



wwPDB EM Validation Summary Report ⓘ

Sep 13, 2026 – 10:25 am BST

PDB ID : 31FZ / pdb_000031fz
EMDB ID : EMD-58363
Title : Mouse 80S ribosome, eL41 KO
Authors : Rabl, J.; Valdivia Francia, F.; Sendoel, A.
Deposited on : 2026-06-02
Resolution : 2.89 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

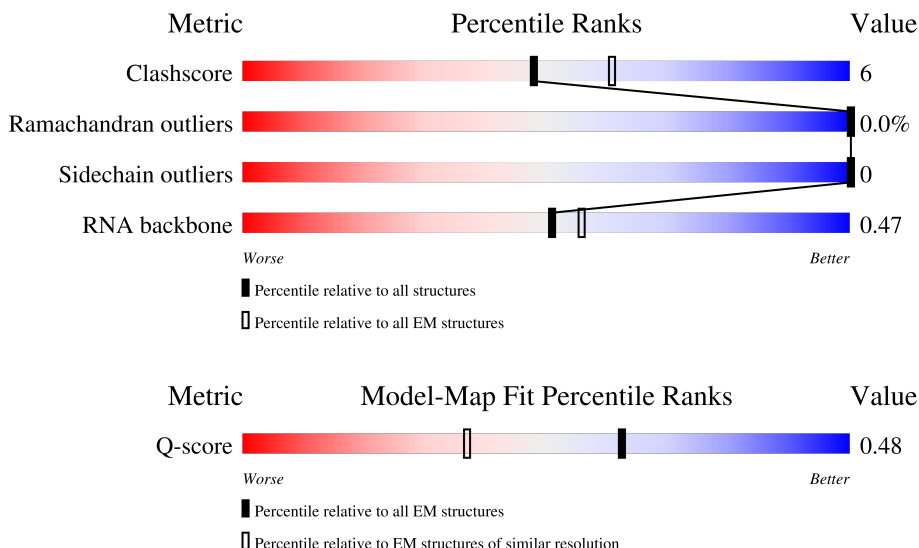
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 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	12148 (2.39 - 3.39)

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	AA	257	
2	AB	403	
3	AC	419	

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Mol	Chain	Length	Quality of chain
4	AD	297	
5	AE	296	
6	AF	203	
7	AG	184	
8	AH	188	
9	AI	196	
10	AJ	176	
11	AK	160	
12	AL	128	
13	AM	140	
14	AN	157	
15	AO	156	
16	AP	145	
17	AQ	136	
18	AR	148	
19	AS	160	
20	AT	115	
21	AU	125	
22	AV	135	
23	AW	110	
24	AX	117	
25	AY	123	
26	AZ	105	
27	Aa	97	
28	Ab	70	

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Mol	Chain	Length	Quality of chain
29	Ac	51	
30	Ad	128	
31	Ae	106	
32	Af	92	
33	Ag	137	
34	BA	69	
35	BB	56	
36	BC	1871	
37	BE	243	
38	BH	135	
39	BJ	204	
40	BK	165	
41	BL	145	
42	BM	146	
43	BN	152	
44	BO	145	
45	BP	119	
46	BT	317	
47	BX	132	
48	Bc	125	
49	Bf	156	
50	BD	264	
51	BF	263	
52	BG	158	
53	BI	295	

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Mol	Chain	Length	Quality of chain
54	BQ	83	
55	BR	143	
56	BS	115	
57	BU	293	
58	BV	249	
59	BW	194	
60	BY	151	
61	BZ	151	
62	Ba	130	
63	Bb	133	
64	Bd	84	
65	Be	133	
66	Bg	194	
67	Bh	208	
68	CA	270	
69	CB	266	
70	CC	192	
71	CD	214	
72	CE	178	
73	CF	211	
74	CG	217	
75	CH	204	
76	CI	4731	
77	CJ	121	
78	CK	156	

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 362477 atoms, of which 154374 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	AA	251	Total	C	H	N	O	S	0	0
			3943	1204	2022	393	318	6		

- Molecule 2 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AB	402	Total	C	H	N	O	S	0	0
			6618	2060	3380	609	555	14		

- Molecule 3 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	AC	367	Total	C	H	N	O	S	0	0
			6039	1842	3111	583	488	15		

- Molecule 4 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AD	293	Total	C	H	N	O	S	0	0
			4794	1506	2409	440	425	14		

- Molecule 5 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	AE	221	Total	C	H	N	O	S	0	0
			3721	1145	1932	342	298	4		

- Molecule 6 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	AF	201	Total	C	H	N	O	S	0	0
			3430	1055	1790	320	259	6		

- Molecule 7 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	AG	153	Total	C	H	N	O	S	0	0
			2516	777	1274	241	215	9		

- Molecule 8 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	AH	186	Total	C	H	N	O	S	0	0
			3147	946	1636	313	248	4		

- Molecule 9 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	AI	184	Total	C	H	N	O	S	0	0
			3240	955	1698	332	246	9		

- Molecule 10 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	AJ	175	Total	C	H	N	O	S	0	0
			2938	924	1488	283	233	10		

- Molecule 11 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AK	158	Total	C	H	N	O	S	0	0
			2657	821	1364	251	215	6		

- Molecule 12 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AL	101	Total	C	H	N	O	S	0	0
			1675	529	850	144	150	2		

- Molecule 13 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AM	129	Total	C	H	N	O	S	0	0
			2000	613	1031	182	169	5		

- Molecule 14 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AN	61	Total	C	H	N	O	S	0	0
			1045	330	530	100	82	3		

- Molecule 15 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AO	118	Total	C	H	N	O	S	0	0
			2007	618	1040	181	167	1		

- Molecule 16 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	AP	134	Total	C	H	N	O	S	0	0
			2320	700	1205	226	186	3		

- Molecule 17 is a protein called Large ribosomal subunit protein eL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	AQ	135	Total	C	H	N	O	S	0	0
			2289	714	1182	208	182	3		

- Molecule 18 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	AR	147	Total	C	H	N	O	S	0	0
			2377	736	1213	239	185	4		

- Molecule 19 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	AS	117	Total	C	H	N	O	S	0	0
			1982	596	1037	198	146	5		

- Molecule 20 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	AT	94	Total	C	H	N	O	S	0	0
			1501	465	769	130	131	6		

- Molecule 21 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	AU	107	Total	C	H	N	O	S	0	0
			1817	560	929	171	155	2		

- Molecule 22 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	AV	128	Total	C	H	N	O	S	0	0
			2199	667	1146	216	165	5		

- Molecule 23 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AW	109	Total	C	H	N	O	S	0	0
			1788	555	912	174	143	4		

- Molecule 24 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AX	114	Total	C	H	N	O	S	0	0
			1903	565	997	187	148	6		

- Molecule 25 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	AY	120	Total	C	H	N	O	S	0	0
			2139	634	1138	201	165	1		

- Molecule 26 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AZ	102	Total	C	H	N	O	S	0	0
			1749	521	917	177	129	5		

- Molecule 27 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	Aa	86	Total	C	H	N	O	S	0	0
			1442	434	737	155	111	5		

- Molecule 28 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	Ab	69	Total	C	H	N	O	S	0	0
			1203	365	635	103	99	1		

- Molecule 29 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	Ac	50	Total	C	H	N	O	S	0	0
			927	281	483	98	64	1		

- Molecule 30 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	Ad	52	Total	C	H	N	O	S	0	0
			895	267	465	90	67	6		

- Molecule 31 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	Ae	103	Total	C	H	N	O	S	0	0
			1753	528	911	172	136	6		

- Molecule 32 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	Af	89	Total	C	H	N	O	S	0	0
			1432	436	738	133	118	7		

- Molecule 33 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	Ag	125	Total	C	H	N	O	S	0	0
			2067	621	1066	207	168	5		

- Molecule 34 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	BA	61	Total	C	H	N	O	S	0	0
			986	292	507	95	90	2		

- Molecule 35 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	BB	54	Total	C	H	N	O	S	0	0
			902	284	447	93	73	5		

- Molecule 36 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	BC	1691	Total	C	H	N	O	P	0	0
			54345	16127	18227	6484	11817	1690		

- Molecule 37 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	BE	226	Total	C	H	N	O	S	0	0
			3607	1119	1851	316	314	7		

- Molecule 38 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	BH	131	Total	C	H	N	O	S	0	0
			2182	668	1118	198	194	4		

- Molecule 39 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	BJ	189	Total	C	H	N	O	S	0	0
			3044	934	1549	284	270	7		

- Molecule 40 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	BK	97	Total	C	H	N	O	S	0	0
			1661	534	842	147	133	5		

- Molecule 41 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	BL	130	Total	C	H	N	O	S	0	0
			2201	681	1128	205	180	7		

- Molecule 42 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	BM	140	Total	C	H	N	O	S	0	0
			2302	710	1185	211	193	3		

- Molecule 43 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	BN	144	Total	C	H	N	O	S	0	0
			2440	746	1250	241	202	1		

- Molecule 44 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	BO	141	Total	C	H	N	O	S	0	0
			2243	691	1139	215	196	2		

- Molecule 45 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	BP	102	Total	C	H	N	O	S	0	0
			1681	507	874	153	143	4		

- Molecule 46 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	BT	313	Total	C	H	N	O	S	0	0
			4829	1535	2393	424	465	12		

- Molecule 47 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	BX	119	Total	C	H	N	O	S	0	0
			1860	576	943	161	172	8		

- Molecule 48 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	Bc	75	Total	C	H	N	O	S	0	0
			1254	382	656	111	104	1		

- Molecule 49 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	Bf	62	Total	C	H	N	O	S	0	0
			1011	317	506	96	85	7		

- Molecule 50 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	BD	214	Total	C	H	N	O	S	0	0
			3545	1103	1807	310	311	14		

- Molecule 51 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	BF	241	Total	C	H	N	O	S	0	0
			3921	1228	2006	353	326	8		

- Molecule 52 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	BG	153	Total	C	H	N	O	S	0	0
			2570	793	1323	234	214	6		

- Molecule 53 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	BI	214	Total	C	H	N	O	S	0	0
			3390	1077	1696	297	312	8		

- Molecule 54 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	BQ	83	Total	C	H	N	O	S	0	0
			1273	392	635	119	122	5		

- Molecule 55 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	BR	141	Total	C	H	N	O	S	0	0
			2266	693	1168	219	183	3		

- Molecule 56 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	BS	100	Total	C	H	N	O	S	1	0
			1677	506	866	169	131	5		

- Molecule 57 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	BU	222	Total	C	H	N	O	S	0	0
			3540	1116	1815	298	302	9		

- Molecule 58 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	BV	227	Total	C	H	N	O	S	0	0
			3829	1149	1989	367	317	7		

- Molecule 59 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	BW	82	Total	C	H	N	O	S	0	0
			1450	445	751	140	113	1		

- Molecule 60 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	BY	150	Total	C	H	N	O	S	0	0
			2502	773	1294	229	205	1		

- Molecule 61 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	BZ	134	Total	C	H	N	O	S	0	0
			2023	612	1021	197	187	6		

- Molecule 62 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	Ba	129	Total	C	H	N	O	S	0	0
			2114	659	1080	193	176	6		

- Molecule 63 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	Bb	129	Total	C	H	N	O	S	0	0
			2171	662	1122	206	176	5		

- Molecule 64 is a protein called Small ribosomal subunit protein eS27-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	Bd	83	Total	C	H	N	O	S	0	0
			1328	409	676	121	115	7		

- Molecule 65 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	Be	15	Total	C	H	N	O	S	0	0
			232	67	123	24	18			

- Molecule 66 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	Bg	183	Total	C	H	N	O	S	0	0
			3044	944	1567	270	262	1		

- Molecule 67 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	Bh	206	Total	C	H	N	O	S	0	0
			3458	1058	1772	332	291	5		

- Molecule 68 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	CA	222	Total	C	H	N	O	S	1	0
			3839	1190	1988	356	297	8		

- Molecule 69 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	CB	230	Total	C	H	N	O	S	1	0
			3866	1188	2003	359	312	4		

- Molecule 70 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	CC	190	Total	C	H	N	O	S	0	0
			3122	956	1603	284	273	6		

- Molecule 71 is a protein called Large ribosomal subunit protein uL16-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	CD	204	Total	C	H	N	O	S	0	0
			3363	1052	1709	319	271	12		

- Molecule 72 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	CE	174	Total	C	H	N	O	S	0	0
			2822	880	1425	260	251	6		

- Molecule 73 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	CF	207	Total	C	H	N	O	S	0	0
			3453	1048	1777	344	280	4		

- Molecule 74 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	CG	139	Total	C	H	N	O	S	0	0
			2360	732	1217	221	183	7		

- Molecule 75 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	CH	203	Total	C	H	N	O	S	0	0
			3450	1072	1749	359	266	4		

- Molecule 76 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	CI	3558	Total	C	H	N	O	P	0	0
			114907	34045	38565	13907	24833	3557		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CI	248	C	-	insertion	GB 120444900
CI	?	-	C	deletion	GB 120444900
CI	?	-	C	deletion	GB 120444900
CI	831	U	-	insertion	GB 120444900
CI	1887	G	-	insertion	GB 120444900
CI	2324	C	-	insertion	GB 120444900
CI	2325	G	-	insertion	GB 120444900
CI	2326	U	-	insertion	GB 120444900
CI	?	-	G	deletion	GB 120444900
CI	?	-	A	deletion	GB 120444900
CI	?	-	A	deletion	GB 120444900

- Molecule 77 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	CJ	120	Total	C	H	N	O	P	0	0
			3853	1141	1295	456	842	119		

- Molecule 78 is a RNA chain called 5.8S rRNA.

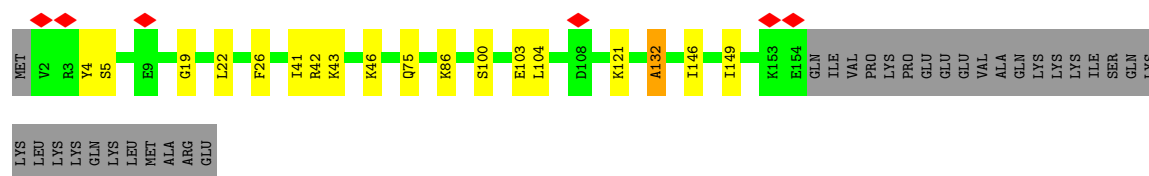
Mol	Chain	Residues	Atoms						AltConf	Trace
78	CK	156	Total	C	H	N	O	P	0	0
			4997	1481	1682	585	1094	155		

- Molecule 79 is ZINC ION (CCD ID: ZN) (formula: Zn).

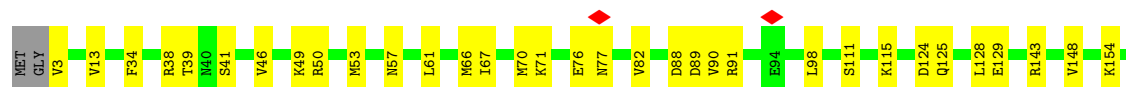
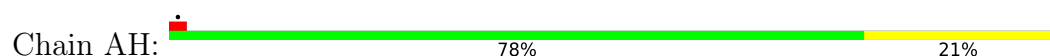
Mol	Chain	Residues	Atoms		AltConf
79	Aa	1	Total	Zn	0
			1	1	
79	Ad	1	Total	Zn	0
			1	1	
79	Ae	1	Total	Zn	0
			1	1	
79	Af	1	Total	Zn	0
			1	1	
79	BB	1	Total	Zn	0
			1	1	
79	Bf	1	Total	Zn	0
			1	1	
79	BS	1	Total	Zn	0
			1	1	

- Molecule 80 is water.

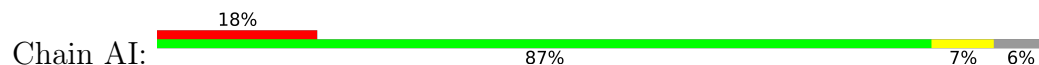
Mol	Chain	Residues	Atoms		AltConf
80	BC	2	Total 2	O 2	0
80	CB	1	Total 1	O 1	0
80	CI	1	Total 1	O 1	0



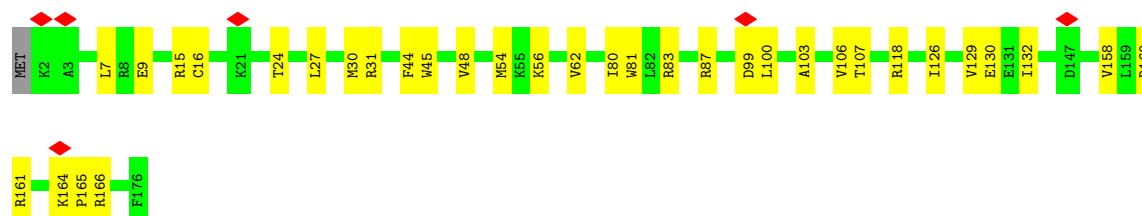
- Molecule 8: Large ribosomal subunit protein eL18



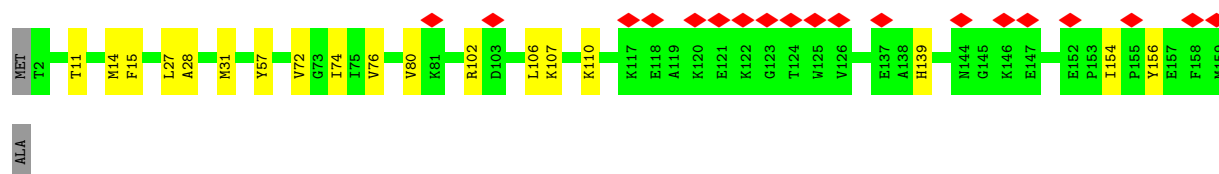
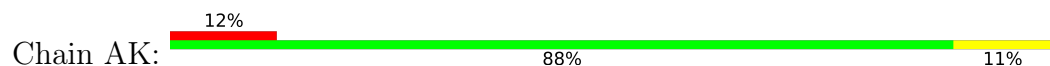
- Molecule 9: Large ribosomal subunit protein eL19



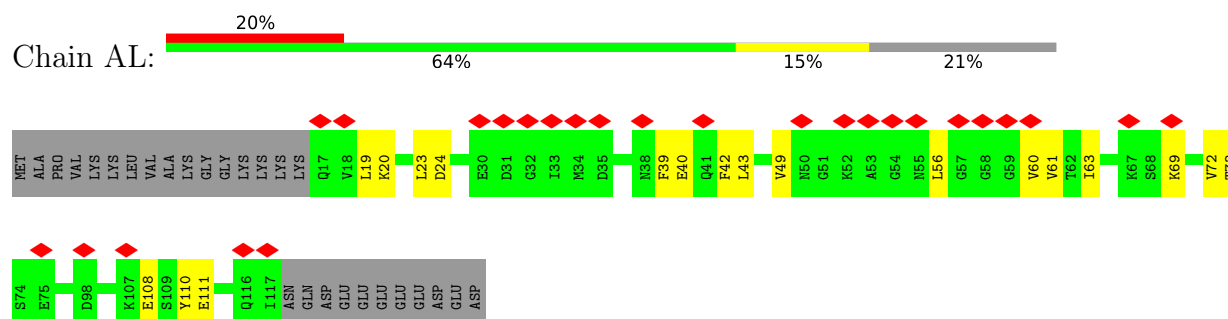
- Molecule 10: Large ribosomal subunit protein eL20



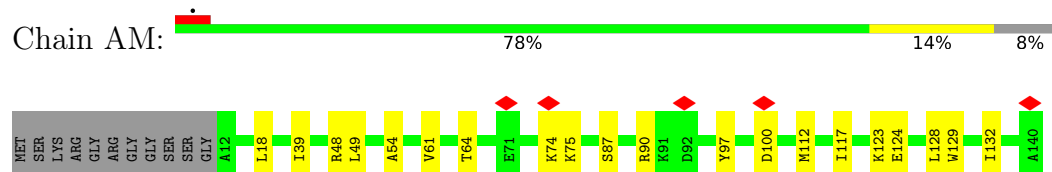
- Molecule 11: Large ribosomal subunit protein eL21



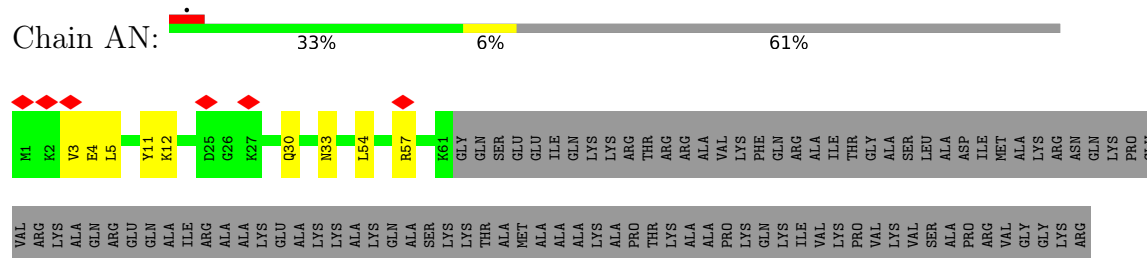
- Molecule 12: Large ribosomal subunit protein eL22



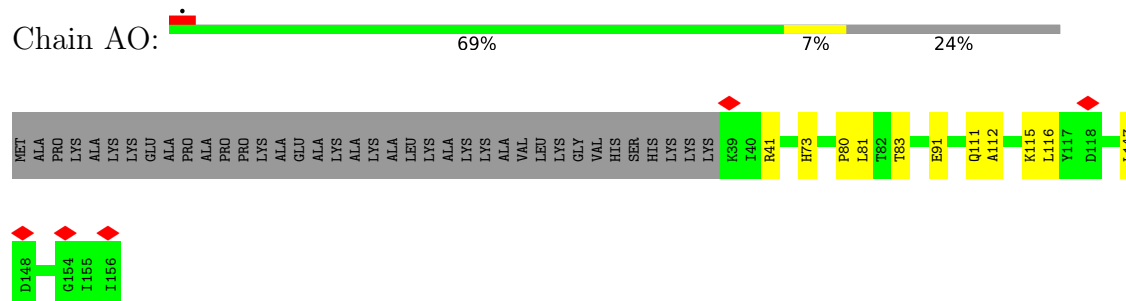
- Molecule 13: Large ribosomal subunit protein uL14



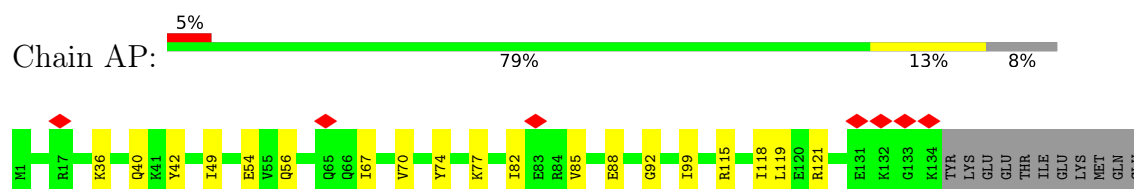
- Molecule 14: Large ribosomal subunit protein eL24



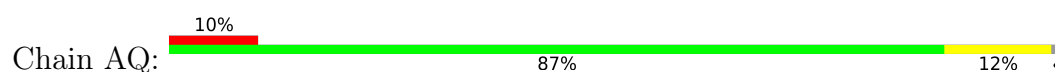
- Molecule 15: Large ribosomal subunit protein uL23



- Molecule 16: Large ribosomal subunit protein uL24



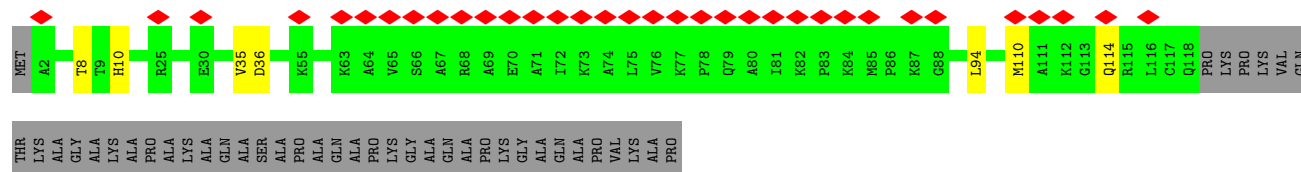
- Molecule 17: Large ribosomal subunit protein eL27



- Molecule 18: Large ribosomal subunit protein uL15



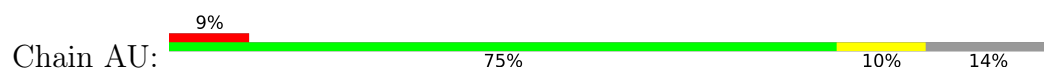
- Molecule 19: Large ribosomal subunit protein eL29



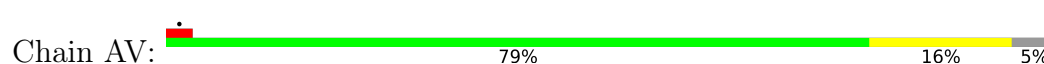
- Molecule 20: Large ribosomal subunit protein eL30



- Molecule 21: Large ribosomal subunit protein eL31

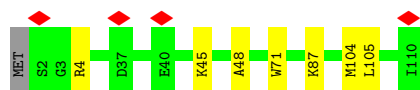


- Molecule 22: Large ribosomal subunit protein eL32

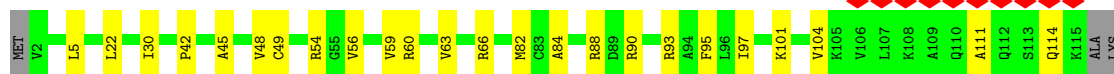
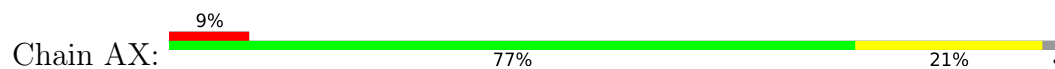


- Molecule 23: Large ribosomal subunit protein eL33

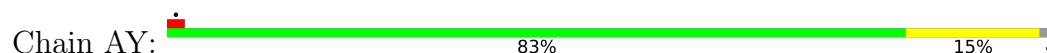




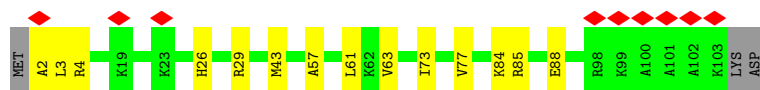
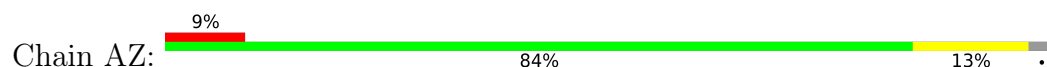
- Molecule 24: Large ribosomal subunit protein eL34



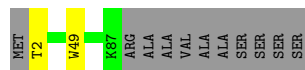
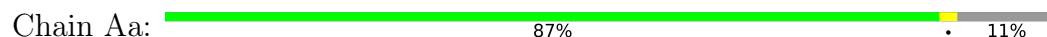
- Molecule 25: Large ribosomal subunit protein uL29



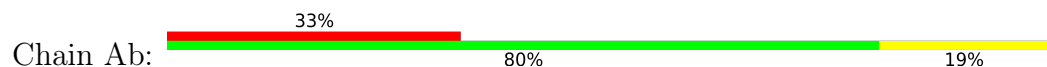
- Molecule 26: Large ribosomal subunit protein eL36



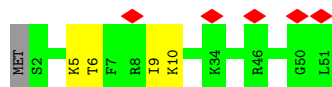
- Molecule 27: Large ribosomal subunit protein eL37



- Molecule 28: Large ribosomal subunit protein eL38



- Molecule 29: Large ribosomal subunit protein eL39



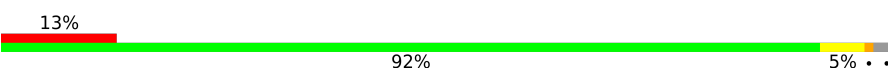
- Molecule 30: Ubiquitin-ribosomal protein eL40 fusion protein

Chain Ad: 

MET GLN ILE PHE VAL SER THR LEU THR LEU THR VAL GLU VAL PRO SER ASP THR ILE GLU ASN VAL LYS ALA ILE GLN ASP LYS GLU ILE PRO PRO ASP GLN ARG LEU ILE PHE ALA GLY LYS GLN LEU GLU ASP GLY ARG THR LEU SER ASP TYR ASN

ILE GLN LYS SER THR LEU HIS VAL LEU ARG LEU ARG GLY I77 I78 E79 P80 R83 Q84 M84 K98 R102 L103 H104 P105 R106 G110 C115 T118 K128

- Molecule 31: Large ribosomal subunit protein eL42

Chain Ae: 

MET V2 N3 K30 D31 S32 L33 Y34 A35 K59 K64 M76 C77 R78 M82 K89 D96 K97 K98 R99 K100 G101 Q102 V103 I104 GLN PHE

- Molecule 32: Large ribosomal subunit protein eL43

Chain Af: 

MET ALA LYS R4 R17 Y18 K27 I31 K36 K46 M47 K48 V52 C57 G58 S59 C60 M61 K62 T74 V77 T78 V79 T83 R84 R85 K90 D91 Q92

- Molecule 33: Large ribosomal subunit protein eL28

Chain Ag: 

MET S2 Q6 L17 I18 K19 R20 N41 I44 A55 D56 G57 R67 I82 R83 K84 V124 V125 V126 LYS ARG LYS THR ARG ARG ARG PRO THR LYS SER SER

- Molecule 34: Small ribosomal subunit protein eS28

Chain BA: 

MET ASP THR SER ARG VAL GLN P8 P9 K10 L11 A12 R13 V14 T15 K16 V17 L18 G19 G22 Q26 R31 V32 E33 F34 M35 D36 D37 T38 S39 R40 S41 I42 I43 R44 R45 V46 K47 G48 P49 V50 R51 E52 Q53 D54 V55 L56 T57 L58 L59 E60 S61 E62 R63 E64 A65 R66 R67 R68 ARG

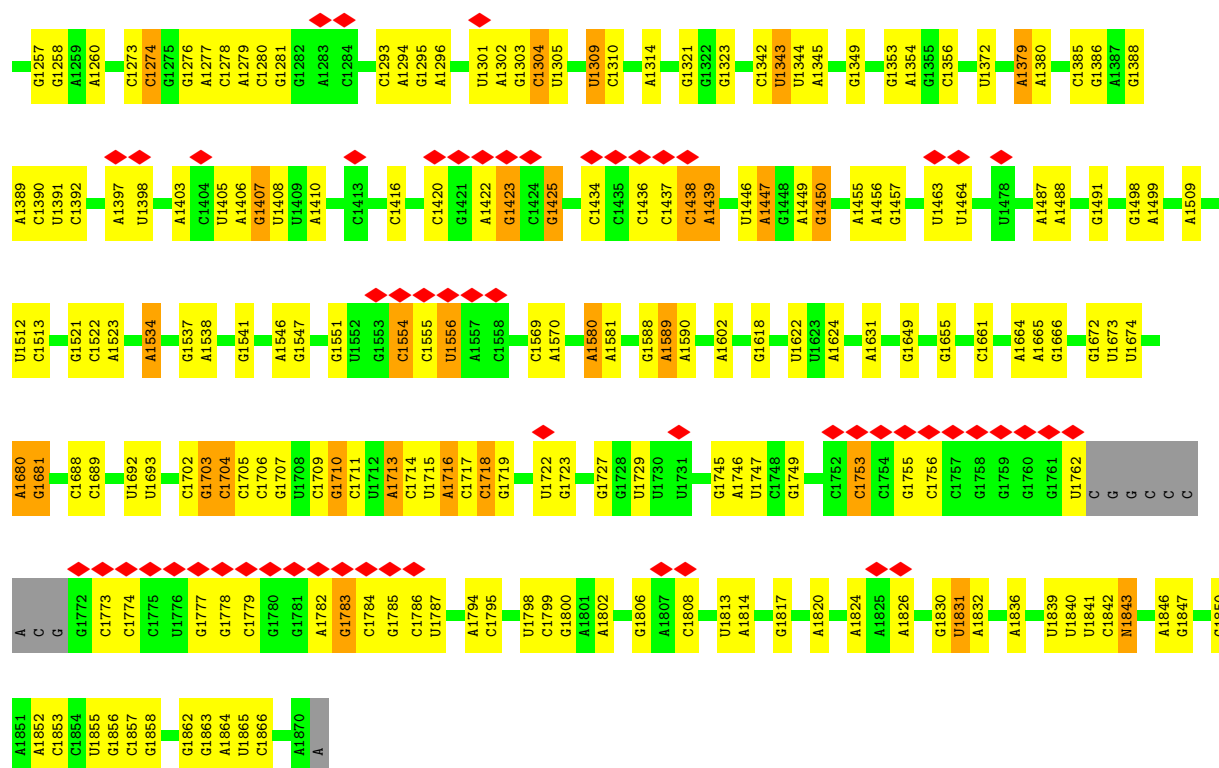
- Molecule 35: Small ribosomal subunit protein uS14

Chain BB: 

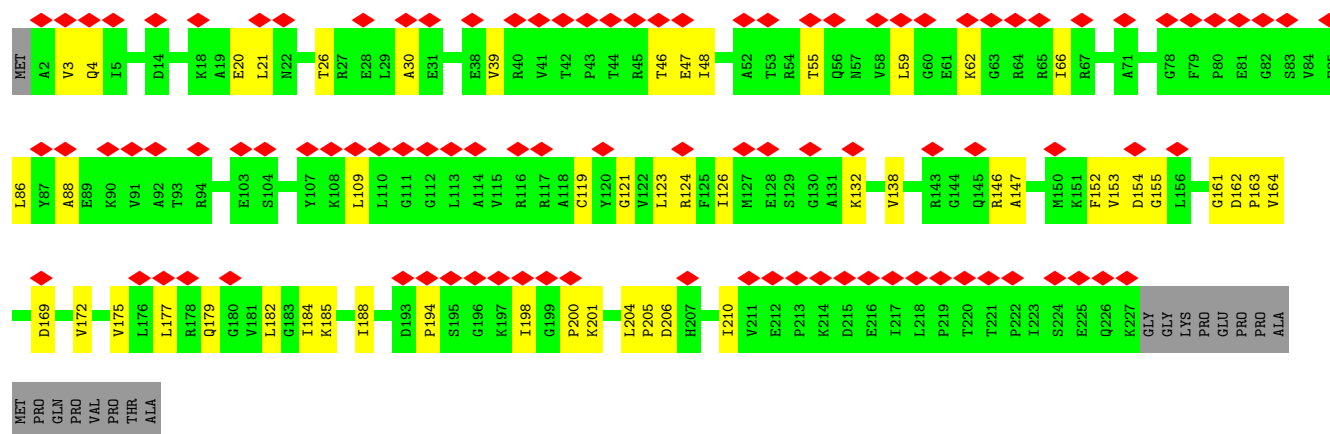
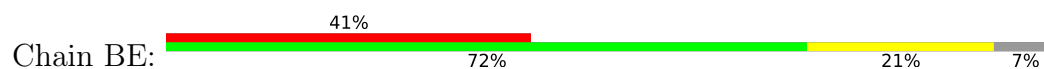
MET GLY H3 Q4 Q5 K13 F14 R22 V23 C24 S25 N26 M37 M38 C39 Y46 I50 L55 D56

- Molecule 36: 18S rRNA

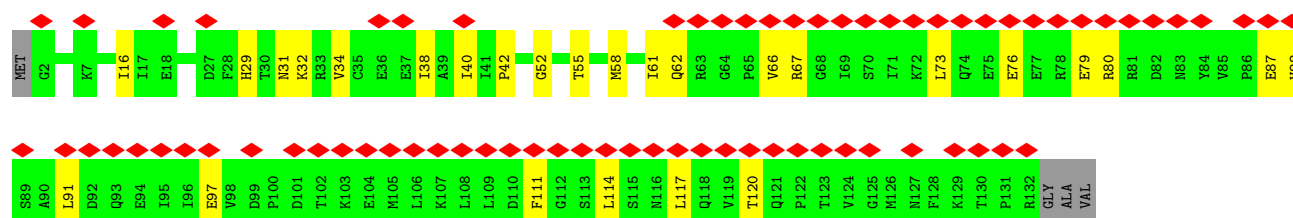
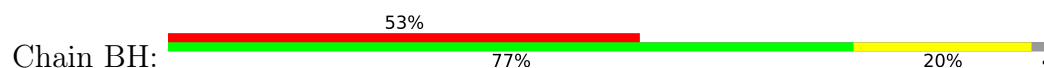




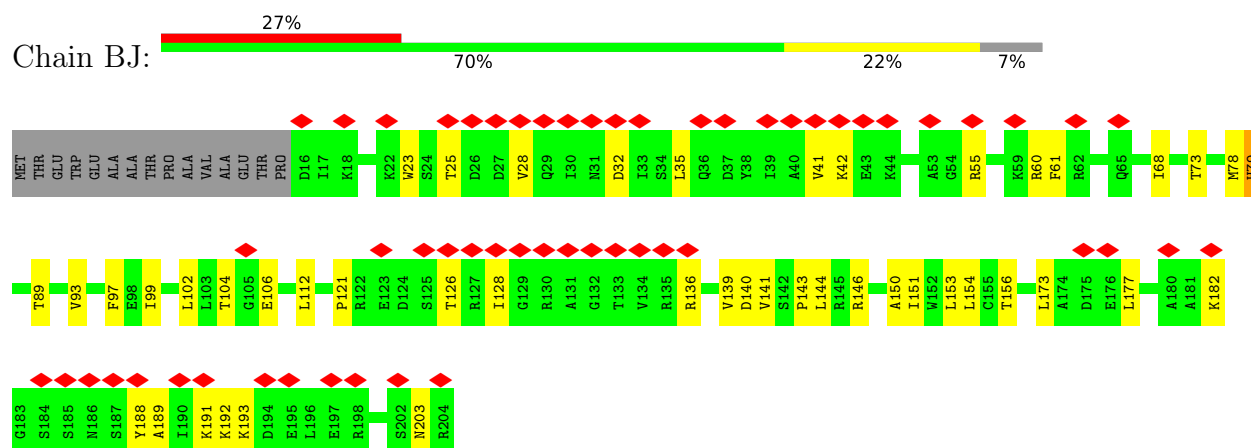
• Molecule 37: Small ribosomal subunit protein uS3



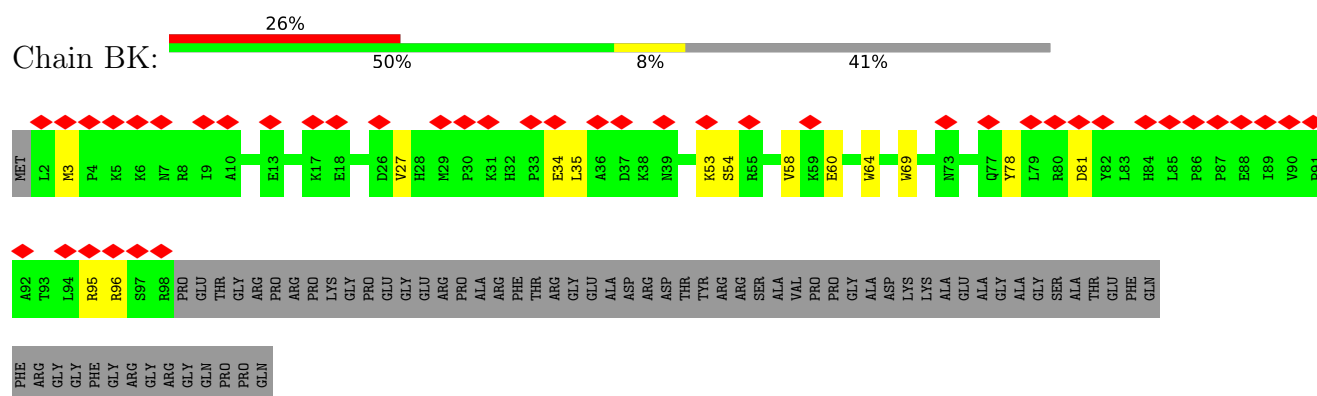
• Molecule 38: Small ribosomal subunit protein eS17



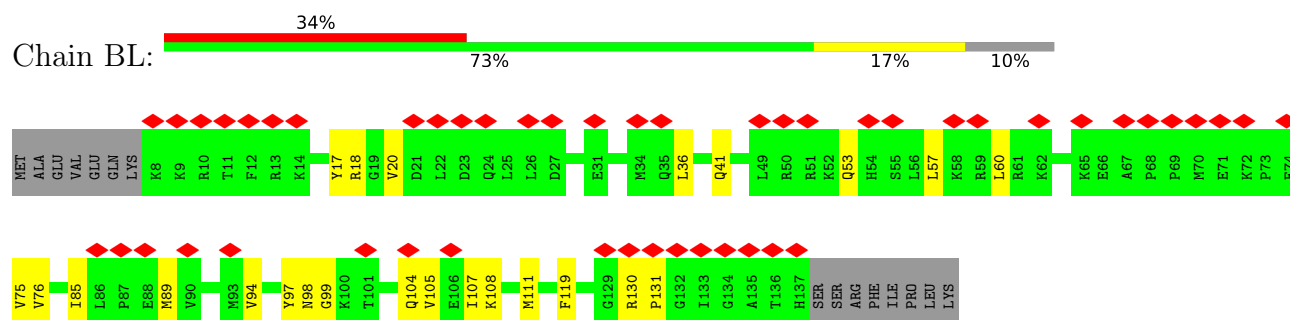
- Molecule 39: Small ribosomal subunit protein uS7



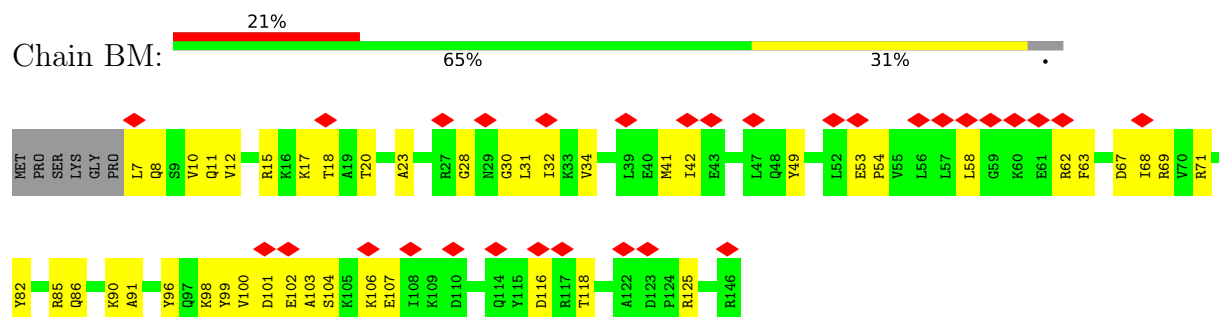
- Molecule 40: Small ribosomal subunit protein eS10



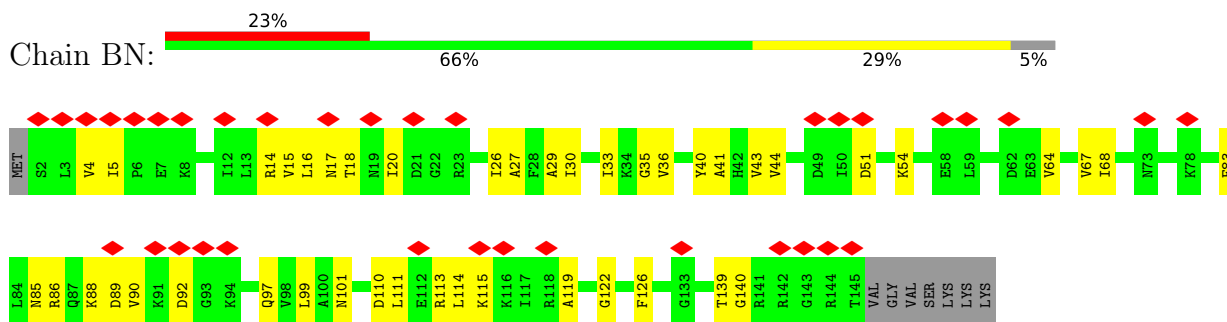
- Molecule 41: Small ribosomal subunit protein uS19



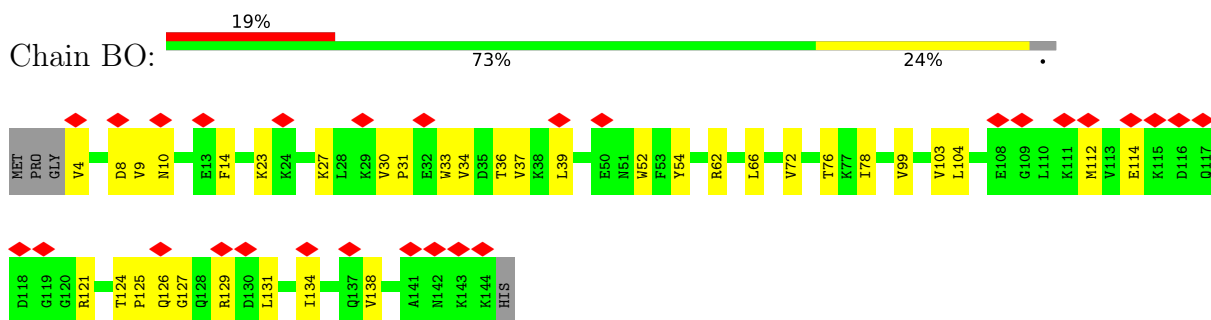
- Molecule 42: Small ribosomal subunit protein uS9



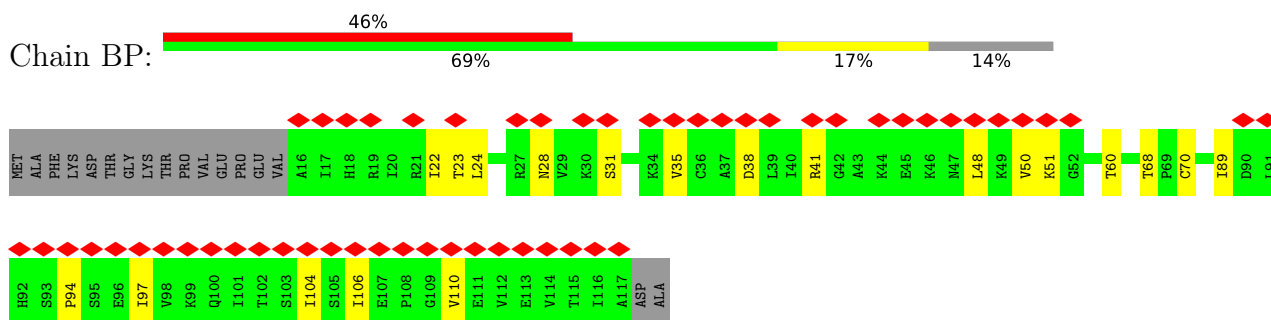
- Molecule 43: Small ribosomal subunit protein uS13



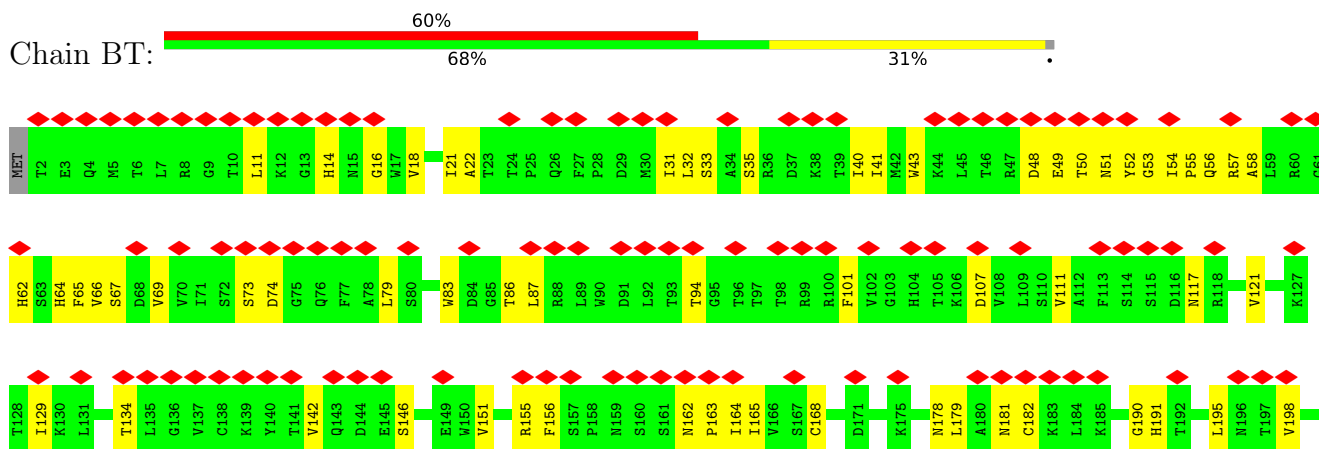
- Molecule 44: Small ribosomal subunit protein eS19

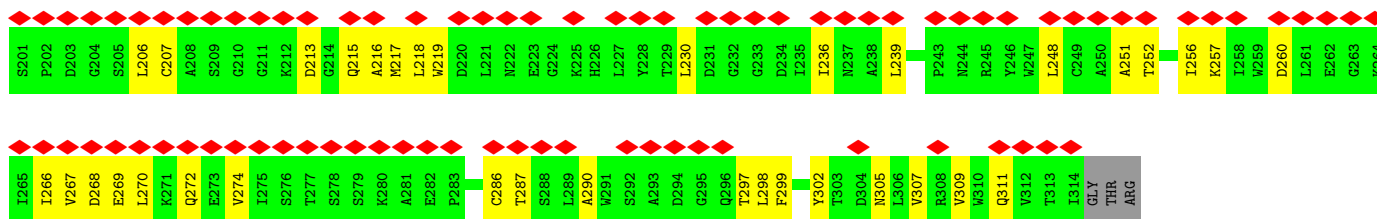


- Molecule 45: Small ribosomal subunit protein uS10

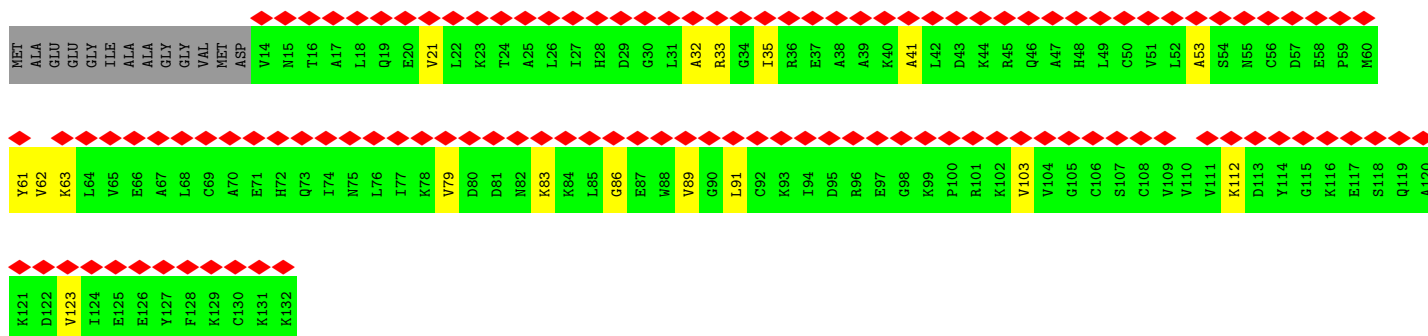
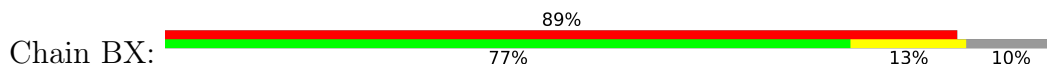


- Molecule 46: Small ribosomal subunit protein RACK1

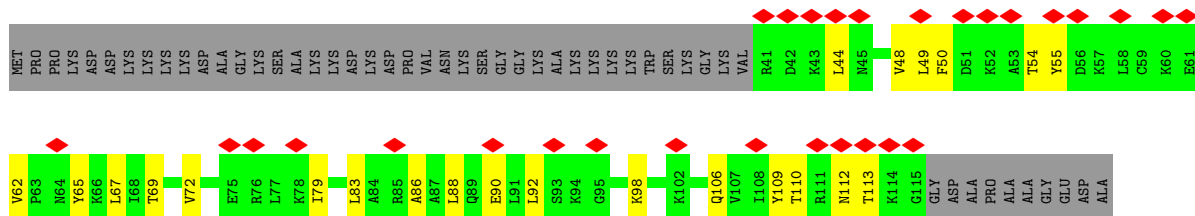
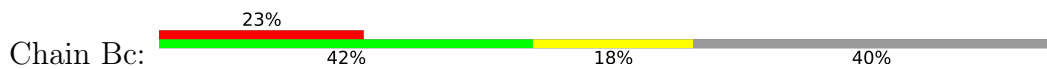




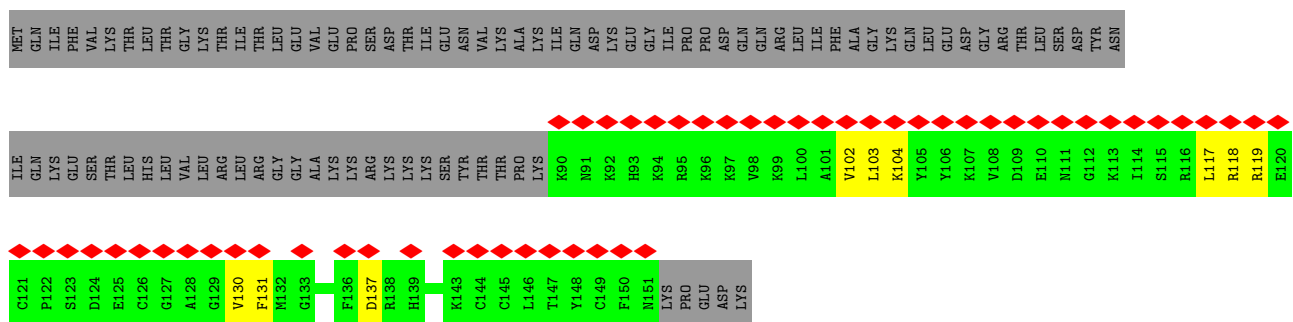
• Molecule 47: Small ribosomal subunit protein eS12



• Molecule 48: Small ribosomal subunit protein eS25

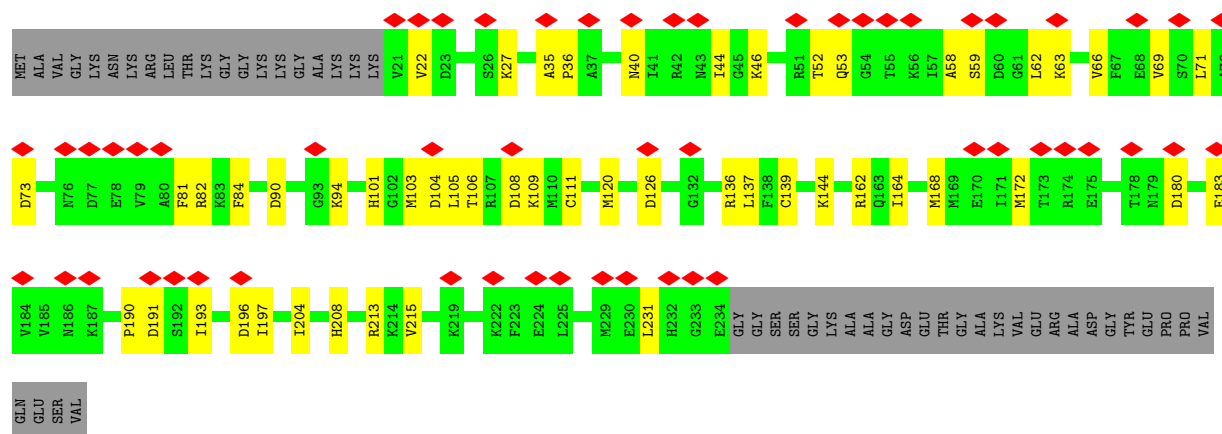


• Molecule 49: Ubiquitin-ribosomal protein eS31 fusion protein

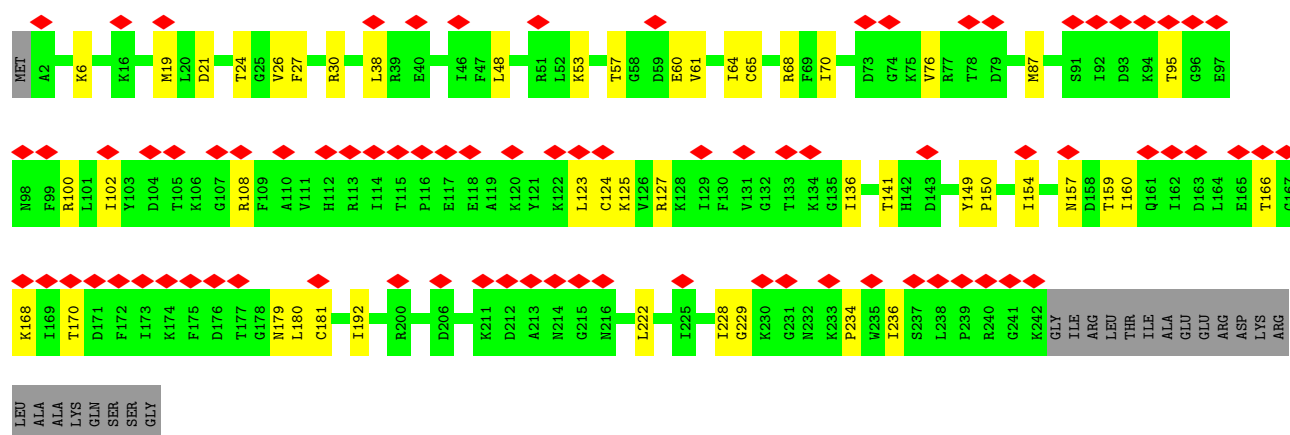
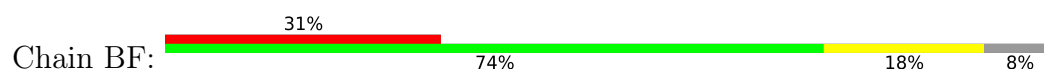


• Molecule 50: 40S ribosomal protein S3a

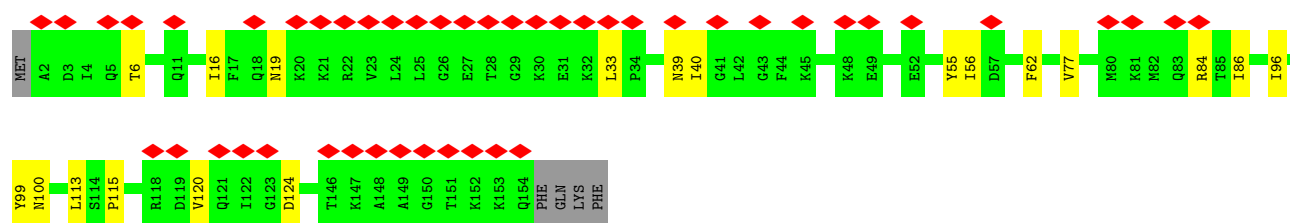
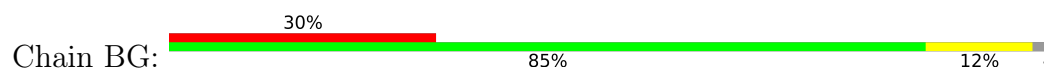




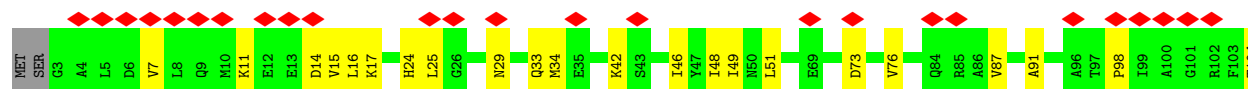
• Molecule 51: Small ribosomal subunit protein eS4

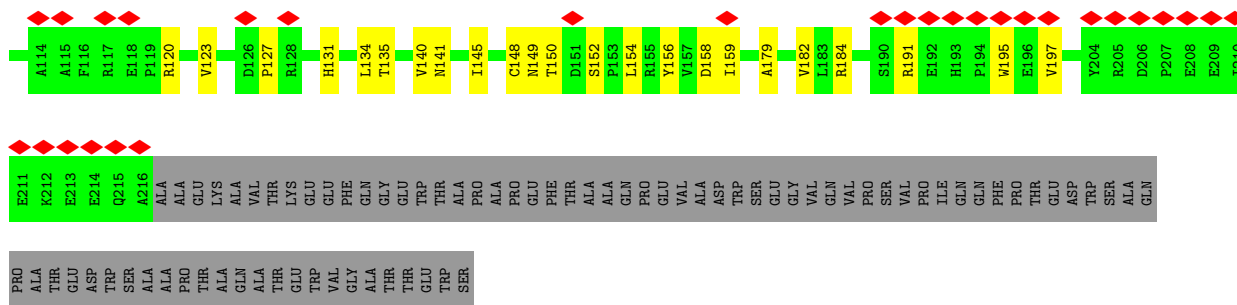


• Molecule 52: Small ribosomal subunit protein uS17

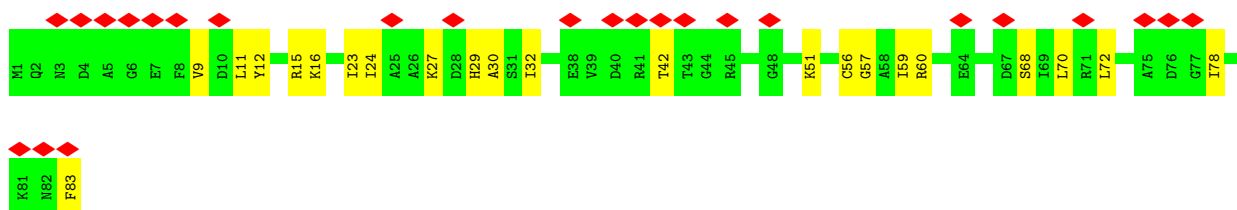
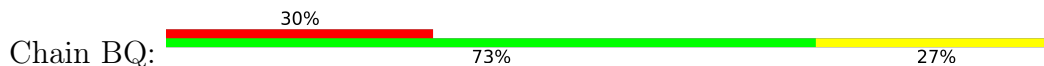


• Molecule 53: Small ribosomal subunit protein uS2

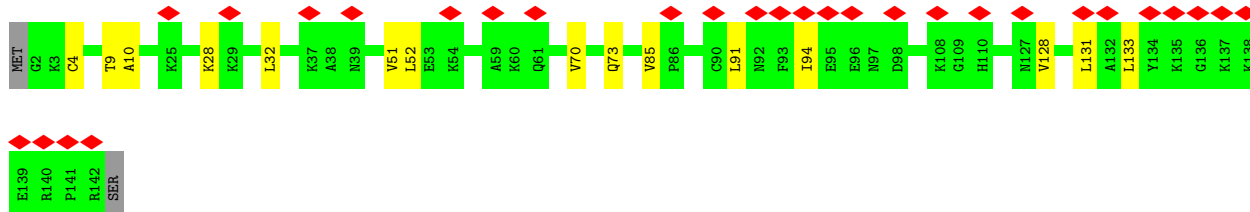
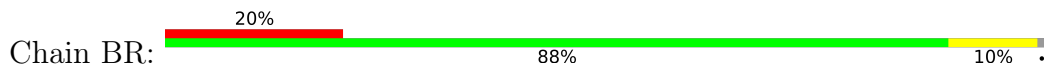




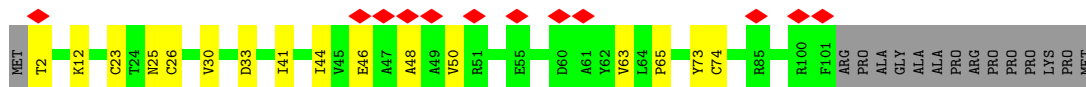
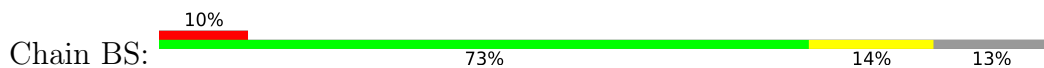
- Molecule 54: Small ribosomal subunit protein eS21



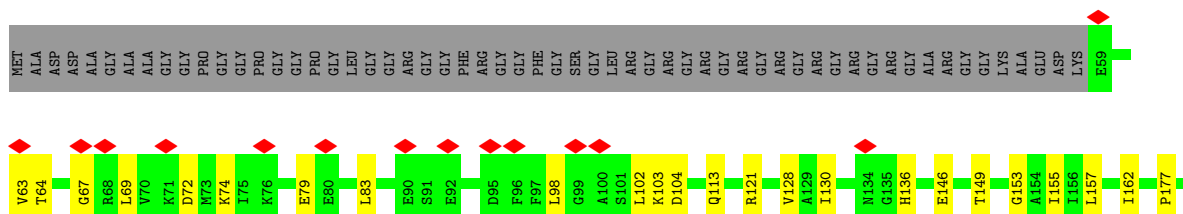
- Molecule 55: Small ribosomal subunit protein uS12

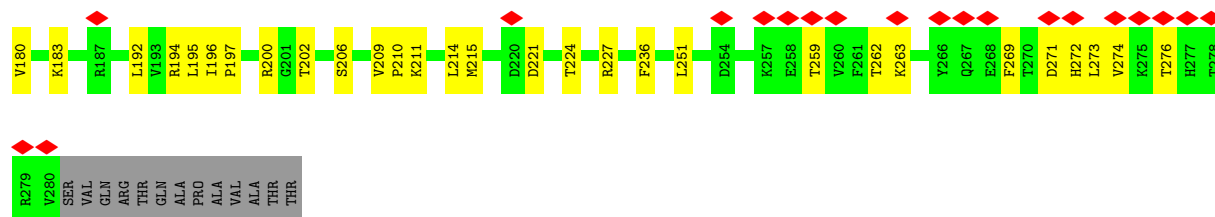


- Molecule 56: Small ribosomal subunit protein eS26



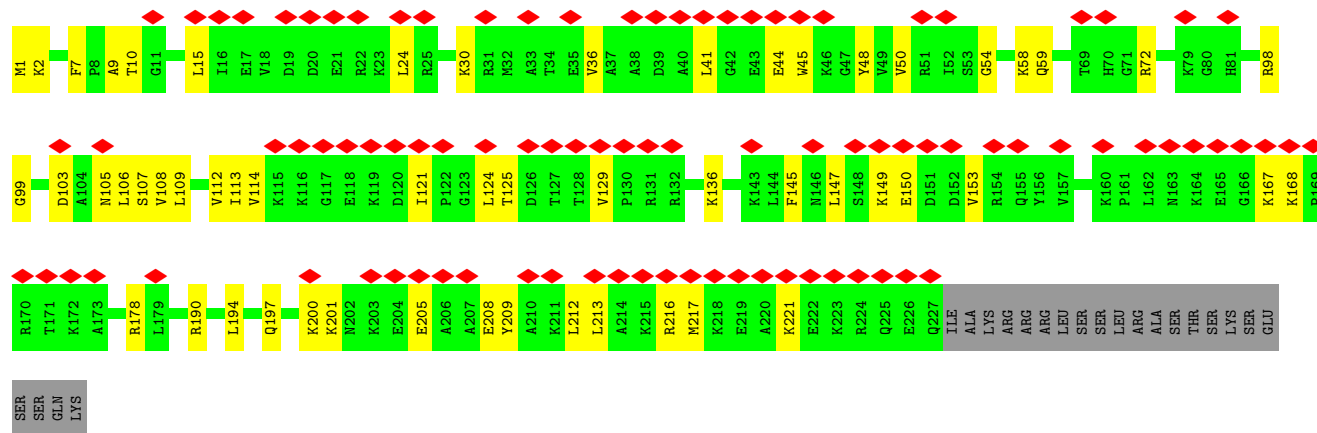
- Molecule 57: Small ribosomal subunit protein uS5





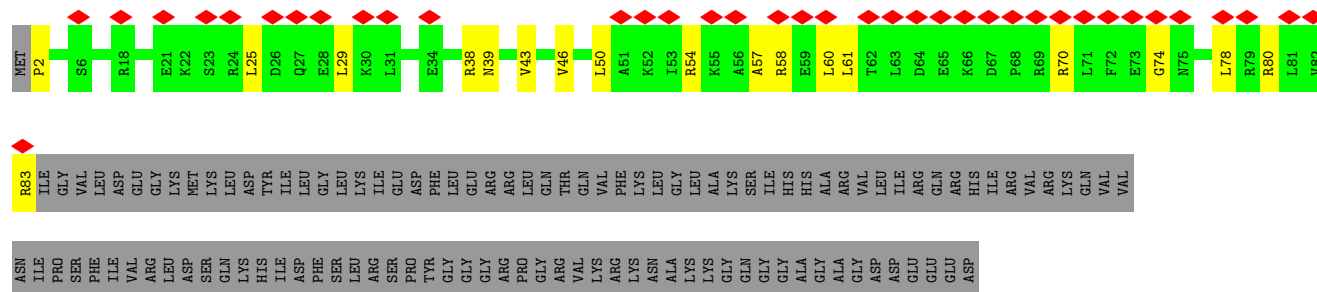
- Molecule 58: Small ribosomal subunit protein eS6

Chain BV: 37% 69% 22% 9%



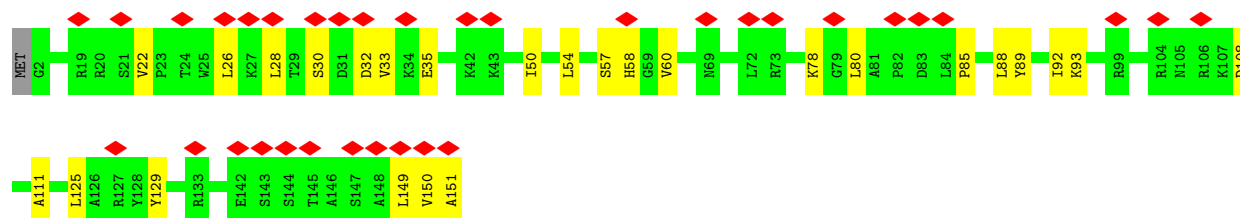
- Molecule 59: Small ribosomal subunit protein uS4

Chain BW: 20% 33% 9% 58%

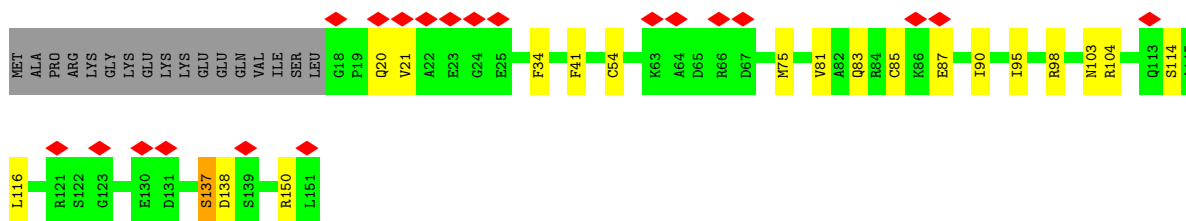
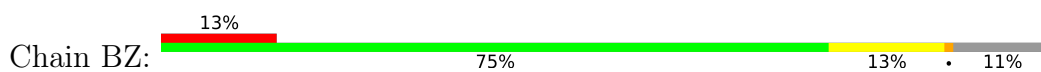


- Molecule 60: Small ribosomal subunit protein uS15

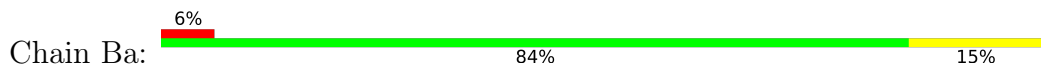
Chain BY: 23% 82% 17%



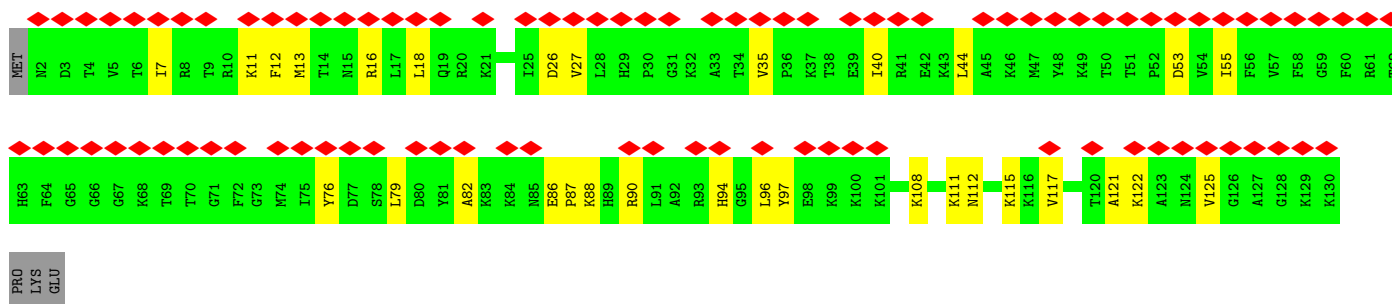
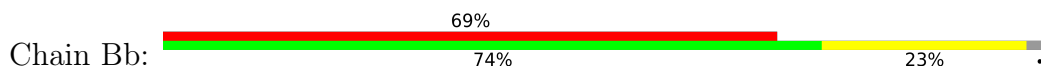
- Molecule 61: Small ribosomal subunit protein uS11



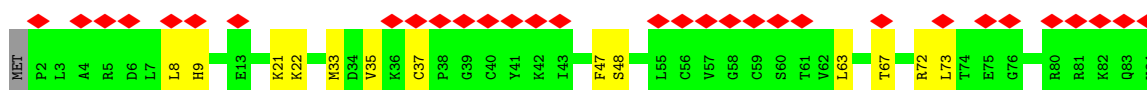
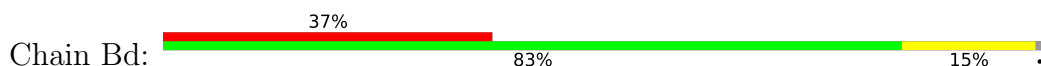
- Molecule 62: Small ribosomal subunit protein uS8



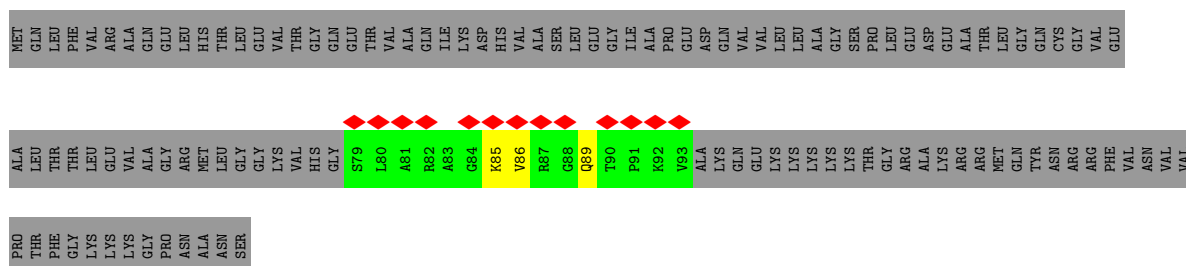
- Molecule 63: Small ribosomal subunit protein eS24



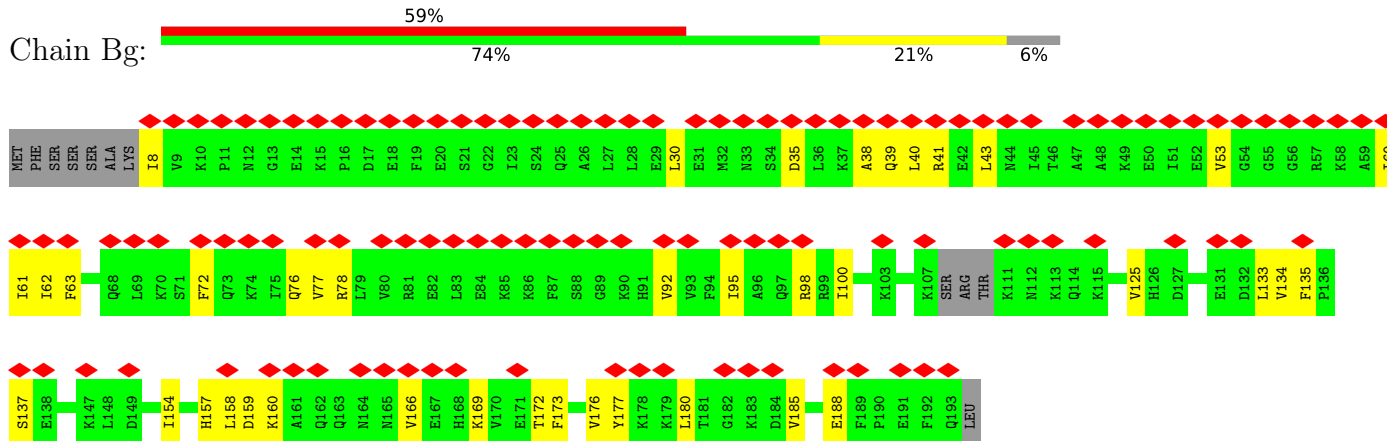
- Molecule 64: Small ribosomal subunit protein eS27-like



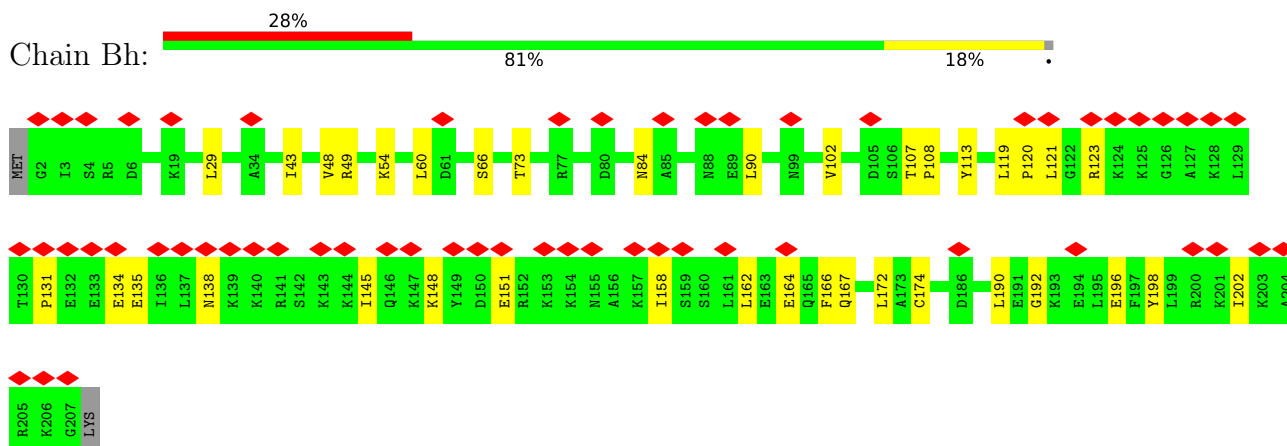
- Molecule 65: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein



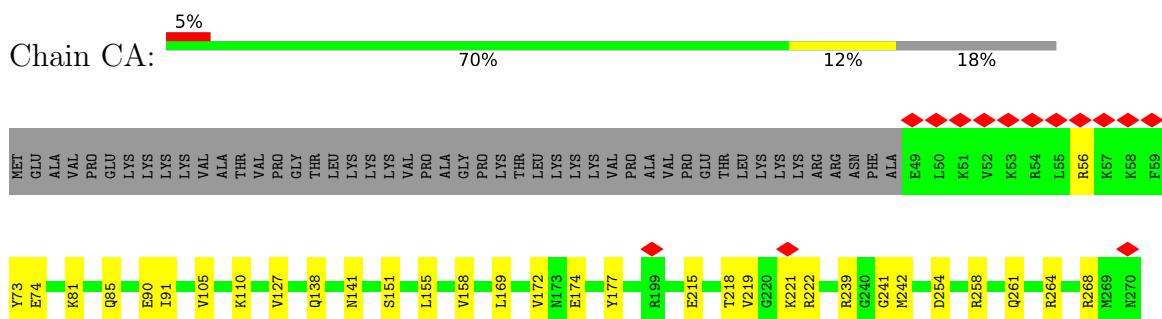
- Molecule 66: Small ribosomal subunit protein eS7



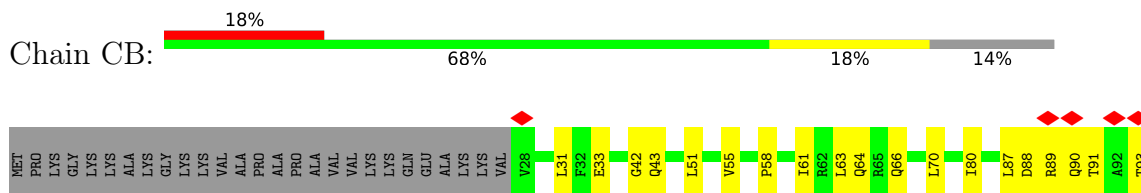
- Molecule 67: Small ribosomal subunit protein eS8

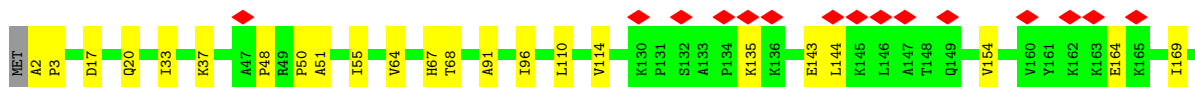


- Molecule 68: Large ribosomal subunit protein uL30



- Molecule 69: Large ribosomal subunit protein eL8

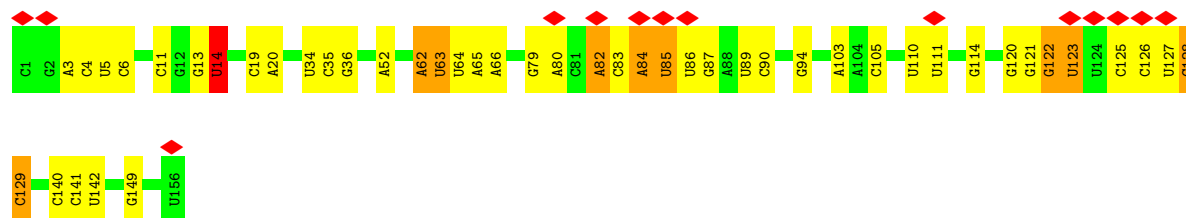












4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58734	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60.3	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.429	Depositor
Minimum map value	-1.756	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.096	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	633.2416, 633.2416, 633.2416	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2368, 1.2368, 1.2368	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, B9B, 1MA, MLZ, MHG, UR3, B8Q, I4U, 5MC, G7M, 2MG, B9H, B8T, E6G, PSU, E7G, B8N, B8W, P7G, A2M, OMU, 6MZ, 4AC, OMG, OMC

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	AA	0.16	0/1959	0.38	0/2627
2	AB	0.15	0/3305	0.39	0/4422
3	AC	0.18	0/2971	0.39	0/3987
4	AD	0.16	0/2431	0.37	0/3256
5	AE	0.15	0/1822	0.34	0/2443
6	AF	0.18	0/1670	0.40	0/2232
7	AG	0.15	0/1268	0.37	0/1700
8	AH	0.20	0/1535	0.45	0/2048
9	AI	0.18	0/1558	0.38	0/2059
10	AJ	0.17	0/1490	0.41	0/2000
11	AK	0.15	0/1321	0.36	0/1764
12	AL	0.17	0/839	0.42	0/1126
13	AM	0.16	0/983	0.37	0/1319
14	AN	0.27	0/528	0.45	0/703
15	AO	0.15	0/984	0.35	0/1323
16	AP	0.17	0/1132	0.39	0/1504
17	AQ	0.15	0/1130	0.37	0/1507
18	AR	0.16	0/1193	0.33	0/1593
19	AS	0.18	0/963	0.37	0/1275
20	AT	0.17	0/742	0.42	0/996
21	AU	0.16	0/903	0.44	0/1216
22	AV	0.17	0/1071	0.42	0/1429
23	AW	0.14	0/895	0.38	0/1198
24	AX	0.15	0/916	0.34	0/1221
25	AY	0.16	0/1009	0.38	0/1332
26	AZ	0.18	0/843	0.39	0/1115
27	Aa	0.14	0/720	0.35	0/952
28	Ab	0.18	0/574	0.42	0/760
29	Ac	0.15	0/454	0.37	0/599
30	Ad	0.14	0/425	0.36	0/561
31	Ae	0.14	0/855	0.43	1/1128 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Af	0.17	0/704	0.38	0/935
33	Ag	0.22	0/1016	0.40	0/1363
34	BA	0.16	0/481	0.39	0/643
35	BB	0.18	0/466	0.38	0/618
36	BC	0.14	0/39990	0.29	0/62326
37	BE	0.20	0/1784	0.46	0/2402
38	BH	0.20	0/1078	0.51	0/1447
39	BJ	0.19	0/1516	0.48	0/2037
40	BK	0.17	0/843	0.48	0/1137
41	BL	0.16	0/1094	0.42	0/1460
42	BM	0.21	0/1134	0.54	0/1517
43	BN	0.17	0/1208	0.46	0/1618
44	BO	0.19	0/1122	0.43	0/1503
45	BP	0.16	0/817	0.39	0/1097
46	BT	0.19	0/2493	0.47	0/3394
47	BX	0.16	0/927	0.34	0/1244
48	Bc	0.18	0/604	0.50	0/810
49	Bf	0.13	0/515	0.38	0/682
50	BD	0.18	0/1765	0.43	0/2362
51	BF	0.14	0/1957	0.39	0/2637
52	BG	0.15	0/1268	0.38	0/1696
53	BI	0.16	0/1731	0.38	0/2352
54	BQ	0.15	0/645	0.40	0/863
55	BR	0.16	0/1116	0.42	0/1490
56	BS	0.17	0/828	0.40	0/1109
57	BU	0.23	0/1762	0.45	0/2382
58	BV	0.21	0/1863	0.47	0/2481
59	BW	0.20	0/711	0.47	0/951
60	BY	0.20	0/1232	0.43	0/1656
61	BZ	0.17	0/1015	0.41	0/1361
62	Ba	0.18	0/1051	0.40	0/1406
63	Bb	0.17	0/1066	0.45	0/1415
64	Bd	0.13	0/665	0.37	0/890
65	Be	0.13	0/109	0.31	0/144
66	Bg	0.16	0/1499	0.43	0/2007
67	Bh	0.17	0/1715	0.43	0/2287
68	CA	0.18	0/1888	0.39	0/2516
69	CB	0.20	0/1898	0.46	0/2553
70	CC	0.18	0/1537	0.44	0/2065
71	CD	0.15	0/1692	0.35	0/2258
72	CE	0.19	0/1420	0.45	0/1899
73	CF	0.17	0/1707	0.41	0/2286
74	CG	0.20	0/1165	0.45	0/1558

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	CH	0.17	0/1746	0.40	0/2338
76	CI	0.14	1/83322 (0.0%)	0.26	0/129924
77	CJ	0.13	0/2858	0.26	0/4455
78	CK	0.15	0/3679	0.27	0/5732
All	All	0.16	1/221191 (0.0%)	0.33	1/324701 (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
61	BZ	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
76	CI	3382	A2M	O3'-P	5.14	1.61	1.56

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	Ae	64	LYS	CG-CD-CE	5.78	124.60	111.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
61	BZ	137	SER	Peptide

5.2 Too-close contacts [i](#)

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	AA	1921	2022	2022	30	0
2	AB	3238	3380	3380	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	AC	2928	3111	3110	49	0
4	AD	2385	2409	2409	38	0
5	AE	1789	1932	1932	18	0
6	AF	1640	1790	1790	32	0
7	AG	1242	1274	1274	14	0
8	AH	1511	1636	1636	34	0
9	AI	1542	1698	1698	10	0
10	AJ	1450	1488	1488	29	0
11	AK	1293	1364	1363	14	0
12	AL	825	850	850	15	0
13	AM	969	1031	1031	13	0
14	AN	515	530	530	7	0
15	AO	967	1040	1040	10	0
16	AP	1115	1205	1205	12	0
17	AQ	1107	1182	1182	11	0
18	AR	1164	1213	1213	13	0
19	AS	945	1037	1037	4	0
20	AT	732	769	769	11	0
21	AU	888	929	929	9	0
22	AV	1053	1146	1145	19	0
23	AW	876	912	912	9	0
24	AX	906	997	997	16	0
25	AY	1001	1138	1138	15	0
26	AZ	832	917	917	13	0
27	Aa	705	737	737	2	0
28	Ab	568	635	635	9	0
29	Ac	444	483	483	2	0
30	Ad	430	465	465	7	0
31	Ae	842	911	912	8	0
32	Af	694	738	738	13	0
33	Ag	1001	1066	1066	6	0
34	BA	479	507	507	14	0
35	BB	455	447	446	7	0
36	BC	36118	18227	18245	209	0
37	BE	1756	1851	1851	50	0
38	BH	1064	1118	1118	20	0
39	BJ	1495	1549	1549	41	0
40	BK	819	842	842	14	0
41	BL	1073	1128	1128	22	0
42	BM	1117	1185	1185	36	0
43	BN	1190	1250	1249	40	0
44	BO	1104	1139	1139	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	BP	807	874	874	16	0
46	BT	2436	2393	2393	75	0
47	BX	917	943	943	9	0
48	Bc	598	656	656	24	0
49	Bf	505	506	505	6	0
50	BD	1738	1807	1809	39	0
51	BF	1915	2006	2006	36	0
52	BG	1247	1323	1323	16	0
53	BI	1694	1696	1696	29	0
54	BQ	638	635	635	17	0
55	BR	1098	1168	1167	12	0
56	BS	811	866	866	10	0
57	BU	1725	1815	1815	39	0
58	BV	1840	1989	1989	44	0
59	BW	699	751	751	13	0
60	BY	1208	1294	1294	19	0
61	BZ	1002	1021	1021	14	0
62	Ba	1034	1080	1080	15	0
63	Bb	1049	1122	1122	25	0
64	Bd	652	676	676	11	0
65	Be	109	123	123	3	0
66	Bg	1477	1567	1567	33	0
67	Bh	1686	1772	1772	30	0
68	CA	1851	1988	1988	28	0
69	CB	1863	2003	2003	36	0
70	CC	1519	1603	1603	24	0
71	CD	1654	1709	1709	19	0
72	CE	1397	1425	1425	36	0
73	CF	1676	1777	1777	18	0
74	CG	1143	1217	1217	14	0
75	CH	1701	1749	1749	21	0
76	CI	76342	38565	38464	524	0
77	CJ	2558	1295	1296	15	0
78	CK	3315	1682	1685	26	0
79	Aa	1	0	0	0	0
79	Ad	1	0	0	0	0
79	Ae	1	0	0	0	0
79	Af	1	0	0	0	0
79	BB	1	0	0	0	0
79	BS	1	0	0	0	0
79	Bf	1	0	0	0	0
80	BC	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	CB	1	0	0	0	0
80	CI	1	0	0	0	0
All	All	208103	154374	154291	2119	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 2119 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)
76:CI:2542:B9H:N3	76:CI:2542:B9H:C4	1.70	1.52
16:AP:85:VAL:HG11	16:AP:99:ILE:HD11	1.35	1.05
36:BC:70:G:H21	36:BC:79:A:H62	1.15	0.94
57:BU:104:ASP:OD1	57:BU:130:ILE:HD13	1.69	0.91
67:Bh:158:ILE:HD12	67:Bh:162:LEU:HD23	1.56	0.88

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	249/257 (97%)	237 (95%)	12 (5%)	0	100	100
2	AB	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
3	AC	364/419 (87%)	359 (99%)	5 (1%)	0	100	100
4	AD	291/297 (98%)	288 (99%)	3 (1%)	0	100	100
5	AE	215/296 (73%)	209 (97%)	6 (3%)	0	100	100
6	AF	199/203 (98%)	197 (99%)	2 (1%)	0	100	100
7	AG	151/184 (82%)	149 (99%)	1 (1%)	1 (1%)	18	48
8	AH	184/188 (98%)	177 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	AI	182/196 (93%)	182 (100%)	0	0	100	100
10	AJ	173/176 (98%)	169 (98%)	4 (2%)	0	100	100
11	AK	156/160 (98%)	156 (100%)	0	0	100	100
12	AL	99/128 (77%)	95 (96%)	4 (4%)	0	100	100
13	AM	127/140 (91%)	127 (100%)	0	0	100	100
14	AN	59/157 (38%)	58 (98%)	1 (2%)	0	100	100
15	AO	116/156 (74%)	113 (97%)	3 (3%)	0	100	100
16	AP	132/145 (91%)	131 (99%)	1 (1%)	0	100	100
17	AQ	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
18	AR	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
19	AS	115/160 (72%)	109 (95%)	6 (5%)	0	100	100
20	AT	92/115 (80%)	87 (95%)	5 (5%)	0	100	100
21	AU	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
22	AV	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
23	AW	107/110 (97%)	105 (98%)	2 (2%)	0	100	100
24	AX	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
25	AY	118/123 (96%)	115 (98%)	3 (2%)	0	100	100
26	AZ	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
27	Aa	84/97 (87%)	84 (100%)	0	0	100	100
28	Ab	67/70 (96%)	67 (100%)	0	0	100	100
29	Ac	48/51 (94%)	48 (100%)	0	0	100	100
30	Ad	49/128 (38%)	49 (100%)	0	0	100	100
31	Ae	101/106 (95%)	96 (95%)	5 (5%)	0	100	100
32	Af	87/92 (95%)	84 (97%)	3 (3%)	0	100	100
33	Ag	123/137 (90%)	122 (99%)	1 (1%)	0	100	100
34	BA	59/69 (86%)	58 (98%)	1 (2%)	0	100	100
35	BB	52/56 (93%)	50 (96%)	2 (4%)	0	100	100
37	BE	224/243 (92%)	217 (97%)	7 (3%)	0	100	100
38	BH	129/135 (96%)	121 (94%)	8 (6%)	0	100	100
39	BJ	187/204 (92%)	179 (96%)	7 (4%)	1 (0%)	24	54
40	BK	95/165 (58%)	94 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	BL	128/145 (88%)	124 (97%)	4 (3%)	0	100	100
42	BM	138/146 (94%)	136 (99%)	2 (1%)	0	100	100
43	BN	142/152 (93%)	138 (97%)	4 (3%)	0	100	100
44	BO	139/145 (96%)	139 (100%)	0	0	100	100
45	BP	100/119 (84%)	97 (97%)	3 (3%)	0	100	100
46	BT	311/317 (98%)	297 (96%)	14 (4%)	0	100	100
47	BX	117/132 (89%)	111 (95%)	6 (5%)	0	100	100
48	Bc	73/125 (58%)	72 (99%)	1 (1%)	0	100	100
49	Bf	60/156 (38%)	56 (93%)	4 (7%)	0	100	100
50	BD	212/264 (80%)	208 (98%)	4 (2%)	0	100	100
51	BF	239/263 (91%)	235 (98%)	4 (2%)	0	100	100
52	BG	151/158 (96%)	146 (97%)	5 (3%)	0	100	100
53	BI	212/295 (72%)	209 (99%)	3 (1%)	0	100	100
54	BQ	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
55	BR	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
56	BS	99/115 (86%)	97 (98%)	2 (2%)	0	100	100
57	BU	220/293 (75%)	213 (97%)	7 (3%)	0	100	100
58	BV	225/249 (90%)	218 (97%)	7 (3%)	0	100	100
59	BW	80/194 (41%)	80 (100%)	0	0	100	100
60	BY	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
61	BZ	132/151 (87%)	127 (96%)	5 (4%)	0	100	100
62	Ba	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
63	Bb	127/133 (96%)	123 (97%)	4 (3%)	0	100	100
64	Bd	81/84 (96%)	77 (95%)	4 (5%)	0	100	100
65	Be	13/133 (10%)	12 (92%)	1 (8%)	0	100	100
66	Bg	179/194 (92%)	172 (96%)	7 (4%)	0	100	100
67	Bh	204/208 (98%)	201 (98%)	3 (2%)	0	100	100
68	CA	221/270 (82%)	216 (98%)	5 (2%)	0	100	100
69	CB	227/266 (85%)	222 (98%)	5 (2%)	0	100	100
70	CC	188/192 (98%)	187 (100%)	1 (0%)	0	100	100
71	CD	200/214 (94%)	193 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	CE	172/178 (97%)	167 (97%)	5 (3%)	0	100	100
73	CF	205/211 (97%)	197 (96%)	8 (4%)	0	100	100
74	CG	137/217 (63%)	133 (97%)	4 (3%)	0	100	100
75	CH	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
All	All	10983/12762 (86%)	10714 (98%)	267 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	AG	132	ALA
39	BJ	79	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	193/199 (97%)	193 (100%)	0	100	100
2	AB	347/348 (100%)	347 (100%)	0	100	100
3	AC	307/347 (88%)	307 (100%)	0	100	100
4	AD	245/249 (98%)	245 (100%)	0	100	100
5	AE	198/256 (77%)	198 (100%)	0	100	100
6	AF	172/173 (99%)	172 (100%)	0	100	100
7	AG	134/163 (82%)	134 (100%)	0	100	100
8	AH	164/165 (99%)	164 (100%)	0	100	100
9	AI	163/175 (93%)	163 (100%)	0	100	100
10	AJ	155/156 (99%)	155 (100%)	0	100	100
11	AK	139/140 (99%)	139 (100%)	0	100	100
12	AL	91/114 (80%)	91 (100%)	0	100	100
13	AM	100/107 (94%)	100 (100%)	0	100	100
14	AN	54/126 (43%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	AO	106/133 (80%)	106 (100%)	0	100	100
16	AP	124/135 (92%)	124 (100%)	0	100	100
17	AQ	117/118 (99%)	117 (100%)	0	100	100
18	AR	120/121 (99%)	120 (100%)	0	100	100
19	AS	98/124 (79%)	98 (100%)	0	100	100
20	AT	79/97 (81%)	79 (100%)	0	100	100
21	AU	98/110 (89%)	98 (100%)	0	100	100
22	AV	114/121 (94%)	114 (100%)	0	100	100
23	AW	88/89 (99%)	88 (100%)	0	100	100
24	AX	98/100 (98%)	98 (100%)	0	100	100
25	AY	108/110 (98%)	108 (100%)	0	100	100
26	AZ	86/89 (97%)	86 (100%)	0	100	100
27	Aa	73/80 (91%)	73 (100%)	0	100	100
28	Ab	64/65 (98%)	64 (100%)	0	100	100
29	Ac	47/48 (98%)	47 (100%)	0	100	100
30	Ad	47/115 (41%)	47 (100%)	0	100	100
31	Ae	91/94 (97%)	91 (100%)	0	100	100
32	Af	73/75 (97%)	73 (100%)	0	100	100
33	Ag	109/121 (90%)	109 (100%)	0	100	100
34	BA	54/62 (87%)	54 (100%)	0	100	100
35	BB	48/49 (98%)	48 (100%)	0	100	100
37	BE	189/202 (94%)	189 (100%)	0	100	100
38	BH	119/121 (98%)	119 (100%)	0	100	100
39	BJ	159/170 (94%)	159 (100%)	0	100	100
40	BK	88/136 (65%)	88 (100%)	0	100	100
41	BL	116/130 (89%)	116 (100%)	0	100	100
42	BM	116/121 (96%)	116 (100%)	0	100	100
43	BN	125/132 (95%)	125 (100%)	0	100	100
44	BO	112/115 (97%)	112 (100%)	0	100	100
45	BP	93/107 (87%)	93 (100%)	0	100	100
46	BT	272/275 (99%)	272 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	BX	99/108 (92%)	99 (100%)	0	100	100
48	Bc	66/103 (64%)	66 (100%)	0	100	100
49	Bf	55/140 (39%)	55 (100%)	0	100	100
50	BD	195/229 (85%)	195 (100%)	0	100	100
51	BF	208/225 (92%)	208 (100%)	0	100	100
52	BG	137/142 (96%)	137 (100%)	0	100	100
53	BI	179/242 (74%)	179 (100%)	0	100	100
54	BQ	67/67 (100%)	67 (100%)	0	100	100
55	BR	113/115 (98%)	113 (100%)	0	100	100
56	BS	88/98 (90%)	88 (100%)	0	100	100
57	BU	188/224 (84%)	188 (100%)	0	100	100
58	BV	198/218 (91%)	198 (100%)	0	100	100
59	BW	74/168 (44%)	74 (100%)	0	100	100
60	BY	130/131 (99%)	130 (100%)	0	100	100
61	BZ	104/119 (87%)	104 (100%)	0	100	100
62	Ba	112/113 (99%)	112 (100%)	0	100	100
63	Bb	111/115 (96%)	111 (100%)	0	100	100
64	Bd	75/76 (99%)	75 (100%)	0	100	100
65	Be	11/106 (10%)	11 (100%)	0	100	100
66	Bg	164/174 (94%)	164 (100%)	0	100	100
67	Bh	178/180 (99%)	178 (100%)	0	100	100
68	CA	194/234 (83%)	194 (100%)	0	100	100
69	CB	198/223 (89%)	198 (100%)	0	100	100
70	CC	169/171 (99%)	169 (100%)	0	100	100
71	CD	173/180 (96%)	173 (100%)	0	100	100
72	CE	147/149 (99%)	147 (100%)	0	100	100
73	CF	174/178 (98%)	174 (100%)	0	100	100
74	CG	118/157 (75%)	118 (100%)	0	100	100
75	CH	171/172 (99%)	171 (100%)	0	100	100
All	All	9589/10840 (88%)	9589 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 106 such sidechains are listed below:

Mol	Chain	Res	Type
46	BT	305	ASN
57	BU	113	GLN
71	CD	73	ASN
49	Bf	135	HIS
51	BF	142	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
36	BC	1683/1871 (89%)	324 (19%)	7 (0%)
76	CI	3541/4731 (74%)	876 (24%)	17 (0%)
77	CJ	119/121 (98%)	9 (7%)	0
78	CK	155/156 (99%)	26 (16%)	0
All	All	5498/6879 (79%)	1235 (22%)	24 (0%)

5 of 1235 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
36	BC	8	U
36	BC	17	C
36	BC	33	G
36	BC	42	A
36	BC	46	A

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
76	CI	1438	OMG
76	CI	1893	C
76	CI	1714	G
76	CI	2431	G
36	BC	1703	G

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

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
76	B8W	CI	3840	76	23,26,27	1.84	4 (17%)	33,38,41	2.61	16 (48%)
76	P7G	CI	1711	77,76	24,28,29	5.14	9 (37%)	27,41,44	1.57	1 (3%)
76	2MG	CI	4519	76	23,26,27	0.47	0	32,38,41	0.57	0
76	PSU	CI	4058	76	18,21,22	1.05	1 (5%)	22,30,33	1.80	4 (18%)
36	UR3	BC	1831	36	19,22,23	3.10	8 (42%)	26,32,35	1.37	3 (11%)
76	5MC	CI	3441	76	18,22,23	0.55	0	26,32,35	0.53	0
3	MLZ	AC	333	3	8,9,10	0.83	0	4,9,11	0.72	0
76	OMC	CI	4191	76	19,22,23	0.54	0	26,31,34	0.68	0
76	OMG	CI	4292	76	23,26,27	0.50	0	33,38,41	0.44	0
36	PSU	BC	1082	36	18,21,22	1.08	1 (5%)	22,30,33	1.74	5 (22%)
36	OMC	BC	518	36	19,22,23	0.53	0	26,31,34	0.61	0
76	OMC	CI	3568	76	19,22,23	0.52	0	26,31,34	0.67	0
76	6MZ	CI	3875	76	22,25,26	3.83	8 (36%)	30,36,39	2.32	10 (33%)
76	OMG	CI	4517	76	23,26,27	0.43	0	33,38,41	0.76	0
76	PSU	CI	3423	76	18,21,22	1.06	1 (5%)	22,30,33	1.82	5 (22%)
76	5MC	CI	3990	76	18,22,23	0.53	0	26,32,35	0.53	0
76	OMG	CI	3451	76	23,26,27	0.49	0	33,38,41	0.43	0
36	PSU	BC	824	36	18,21,22	1.14	1 (5%)	22,30,33	1.82	5 (22%)
76	A2M	CI	2119	76	22,25,26	3.43	9 (40%)	31,36,39	2.64	14 (45%)
76	PSU	CI	1496	76	18,21,22	1.06	1 (5%)	22,30,33	1.83	5 (22%)
36	OMU	BC	116	36	19,22,23	3.56	8 (42%)	26,31,34	1.63	5 (19%)
36	PSU	BC	1244	36	18,21,22	1.08	1 (5%)	22,30,33	1.91	5 (22%)
76	PSU	CI	4283	76	18,21,22	1.03	1 (5%)	22,30,33	1.86	4 (18%)
76	PSU	CI	2264	76	18,21,22	1.05	1 (5%)	22,30,33	1.96	4 (18%)
76	I4U	CI	3849	76	21,24,25	3.55	9 (42%)	27,34,37	1.01	1 (3%)
76	G7M	CI	1418	76	23,26,27	2.96	9 (39%)	35,39,42	2.56	10 (28%)
76	A2M	CI	1337	76	22,25,26	3.40	9 (40%)	31,36,39	2.67	12 (38%)
76	B9B	CI	237	76	25,28,29	1.76	6 (24%)	35,40,43	2.81	12 (34%)
76	G7M	CI	4205	76	23,26,27	2.96	9 (39%)	35,39,42	2.47	10 (28%)
76	PSU	CI	3948	76	18,21,22	1.07	1 (5%)	22,30,33	2.11	5 (22%)
76	A2M	CI	398	76	22,25,26	3.43	9 (40%)	31,36,39	2.61	11 (35%)
76	OMC	CI	2178	76	19,22,23	0.54	0	26,31,34	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	A2M	BC	27	36	22,25,26	3.41	9 (40%)	31,36,39	2.64	12 (38%)
76	PSU	CI	3388	76	18,21,22	1.11	1 (5%)	22,30,33	1.86	5 (22%)
76	P7G	CI	3539	76	24,28,29	5.12	9 (37%)	27,41,44	1.58	2 (7%)
76	PSU	CI	1395	76	18,21,22	1.08	1 (5%)	22,30,33	1.72	3 (13%)
76	5MC	CI	4102	76	18,22,23	0.55	0	26,32,35	0.58	0
76	PSU	CI	4155	76	18,21,22	1.07	1 (5%)	22,30,33	1.67	4 (18%)
76	OMC	CI	3546	76	19,22,23	0.60	0	26,31,34	0.76	1 (3%)
76	G7M	CI	2278	76	23,26,27	2.95	9 (39%)	35,39,42	2.53	10 (28%)
76	OMC	CI	2617	76	19,22,23	0.51	0	26,31,34	0.61	0
76	OMG	CI	4149	76	23,26,27	0.50	0	33,38,41	0.47	0
76	PSU	CI	1490	76	18,21,22	1.08	1 (5%)	22,30,33	1.80	4 (18%)
76	A2M	CI	1673	76	22,25,26	3.44	9 (40%)	31,36,39	2.58	10 (32%)
76	E7G	CI	2053	76	24,27,28	5.67	10 (41%)	30,40,43	2.21	9 (30%)
36	PSU	BC	823	36	18,21,22	1.03	1 (5%)	22,30,33	1.68	3 (13%)
36	4AC	BC	1843	36	21,24,25	3.81	10 (47%)	29,34,37	1.05	4 (13%)
76	OMC	CI	3360	76	19,22,23	0.53	0	26,31,34	0.56	0
76	OMG	CI	2529	76	23,26,27	0.53	0	33,38,41	0.51	0
76	A2M	CI	3444	76	22,25,26	3.36	8 (36%)	31,36,39	2.67	12 (38%)
76	OMC	CI	3528	76	19,22,23	0.53	0	26,31,34	0.56	0
76	A2M	CI	3526	76	22,25,26	3.42	9 (40%)	31,36,39	2.65	12 (38%)
36	B8N	BC	1249	36	24,29,30	3.28	5 (20%)	29,42,45	1.84	6 (20%)
76	E6G	CI	4010	76	24,27,28	2.14	5 (20%)	34,39,42	5.96	15 (44%)
76	B8T	CI	4138	76	19,22,23	3.25	8 (42%)	26,31,34	0.79	1 (3%)
36	OMG	BC	684	36	23,26,27	0.49	0	33,38,41	0.51	0
76	A2M	CI	1347	76	22,25,26	3.43	9 (40%)	31,36,39	2.62	11 (35%)
76	OMG	CI	373	76	23,26,27	0.49	0	33,38,41	0.47	0
76	OMG	CI	1335	76	23,26,27	0.51	0	33,38,41	0.54	0
36	PSU	BC	613	36	18,21,22	1.07	1 (5%)	22,30,33	1.93	6 (27%)
76	OMG	CI	2180	76	23,26,27	0.50	0	33,38,41	0.44	0
76	OMG	CI	4278	76	23,26,27	0.50	0	33,38,41	0.47	0
76	B9B	CI	1387	76	25,28,29	1.75	6 (24%)	35,40,43	3.01	11 (31%)
76	A2M	CI	3382	76	22,25,26	3.33	9 (40%)	31,36,39	2.84	13 (41%)
76	2MG	CI	1330	76	23,26,27	0.52	0	32,38,41	0.58	0
76	UR3	CI	4252	76	19,22,23	3.06	8 (42%)	26,32,35	1.36	3 (11%)
76	PSU	CI	3374	76	18,21,22	1.06	1 (5%)	22,30,33	1.89	4 (18%)
76	A2M	CI	1140	76	22,25,26	3.37	9 (40%)	31,36,39	2.76	13 (41%)
76	I4U	CI	1472	76	21,24,25	3.55	9 (42%)	27,34,37	0.99	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
76	A2M	CI	2157	76	22,25,26	3.41	10 (45%)	31,36,39	2.67	13 (41%)
76	A2M	CI	3484	76	22,25,26	3.42	9 (40%)	31,36,39	2.62	11 (35%)
76	PSU	CI	4291	76	18,21,22	1.04	1 (5%)	22,30,33	1.84	5 (22%)
76	PSU	CI	4105	76	18,21,22	1.05	1 (5%)	22,30,33	1.79	5 (22%)
76	OMG	CI	3851	76	23,26,27	0.48	0	33,38,41	0.54	0
76	OMC	CI	2121	76	19,22,23	0.58	0	26,31,34	1.19	4 (15%)
76	UR3	CI	1668	76	19,22,23	2.99	8 (42%)	26,32,35	1.25	1 (3%)
36	A2M	BC	1032	36	22,25,26	3.42	9 (40%)	31,36,39	2.65	12 (38%)
30	MLZ	Ad	98	30	8,9,10	0.76	0	4,9,11	0.71	0
36	OMG	BC	645	36	23,26,27	0.49	0	33,38,41	0.46	0
76	E7G	CI	1599	76	24,27,28	5.65	10 (41%)	30,40,43	2.26	9 (30%)
76	OMG	CI	1685	76	23,26,27	0.47	0	33,38,41	0.62	0
78	OMU	CK	14	78	19,22,23	3.44	8 (42%)	26,31,34	1.53	5 (19%)
76	2MG	CI	877	76	23,26,27	0.49	0	32,38,41	0.50	0
76	OMG	CI	1438	76	23,26,27	0.52	0	33,38,41	0.47	0
76	B9H	CI	2542	76	20,25,26	4.81	4 (20%)	22,35,38	1.26	2 (9%)
76	OMG	CI	2120	76	23,26,27	0.49	0	33,38,41	0.44	0
76	OMC	CI	2560	76	19,22,23	0.56	0	26,31,34	0.65	0
76	PSU	CI	4097	76	18,21,22	1.11	1 (5%)	22,30,33	1.81	5 (22%)
76	PSU	CI	4186	76	18,21,22	1.04	1 (5%)	22,30,33	1.92	5 (22%)
36	A2M	BC	669	36	22,25,26	3.36	8 (36%)	31,36,39	2.54	10 (32%)
76	OMU	CI	3961	76	19,22,23	3.57	8 (42%)	26,31,34	1.68	5 (19%)
76	1MA	CI	4070	76	21,25,26	0.51	0	31,37,40	0.76	1 (3%)
76	A2M	CI	4226	76	22,25,26	3.41	9 (40%)	31,36,39	2.65	12 (38%)
76	OMU	CI	4275	76	19,22,23	3.52	8 (42%)	26,31,34	1.65	5 (19%)
76	OMG	CI	4025	76	23,26,27	0.49	0	33,38,41	0.65	0
76	B8Q	CI	1269	76	17,22,23	4.65	5 (29%)	22,32,35	2.01	5 (22%)
76	A2M	CI	3377	76	22,25,26	3.38	10 (45%)	31,36,39	2.64	11 (35%)
76	OMG	CI	1852	76	23,26,27	0.53	0	33,38,41	0.49	0
76	MHG	CI	4026	76	29,32,33	5.59	12 (41%)	34,46,49	2.48	11 (32%)
36	A2M	BC	166	36	22,25,26	3.43	9 (40%)	31,36,39	2.63	11 (35%)

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
76	B8W	CI	3840	76	-	2/9/27/28	0/3/3/3
76	P7G	CI	1711	77,76	-	0/10/40/41	0/3/3/3
76	2MG	CI	4519	76	-	0/9/27/28	0/3/3/3
76	PSU	CI	4058	76	-	0/7/25/26	0/2/2/2
36	UR3	BC	1831	36	-	3/7/25/26	0/2/2/2
76	5MC	CI	3441	76	-	0/7/25/26	0/2/2/2
3	MLZ	AC	333	3	-	1/7/8/10	-
76	OMC	CI	4191	76	-	0/9/27/28	0/2/2/2
76	OMG	CI	4292	76	-	2/9/27/28	0/3/3/3
36	PSU	BC	1082	36	-	4/7/25/26	0/2/2/2
36	OMC	BC	518	36	-	2/9/27/28	0/2/2/2
76	OMC	CI	3568	76	-	2/9/27/28	0/2/2/2
76	6MZ	CI	3875	76	-	0/9/27/28	0/3/3/3
76	OMG	CI	4517	76	-	2/9/27/28	0/3/3/3
76	PSU	CI	3423	76	-	1/7/25/26	0/2/2/2
76	5MC	CI	3990	76	-	0/7/25/26	0/2/2/2
76	OMG	CI	3451	76	-	0/9/27/28	0/3/3/3
36	PSU	BC	824	36	-	2/7/25/26	0/2/2/2
76	A2M	CI	2119	76	-	0/9/27/28	0/3/3/3
76	PSU	CI	1496	76	-	0/7/25/26	0/2/2/2
36	OMU	BC	116	36	-	1/9/27/28	0/2/2/2
36	PSU	BC	1244	36	-	0/7/25/26	0/2/2/2
76	PSU	CI	4283	76	-	0/7/25/26	0/2/2/2
76	PSU	CI	2264	76	-	1/7/25/26	0/2/2/2
76	I4U	CI	3849	76	-	2/9/29/30	0/2/2/2
76	G7M	CI	1418	76	-	0/7/25/26	0/3/3/3
76	A2M	CI	1337	76	-	1/9/27/28	0/3/3/3
76	B9B	CI	237	76	-	6/11/29/30	0/3/3/3
76	G7M	CI	4205	76	-	3/7/25/26	0/3/3/3
76	PSU	CI	3948	76	-	0/7/25/26	0/2/2/2
76	A2M	CI	398	76	-	2/9/27/28	0/3/3/3
76	OMC	CI	2178	76	-	1/9/27/28	0/2/2/2
36	A2M	BC	27	36	-	1/9/27/28	0/3/3/3
76	PSU	CI	3388	76	-	2/7/25/26	0/2/2/2
76	P7G	CI	3539	76	-	1/10/40/41	0/3/3/3
76	PSU	CI	1395	76	-	0/7/25/26	0/2/2/2
76	5MC	CI	4102	76	-	4/7/25/26	0/2/2/2
76	PSU	CI	4155	76	-	1/7/25/26	0/2/2/2
76	OMC	CI	3546	76	-	3/9/27/28	0/2/2/2
76	G7M	CI	2278	76	-	0/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
76	OMC	CI	2617	76	-	0/9/27/28	0/2/2/2
76	OMG	CI	4149	76	-	0/9/27/28	0/3/3/3
76	PSU	CI	1490	76	-	2/7/25/26	0/2/2/2
76	A2M	CI	1673	76	-	0/9/27/28	0/3/3/3
76	E7G	CI	2053	76	-	0/9/39/40	0/3/3/3
36	PSU	BC	823	36	-	0/7/25/26	0/2/2/2
36	4AC	BC	1843	36	-	0/11/29/30	0/2/2/2
76	OMC	CI	3360	76	-	4/9/27/28	0/2/2/2
76	OMG	CI	2529	76	-	3/9/27/28	0/3/3/3
76	A2M	CI	3444	76	-	2/9/27/28	0/3/3/3
76	OMC	CI	3528	76	-	2/9/27/28	0/2/2/2
76	A2M	CI	3526	76	-	3/9/27/28	0/3/3/3
36	B8N	BC	1249	36	-	6/16/34/35	0/2/2/2
76	E6G	CI	4010	76	-	3/10/28/29	0/3/3/3
76	B8T	CI	4138	76	-	1/7/27/28	0/2/2/2
36	OMG	BC	684	36	-	0/9/27/28	0/3/3/3
76	A2M	CI	1347	76	-	0/9/27/28	0/3/3/3
76	OMG	CI	373	76	-	1/9/27/28	0/3/3/3
76	OMG	CI	1335	76	-	0/9/27/28	0/3/3/3
36	PSU	BC	613	36	-	2/7/25/26	0/2/2/2
76	OMG	CI	2180	76	-	0/9/27/28	0/3/3/3
76	OMG	CI	4278	76	-	0/9/27/28	0/3/3/3
76	B9B	CI	1387	76	-	5/11/29/30	0/3/3/3
76	A2M	CI	3382	76	-	1/9/27/28	0/3/3/3
76	2MG	CI	1330	76	-	0/9/27/28	0/3/3/3
76	UR3	CI	4252	76	-	1/7/25/26	0/2/2/2
76	PSU	CI	3374	76	-	0/7/25/26	0/2/2/2
76	A2M	CI	1140	76	-	2/9/27/28	0/3/3/3
76	I4U	CI	1472	76	-	2/9/29/30	0/2/2/2
76	A2M	CI	2157	76	-	0/9/27/28	0/3/3/3
76	A2M	CI	3484	76	-	1/9/27/28	0/3/3/3
76	PSU	CI	4291	76	-	6/7/25/26	0/2/2/2
76	PSU	CI	4105	76	-	4/7/25/26	0/2/2/2
76	OMG	CI	3851	76	-	2/9/27/28	0/3/3/3
76	OMC	CI	2121	76	-	0/9/27/28	0/2/2/2
76	UR3	CI	1668	76	-	0/7/25/26	0/2/2/2
36	A2M	BC	1032	36	-	0/9/27/28	0/3/3/3
30	MLZ	Ad	98	30	-	0/7/8/10	-
36	OMG	BC	645	36	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
76	E7G	CI	1599	76	-	0/9/39/40	0/3/3/3
76	OMG	CI	1685	76	-	3/9/27/28	0/3/3/3
78	OMU	CK	14	78	-	2/9/27/28	0/2/2/2
76	2MG	CI	877	76	-	1/9/27/28	0/3/3/3
76	OMG	CI	1438	76	-	2/9/27/28	0/3/3/3
76	B9H	CI	2542	76	-	2/12/47/48	0/2/2/2
76	OMG	CI	2120	76	-	2/9/27/28	0/3/3/3
76	OMC	CI	2560	76	-	0/9/27/28	0/2/2/2
76	PSU	CI	4097	76	-	2/7/25/26	0/2/2/2
76	PSU	CI	4186	76	-	5/7/25/26	0/2/2/2
36	A2M	BC	669	36	-	3/9/27/28	0/3/3/3
76	OMU	CI	3961	76	-	3/9/27/28	0/2/2/2
76	1MA	CI	4070	76	-	2/7/25/26	0/3/3/3
76	A2M	CI	4226	76	-	1/9/27/28	0/3/3/3
76	OMU	CI	4275	76	-	0/9/27/28	0/2/2/2
76	OMG	CI	4025	76	-	3/9/27/28	0/3/3/3
76	B8Q	CI	1269	76	-	0/7/42/43	0/2/2/2
76	A2M	CI	3377	76	-	2/9/27/28	0/3/3/3
76	OMG	CI	1852	76	-	0/9/27/28	0/3/3/3
76	MHG	CI	4026	76	-	5/16/46/47	0/3/3/3
36	A2M	BC	166	36	-	0/9/27/28	0/3/3/3

The worst 5 of 385 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
76	CI	2053	E7G	C8-N9	23.18	1.58	1.46
76	CI	1599	E7G	C8-N9	23.01	1.58	1.46
76	CI	4026	MHG	C8-N9	19.71	1.57	1.46
76	CI	3539	P7G	C8-N9	17.75	1.55	1.46
76	CI	1711	P7G	C8-N9	17.73	1.55	1.46

The worst 5 of 470 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	CI	4010	E6G	O6-C6-C5	21.18	143.38	116.57
76	CI	4010	E6G	O6-C6-N1	-18.01	94.92	120.00
76	CI	4010	E6G	C1'-N9-C8	-10.42	103.61	127.14
76	CI	4010	E6G	C4-N9-C1'	9.09	148.26	126.59
76	CI	4010	E6G	N2-C2-N3	8.84	131.00	117.25

There are no chirality outliers.

5 of 142 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
76	CI	237	B9B	C5-C6-O6-C61
76	CI	237	B9B	N1-C6-O6-C61
76	CI	237	B9B	C4'-C5'-O5'-P
76	CI	237	B9B	C62-C61-O6-C6
76	CI	1140	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

42 monomers are involved in 76 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
76	CI	4191	OMC	2	0
76	CI	3568	OMC	2	0
76	CI	3875	6MZ	2	0
76	CI	4517	OMG	5	0
76	CI	2119	A2M	2	0
36	BC	116	OMU	3	0
76	CI	4283	PSU	2	0
76	CI	237	B9B	2	0
76	CI	4205	G7M	1	0
76	CI	398	A2M	1	0
36	BC	27	A2M	1	0
76	CI	3388	PSU	1	0
76	CI	3546	OMC	1	0
76	CI	2617	OMC	1	0
76	CI	4149	OMG	1	0
76	CI	1673	A2M	1	0
36	BC	823	PSU	2	0
36	BC	1843	4AC	2	0
76	CI	3444	A2M	2	0
76	CI	3526	A2M	2	0
36	BC	1249	B8N	1	0
76	CI	373	OMG	1	0
36	BC	613	PSU	1	0
76	CI	3382	A2M	1	0
76	CI	4252	UR3	1	0
76	CI	1140	A2M	1	0
76	CI	4291	PSU	1	0
76	CI	3851	OMG	1	0
76	CI	2121	OMC	1	0
76	CI	1668	UR3	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	Ad	98	MLZ	1	0
76	CI	1685	OMG	3	0
78	CK	14	OMU	5	0
76	CI	1438	OMG	1	0
76	CI	2542	B9H	5	0
76	CI	2120	OMG	1	0
76	CI	2560	OMC	1	0
76	CI	4070	1MA	1	0
76	CI	4275	OMU	2	0
76	CI	4025	OMG	6	0
76	CI	1269	B8Q	1	0
76	CI	3377	A2M	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 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.

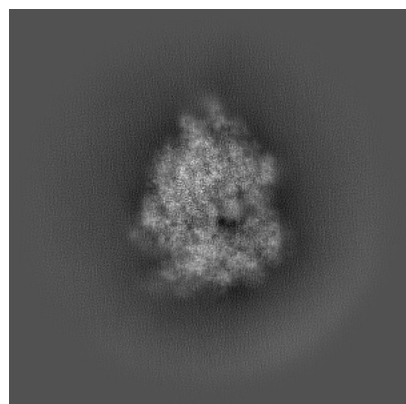
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-58363. These allow visual inspection of the internal detail of the map and identification of artifacts.

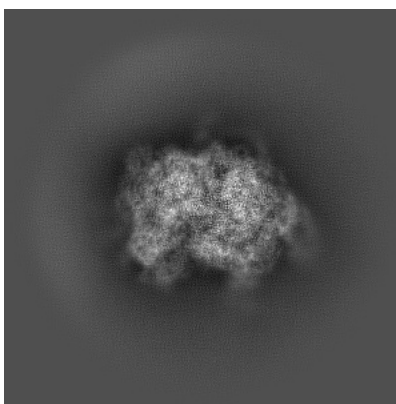
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

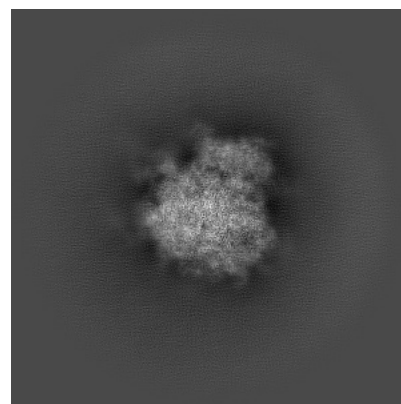
6.1.1 Primary map



X

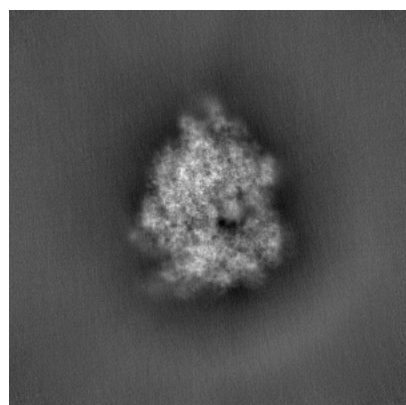


Y

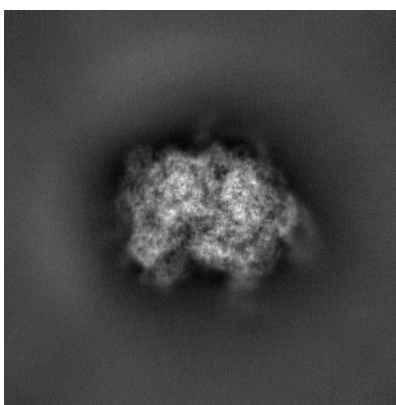


Z

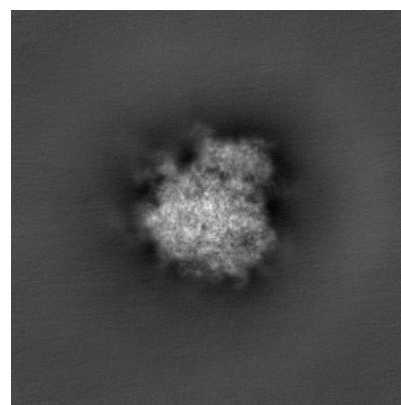
6.1.2 Raw map



X



Y

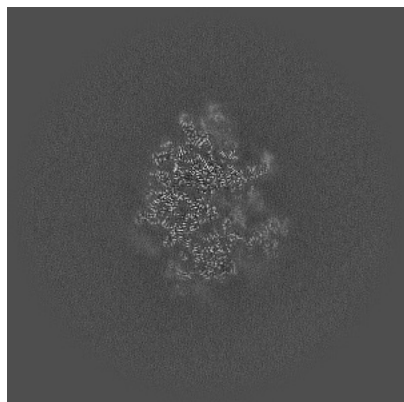


Z

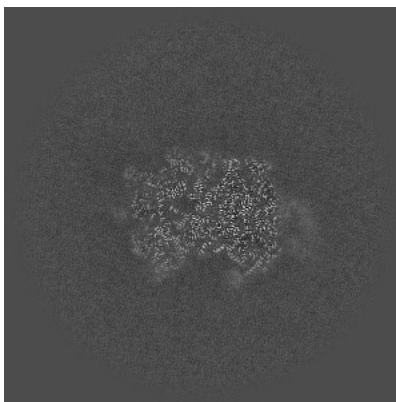
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

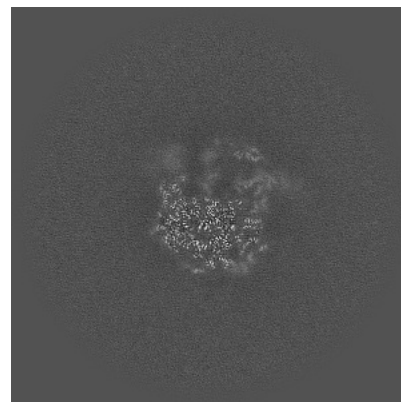
6.2.1 Primary map



X Index: 256

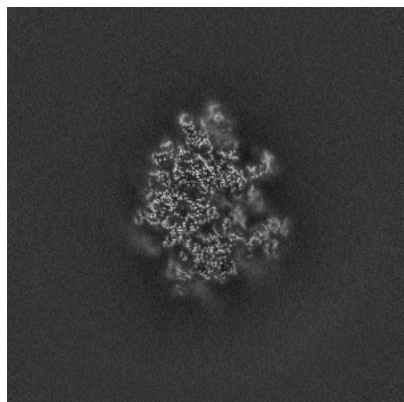


Y Index: 256

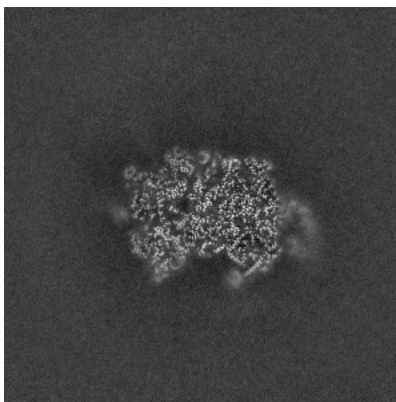


Z Index: 256

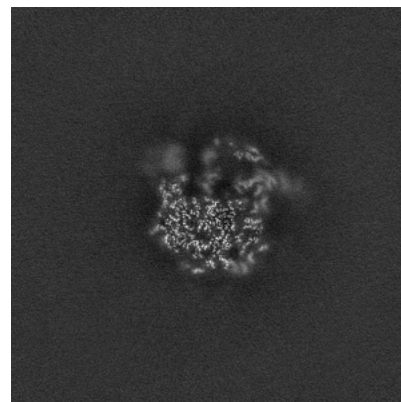
6.2.2 Raw map



X Index: 256



Y Index: 256

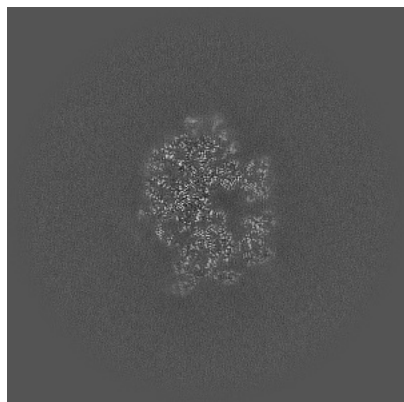


Z Index: 256

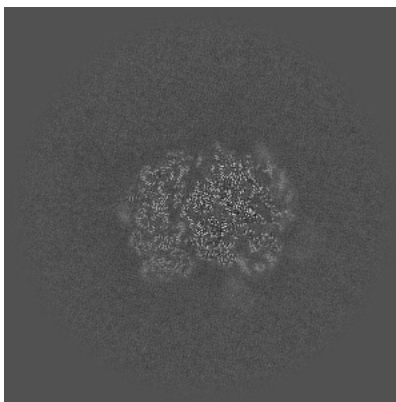
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

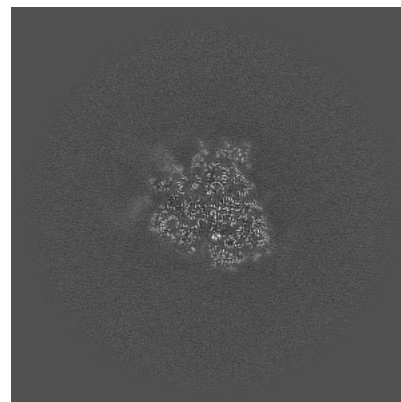
6.3.1 Primary map



X Index: 271

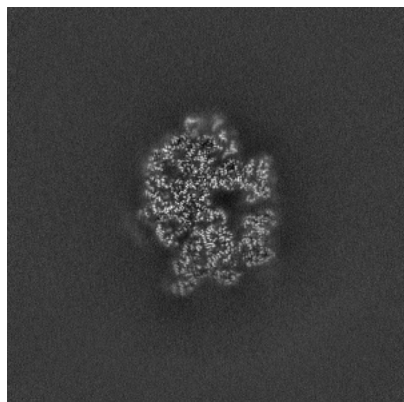


Y Index: 243

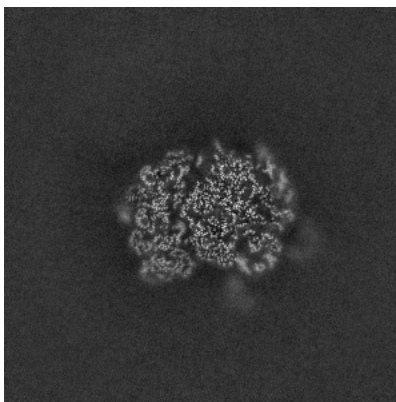


Z Index: 290

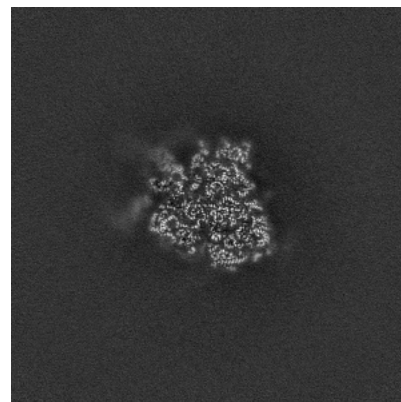
6.3.2 Raw map



X Index: 272



Y Index: 243

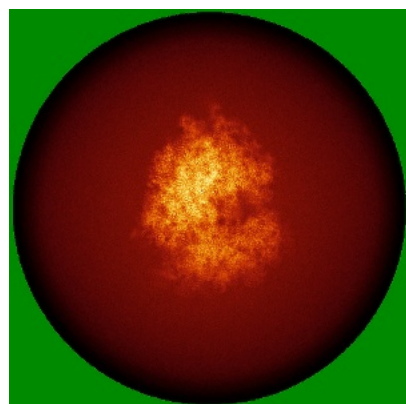


Z Index: 290

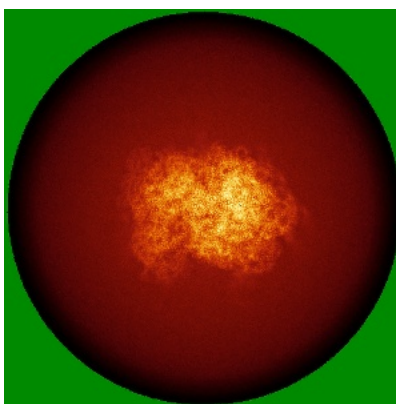
The images above show the largest variance slices of the map in three orthogonal directions.

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

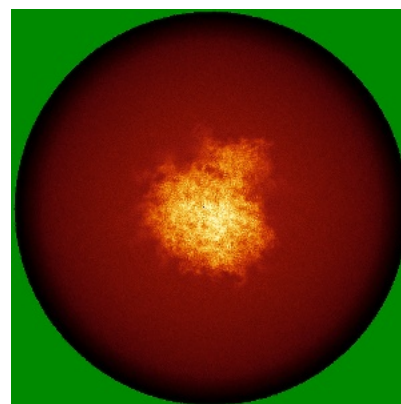
6.4.1 Primary map



X



Y

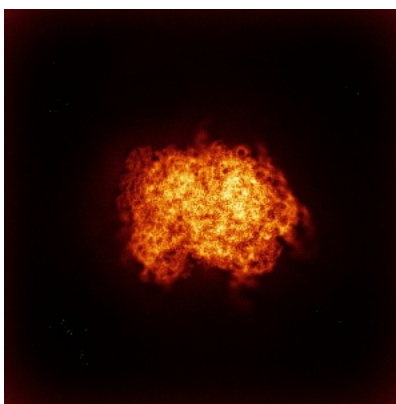


Z

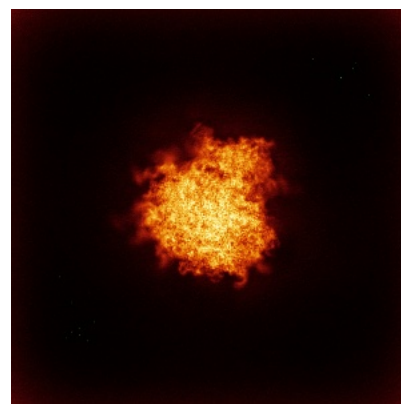
6.4.2 Raw map



X



Y

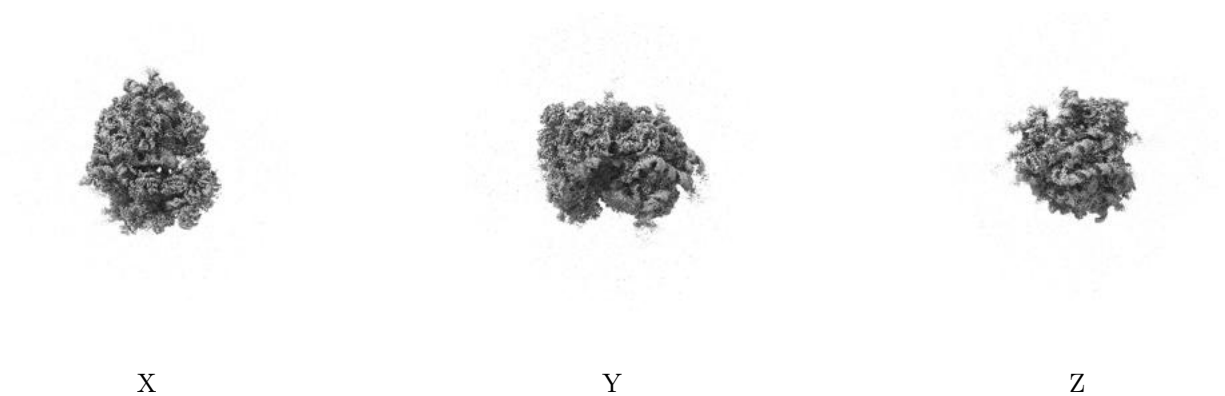


Z

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 0.4. 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.

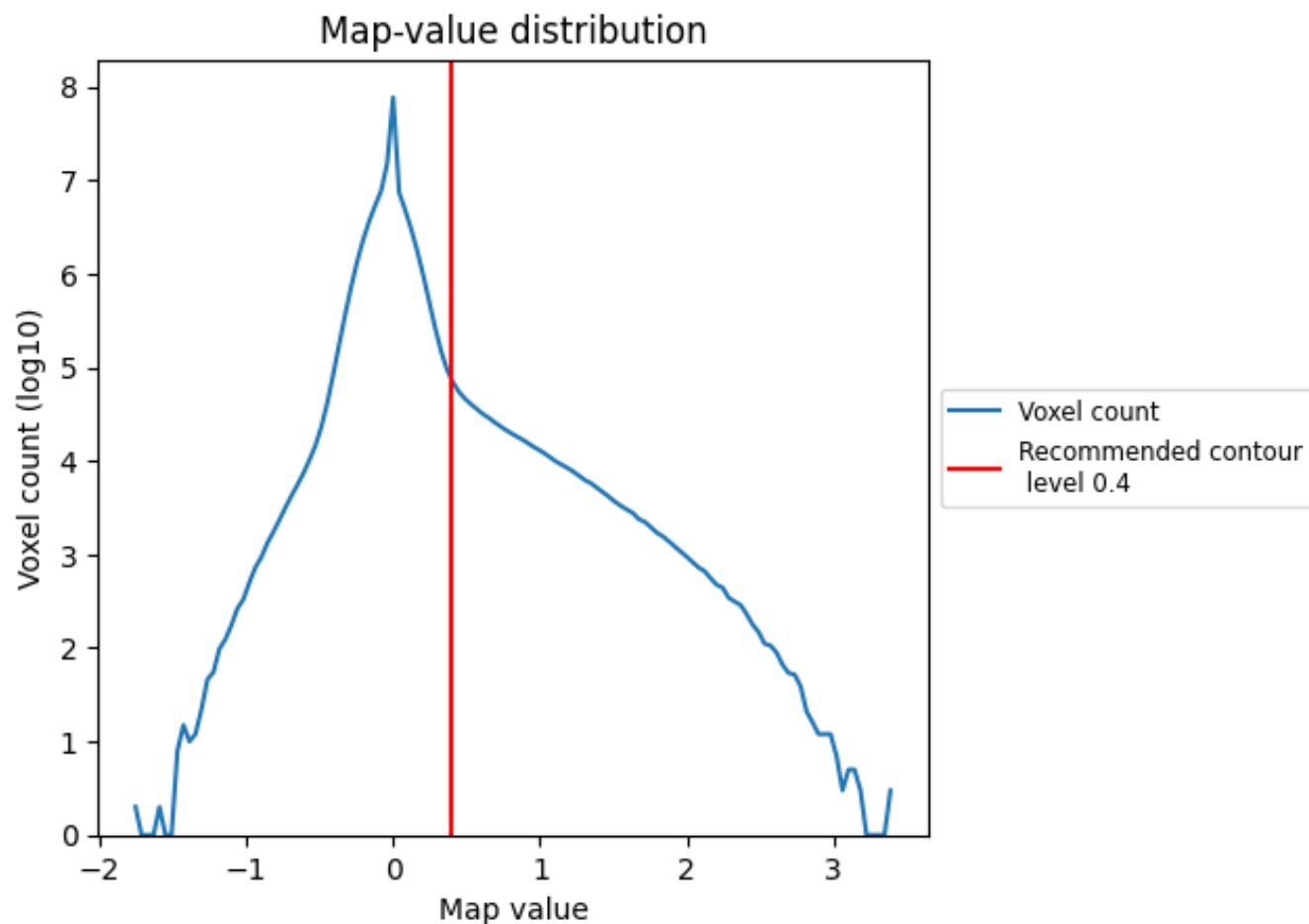
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

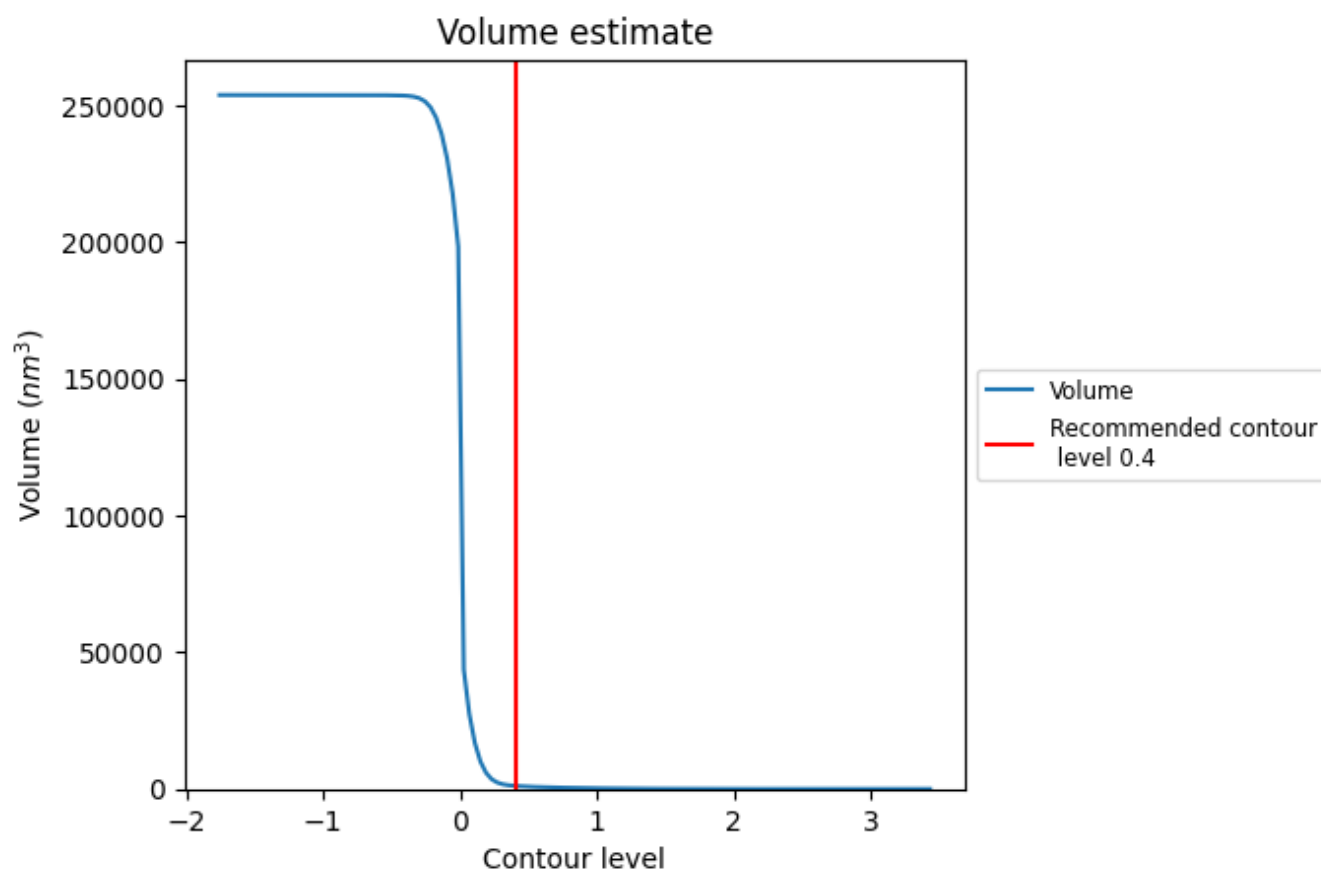
This section contains the results of statistical analysis of the map.

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.

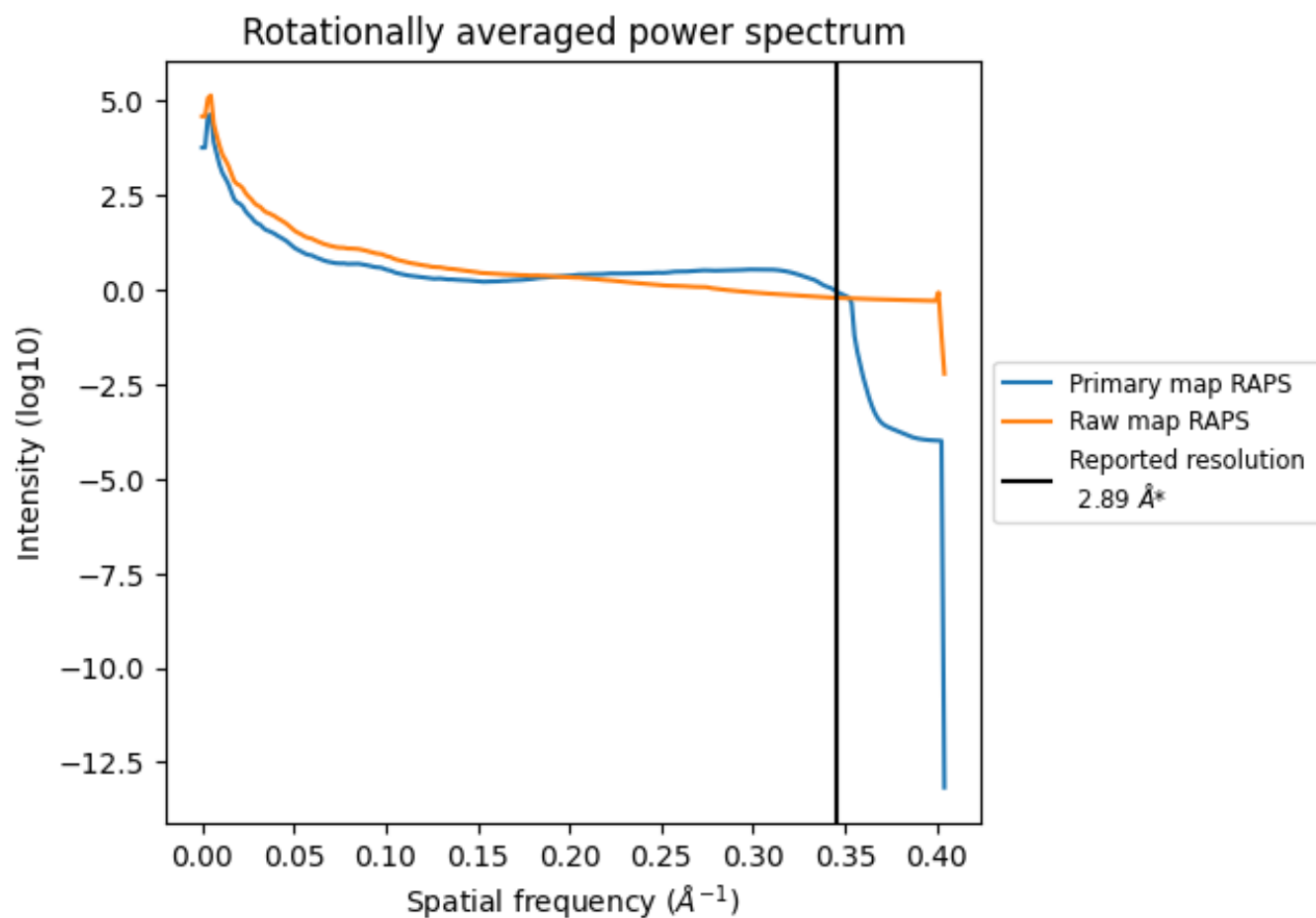
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1136 nm^3 ; this corresponds to an approximate mass of 1026 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 ⓘ

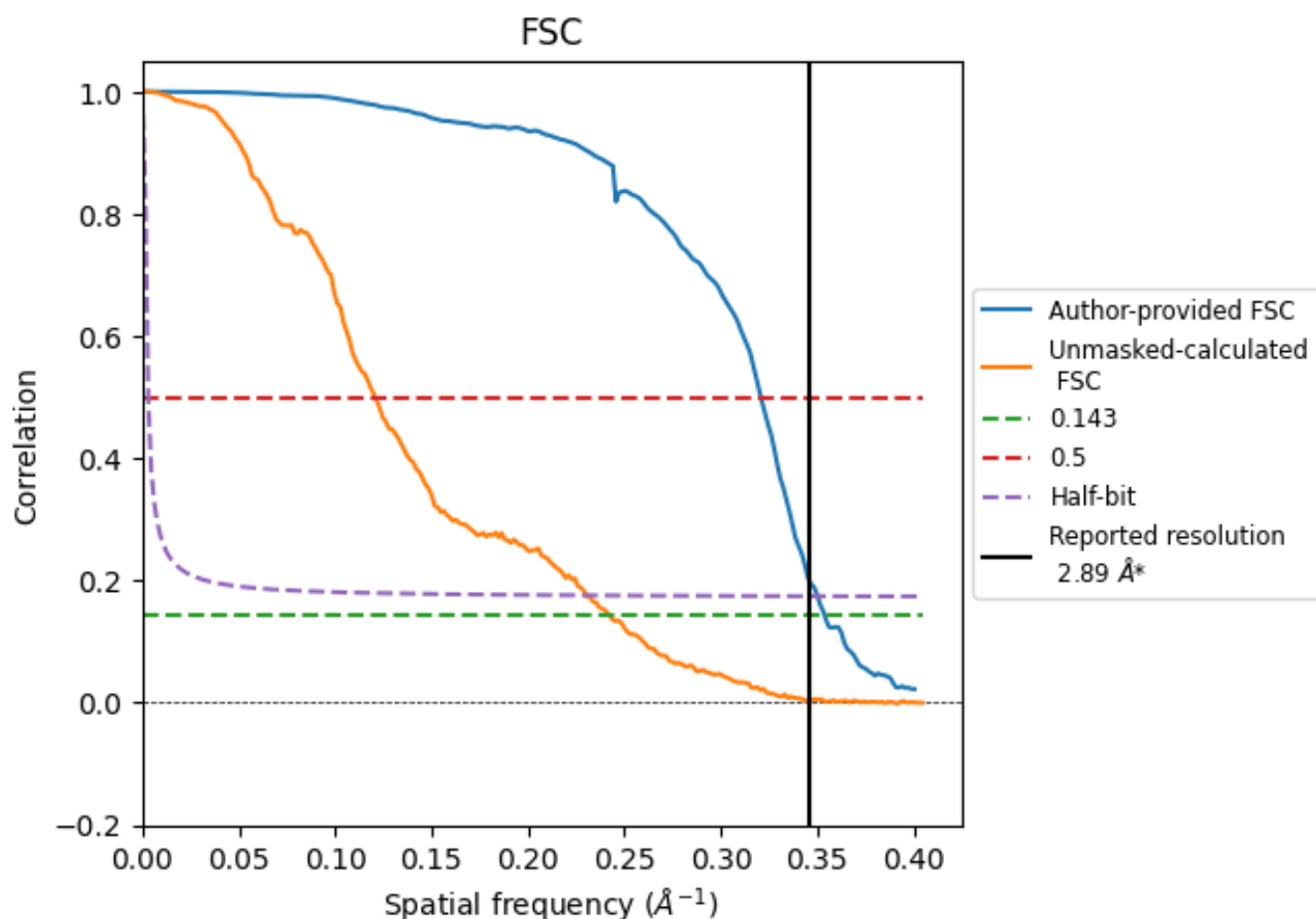


*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

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 $0.346 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

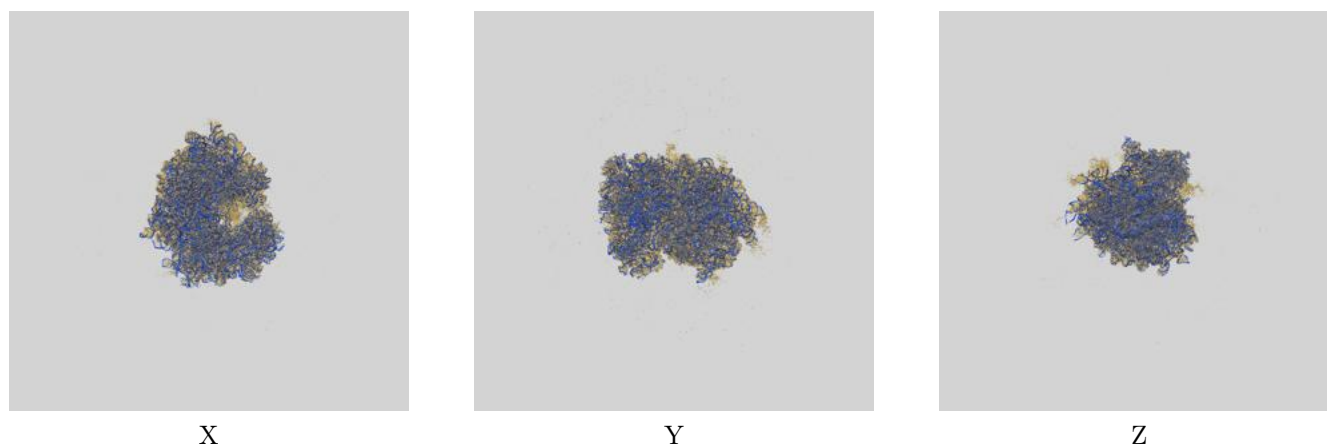
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	2.83	3.12	2.86
Unmasked-calculated*	4.13	8.28	4.34

*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 4.13 differs from the reported value 2.89 by more than 10 %

9 Map-model fit [i](#)

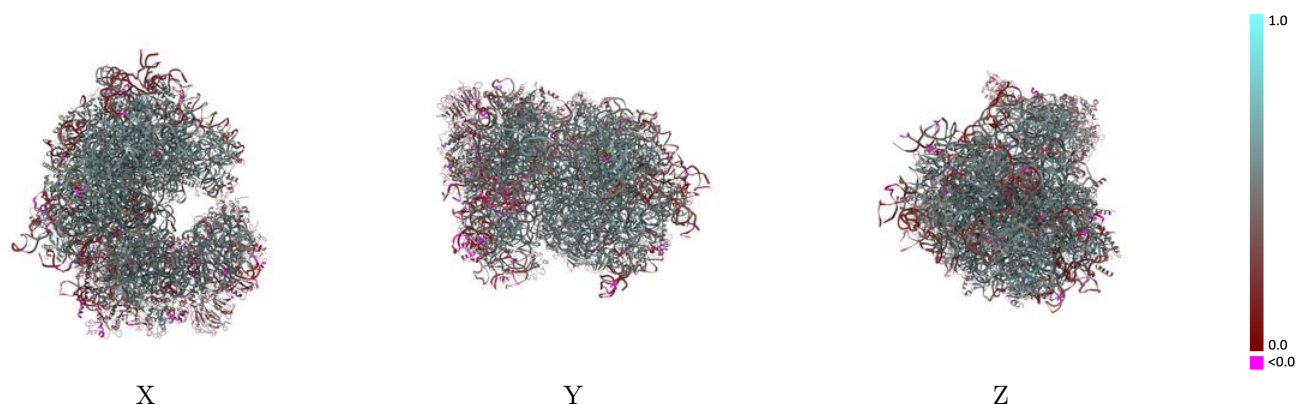
This section contains information regarding the fit between EMDB map EMD-58363 and PDB model 31FZ. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

9.1 Map-model overlay [i](#)



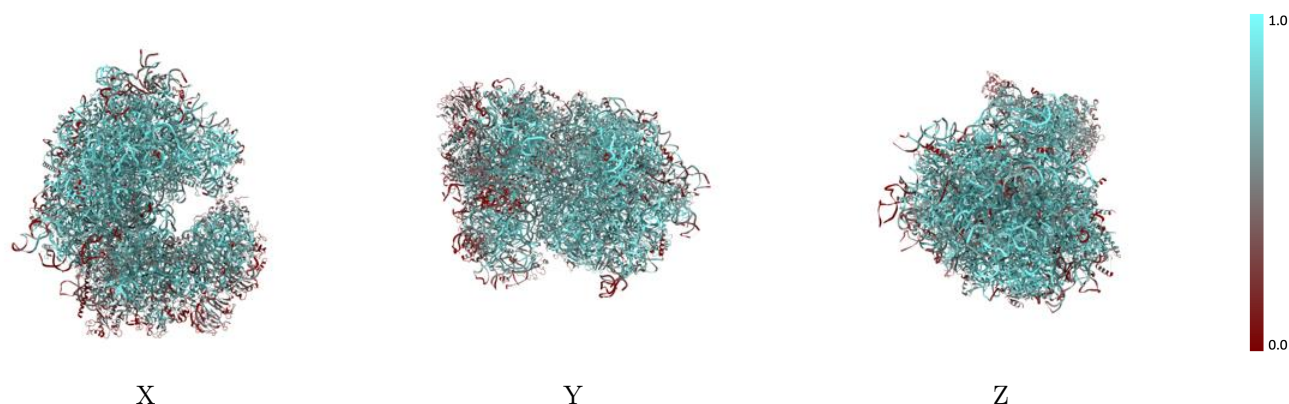
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



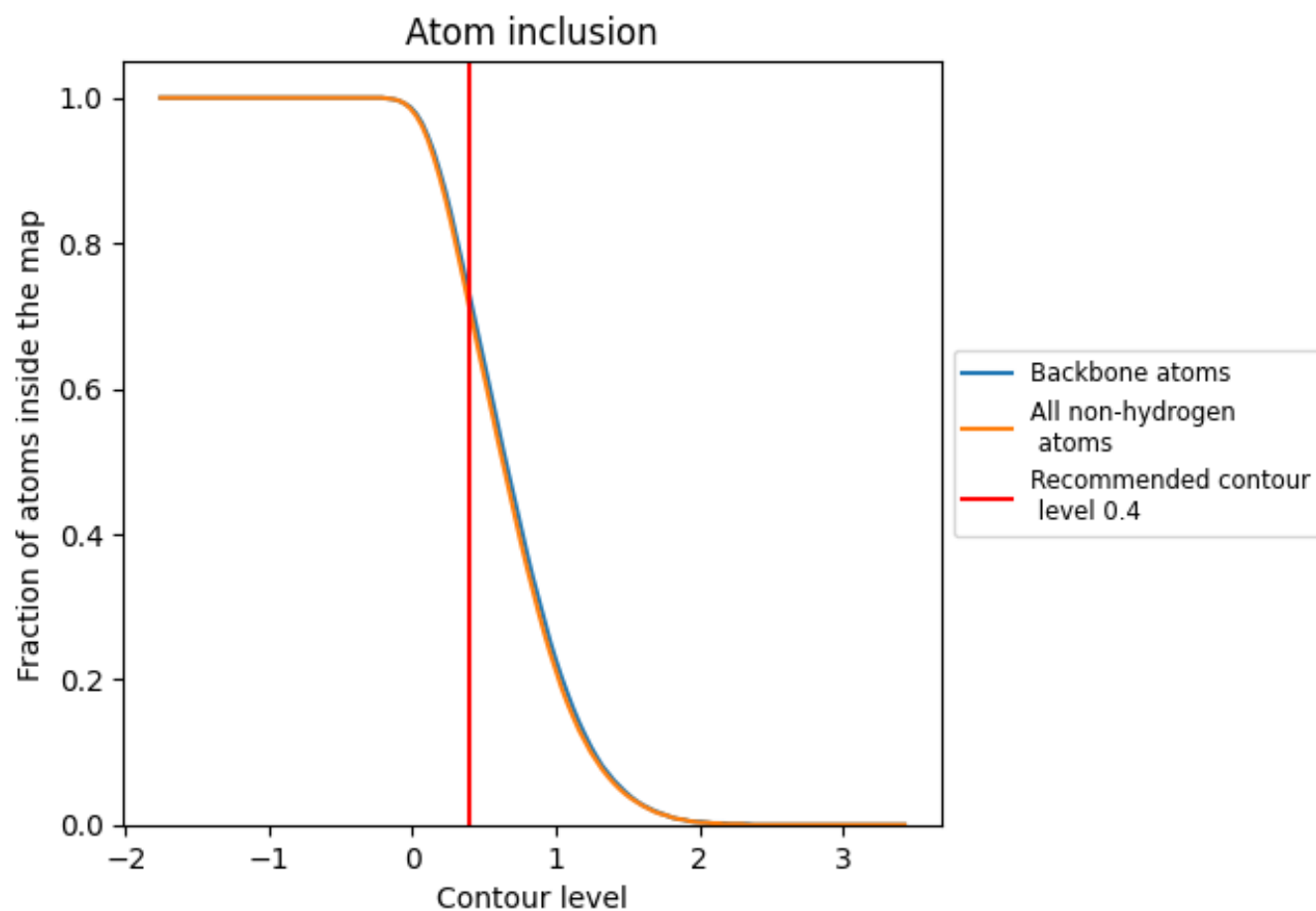
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 71% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7080	 0.4800
AA	 0.7670	 0.5620
AB	 0.7550	 0.5220
AC	 0.7630	 0.5380
AD	 0.7260	 0.4790
AE	 0.6900	 0.4810
AF	 0.7640	 0.5430
AG	 0.7800	 0.5520
AH	 0.7880	 0.5660
AI	 0.6430	 0.4750
AJ	 0.7880	 0.5410
AK	 0.7190	 0.5190
AL	 0.5690	 0.4100
AM	 0.7470	 0.5480
AN	 0.7280	 0.5340
AO	 0.7320	 0.5420
AP	 0.7590	 0.5220
AQ	 0.7050	 0.5040
AR	 0.8150	 0.5680
AS	 0.5910	 0.4400
AT	 0.6520	 0.4740
AU	 0.7210	 0.5090
AV	 0.7890	 0.5630
AW	 0.8280	 0.5680
AX	 0.7090	 0.5300
AY	 0.7250	 0.5270
AZ	 0.6620	 0.4870
Aa	 0.8230	 0.5760
Ab	 0.5470	 0.4330
Ac	 0.7610	 0.5600
Ad	 0.7150	 0.4820
Ae	 0.6880	 0.5150
Af	 0.7070	 0.5370
Ag	 0.7950	 0.5510
BA	 0.3560	 0.2770



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Chain	Atom inclusion	Q-score
BB	 0.6940	 0.4820
BC	 0.7570	 0.4740
BD	 0.5730	 0.4390
BE	 0.4290	 0.3490
BF	 0.4950	 0.3630
BG	 0.5380	 0.4250
BH	 0.3640	 0.3510
BI	 0.5300	 0.4430
BJ	 0.5190	 0.3940
BK	 0.4440	 0.3650
BL	 0.4900	 0.3590
BM	 0.5870	 0.4440
BN	 0.5740	 0.4210
BO	 0.6130	 0.4540
BP	 0.3860	 0.3230
BQ	 0.5050	 0.4310
BR	 0.5990	 0.4250
BS	 0.6530	 0.4890
BT	 0.3300	 0.3050
BU	 0.6190	 0.4870
BV	 0.4450	 0.3510
BW	 0.4570	 0.2980
BX	 0.0800	 0.1570
BY	 0.5810	 0.4700
BZ	 0.6210	 0.4740
Ba	 0.6730	 0.5210
Bb	 0.2660	 0.1230
Bc	 0.4700	 0.3540
Bd	 0.4730	 0.3780
Be	 0.2190	 0.0740
Bf	 0.1240	 0.1550
Bg	 0.3250	 0.3030
Bh	 0.5430	 0.4150
CA	 0.7660	 0.5420
CB	 0.6340	 0.4450
CC	 0.6610	 0.4990
CD	 0.7060	 0.5190
CE	 0.5870	 0.3960
CF	 0.7020	 0.5070
CG	 0.7320	 0.5070
CH	 0.8300	 0.5820
CI	 0.8070	 0.5010

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Chain	Atom inclusion	Q-score
CJ	 0.9400	 0.5730
CK	 0.8630	 0.5410