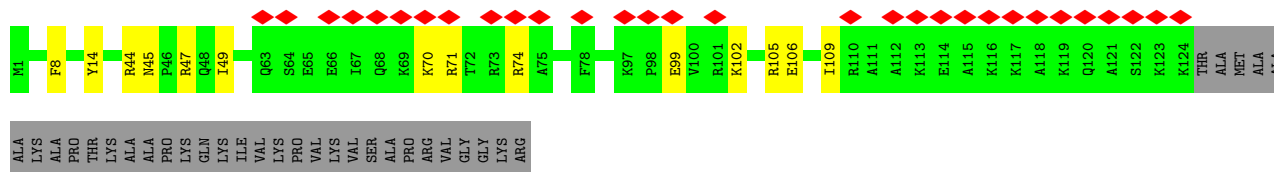
- Molecule 24: 60S ribosomal protein L23

Chain LV:  84% 9% 6%



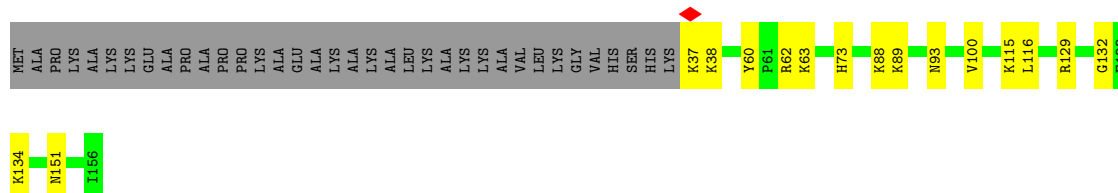
- Molecule 25: 60S ribosomal protein L24

Chain LW:  19% 70% 9% 21%



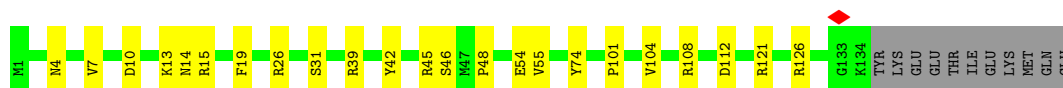
- Molecule 26: 60S ribosomal protein L23a

Chain LX:  67% 10% 23%



- Molecule 27: 60S ribosomal protein L26

Chain LY:  77% 16% 8%

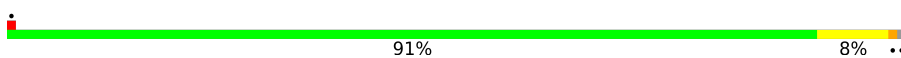


- Molecule 28: 60S ribosomal protein L27

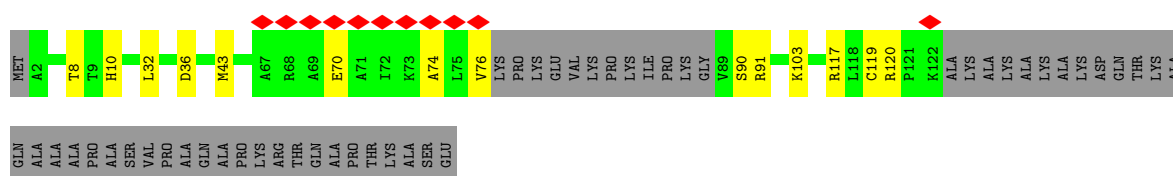
Chain LZ:  87% 12% 1%



• Molecule 29: 60S ribosomal protein L27a

Chain La:  91% 8% ..

• Molecule 30: 60S ribosomal protein L29

Chain Lb:  7% 60% 9% 31%

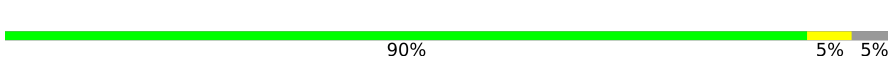
• Molecule 31: 60S ribosomal protein L30

Chain Lc:  72% 13% 15%

• Molecule 32: 60S ribosomal protein L31

Chain Ld:  74% 11% 14%

• Molecule 33: 60S ribosomal protein L32

Chain Le:  90% 5% 5%

• Molecule 34: 60S ribosomal protein L35a

Chain Lf:  84% 15% ..

• Molecule 35: 60S ribosomal protein L34

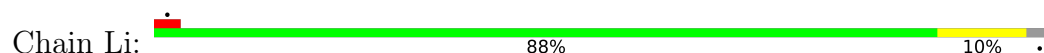
Chain Lg:  5% 83% 15% .



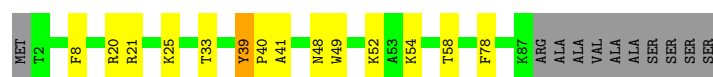
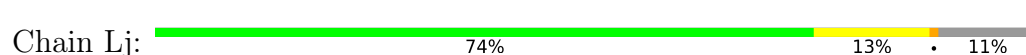
- Molecule 36: 60S ribosomal protein L35



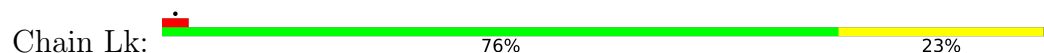
- Molecule 37: 60S ribosomal protein L36



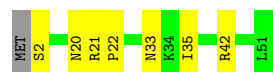
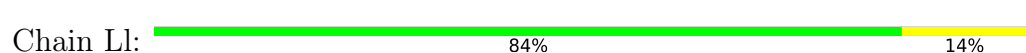
- Molecule 38: 60S ribosomal protein L37



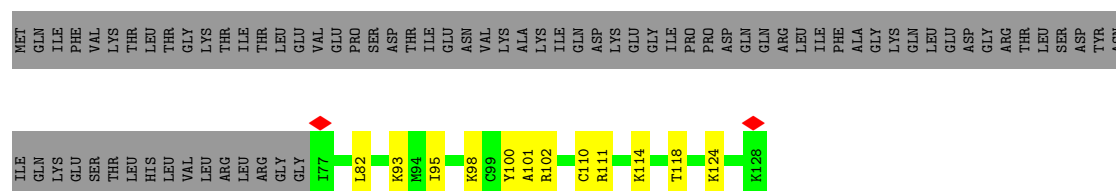
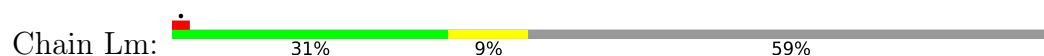
- Molecule 39: 60S ribosomal protein L38

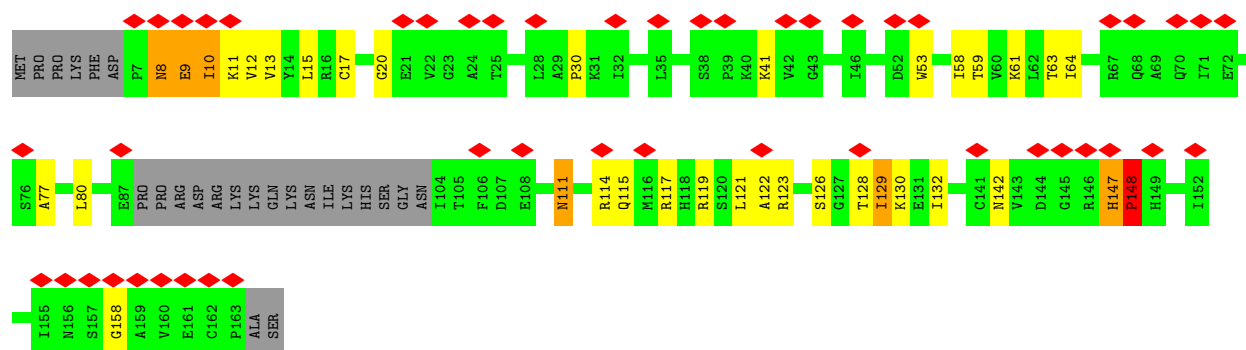


- Molecule 40: 60S ribosomal protein L39

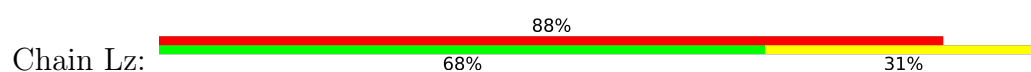


- Molecule 41: Ubiquitin-60S ribosomal protein L40

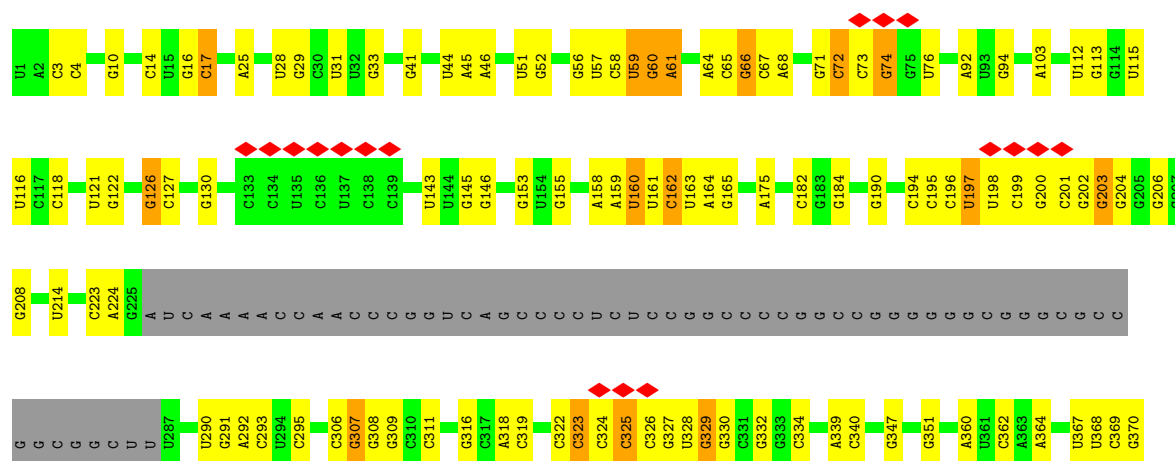




• Molecule 48: 60S ribosomal protein L10a



• Molecule 49: 18S ribosomal RNA

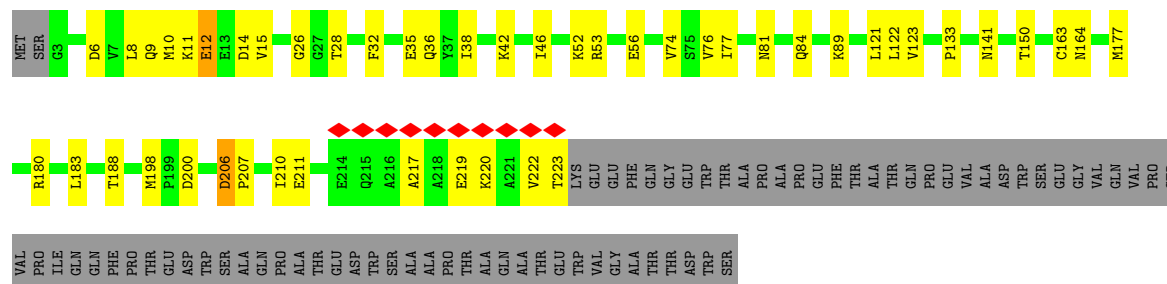


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U1761	G1658	A1556	A1438	G1207	U1061	A920	C835	G	G694	G589	C503	U372
C1762	U1659	C1557	A1439	A1208	U1062	G921	G836	C	C695	A590	G504	G373
G1763	C1660	C1558	G1449	G1211	G1076	A922	A837	C	G696	U591	G504	G374
G1764	A1663	C1562	G1450	C1215	A1080	G925	G838	C	G697	C593	A508	G377
C1765	G1664	G1563	G1451	C1216	A1081	G928	C839	U	A594	A594	G509	G380
C1766	A1665	G1566	A1452	C1217	A1083	G929	C840	C	G597	G597	A516	C381
C1767	U1666	U1307	A1453	C1218	A1084	G930	G841	C	G	A604	A520	C382
U1768	U1667	U1308	A1454	C1219	C1085	C931	C942	A	G	G605	A521	G383
C1769	G1668	U1309	C1086	G933	G1087	G934	G846	U	G	G606	G385	U384
G1770	G1669	G1312	U1088	G934	A1087	G934	A847	C	G	U607	A825	C386
G1771	U1462	G1318	U1089	U943	U1088	U943	U857	U	C	C608	A529	U396
C1772	U1472	U1342	A1093	A944	A1093	A944	A858	U	C	G610	U530	A408
C1773	A1476	U1343	C1094	C951	C1095	C951	A869	U	C	C614	A531	C409
C1774	A1480	G1348	C1096	G959	G1097	G959	U871	C	C	C615	C532	C417
A1675	U1487	U1371	C1098	G1229	C1097	G1229	A872	G	G	G623	A536	G419
U1676	A1488	U1372	C1099	C1230	C1098	C1230	G873	U	C	G627	C537	G420
G1680	A1489	C1373	G1099	U1232	C1099	U1232	G874	A	A	A628	U538	G421
G1686	G1490	C1374	C1106	G1233	C1106	A972	A875	G	G	U631	C539	
U1694	U1494	G1375	C1109	U1242	C1109	A981	C876	U	C	C632	U540	A433
U1699	G1497	A1378	U1115	U1243	U1115	G982	C877	U	C	G639	U541	G438
A1601	A1498	A1396	C1116	A1251	C1116	A990	C879	C	A	A640	U542	
U1602	A1506	G1406	C1117	C1252	C1117	G991	G881	C	C	A641	C543	A445
C1609	A1507	G1406	C1118	A1253	C1118	A992	U883	C	C	U642	G546	A448
G1613	U1508	U1405	G1121	G1256	G1121	A996	C884	C	C	G644	G547	A449
G1617	U1509	A1405	U1129	A1257	U1129	A997	A886	C	C	A655	U551	A450
U1720	U1512	G1406	G1130	A1258	G1130	G999	U887	C	C	A656	U556	A451
U1721	G1513	U1406	A1133	A1260	A1133	A1001	U888	C	C	G659	U557	G452
G1722	G1514	C1412	C1138	C1261	C1138	G1010	U889	C	C	C660	U558	A464
A1735	G1517	A1413	C1139	A1265	C1139	A1011	G891	C	C	U661	G559	A465
C1742	G1520	C1415	A1148	G1274	A1148	U1013	U892	C	C	G662	A560	G471
G1743	C1521	C1416	A1149	G1275	A1149	G1014	G895	C	C	C734	U561	C472
A1831	A1531	C1417	A1150	C1276	A1150	U1015	U896	C	C	C735	G563	A473
C1833	C1532	C1418	C1153	C1277	C1153	U1016	U897	C	C	C736	A564	G474
A1835	A1533	C1419	C1154	C1278	C1154	U1017	U898	C	C	C737	U565	C475
U1838	G1536	G1420	U1155	C1279	U1155	U1018	U899	C	C	C738	U566	A476
G1843	A1537	A1421	U1156	G1280	U1156	U1019	C900	C	C	A670	C567	
A1845	U1542	G1422	G1158	G1281	G1158	A1023	G901	C	C	A671	C568	G482
G1846	G1543	G1423	G1159	C1282	G1159	A1024	G902	U	U	A672	A569	A485
G1849	C1544	G1424	G1160	C1283	G1160	A1025	A903	C	C	G673	C570	A486
A1850	G1545	G1425	G1161	C1284	G1161	A1026	U906	U	U	U681	U576	U488
C1852	G1546	G1426	G1162	C1285	G1162	A1027	G907	C	C	U688	U581	C492
G1855	G1547	G1427	G1163	C1286	G1163	A1028	A908	C	C	U689	U582	A493
G1858	G1548	G1428	G1164	G1287	G1164	A1029	G909	C	C	G690	A583	C494
G1861	G1549	G1429	G1165	A1287	G1165	A1030	A913	C	C	G692	A584	U495
	G1550	C1433	G1166	A1288	G1166	A1031	U914	C	C		G585	
	G1551	C1434	G1167	G1289	G1167	A1032		C	C		A587	
	G1552	C1435	G1168	A1290	G1168	C1047		C	C			
	G1553	C1436	G1169	A1291	G1169			C	C			
	G1554	C1437	G1170	A1292	G1170			C	C			
	G1555	C1438	G1171	A1293	G1171			C	C			
	G1556	C1439	G1172	A1294	G1172			C	C			
	G1557	C1440	G1173	A1295	G1173			C	C			
	G1558	C1441	G1174	A1296	G1174			C	C			
	G1559	C1442	G1175	A1297	G1175			C	C			
	G1560	C1443	G1176	A1298	G1176			C	C			
	G1561	C1444	G1177	A1299	G1177			C	C			
	G1562	C1445	G1178	A1300	G1178			C	C			
	G1563	C1446	G1179	A1301	G1179			C	C			
	G1564	C1447	G1180	A1302	G1180			C	C			
	G1565	C1448	G1181	A1303	G1181			C	C			
	G1566	C1449	G1182	A1304	G1182			C	C			
	G1567	C1450	G1183	A1305	G1183			C	C			
	G1568	C1451	G1184	A1306	G1184			C	C			
	G1569	C1452	G1185	A1307	G1185			C	C			
	G1570	C1453	G1186	A1308	G1186			C	C			
	G1571	C1454	G1187	A1309	G1187			C	C			
	G1572	C1455	G1188	A1310	G1188			C	C			
	G1573	C1456	G1189	A1311	G1189			C	C			
	G1574	C1457	G1190	A1312	G1190			C	C			
	G1575	C1458	G1191	A1313	G1191			C	C			
	G1576	C1459	G1192	A1314	G1192			C	C			
	G1577	C1460	G1193	A1315	G1193			C	C			
	G1578	C1461	G1194	A1316	G1194			C	C			
	G1579	C1462	G1195	A1317	G1195			C	C			
	G1580	C1463	G1196	A1318	G1196			C	C			
	G1581	C1464	G1197	A1319	G1197			C	C			
	G1582	C1465	G1198	A1320	G1198			C	C			
	G1583	C1466	G1199	A1321	G1199			C	C			
	G1584	C1467	G1200	A1322	G1200			C	C			
	G1585	C1468	G1201	A1323	G1201			C	C			
	G1586	C1469	G1202	A1324	G1202			C	C			
	G1587	C1470	G1203	A1325	G1203			C	C			
	G1588	C1471	G1204	A1326	G1204			C	C			
	G1589	C1472	G1205	A1327	G1205			C	C			
	G1590	C1473	G1206	A1328	G1206			C	C			
	G1591	C1474	G1207	A1329	G1207			C	C			
	G1592	C1475	G1208	A1330	G1208			C	C			
	G1593	C1476	G1209	A1331	G1209			C	C			
	G1594	C1477	G1210	A1332	G1210			C	C			
	G1595	C1478	G1211	A1333	G1211			C	C			
	G1596	C1479	G1212	A1334	G1212			C	C			
	G1597	C1480	G1213	A1335	G1213			C	C			
	G1598	C1481	G1214	A1336	G1214			C	C			
	G1599	C1482	G1215	A1337	G1215			C	C			
	G1600	C1483	G1216	A1338	G1216			C	C			
	G1601	C1484	G1217	A1339	G1217			C	C			
	G1602	C1485	G1218	A1340	G1218			C	C			
	G1603	C1486	G1219	A1341	G1219			C	C			
	G1604	C1487	G1220	A1342	G1220			C	C			
	G1605	C1488	G1221	A1343	G1221			C	C			
	G1606	C1489	G1222	A1344	G1222			C	C			
	G1607	C1490	G1223	A1345	G1223			C	C			
	G1608	C1491	G1224	A1346	G1224			C	C			
	G1609	C1492	G1225	A1347	G1225			C	C			
	G1610	C1493	G1226	A1348	G1226			C	C			
	G1611	C1494	G1227	A1349	G1227			C	C			
	G1612	C1495	G1228	A1350	G1228			C	C			
	G1613	C1496	G1229	A1351	G1229			C	C			
	G1614	C1497	G1230	A1352	G1230			C	C			
	G1615	C1498	G1231	A1353	G1231			C	C			
	G1616	C1499	G1232	A1354	G1232			C	C			
	G1617	C1500	G1233	A1355	G1233			C	C			
	G1618	C1501	G1234	A1356	G1234			C	C			
	G1619	C1502	G1235	A1357	G1235			C	C			
	G1620	C1503	G1236	A1358	G1236			C	C			
	G1621	C1504	G1237	A1359	G1237			C	C			
	G1622	C1505	G1238	A1360	G1238			C	C			
	G1623	C1506	G1239	A1361	G1239			C	C			
	G1624	C1507	G1240	A1362	G1240			C	C			
	G1625	C1508	G1241	A1363	G1241			C	C			
	G1626	C1509	G1242	A1364	G1242			C	C			
	G1627	C1510	G1243	A1365	G1243			C	C			
	G1628	C1511	G1244	A1366	G1244			C	C			
	G1629	C1512	G1245	A1367	G1245			C	C			
	G1630	C1513	G1246	A1368	G1246			C	C			
	G1631	C1514	G1247	A1369	G1247			C	C			
	G1632	C1515	G1248	A1370	G1248			C	C			
	G1633	C1516	G1249	A1371	G1249			C	C			
	G1634	C1517	G1250	A1372	G1250			C	C			
	G1635	C1518	G1251	A1373	G1251			C	C			
	G1636	C1519	G1252	A1374	G1252			C	C			

G1862
A1863
U1864
C1865
A1869

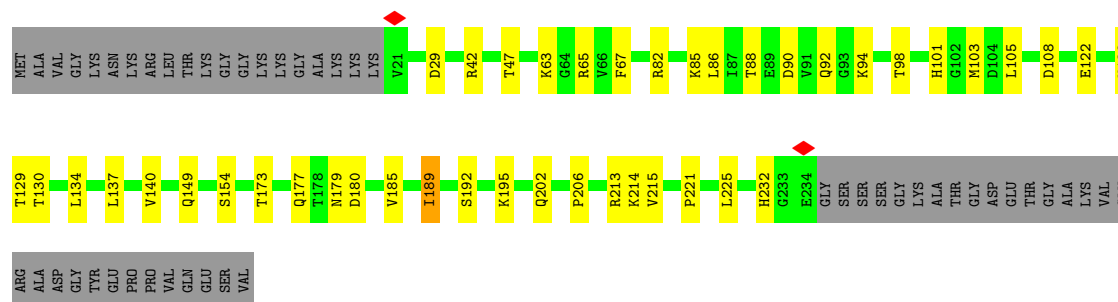
- Molecule 50: 40S ribosomal protein SA

Chain SA:  59% 16% 25%



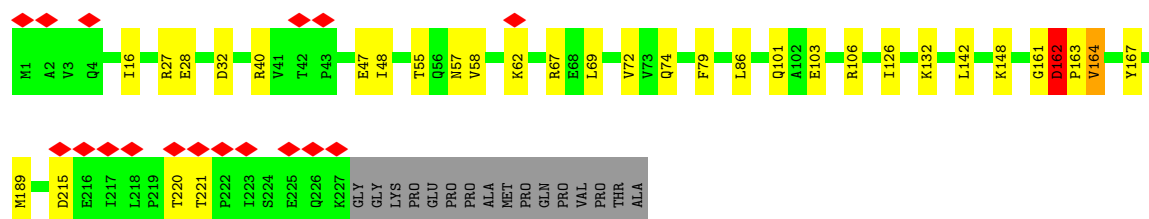
- Molecule 51: 40S ribosomal protein S3a

Chain SB:  65% 16% 19%



- Molecule 52: 40S ribosomal protein S3

Chain SD:  7% 80% 13% 7%



- Molecule 53: 40S ribosomal protein S4, X isoform

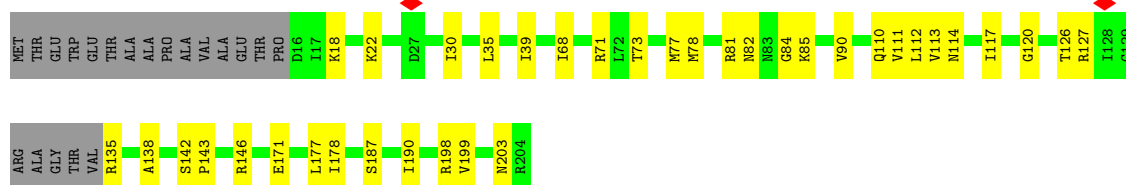
Chain SE:  88% 12%





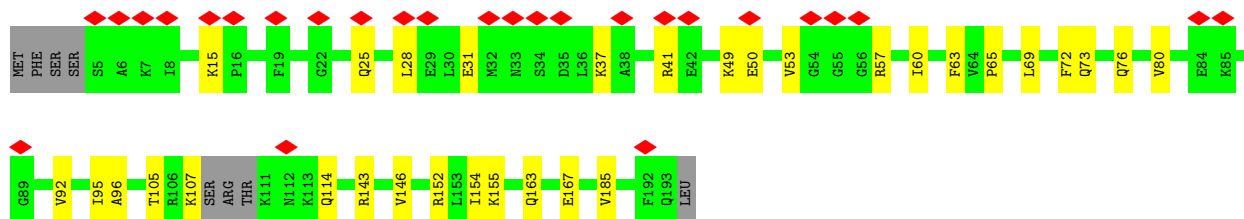
- Molecule 54: 40S ribosomal protein S5

Chain SF: 72% 18% 10%



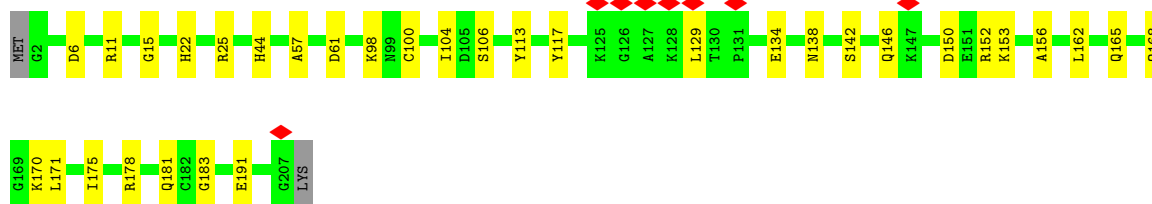
- Molecule 55: 40S ribosomal protein S7

Chain SH: 14% 79% 16%



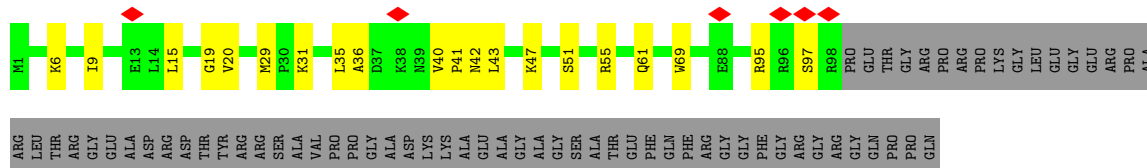
- Molecule 56: 40S ribosomal protein S8

Chain SI: 83% 16%



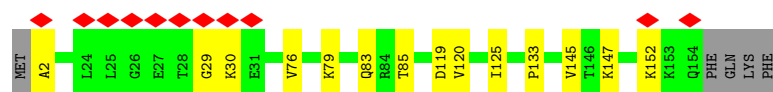
- Molecule 57: 40S ribosomal protein S10

Chain SK: 47% 12% 41%

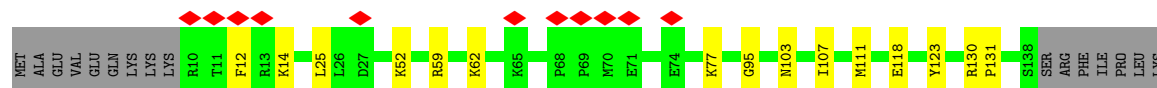
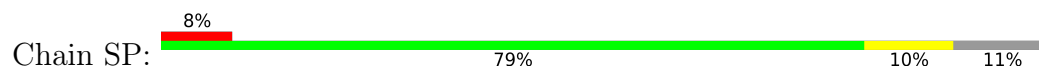


- Molecule 58: 40S ribosomal protein S11

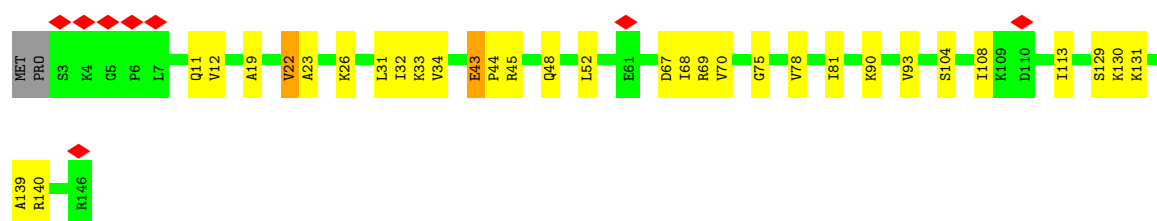
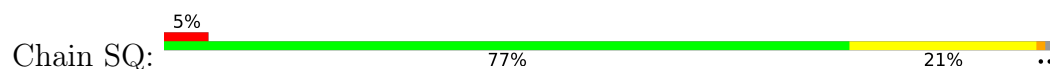
Chain SL: 7% 88% 9%



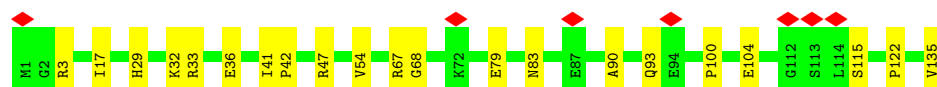
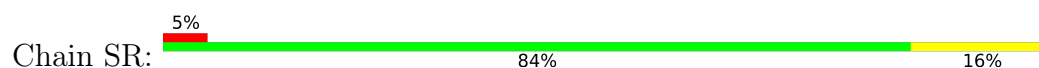
- Molecule 59: 40S ribosomal protein S15



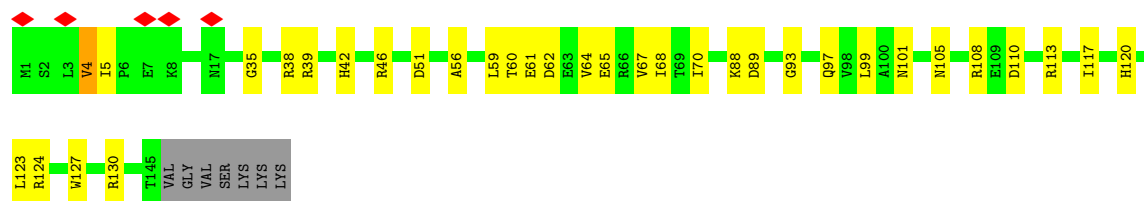
- Molecule 60: 40S ribosomal protein S16



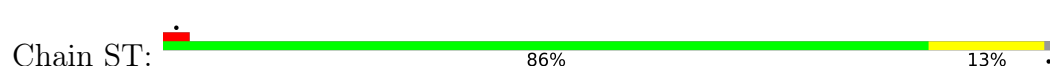
- Molecule 61: 40S ribosomal protein S17



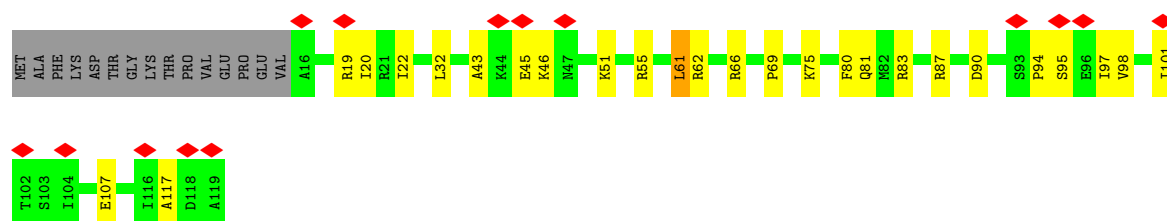
- Molecule 62: 40S ribosomal protein S18



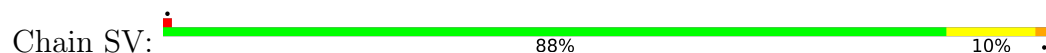
- Molecule 63: 40S ribosomal protein S19



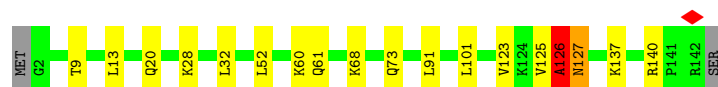
- Molecule 64: 40S ribosomal protein S20



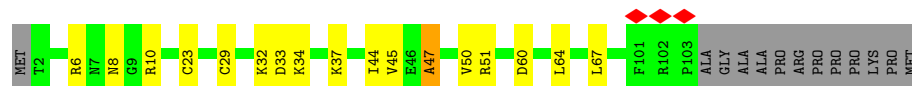
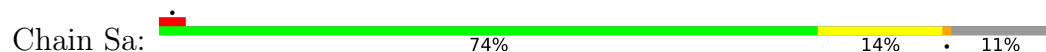
- Molecule 65: 40S ribosomal protein S21



- Molecule 66: 40S ribosomal protein S23



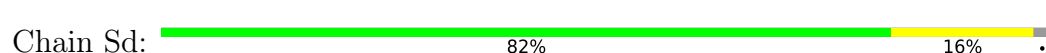
- Molecule 67: 40S ribosomal protein S26



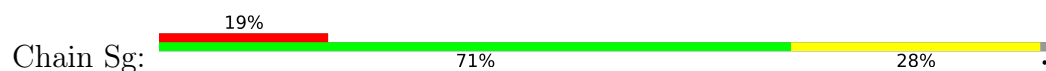
- Molecule 68: 40S ribosomal protein S28

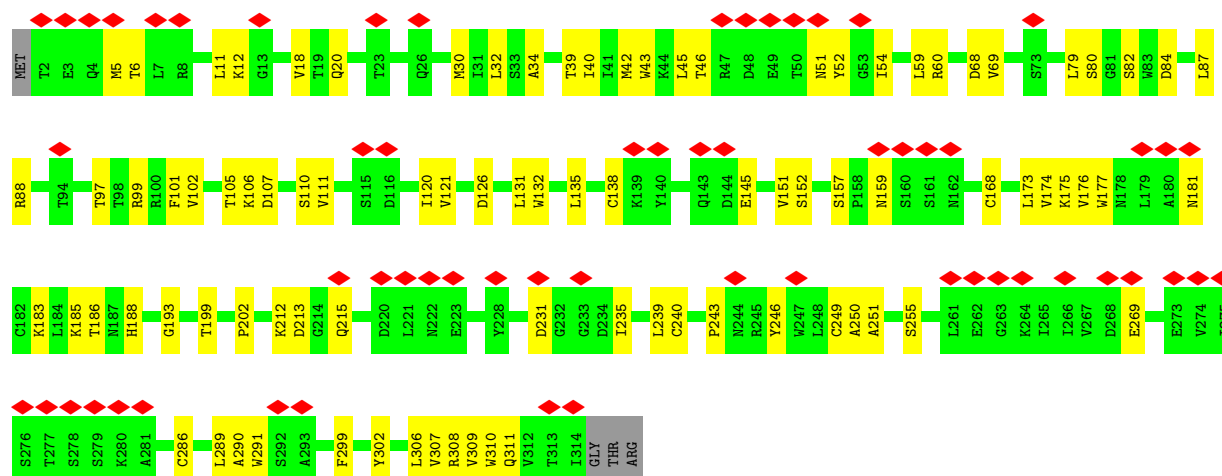


- Molecule 69: 40S ribosomal protein S29



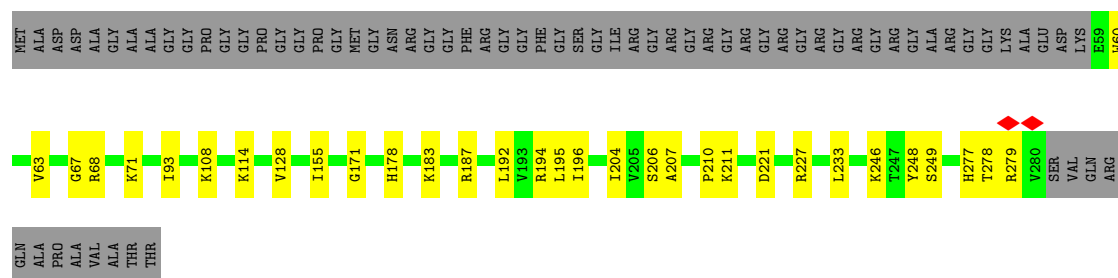
- Molecule 70: Receptor of activated protein C kinase 1





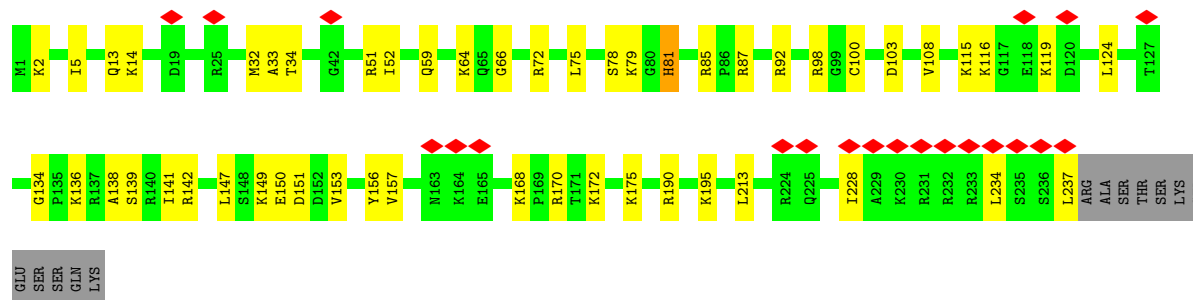
- Molecule 71: 40S ribosomal protein S2

Chain SC: 65% 11% 24%



- Molecule 72: 40S ribosomal protein S6

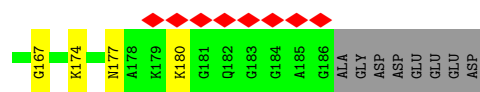
Chain SG: 8% 75% 20% 5%



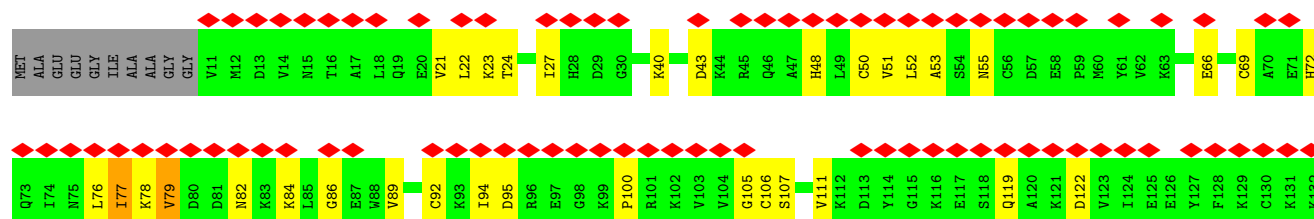
- Molecule 73: 40S ribosomal protein S9

Chain SJ: 5% 78% 17% 5%





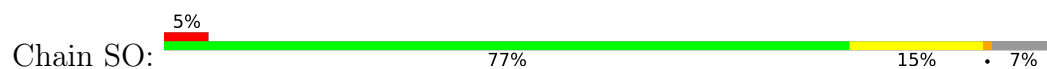
- Molecule 74: 40S ribosomal protein S12



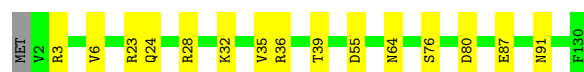
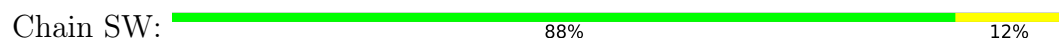
- Molecule 75: 40S ribosomal protein S13



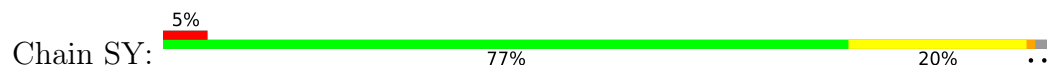
- Molecule 76: 40S ribosomal protein S14



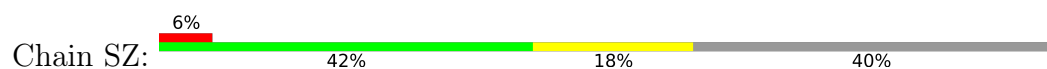
- Molecule 77: 40S ribosomal protein S15a



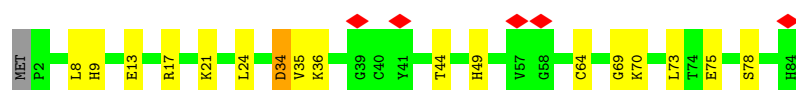
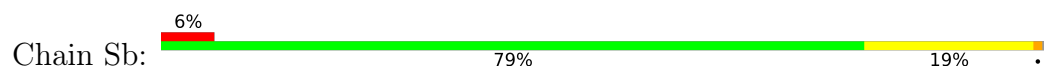
- Molecule 78: 40S ribosomal protein S24



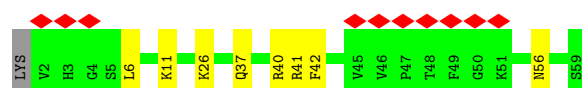
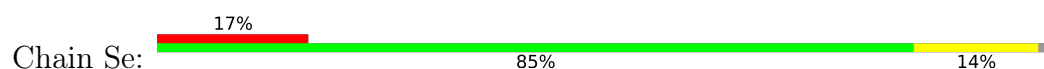
- Molecule 79: 40S ribosomal protein S25



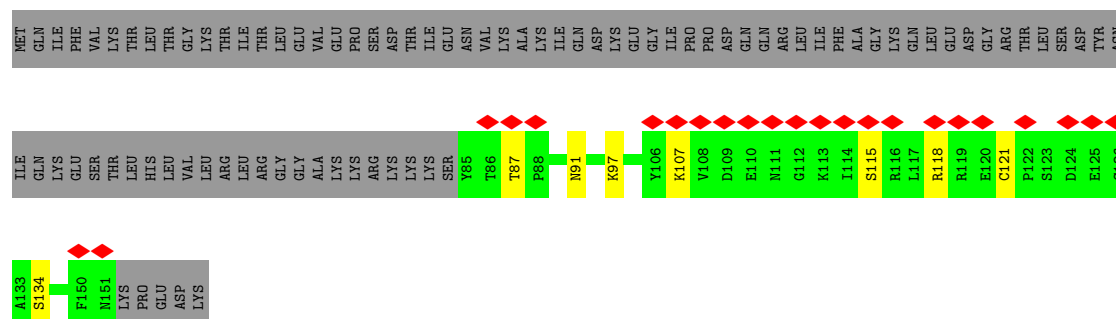
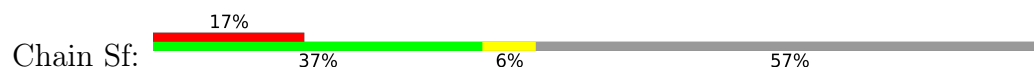
- Molecule 80: 40S ribosomal protein S27



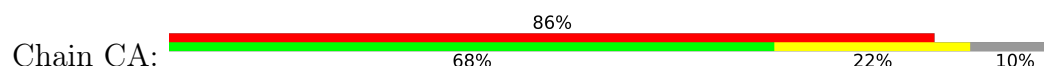
- Molecule 81: 40S ribosomal protein S30

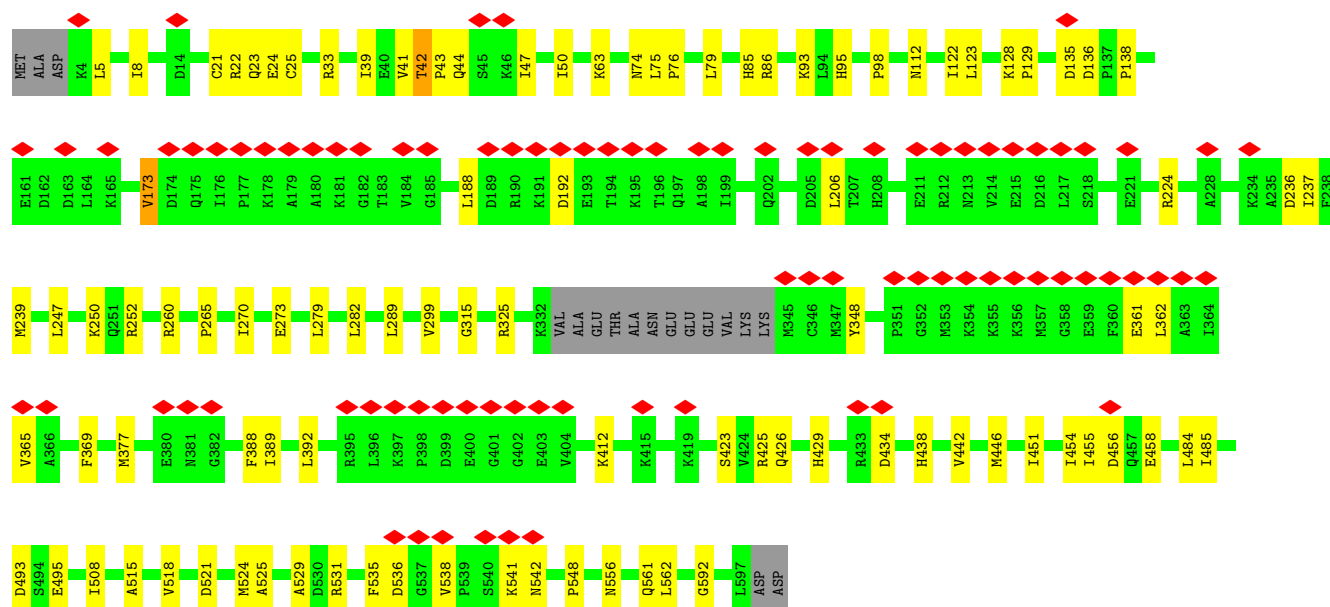


- Molecule 82: Ubiquitin-40S ribosomal protein S27a

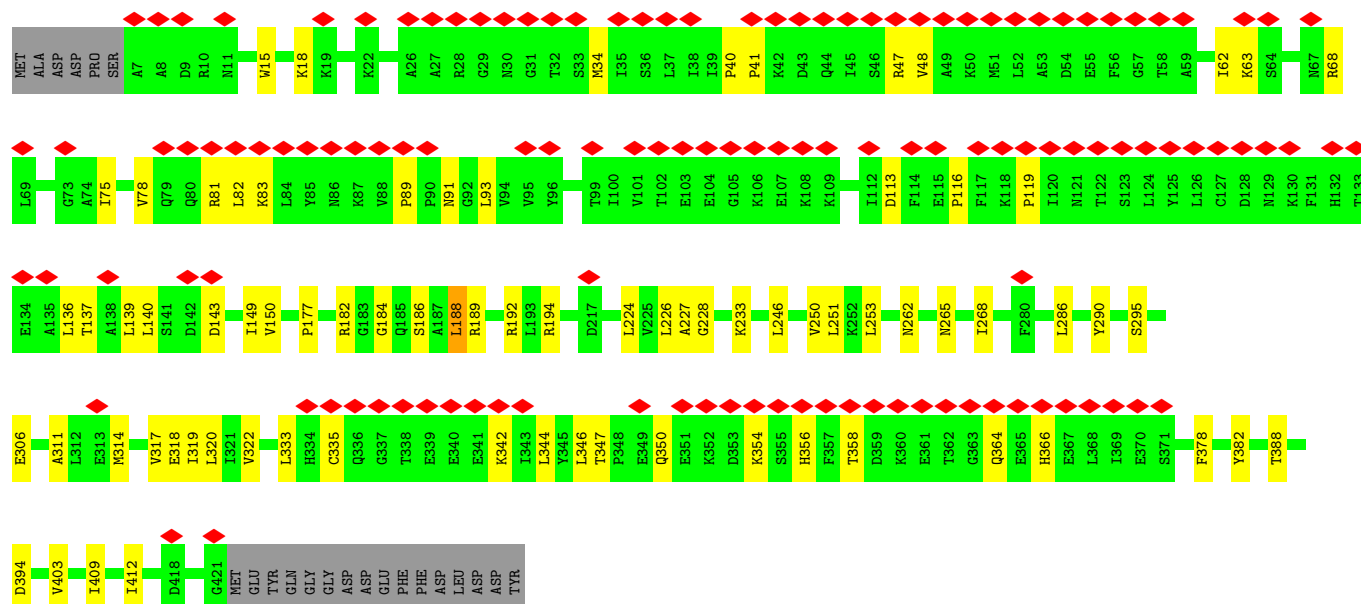
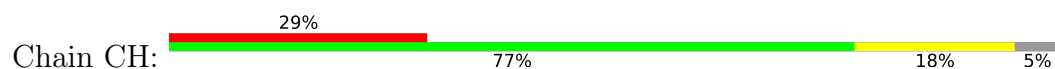


- Molecule 83: Proliferation-associated protein 2G4





- Molecule 88: Eukaryotic peptide chain release factor subunit 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13337	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.457	Depositor
Minimum map value	-0.148	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	423.6, 423.6, 423.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	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, SF4, ADP

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	0.33	2/89595 (0.0%)	0.43	26/139686 (0.0%)
2	L7	0.29	0/2861	0.37	0/4459
3	L8	0.32	0/3701	0.37	0/5766
4	LA	0.37	0/1936	0.66	0/2596
5	LB	0.31	0/3306	0.59	3/4424 (0.1%)
6	LC	0.34	0/2981	0.63	2/4002 (0.0%)
7	LD	0.26	0/2428	0.58	0/3252
8	LE	0.27	0/1942	0.59	0/2606
9	LF	0.33	0/1905	0.60	0/2539
10	LG	0.29	0/1960	0.60	0/2637
11	LH	0.29	0/1537	0.57	0/2066
12	LI	0.29	0/1673	0.55	0/2233
13	LJ	0.27	0/1433	0.67	0/1915
14	LL	0.30	0/1732	0.60	0/2315
15	LM	0.29	0/1161	0.62	2/1554 (0.1%)
16	LN	0.35	0/1746	0.62	0/2338
17	LO	0.32	0/1682	0.51	0/2250
18	LP	0.31	0/1268	0.52	0/1701
19	LQ	0.33	0/1537	0.52	0/2052
20	LR	0.29	0/1582	0.58	2/2091 (0.1%)
21	LS	0.30	0/1493	0.50	0/2003
22	LT	0.34	0/1326	0.61	0/1770
23	LU	0.29	0/839	0.74	2/1126 (0.2%)
24	LV	0.31	0/993	0.56	0/1332
25	LW	0.26	0/1030	0.57	0/1364
26	LX	0.28	0/1002	0.53	0/1345
27	LY	0.29	0/1132	0.53	0/1504
28	LZ	0.28	0/1130	0.49	0/1507
29	La	0.32	0/1191	0.54	0/1591
30	Lb	0.27	0/889	0.58	0/1175
31	Lc	0.30	0/774	0.58	0/1038
32	Ld	0.31	0/903	0.52	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.35	0/1071	0.56	0/1429
34	Lf	0.34	0/895	0.57	0/1198
35	Lg	0.32	0/916	0.56	0/1220
36	Lh	0.26	0/1023	0.48	0/1351
37	Li	0.24	0/843	0.49	0/1115
38	Lj	0.38	0/720	0.63	0/952
39	Lk	0.25	0/575	0.52	0/761
40	Ll	0.33	0/454	0.60	0/599
41	Lm	0.34	0/435	0.55	0/575
42	Ln	0.30	0/231	0.50	0/294
43	Lo	0.28	0/876	0.49	0/1156
44	Lp	0.32	0/718	0.52	0/953
45	Lr	0.30	0/1017	0.54	0/1364
46	Ls	0.28	1/1519 (0.1%)	0.66	0/2052
47	Lt	0.34	0/1058	0.94	4/1430 (0.3%)
48	Lz	0.29	0/1769	0.74	0/2371
49	S2	0.31	3/41245 (0.0%)	0.43	14/64265 (0.0%)
50	SA	0.29	0/1778	0.58	0/2416
51	SB	0.25	0/1765	0.54	0/2362
52	SD	0.26	0/1793	0.63	0/2414
53	SE	0.28	0/2118	0.56	1/2849 (0.0%)
54	SF	0.25	0/1481	0.58	0/1988
55	SH	0.28	0/1519	0.64	0/2033
56	SI	0.30	0/1715	0.59	2/2287 (0.1%)
57	SK	0.24	0/851	0.60	0/1147
58	SL	0.31	0/1268	0.53	0/1696
59	SP	0.23	0/1082	0.71	2/1446 (0.1%)
60	SQ	0.28	0/1160	0.66	0/1553
61	SR	0.25	0/1105	0.67	0/1484
62	SS	0.27	0/1216	0.61	0/1628
63	ST	0.25	0/1131	0.57	0/1515
64	SU	0.28	0/831	0.66	0/1115
65	SV	0.28	0/643	0.63	1/860 (0.1%)
66	SX	0.32	0/1116	0.61	1/1490 (0.1%)
67	Sa	0.33	0/836	0.68	0/1121
68	Sc	0.27	0/508	0.77	2/680 (0.3%)
69	Sd	0.27	0/470	0.60	0/623
70	Sg	0.28	0/2493	0.73	2/3394 (0.1%)
71	SC	0.31	0/1762	0.65	3/2381 (0.1%)
72	SG	0.25	0/1946	0.61	3/2590 (0.1%)
73	SJ	0.29	0/1550	0.59	0/2069
74	SM	0.29	0/950	0.74	0/1275
75	SN	0.28	0/1232	0.52	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SO	0.31	0/1062	0.71	4/1425 (0.3%)
77	SW	0.32	0/1051	0.55	0/1406
78	SY	0.26	0/1083	0.55	0/1438
79	SZ	0.32	0/604	0.80	0/810
80	Sb	0.26	0/665	0.54	0/891
81	Se	0.23	0/444	0.60	0/588
82	Sf	0.24	0/560	0.70	0/745
83	CA	0.31	0/2810	0.79	3/3780 (0.1%)
84	CC	0.18	0/1773	0.39	1/2759 (0.0%)
85	CE	0.23	0/1010	0.57	0/1339
86	CF	0.25	0/244	0.46	0/328
87	CI	0.24	0/4672	0.59	1/6308 (0.0%)
88	CH	0.33	0/3309	0.66	2/4450 (0.0%)
All	All	0.31	6/249639 (0.0%)	0.51	83/364877 (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
4	LA	0	1
5	LB	0	3
8	LE	0	1
11	LH	0	1
12	LI	0	3
14	LL	0	1
15	LM	0	3
17	LO	0	2
22	LT	0	1
34	Lf	0	1
36	Lh	0	1
38	Lj	0	1
46	Ls	0	1
47	Lt	0	6
51	SB	0	1
52	SD	0	2
54	SF	0	2
55	SH	0	1
60	SQ	0	1
63	ST	0	1
64	SU	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
65	SV	0	1
66	SX	0	3
73	SJ	0	1
74	SM	0	1
76	SO	0	1
79	SZ	0	1
80	Sb	0	1
87	CI	0	5
88	CH	0	1
All	All	0	51

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	S2	61	A	O3'-P	-6.44	1.51	1.61
1	L5	2113	G	C1'-N9	-6.33	1.37	1.47
1	L5	4546	A	O3'-P	-5.58	1.52	1.61
46	Ls	79	LEU	C-N	5.23	1.37	1.33
49	S2	59	U	O3'-P	-5.22	1.53	1.61

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	S2	1094	C	C1'-C2'-O2'	-13.11	88.74	108.40
1	L5	4905	C	C1'-C2'-O2'	-12.78	89.22	108.40
1	L5	4915	G	C1'-C2'-O2'	-11.00	91.90	108.40
1	L5	4547	C	C1'-C2'-O2'	-10.24	93.05	108.40
49	S2	61	A	C1'-C2'-O2'	-9.59	94.02	108.40

There are no chirality outliers.

5 of 51 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	258	HIS	Peptide
5	LB	301	ASN	Peptide
8	LE	129	GLY	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	80138	0	40378	400	0
2	L7	2561	0	1295	10	0
3	L8	3314	0	1683	8	0
4	LA	1898	0	1993	22	0
5	LB	3238	0	3376	34	0
6	LC	2927	0	3104	21	0
7	LD	2382	0	2410	30	0
8	LE	1904	0	2055	29	0
9	LF	1870	0	1996	16	0
10	LG	1927	0	2074	35	0
11	LH	1518	0	1601	24	0
12	LI	1634	0	1671	27	0
13	LJ	1410	0	1441	18	0
14	LL	1701	0	1818	24	0
15	LM	1138	0	1204	17	0
16	LN	1701	0	1749	18	0
17	LO	1650	0	1794	13	0
18	LP	1242	0	1269	8	0
19	LQ	1513	0	1628	13	0
20	LR	1566	0	1729	15	0
21	LS	1453	0	1490	12	0
22	LT	1298	0	1366	15	0
23	LU	825	0	850	5	0
24	LV	979	0	1039	7	0
25	LW	1015	0	1079	14	0
26	LX	985	0	1066	11	0
27	LY	1115	0	1205	16	0
28	LZ	1107	0	1182	10	0
29	La	1162	0	1213	11	0
30	Lb	876	0	948	11	0
31	Lc	764	0	804	12	0
32	Ld	888	0	930	9	0
33	Le	1053	0	1147	6	0
34	Lf	876	0	912	10	0
35	Lg	906	0	1000	13	0
36	Lh	1015	0	1148	8	0
37	Li	832	0	917	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lj	705	0	738	10	0
39	Lk	569	0	637	10	0
40	Ll	444	0	483	4	0
41	Lm	429	0	465	11	0
42	Ln	230	0	276	2	0
43	Lo	862	0	930	9	0
44	Lp	708	0	756	5	0
45	Lr	1002	0	1068	9	0
46	Ls	1496	0	1540	18	0
47	Lt	1046	0	1076	19	0
48	Lz	1741	0	1854	48	0
49	S2	36899	0	18600	255	0
50	SA	1741	0	1746	29	0
51	SB	1738	0	1809	29	0
52	SD	1765	0	1865	19	0
53	SE	2076	0	2177	20	0
54	SF	1461	0	1511	24	0
55	SH	1497	0	1590	20	0
56	SI	1686	0	1772	23	0
57	SK	827	0	854	12	0
58	SL	1247	0	1323	10	0
59	SP	1061	0	1107	9	0
60	SQ	1142	0	1213	19	0
61	SR	1090	0	1149	14	0
62	SS	1198	0	1261	25	0
63	ST	1112	0	1146	14	0
64	SU	821	0	883	17	0
65	SV	636	0	637	6	0
66	SX	1098	0	1167	11	0
67	Sa	821	0	870	12	0
68	Sc	506	0	536	15	0
69	Sd	459	0	449	9	0
70	Sg	2436	0	2393	48	0
71	SC	1725	0	1813	17	0
72	SG	1923	0	2089	36	0
73	SJ	1525	0	1640	25	0
74	SM	940	0	965	27	0
75	SN	1208	0	1294	10	0
76	SO	1049	0	1073	17	0
77	SW	1034	0	1080	11	0
78	SY	1065	0	1142	21	0
79	SZ	598	0	656	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	Sb	651	0	672	11	0
81	Se	439	0	458	7	0
82	Sf	548	0	555	6	0
83	CA	2764	0	2779	55	0
84	CC	1589	0	810	23	0
85	CE	998	0	1016	6	0
86	CF	239	0	211	2	0
87	CI	4586	0	4717	54	0
88	CH	3257	0	3297	51	0
89	L5	210	0	0	0	0
89	L7	3	0	0	0	0
89	L8	4	0	0	0	0
89	LA	1	0	0	0	0
89	LB	1	0	0	0	0
89	LI	1	0	0	0	0
89	LP	1	0	0	0	0
89	LV	1	0	0	0	0
89	LX	1	0	0	0	0
89	Le	2	0	0	0	0
89	Lg	1	0	0	0	0
89	S2	29	0	0	0	0
89	SG	1	0	0	0	0
90	Lg	1	0	0	0	0
90	Lj	1	0	0	0	0
90	Lm	1	0	0	0	0
90	Lo	1	0	0	0	0
90	Lp	1	0	0	0	0
90	Sa	1	0	0	0	0
90	Sd	1	0	0	0	0
90	Sf	1	0	0	0	0
91	CI	16	0	0	0	0
92	CI	27	0	12	0	0
All	All	233375	0	176724	1809	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1809 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4904:G:O2'	1:L5:4905:C:H5'	1.37	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Lm:98:LYS:HD2	41:Lm:118:THR:HG21	1.27	1.13
49:S2:1756:C:H42	49:S2:1776:G:N2	1.49	1.07
49:S2:1756:C:N4	49:S2:1776:G:H22	1.54	1.05
49:S2:886:A:N6	49:S2:901:G:C4	2.24	1.04

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	246/257 (96%)	223 (91%)	22 (9%)	1 (0%)	30	65
5	LB	400/403 (99%)	374 (94%)	25 (6%)	1 (0%)	36	70
6	LC	366/427 (86%)	337 (92%)	29 (8%)	0	100	100
7	LD	291/297 (98%)	266 (91%)	25 (9%)	0	100	100
8	LE	232/288 (81%)	212 (91%)	20 (9%)	0	100	100
9	LF	223/248 (90%)	216 (97%)	7 (3%)	0	100	100
10	LG	239/266 (90%)	223 (93%)	16 (7%)	0	100	100
11	LH	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
12	LI	198/214 (92%)	182 (92%)	16 (8%)	0	100	100
13	LJ	174/178 (98%)	154 (88%)	20 (12%)	0	100	100
14	LL	208/211 (99%)	190 (91%)	18 (9%)	0	100	100
15	LM	137/215 (64%)	125 (91%)	11 (8%)	1 (1%)	18	53
16	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	12	45
17	LO	199/203 (98%)	186 (94%)	13 (6%)	0	100	100
18	LP	151/184 (82%)	141 (93%)	10 (7%)	0	100	100
19	LQ	185/188 (98%)	175 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	LR	185/196 (94%)	176 (95%)	9 (5%)	0	100	100
21	LS	173/176 (98%)	163 (94%)	10 (6%)	0	100	100
22	LT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
23	LU	99/128 (77%)	84 (85%)	13 (13%)	2 (2%)	6	28
24	LV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
25	LW	122/157 (78%)	113 (93%)	9 (7%)	0	100	100
26	LX	118/156 (76%)	113 (96%)	5 (4%)	0	100	100
27	LY	132/145 (91%)	123 (93%)	9 (7%)	0	100	100
28	LZ	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
29	La	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
30	Lb	105/159 (66%)	97 (92%)	8 (8%)	0	100	100
31	Lc	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
32	Ld	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
33	Le	126/135 (93%)	117 (93%)	9 (7%)	0	100	100
34	Lf	107/110 (97%)	97 (91%)	8 (8%)	2 (2%)	6	30
35	Lg	112/117 (96%)	110 (98%)	2 (2%)	0	100	100
36	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
38	Lj	84/97 (87%)	76 (90%)	8 (10%)	0	100	100
39	Lk	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	97 (94%)	6 (6%)	0	100	100
44	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
45	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
46	Ls	194/317 (61%)	173 (89%)	20 (10%)	1 (0%)	24	60
47	Lt	137/165 (83%)	107 (78%)	27 (20%)	3 (2%)	5	26
48	Lz	215/217 (99%)	159 (74%)	56 (26%)	0	100	100
50	SA	219/295 (74%)	194 (89%)	24 (11%)	1 (0%)	24	60
51	SB	212/264 (80%)	199 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	SD	225/243 (93%)	200 (89%)	25 (11%)	0	100	100
53	SE	260/263 (99%)	242 (93%)	18 (7%)	0	100	100
54	SF	180/204 (88%)	163 (91%)	17 (9%)	0	100	100
55	SH	182/194 (94%)	157 (86%)	25 (14%)	0	100	100
56	SI	204/208 (98%)	194 (95%)	10 (5%)	0	100	100
57	SK	96/165 (58%)	86 (90%)	10 (10%)	0	100	100
58	SL	151/158 (96%)	140 (93%)	11 (7%)	0	100	100
59	SP	127/145 (88%)	116 (91%)	11 (9%)	0	100	100
60	SQ	142/146 (97%)	124 (87%)	17 (12%)	1 (1%)	18	53
61	SR	133/135 (98%)	117 (88%)	16 (12%)	0	100	100
62	SS	143/152 (94%)	132 (92%)	11 (8%)	0	100	100
63	ST	141/145 (97%)	129 (92%)	11 (8%)	1 (1%)	18	53
64	SU	102/119 (86%)	89 (87%)	13 (13%)	0	100	100
65	SV	81/83 (98%)	72 (89%)	8 (10%)	1 (1%)	10	40
66	SX	139/143 (97%)	130 (94%)	7 (5%)	2 (1%)	9	36
67	Sa	100/115 (87%)	90 (90%)	9 (9%)	1 (1%)	12	45
68	Sc	62/69 (90%)	49 (79%)	12 (19%)	1 (2%)	7	34
69	Sd	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
70	Sg	311/317 (98%)	269 (86%)	41 (13%)	1 (0%)	36	70
71	SC	220/293 (75%)	206 (94%)	14 (6%)	0	100	100
72	SG	235/249 (94%)	219 (93%)	16 (7%)	0	100	100
73	SJ	183/194 (94%)	171 (93%)	12 (7%)	0	100	100
74	SM	120/132 (91%)	109 (91%)	11 (9%)	0	100	100
75	SN	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
76	SO	138/151 (91%)	126 (91%)	11 (8%)	1 (1%)	18	53
77	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
78	SY	129/133 (97%)	122 (95%)	7 (5%)	0	100	100
79	SZ	73/125 (58%)	59 (81%)	13 (18%)	1 (1%)	9	36
80	Sb	81/84 (96%)	72 (89%)	9 (11%)	0	100	100
81	Se	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
82	Sf	65/156 (42%)	54 (83%)	11 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
83	CA	350/394 (89%)	331 (95%)	18 (5%)	1 (0%)	36	70
85	CE	113/223 (51%)	109 (96%)	4 (4%)	0	100	100
86	CF	27/180 (15%)	26 (96%)	1 (4%)	0	100	100
87	CI	578/599 (96%)	537 (93%)	39 (7%)	2 (0%)	36	70
88	CH	413/437 (94%)	388 (94%)	24 (6%)	1 (0%)	43	76
All	All	13353/15220 (88%)	12258 (92%)	1067 (8%)	28 (0%)	44	76

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
66	SX	127	ASN
15	LM	88	ALA
23	LU	59	GLY
47	Lt	10	ILE

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%)	187 (98%)	3 (2%)	55	79
5	LB	348/349 (100%)	348 (100%)	0	100	100
6	LC	306/348 (88%)	303 (99%)	3 (1%)	68	84
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	209/252 (83%)	208 (100%)	1 (0%)	81	89
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	203/223 (91%)	202 (100%)	1 (0%)	81	89
11	LH	169/171 (99%)	168 (99%)	1 (1%)	78	88
12	LI	172/181 (95%)	172 (100%)	0	100	100
13	LJ	148/149 (99%)	148 (100%)	0	100	100
14	LL	176/177 (99%)	176 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	LM	118/161 (73%)	117 (99%)	1 (1%)	73	86
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	171 (99%)	2 (1%)	63	82
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	164 (100%)	0	100	100
20	LR	166/175 (95%)	165 (99%)	1 (1%)	78	88
21	LS	156/157 (99%)	155 (99%)	1 (1%)	78	88
22	LT	139/140 (99%)	138 (99%)	1 (1%)	76	86
23	LU	91/115 (79%)	90 (99%)	1 (1%)	65	83
24	LV	101/107 (94%)	99 (98%)	2 (2%)	48	76
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	123 (99%)	1 (1%)	73	86
28	LZ	117/118 (99%)	116 (99%)	1 (1%)	70	85
29	La	120/121 (99%)	119 (99%)	1 (1%)	73	86
30	Lb	88/126 (70%)	87 (99%)	1 (1%)	65	83
31	Lc	83/97 (86%)	82 (99%)	1 (1%)	63	82
32	Ld	98/110 (89%)	98 (100%)	0	100	100
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	83
35	Lg	98/100 (98%)	98 (100%)	0	100	100
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	85 (99%)	1 (1%)	63	82
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	63 (98%)	1 (2%)	55	79
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	48/116 (41%)	48 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	92 (99%)	1 (1%)	65	83
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	Ls	162/258 (63%)	159 (98%)	3 (2%)	50	76
47	Lt	112/137 (82%)	109 (97%)	3 (3%)	39	71
48	Lz	195/196 (100%)	194 (100%)	1 (0%)	81	89
50	SA	183/243 (75%)	180 (98%)	3 (2%)	55	79
51	SB	195/231 (84%)	194 (100%)	1 (0%)	81	89
52	SD	190/202 (94%)	188 (99%)	2 (1%)	65	83
53	SE	224/225 (100%)	222 (99%)	2 (1%)	70	85
54	SF	156/170 (92%)	156 (100%)	0	100	100
55	SH	166/174 (95%)	166 (100%)	0	100	100
56	SI	178/180 (99%)	178 (100%)	0	100	100
57	SK	89/136 (65%)	89 (100%)	0	100	100
58	SL	137/142 (96%)	137 (100%)	0	100	100
59	SP	115/130 (88%)	114 (99%)	1 (1%)	70	85
60	SQ	119/121 (98%)	117 (98%)	2 (2%)	53	78
61	SR	122/122 (100%)	121 (99%)	1 (1%)	73	86
62	SS	126/132 (96%)	125 (99%)	1 (1%)	73	86
63	ST	113/115 (98%)	113 (100%)	0	100	100
64	SU	94/107 (88%)	92 (98%)	2 (2%)	47	75
65	SV	67/67 (100%)	67 (100%)	0	100	100
66	SX	113/115 (98%)	112 (99%)	1 (1%)	70	85
67	Sa	89/98 (91%)	89 (100%)	0	100	100
68	Sc	57/62 (92%)	57 (100%)	0	100	100
69	Sd	48/49 (98%)	48 (100%)	0	100	100
70	Sg	272/275 (99%)	268 (98%)	4 (2%)	57	80
71	SC	188/225 (84%)	188 (100%)	0	100	100
72	SG	207/218 (95%)	205 (99%)	2 (1%)	68	84
73	SJ	161/168 (96%)	160 (99%)	1 (1%)	78	88
74	SM	102/108 (94%)	99 (97%)	3 (3%)	37	70
75	SN	130/131 (99%)	129 (99%)	1 (1%)	73	86
76	SO	110/119 (92%)	110 (100%)	0	100	100
77	SW	112/113 (99%)	112 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	SY	113/115 (98%)	112 (99%)	1 (1%)	70	85
79	SZ	66/103 (64%)	65 (98%)	1 (2%)	57	80
80	Sb	75/76 (99%)	74 (99%)	1 (1%)	61	81
81	Se	42/48 (88%)	42 (100%)	0	100	100
82	Sf	60/140 (43%)	59 (98%)	1 (2%)	53	78
83	CA	303/336 (90%)	303 (100%)	0	100	100
85	CE	104/190 (55%)	103 (99%)	1 (1%)	68	84
86	CF	26/151 (17%)	26 (100%)	0	100	100
87	CI	511/526 (97%)	510 (100%)	1 (0%)	87	92
88	CH	353/376 (94%)	351 (99%)	2 (1%)	78	88
All	All	11626/12971 (90%)	11557 (99%)	69 (1%)	76	88

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
74	SM	66	GLU
74	SM	79	VAL
85	CE	33	GLU
37	Li	34	THR
34	Lf	33	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 198 such sidechains are listed below:

Mol	Chain	Res	Type
54	SF	29	GLN
69	Sd	16	GLN
56	SI	87	ASN
61	SR	48	ASN
70	Sg	215	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3705/5066 (73%)	903 (24%)	20 (0%)
2	L7	119/121 (98%)	9 (7%)	0
3	L8	155/157 (98%)	27 (17%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	S2	1715/1869 (91%)	402 (23%)	12 (0%)
84	CC	74/75 (98%)	26 (35%)	2 (2%)
All	All	5768/7288 (79%)	1367 (23%)	34 (0%)

5 of 1367 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	17	A
1	L5	25	A
1	L5	26	C
1	L5	30	C
1	L5	39	A

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	S2	567	C
49	S2	688	U
84	CC	35	U
1	L5	3673	C
1	L5	3614	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 267 ligands modelled in this entry, 264 are monoatomic - leaving 3 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
91	SF4	CI	602	-	0,12,12	-	-	-		
91	SF4	CI	601	-	0,12,12	-	-	-		
92	ADP	CI	603	-	28,29,29	1.42	5 (17%)	43,45,45	1.84	9 (20%)

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
91	SF4	CI	602	-	-	-	0/6/5/5
91	SF4	CI	601	-	-	-	0/6/5/5
92	ADP	CI	603	-	-	6/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	CI	603	ADP	C5-C4	4.60	1.47	1.39
92	CI	603	ADP	C5-C6	2.68	1.48	1.41
92	CI	603	ADP	C8-N7	2.35	1.36	1.31
92	CI	603	ADP	C5-N7	-2.30	1.34	1.39
92	CI	603	ADP	PA-O3A	2.13	1.61	1.59

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
92	CI	603	ADP	C5-C4-N3	-5.81	118.71	126.72
92	CI	603	ADP	N3-C4-N9	4.51	134.84	127.17
92	CI	603	ADP	C2-N3-C4	3.74	120.96	111.83
92	CI	603	ADP	C4-C5-N7	-3.57	106.50	110.58
92	CI	603	ADP	N3-C2-N1	-3.30	123.59	128.58

There are no chirality outliers.

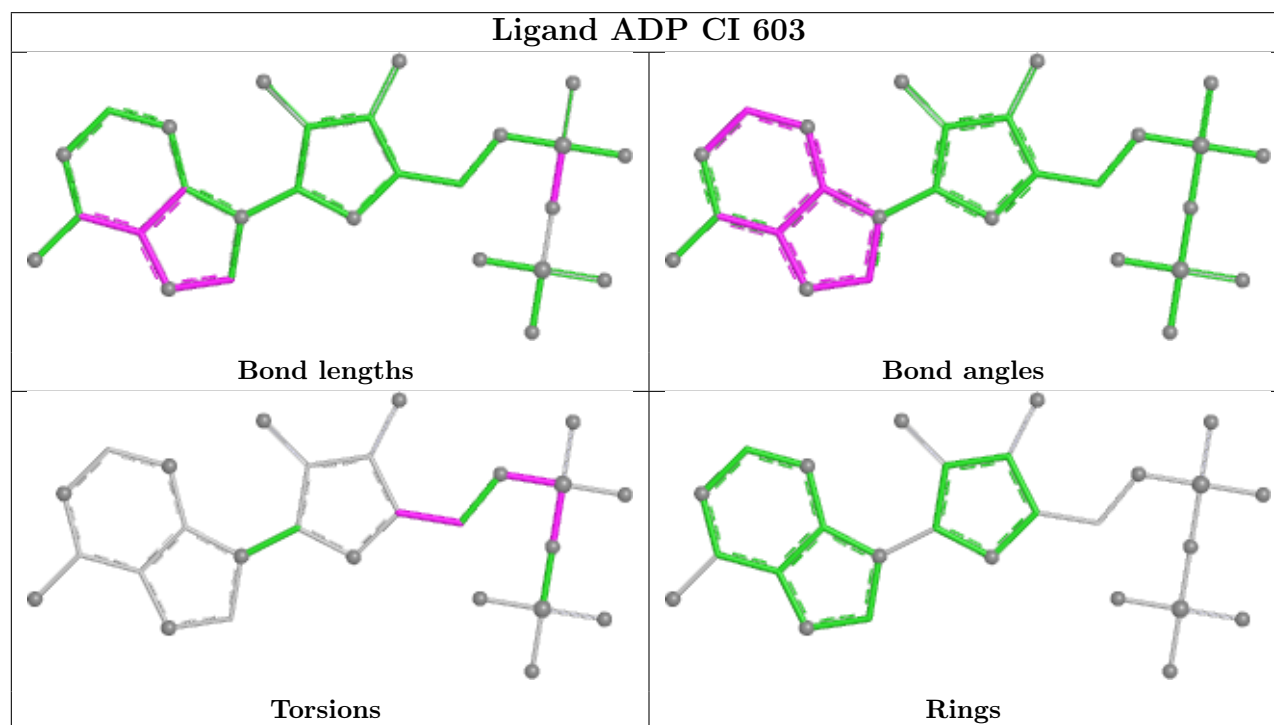
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
92	CI	603	ADP	PB-O3A-PA-O5'
92	CI	603	ADP	C5'-O5'-PA-O1A
92	CI	603	ADP	C5'-O5'-PA-O2A
92	CI	603	ADP	C5'-O5'-PA-O3A
92	CI	603	ADP	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

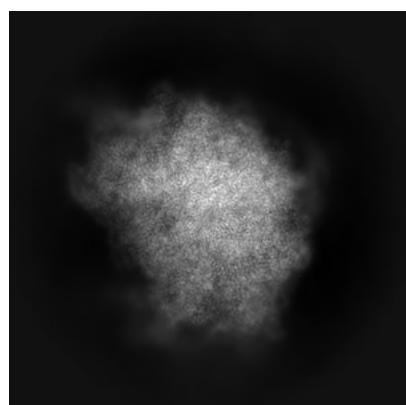
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11289. These allow visual inspection of the internal detail of the map and identification of artifacts.

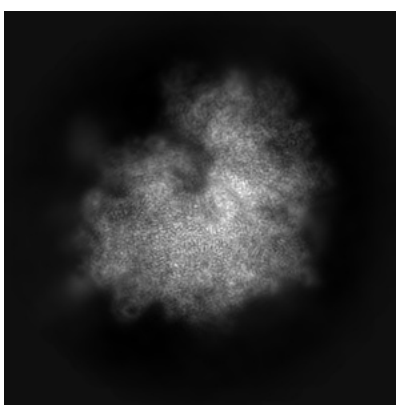
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

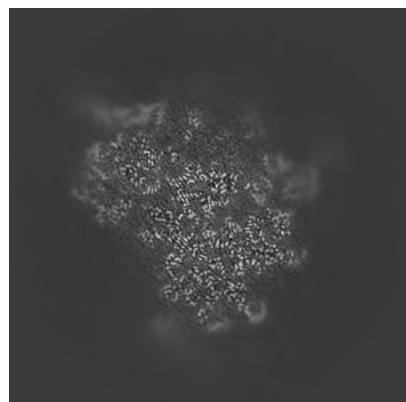


Z

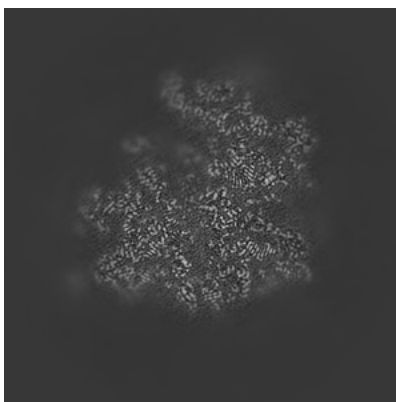
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

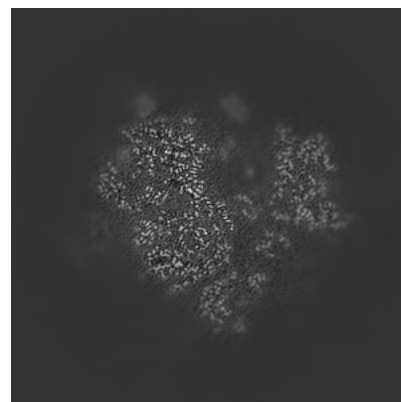
6.2.1 Primary map



X Index: 200



Y Index: 200

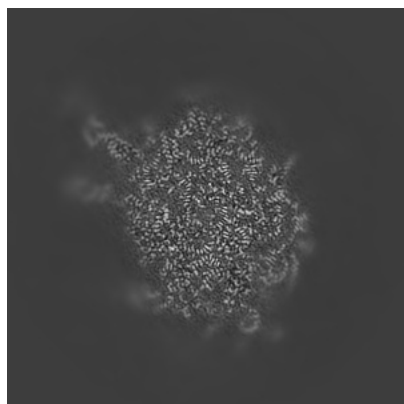


Z Index: 200

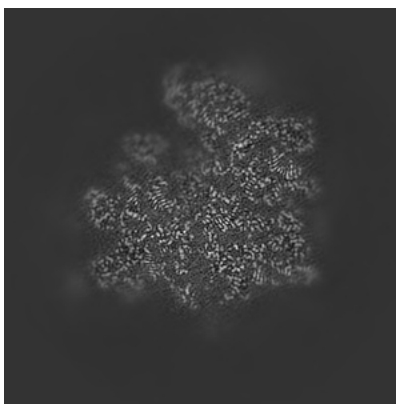
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

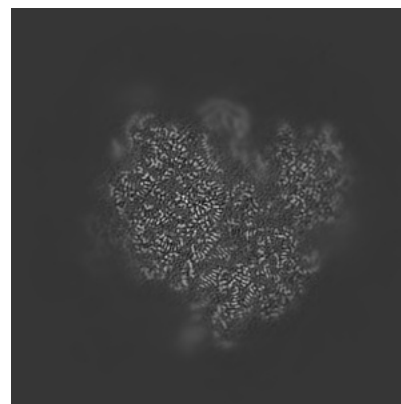
6.3.1 Primary map



X Index: 178



Y Index: 194

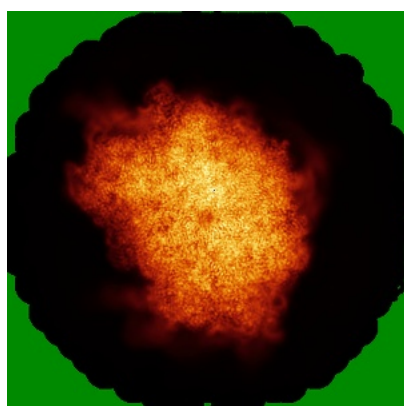


Z Index: 224

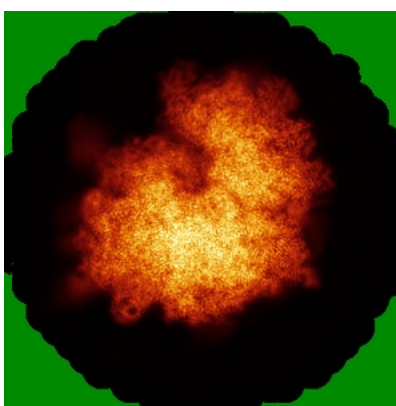
The images above show the largest variance slices of the map in three orthogonal directions.

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

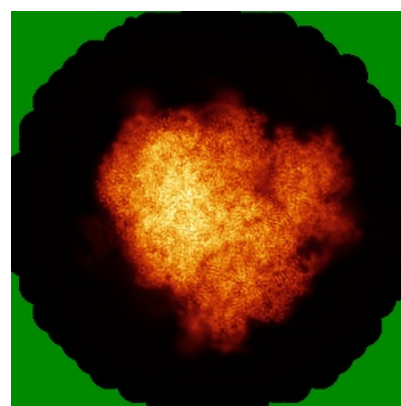
6.4.1 Primary map



X



Y

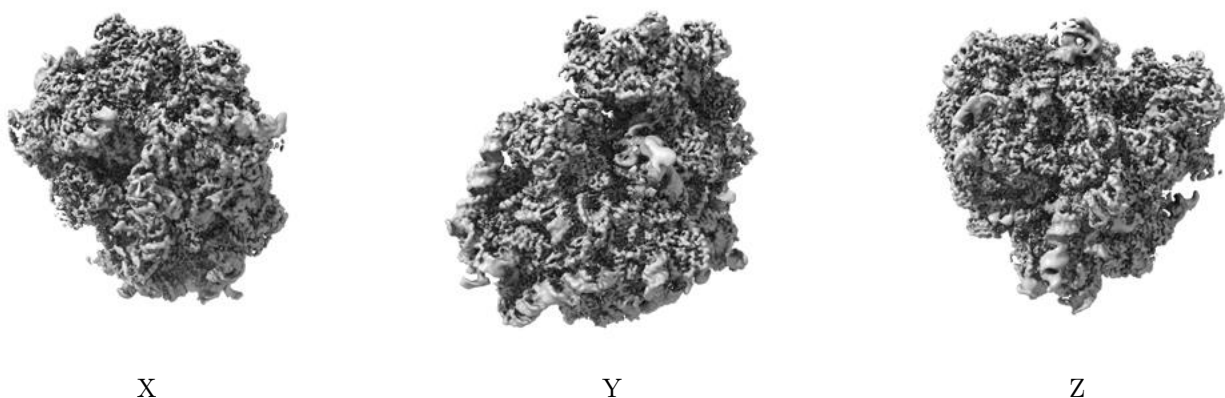


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

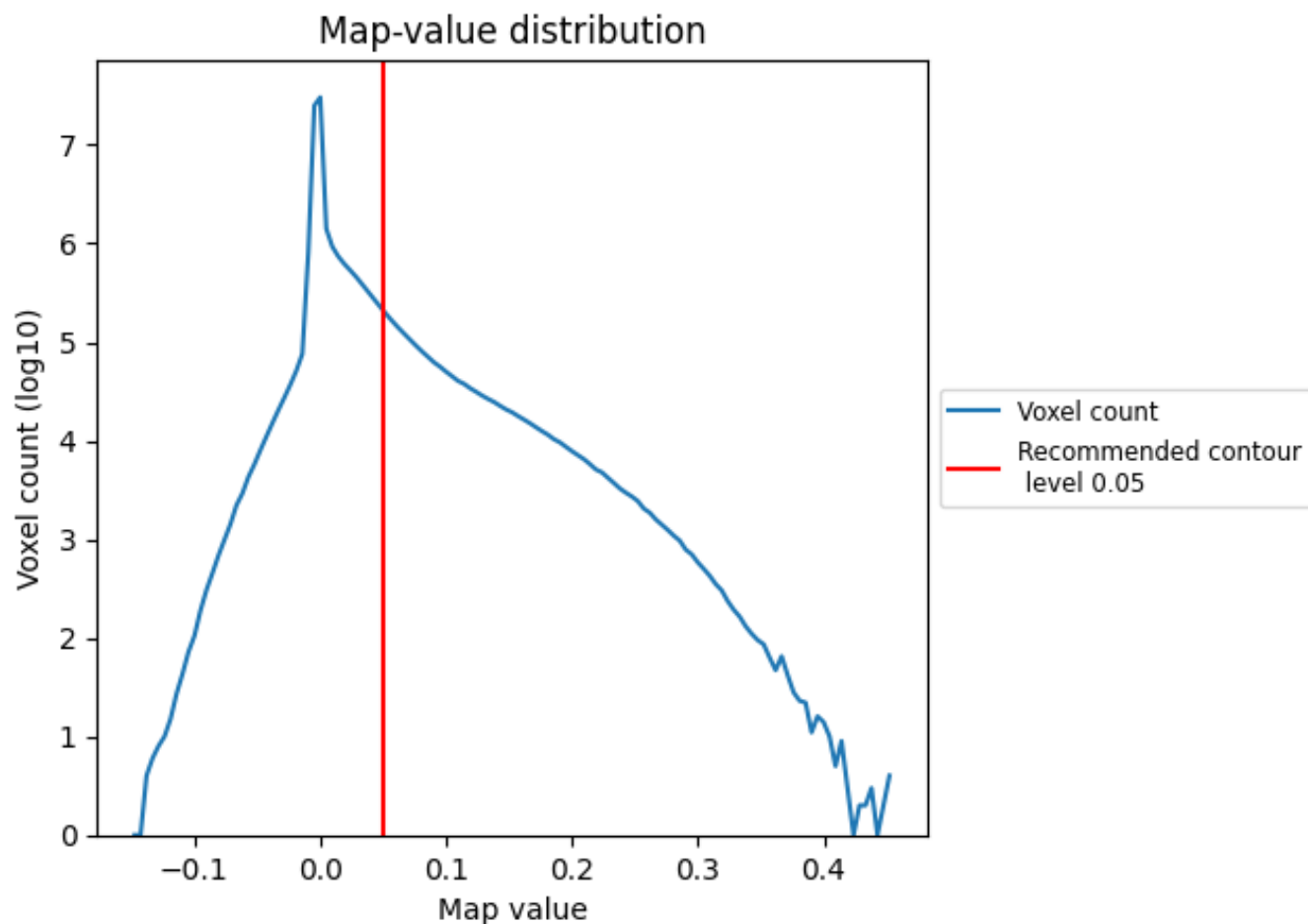
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

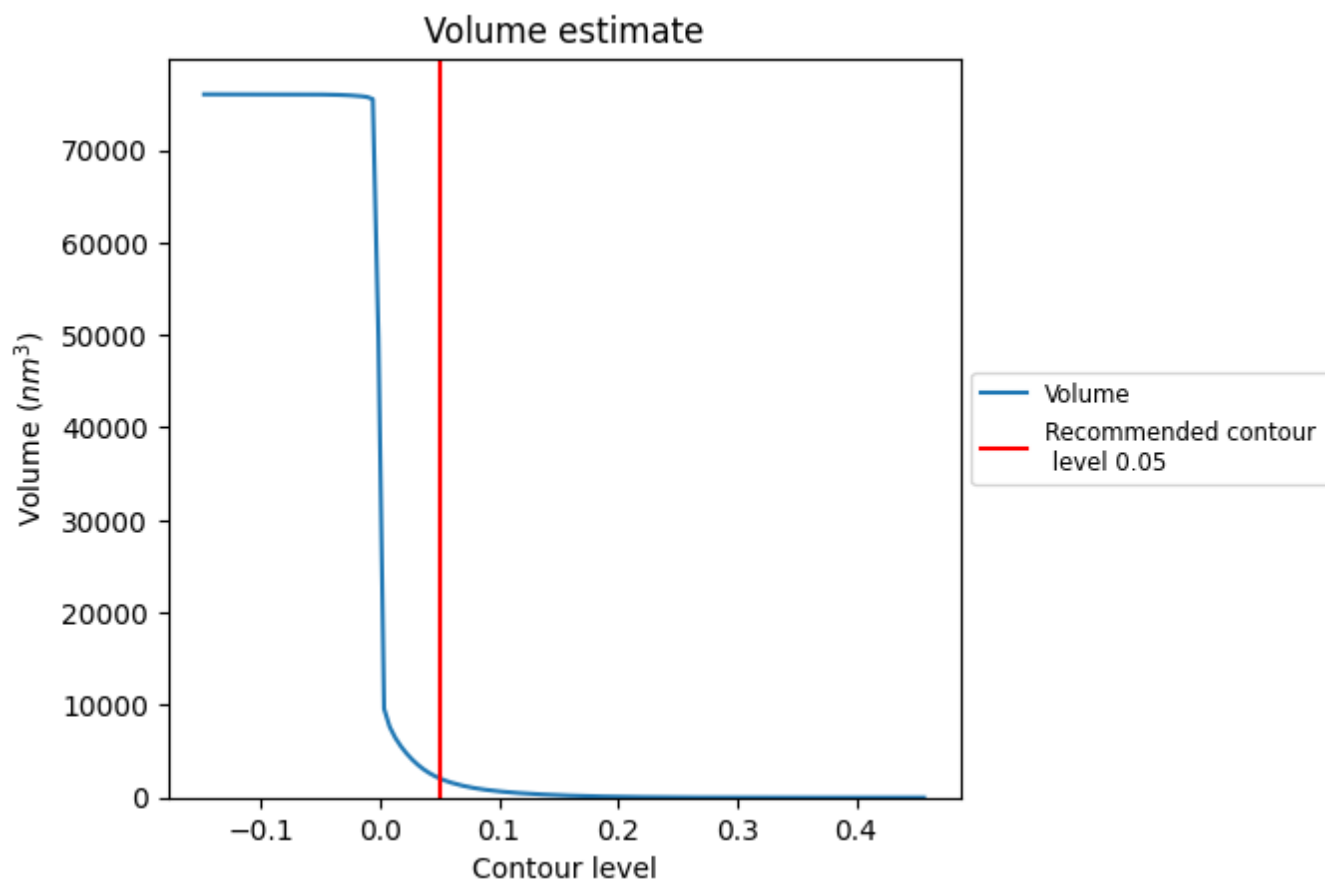
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

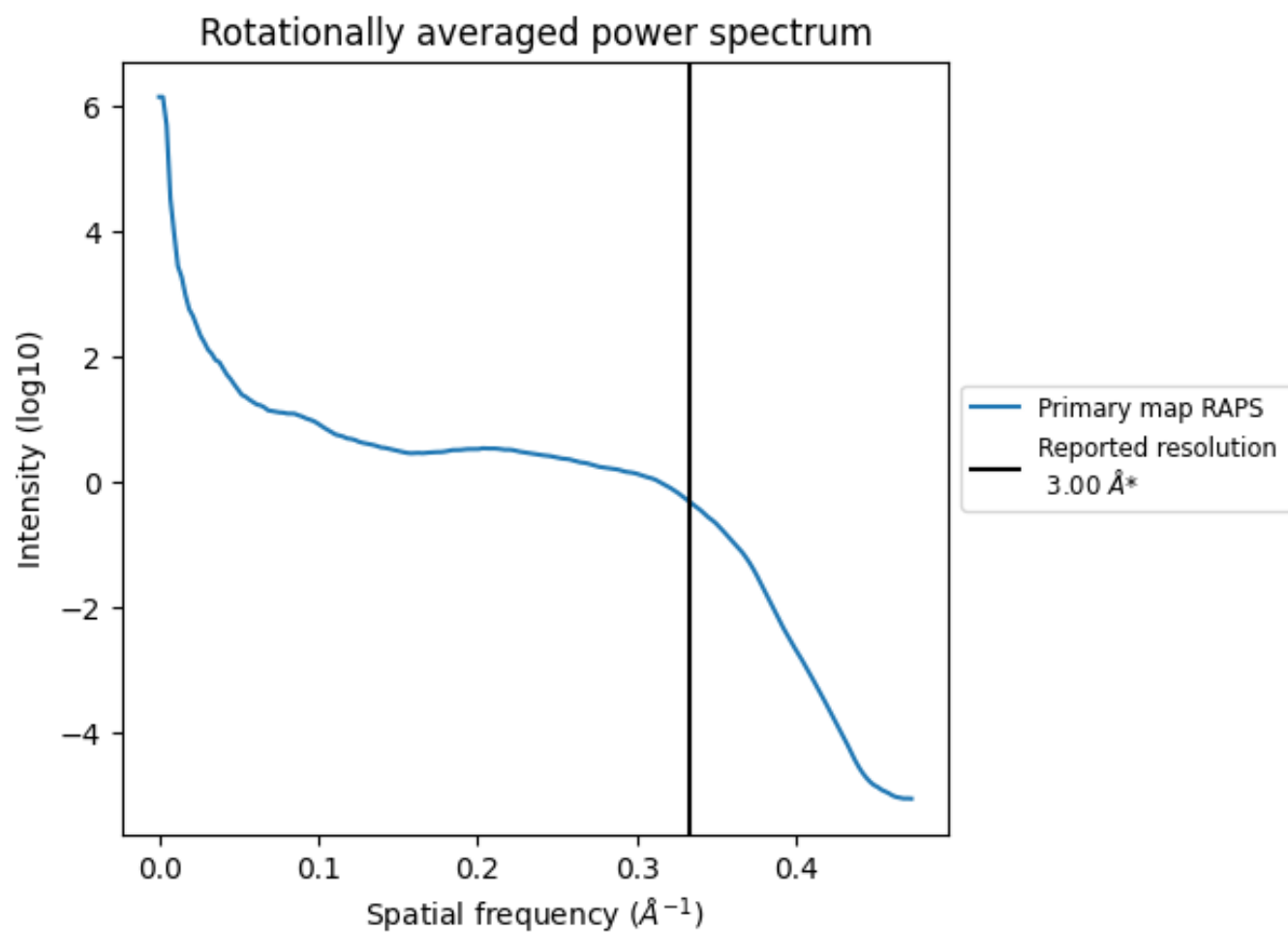
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2092 nm^3 ; this corresponds to an approximate mass of 1890 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 ⓘ

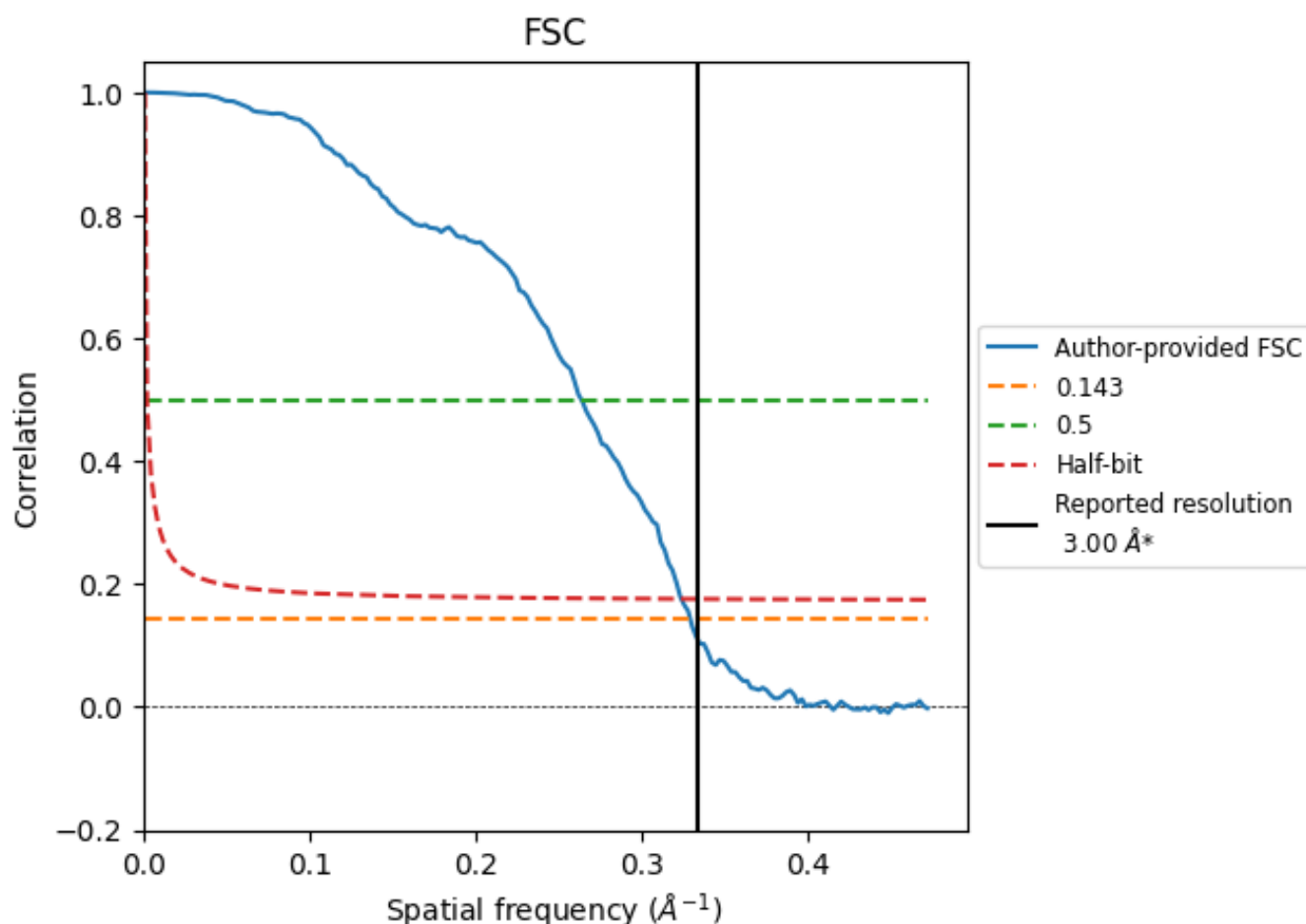


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

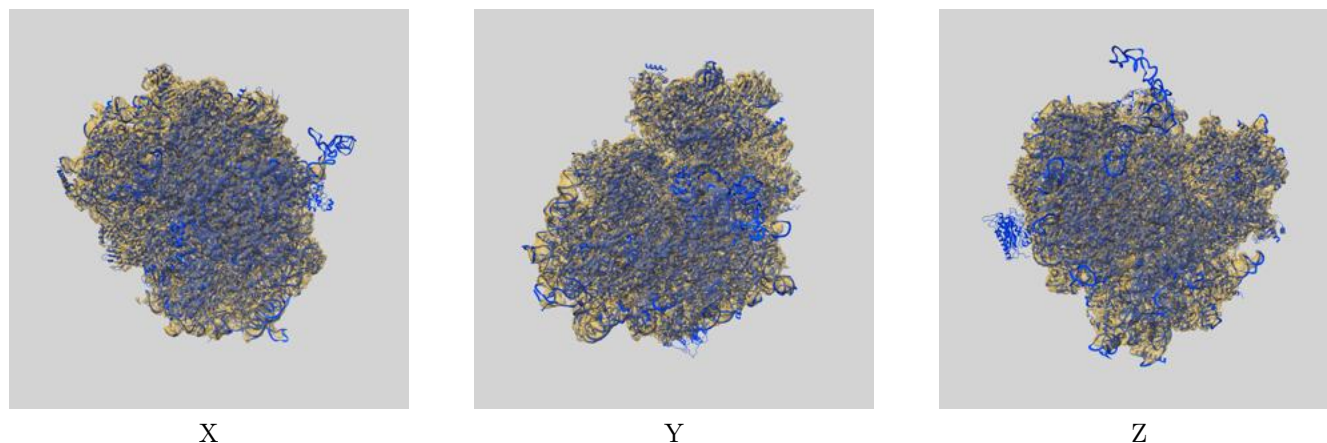
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.79	3.09
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

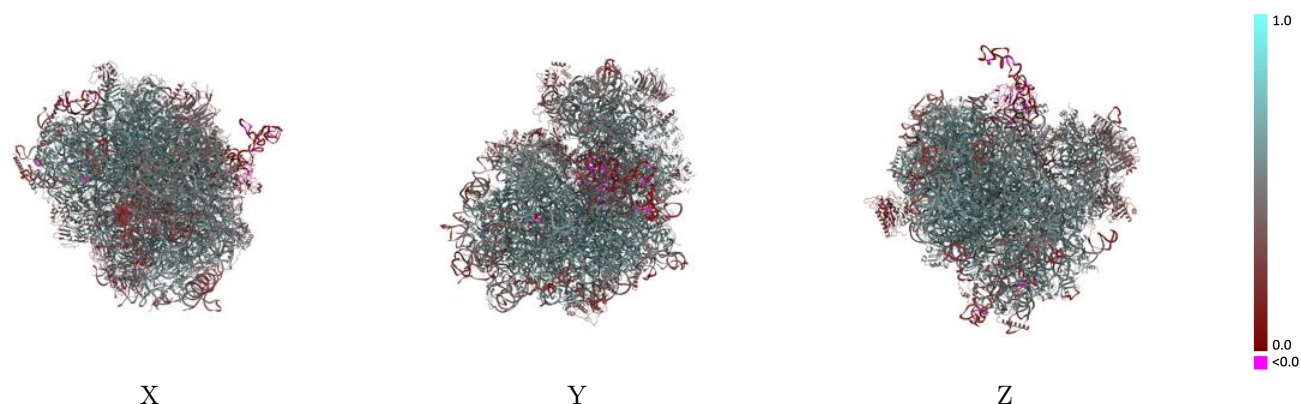
This section contains information regarding the fit between EMDB map EMD-11289 and PDB model 6ZME. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



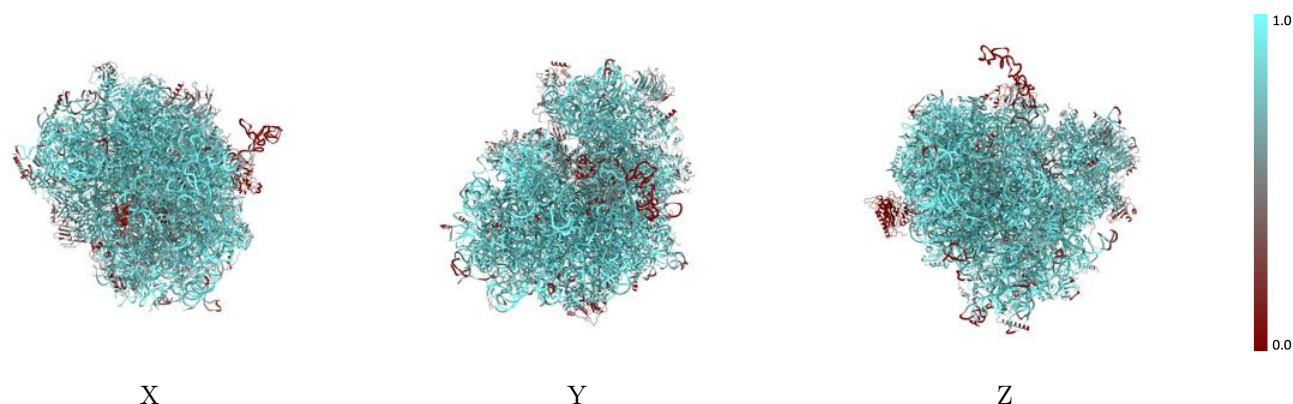
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



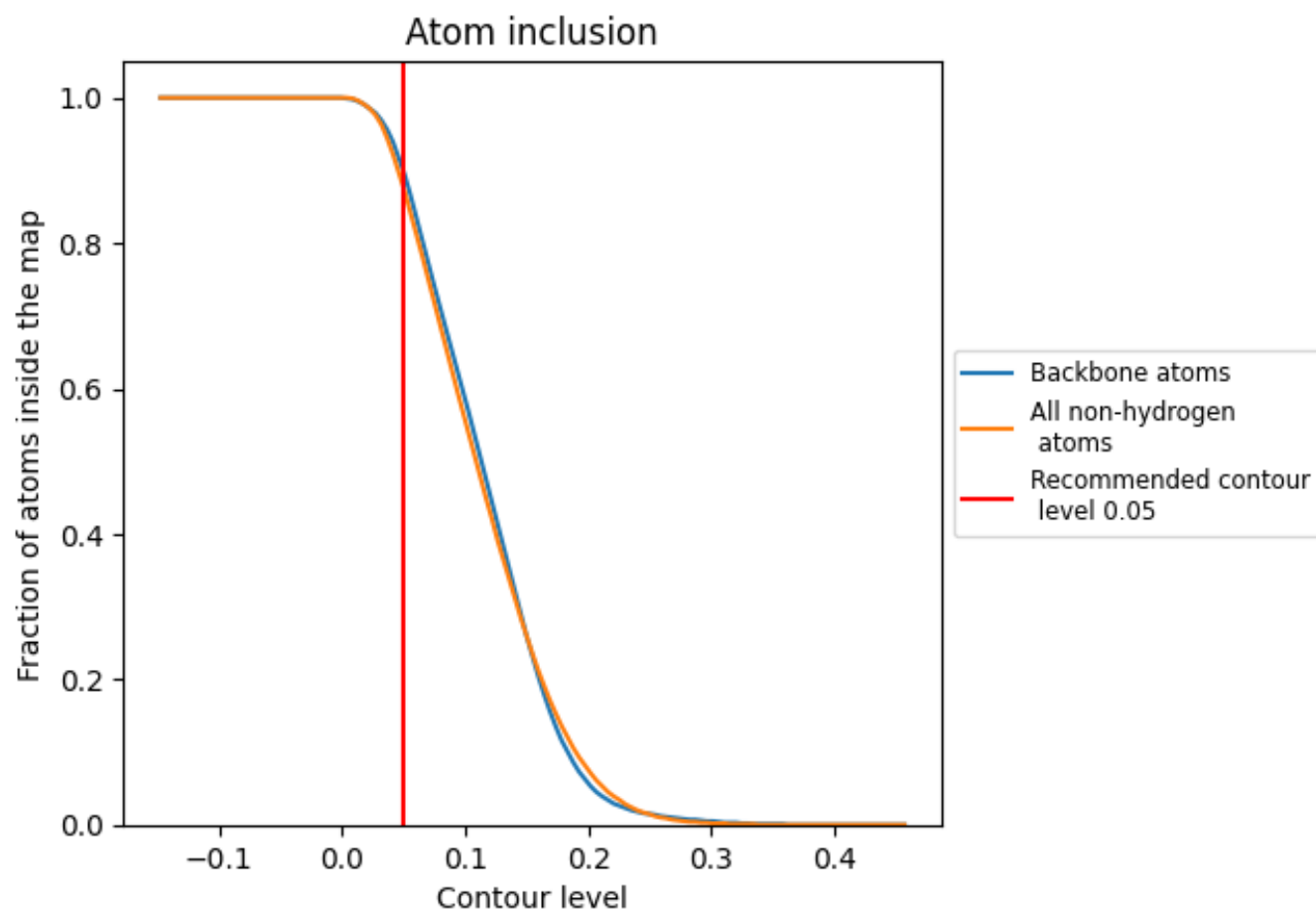
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8750	 0.5200
CA	 0.0420	 0.2520
CC	 0.8740	 0.2970
CE	 0.7320	 0.4260
CF	 0.9230	 0.5470
CH	 0.5680	 0.3700
CI	 0.6840	 0.4610
L5	 0.9330	 0.5400
L7	 0.9860	 0.5750
L8	 0.9660	 0.5680
LA	 0.9810	 0.6180
LB	 0.9340	 0.5870
LC	 0.9280	 0.5780
LD	 0.8680	 0.5220
LE	 0.8250	 0.4970
LF	 0.9630	 0.5860
LG	 0.8070	 0.5060
LH	 0.9050	 0.5490
LI	 0.9360	 0.5660
LJ	 0.7790	 0.4470
LL	 0.8820	 0.5450
LM	 0.9160	 0.5440
LN	 0.9870	 0.6250
LO	 0.9440	 0.5940
LP	 0.9580	 0.6110
LQ	 0.9680	 0.6020
LR	 0.8750	 0.5450
LS	 0.9640	 0.5930
LT	 0.9310	 0.5590
LU	 0.8150	 0.4710
LV	 0.9680	 0.5970
LW	 0.7010	 0.4520
LX	 0.9190	 0.5670
LY	 0.9030	 0.5640
LZ	 0.8990	 0.5590



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Chain	Atom inclusion	Q-score
La	 0.9540	 0.6050
Lb	 0.8300	 0.5030
Lc	 0.9120	 0.5520
Ld	 0.9120	 0.5680
Le	 0.9680	 0.5970
Lf	 0.9670	 0.6100
Lg	 0.9210	 0.5790
Lh	 0.9000	 0.5490
Li	 0.8970	 0.5450
Lj	 0.9810	 0.6110
Lk	 0.7770	 0.5000
Ll	 0.9810	 0.5910
Lm	 0.9330	 0.5710
Ln	 0.9860	 0.6110
Lo	 0.9100	 0.5780
Lp	 0.9460	 0.6000
Lr	 0.9490	 0.5740
Ls	 0.3310	 0.2650
Lt	 0.4750	 0.2590
Lz	 0.1140	 0.1150
S2	 0.9380	 0.5330
SA	 0.8450	 0.5200
SB	 0.8860	 0.5350
SC	 0.9140	 0.5530
SD	 0.7770	 0.4540
SE	 0.9100	 0.5520
SF	 0.8550	 0.4850
SG	 0.7750	 0.4650
SH	 0.7210	 0.4510
SI	 0.8780	 0.5330
SJ	 0.8800	 0.5310
SK	 0.7440	 0.4100
SL	 0.8980	 0.5670
SM	 0.2510	 0.2210
SN	 0.9300	 0.5670
SO	 0.8780	 0.5390
SP	 0.7340	 0.4250
SQ	 0.8090	 0.4820
SR	 0.7600	 0.4670
SS	 0.7860	 0.4500
ST	 0.8270	 0.4790
SU	 0.7340	 0.4230

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Chain	Atom inclusion	Q-score
SV	 0.8760	 0.5390
SW	 0.9460	 0.5830
SX	 0.9420	 0.5810
SY	 0.8180	 0.5020
SZ	 0.7100	 0.4320
Sa	 0.9200	 0.5630
Sb	 0.8390	 0.5140
Sc	 0.7390	 0.4570
Sd	 0.9530	 0.5380
Se	 0.8180	 0.5030
Sf	 0.4490	 0.2880
Sg	 0.6100	 0.3900