



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:46 AM UTC

PDB ID : 6S47 / pdb_00006s47
EMDB ID : EMD-10098
Title : Saccharomyces cerevisiae 80S ribosome bound with ABCF protein New1
Authors : Kasari, V.; Pochopien, A.A.; Margus, T.; Murina, V.; Turnbull, K.; Zhou, Y.; Nissan, T.; Graf, M.; Novacek, J.; Atkinson, G.C.; Johansson, M.J.O.; Wilson, D.N.; Hauryliuk, V.
Deposited on : 2019-06-26
Resolution : 3.28 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:

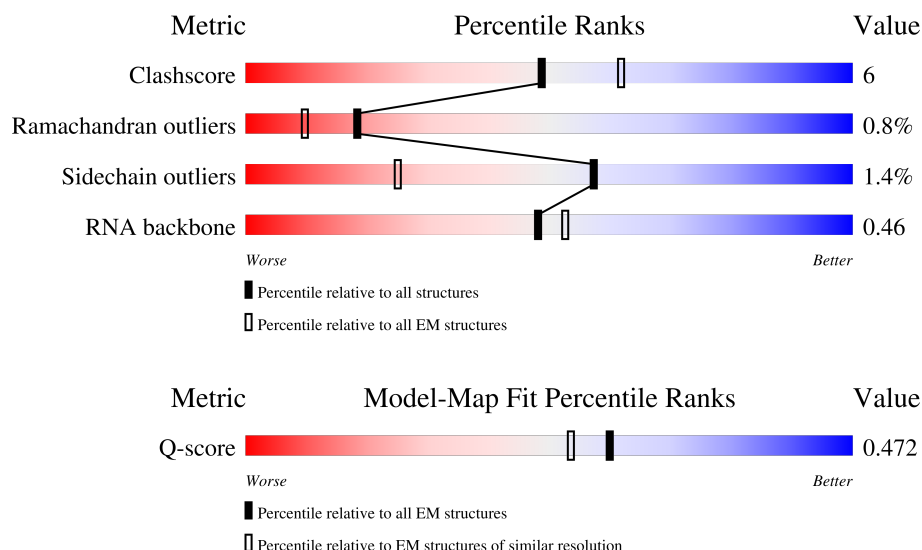
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 3.28 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.



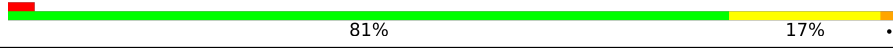
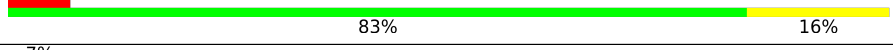
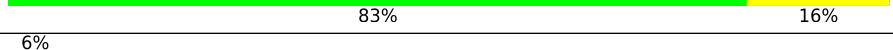
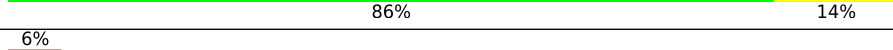
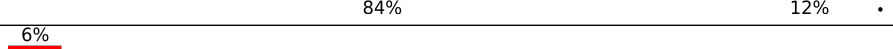
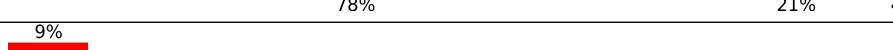
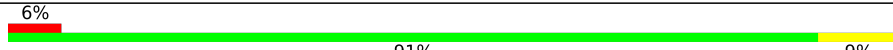
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14492 (2.78 - 3.78)

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	3149	5% 67% 28% .
2	AB	121	77% 21% .
3	AC	158	71% 25% .

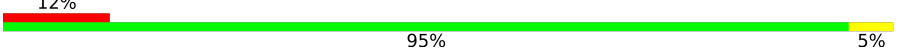
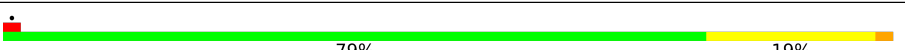
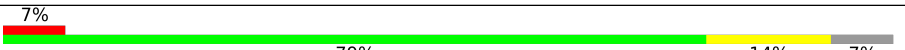
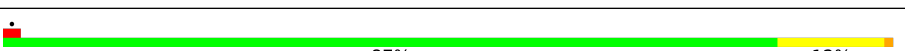
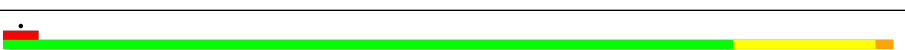
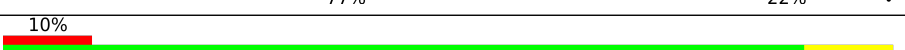
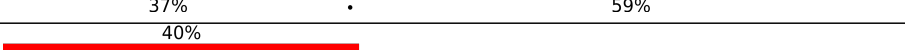
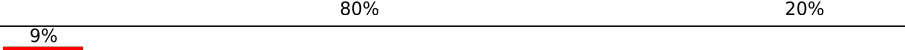
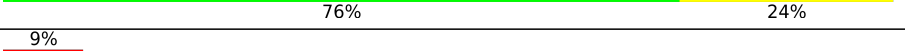
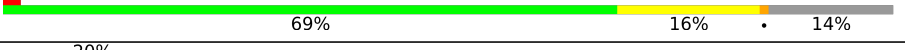
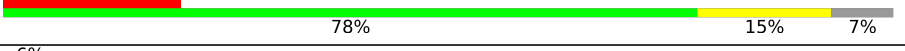
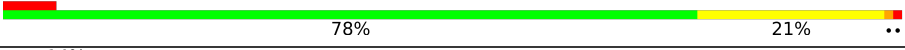
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	AD	252	
5	AE	386	
6	AF	361	
7	AG	296	
8	AH	175	
9	AI	243	
10	AJ	233	
11	AK	191	
12	AL	220	
13	AM	169	
14	AN	198	
15	AO	137	
16	AP	203	
17	AQ	198	
18	AR	183	
19	AS	185	
20	AT	188	
21	AU	172	
22	AV	159	
23	AW	120	
24	AX	136	
25	AY	155	
26	AZ	141	
27	Aa	126	
28	Ab	135	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	Ac	148	
30	Ad	58	
31	Ae	104	
32	Af	112	
33	Ag	129	
34	Ah	106	
35	Ai	121	
36	Aj	119	
37	Ak	99	
38	Al	87	
39	Am	77	
40	An	50	
41	Ao	127	
42	Ap	25	
43	Aq	105	
44	Ar	91	
45	BA	1707	
46	BB	251	
47	BC	254	
48	BD	253	
49	BE	239	
50	BF	260	
51	BG	224	
52	BH	236	
53	BI	189	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	BJ	199	
55	BK	196	
56	BL	105	
57	BM	155	
58	BN	142	
59	BO	150	
60	BP	136	
61	BQ	141	
62	BR	142	
63	BS	135	
64	BT	145	
65	BU	143	
66	BV	120	
67	BW	87	
68	BX	129	
69	BY	144	
70	BZ	134	
71	Ba	107	
72	Bb	118	
73	Bc	81	
74	Bd	66	
75	Be	55	
76	Bf	62	
77	Bg	151	
78	Bh	318	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	Bi	972	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
80	ATP	Bi	1202	-	-	X	-

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 204313 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	AA	3149	Total	C	N	O	P	0	0
			67355	30086	12142	21978	3149		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	211	Total	C	N	O	S	0	0
			1705	1083	322	294	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AN	193	Total	C	N	O	0	0
			1543	962	315	266		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	183	Total	C	N	O	0	0
			1420	882	281	257		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	AT	152	Total	C	N	O	0	0
			1228	763	260	205		

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	100	Total	C	N	O	S	0	0
			796	516	131	149			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	61	Total	C	N	O	S	0	0
			509	328	100	80	1		

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AZ	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Aa	126	Total	C	N	O	S	0	0
			993	625	192	176			

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

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Ab	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ac	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Ad	58	Total	C	N	O	0	0
			462	289	100	73		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ae	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Af	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ag	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ah	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ai	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Aj	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ak	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 38 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Al	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
39	Am	77	Total	C	N	O	0	0
			612	391	115	106		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	An	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ao	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ap	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 43 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Aq	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 44 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ar	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 45 is a RNA chain called 18S rRNA (1707-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BA	1707	Total	C	N	O	P	0	0
			36375	16263	6440	11965	1707		

- Molecule 46 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BB	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 47 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BC	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 48 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BD	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BE	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 50 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BF	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 51 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BG	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 52 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BH	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 53 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	BI	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 54 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BJ	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 55 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BK	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 56 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BL	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

- Molecule 57 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BM	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 58 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BN	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 59 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BO	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 60 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BP	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 61 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BQ	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 62 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	BR	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 63 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BS	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 64 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BT	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 65 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BU	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 66 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	BV	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 67 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BW	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 68 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BX	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 69 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BY	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 70 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	BZ	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 71 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	Ba	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 72 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bb	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 73 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bc	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 74 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bd	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 75 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Be	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 76 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Bf	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 77 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Bg	57	Total	C	N	O	S	0	0
			444	281	82	77	4		

- Molecule 78 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bh	318	Total	C	N	O	S	0	0
			2441	1544	419	470	8		

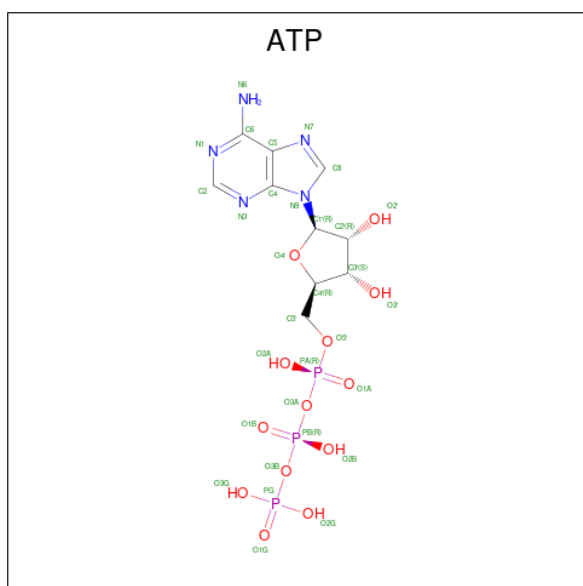
- Molecule 79 is a protein called [NU+] prion formation protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bi	952	Total	C	N	O	S	0	0
			7512	4763	1271	1450	28		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bi	495	ASP	SER	conflict	UNP Q08972
Bi	713	GLN	GLU	conflict	UNP Q08972
Bi	1058	GLN	GLU	conflict	UNP Q08972

- Molecule 80 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



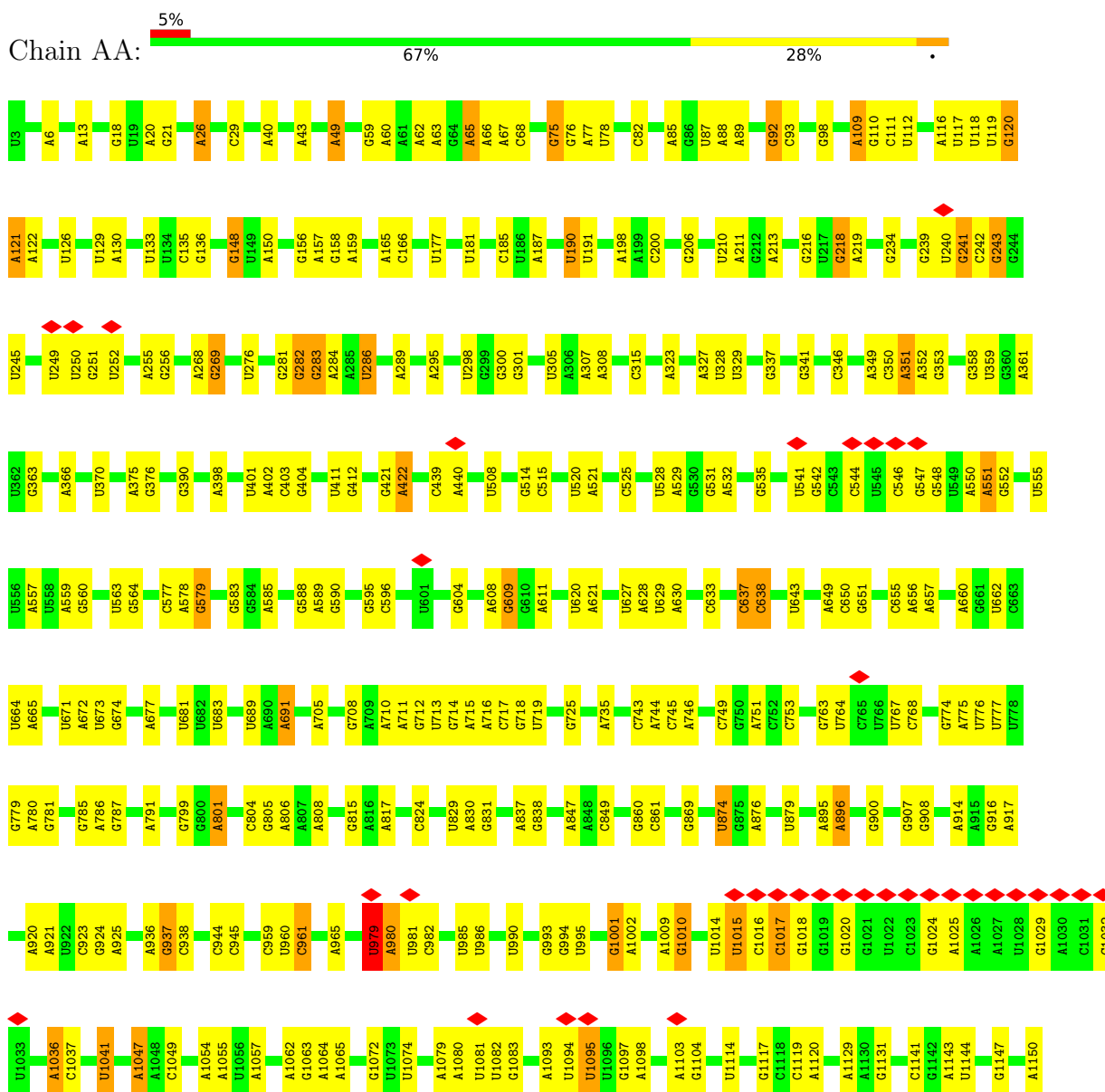
Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
80	Bi	1	31	10	5	13	3	0

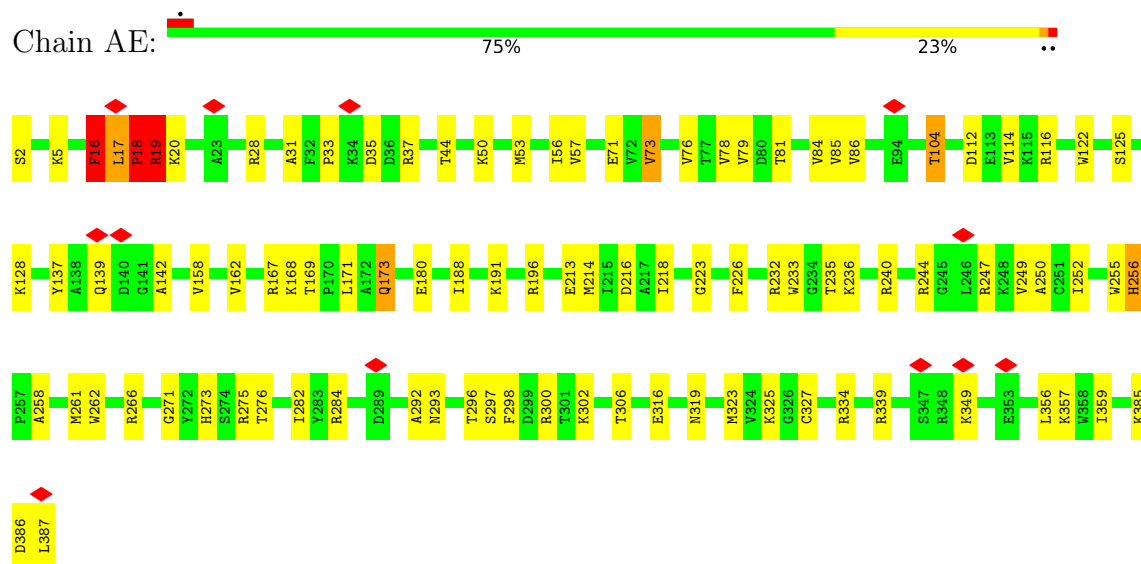
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

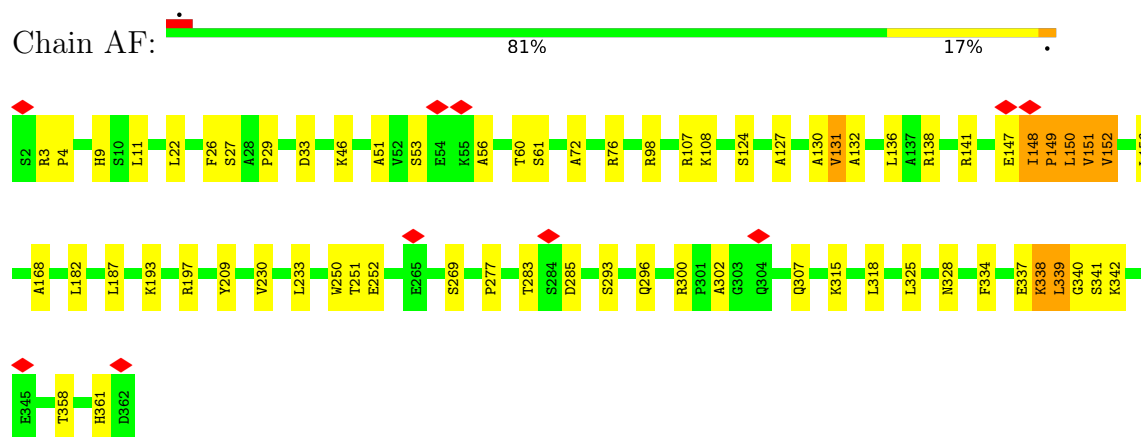
- Molecule 1: 28S ribosomal RNA



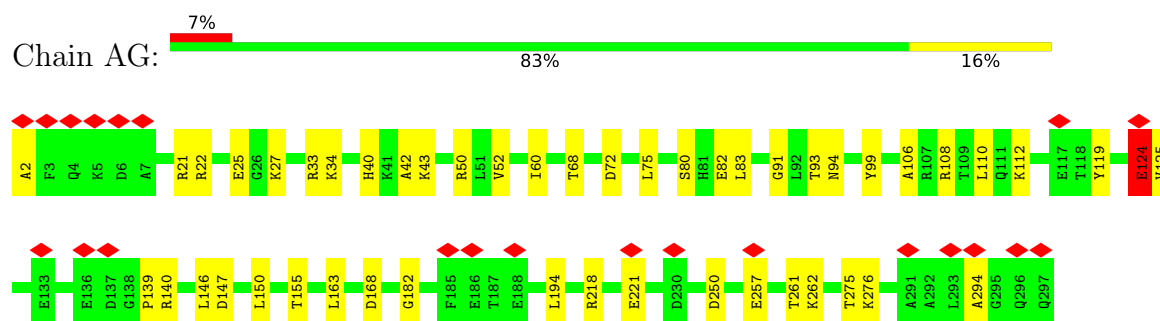




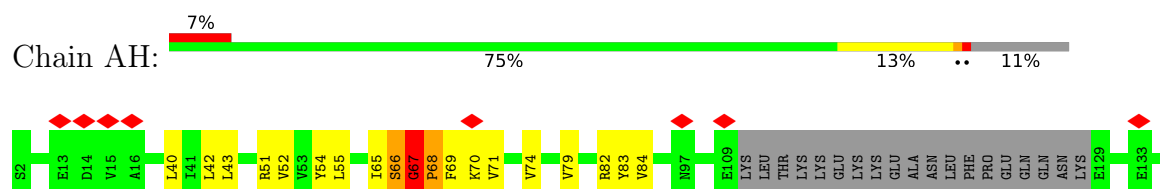
• Molecule 6: 60S ribosomal protein L4-A



• Molecule 7: 60S ribosomal protein L5



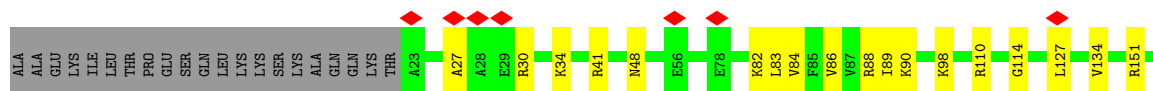
• Molecule 8: 60S ribosomal protein L6-A





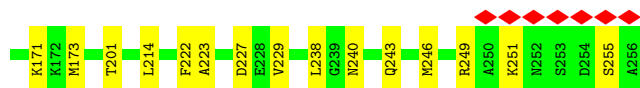
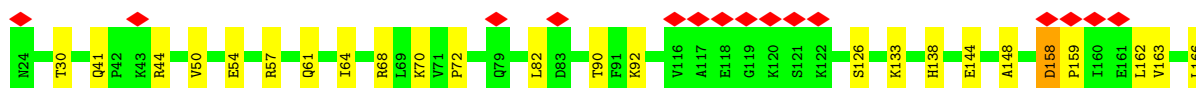
- Molecule 9: 60S ribosomal protein L7-A

Chain AI: 74% 17% 9%



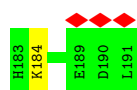
- Molecule 10: 60S ribosomal protein L8-A

Chain AJ: 9% 83% 16%



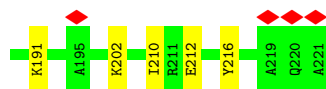
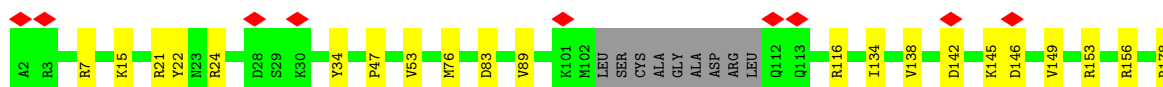
- Molecule 11: 60S ribosomal protein L9-A

Chain AK: 6% 86% 14%

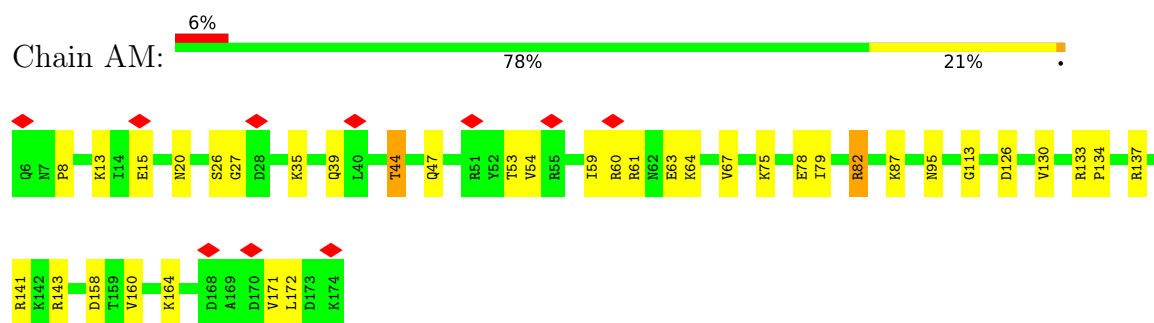


- Molecule 12: 60S ribosomal protein L10

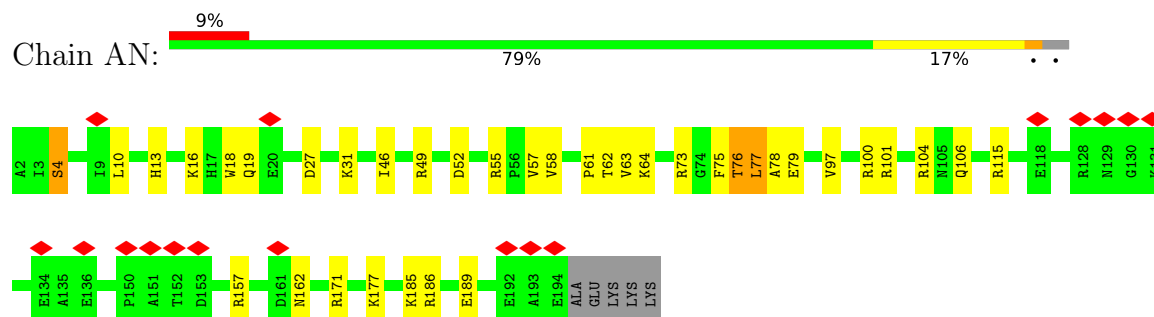
Chain AL: 6% 84% 12%



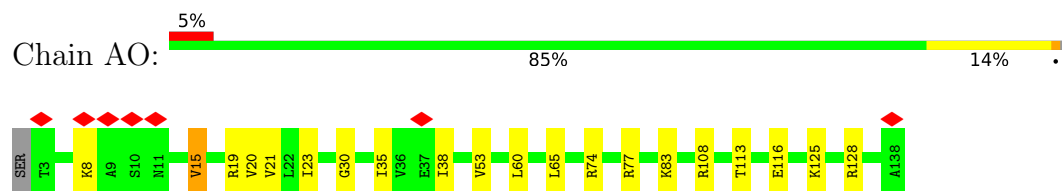
- Molecule 13: 60S ribosomal protein L11-B



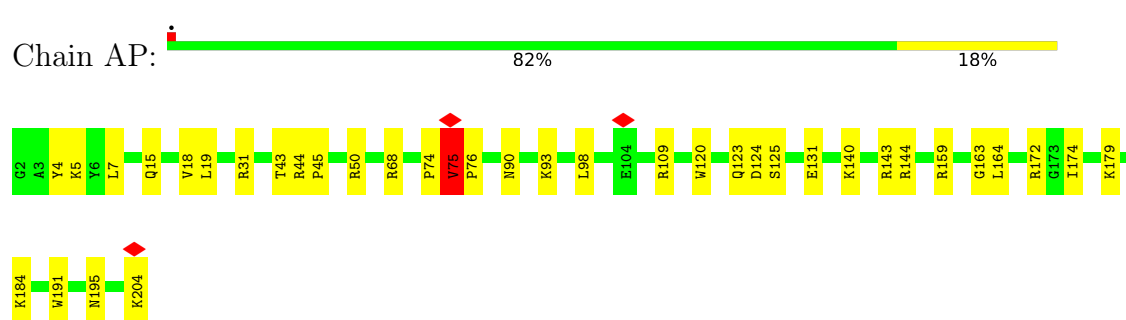
- Molecule 14: 60S ribosomal protein L13-A



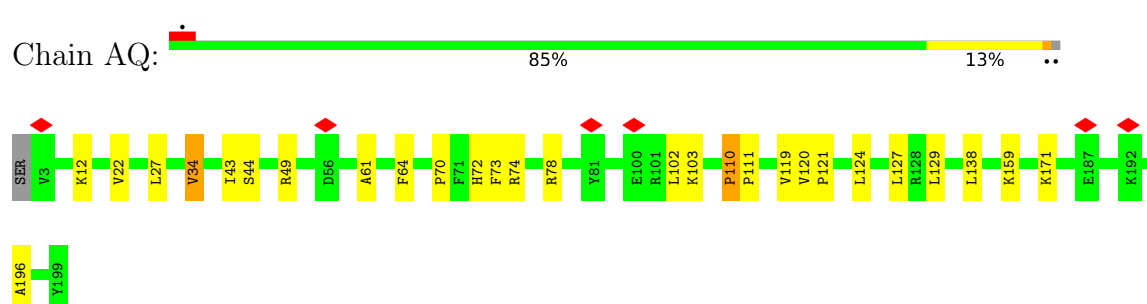
- Molecule 15: 60S ribosomal protein L14-A



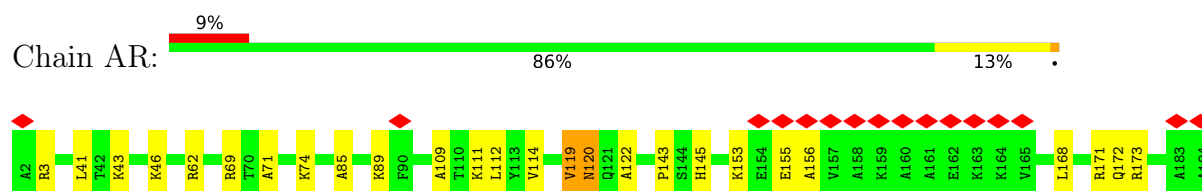
- Molecule 16: 60S ribosomal protein L15-A



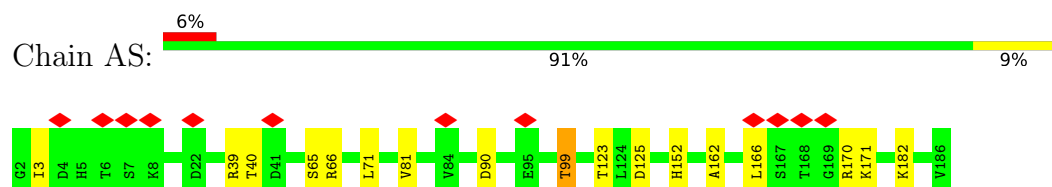
- Molecule 17: 60S ribosomal protein L16-A



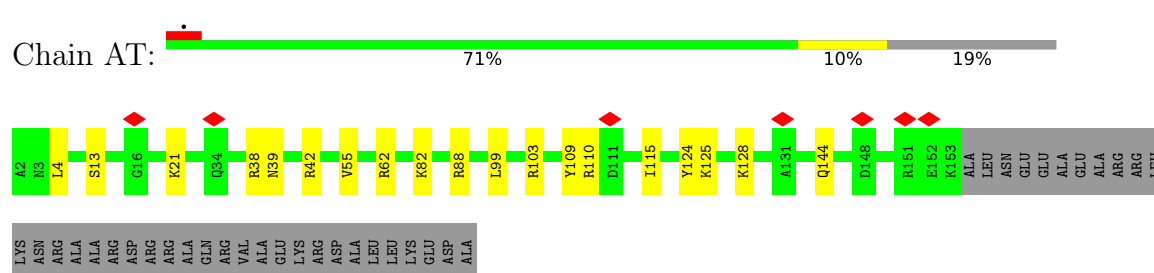
- Molecule 18: 60S ribosomal protein L17-A



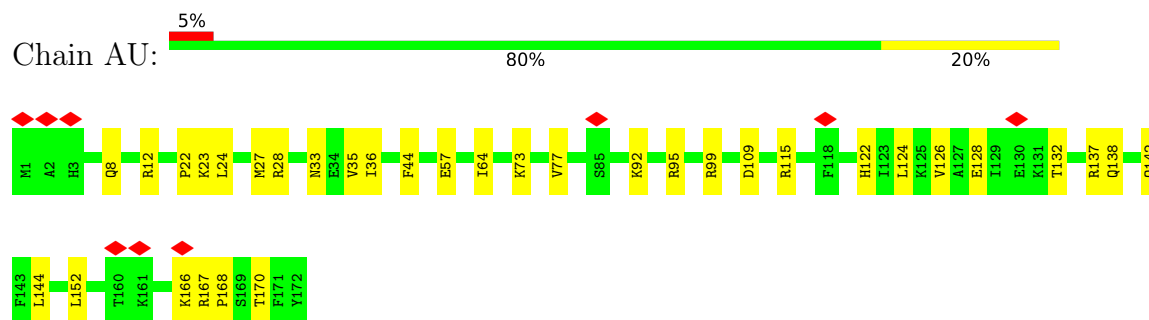
- Molecule 19: 60S ribosomal protein L18-A



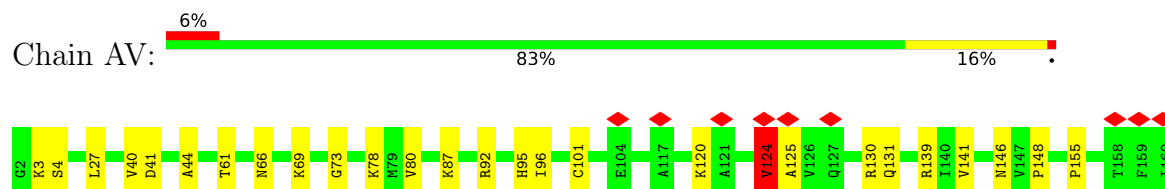
- Molecule 20: 60S ribosomal protein L19-A



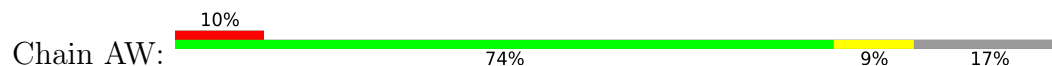
- Molecule 21: 60S ribosomal protein L20-A

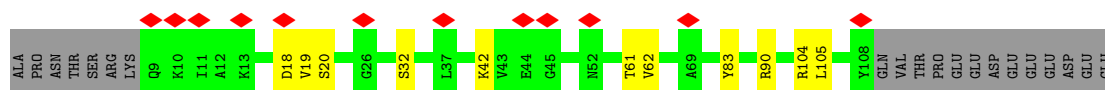


- Molecule 22: 60S ribosomal protein L21-A

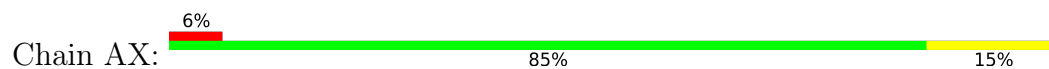


- Molecule 23: 60S ribosomal protein L22-A

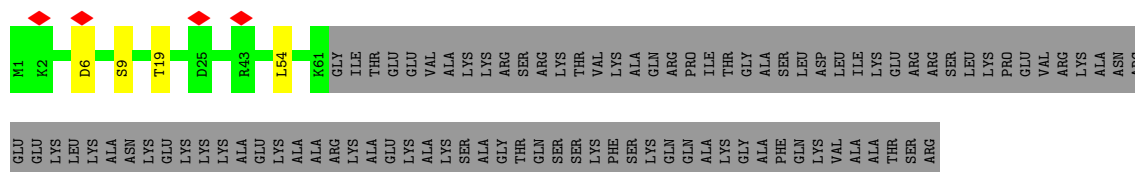




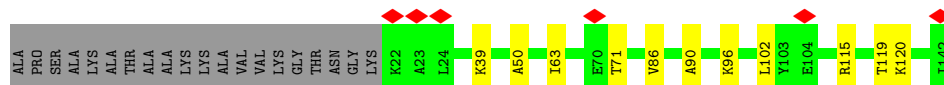
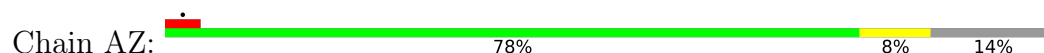
- Molecule 24: 60S ribosomal protein L23-A



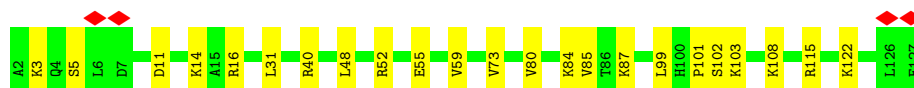
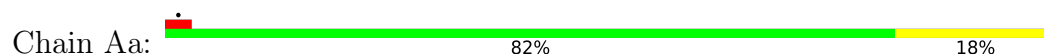
- Molecule 25: 60S ribosomal protein L24-A



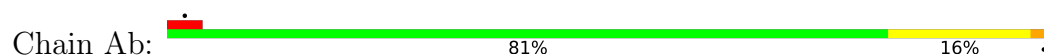
- Molecule 26: 60S ribosomal protein L25



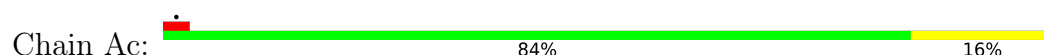
- Molecule 27: 60S ribosomal protein L26-A

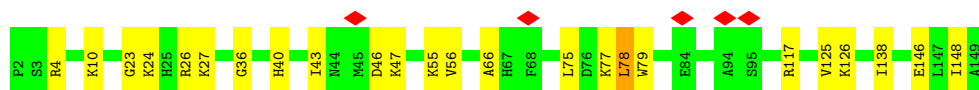


- Molecule 28: 60S ribosomal protein L27-A



- Molecule 29: 60S ribosomal protein L28

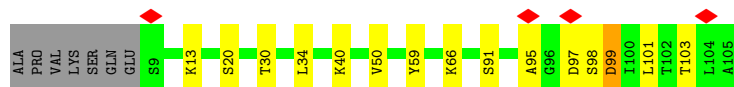
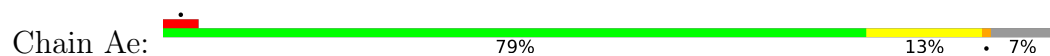




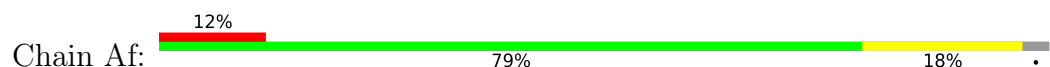
- Molecule 30: 60S ribosomal protein L29



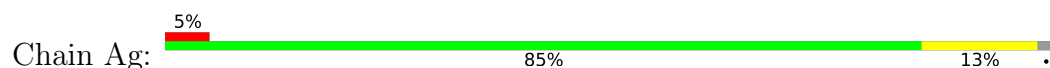
- Molecule 31: 60S ribosomal protein L30



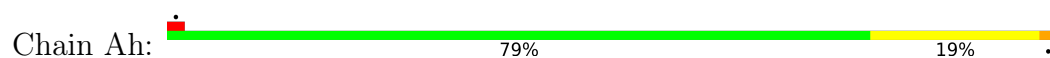
- Molecule 32: 60S ribosomal protein L31-A



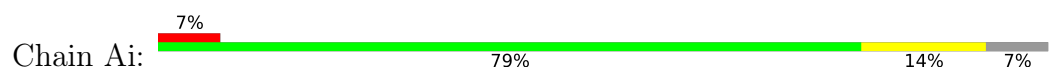
- Molecule 33: 60S ribosomal protein L32



- Molecule 34: 60S ribosomal protein L33-A



- Molecule 35: 60S ribosomal protein L34-A



- Molecule 36: 60S ribosomal protein L35-A

Chain Aj:  87% 12%



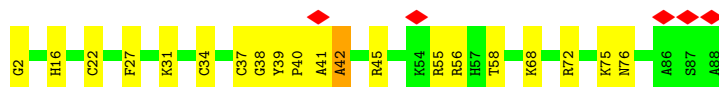
- Molecule 37: 60S ribosomal protein L36-A

Chain Ak:  82% 16%

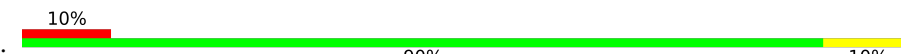


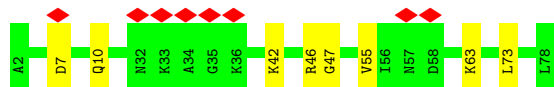
- Molecule 38: 60S ribosomal protein L37-A

Chain Al:  6% 77% 22%



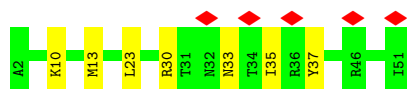
- Molecule 39: 60S ribosomal protein L38

Chain Am:  10% 90% 10%



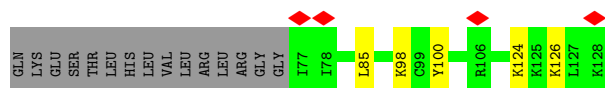
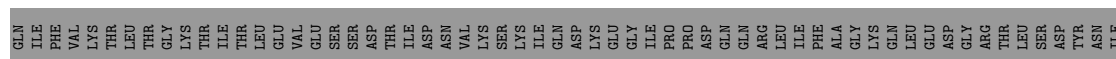
- Molecule 40: 60S ribosomal protein L39

Chain An:  10% 86% 14%



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Ao:  37% 59%

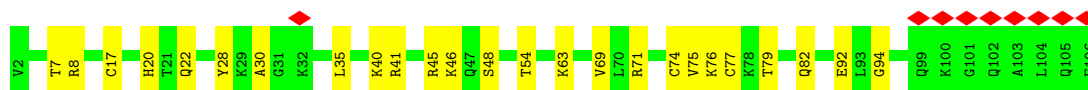
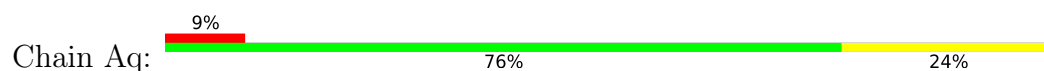


- Molecule 42: 60S ribosomal protein L41-B

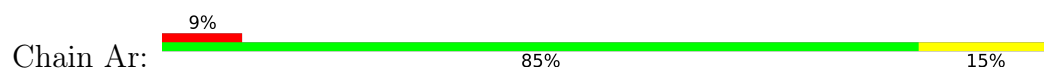
Chain Ap:  40% 80% 20%



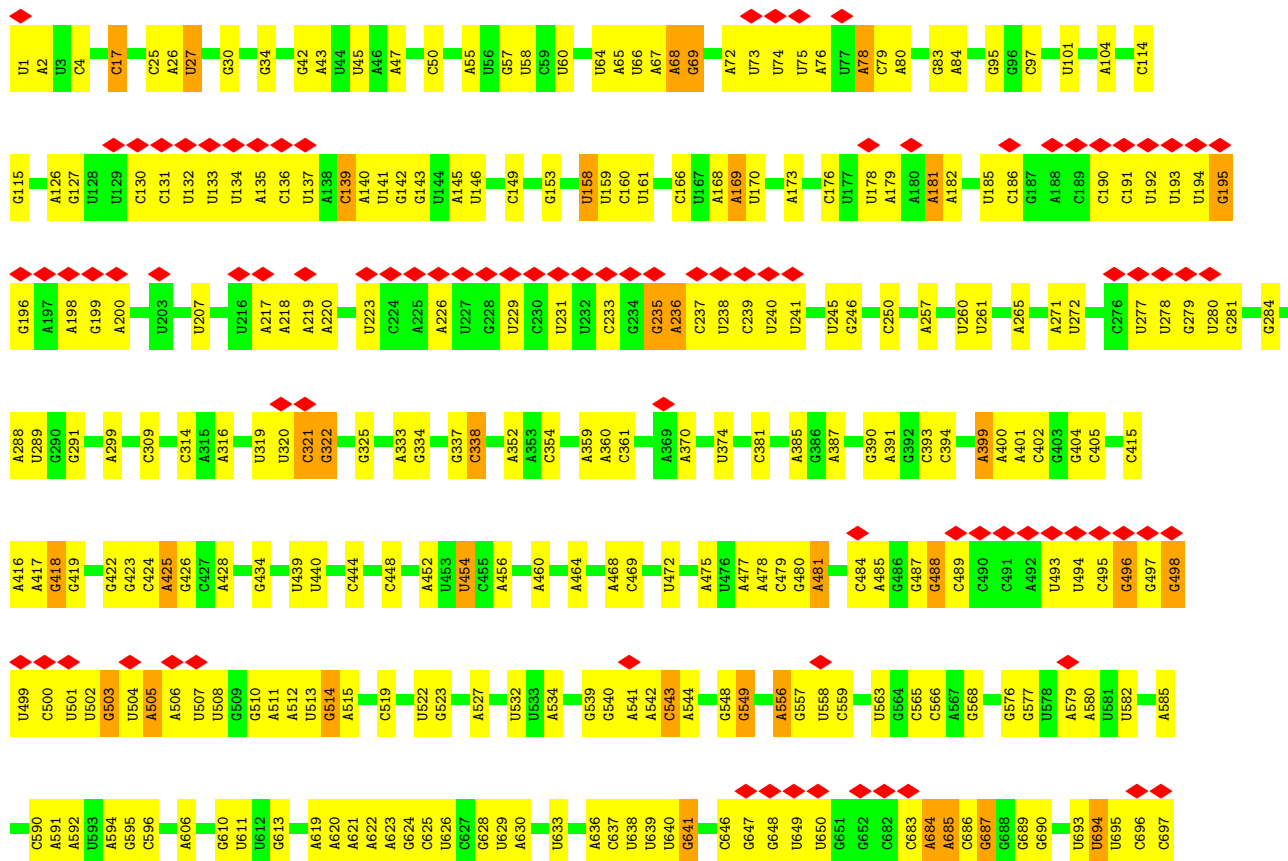
- Molecule 43: 60S ribosomal protein L42-A

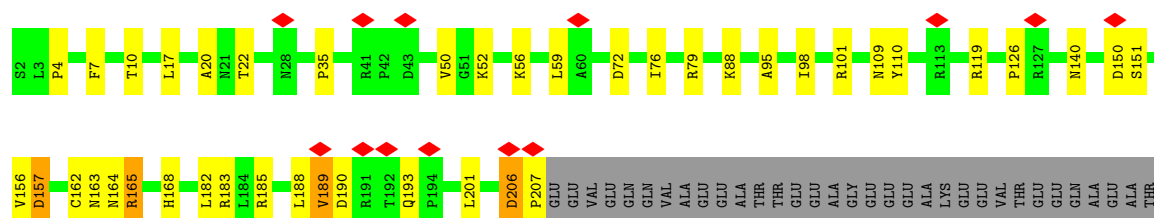


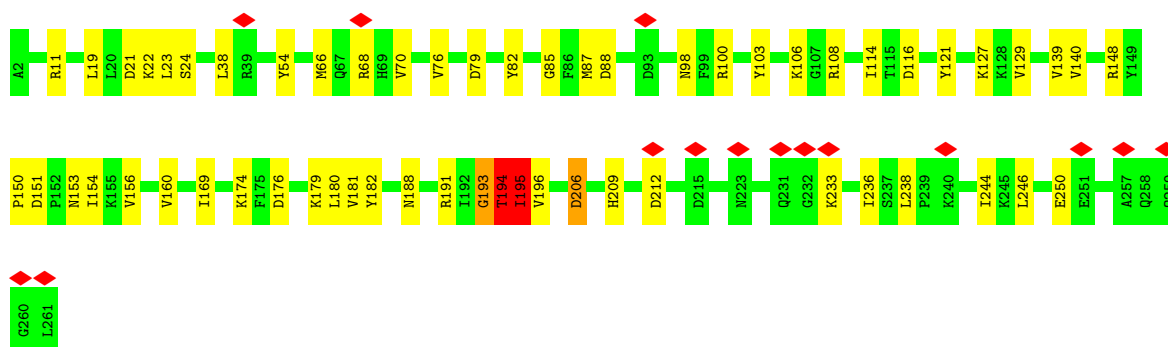
- Molecule 44: 60S ribosomal protein L43-A



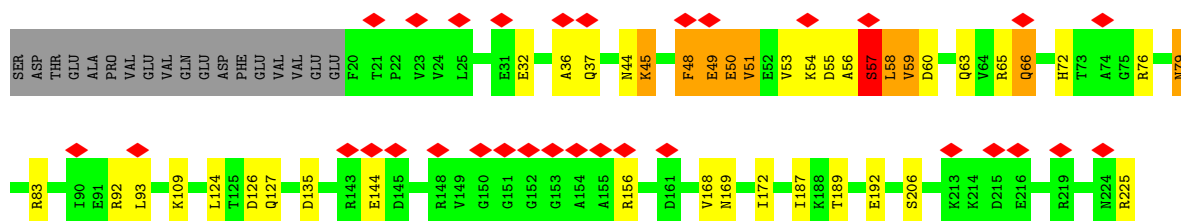
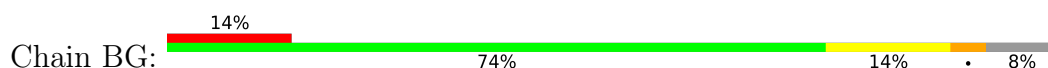
- Molecule 45: 18S rRNA (1707-MER)



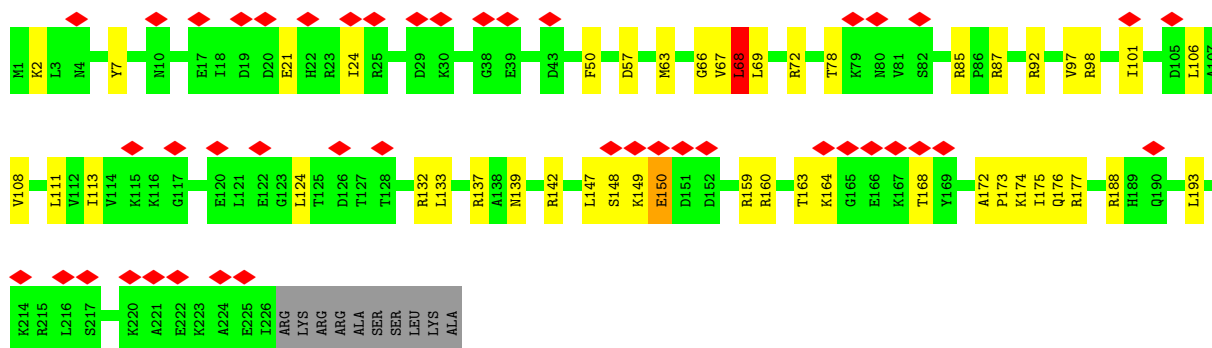
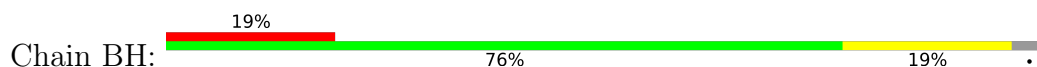




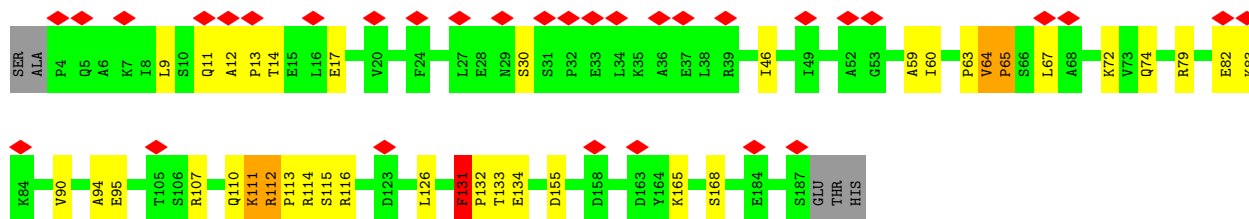
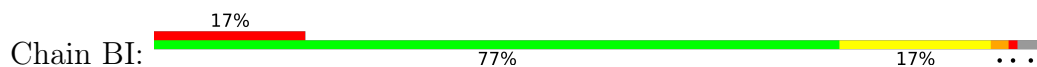
• Molecule 51: Rps5p



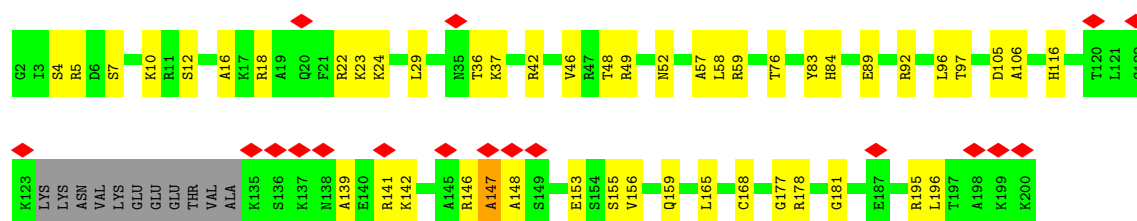
• Molecule 52: 40S ribosomal protein S6-A



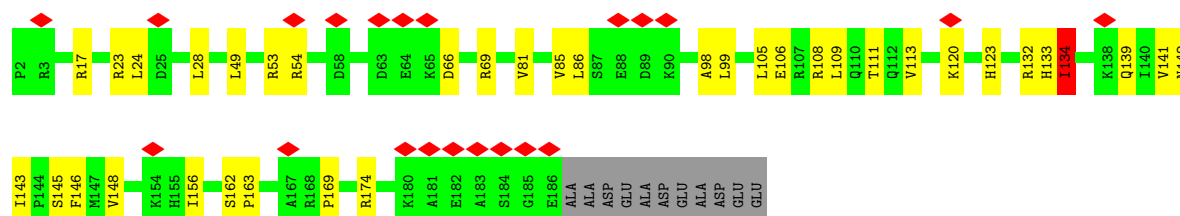
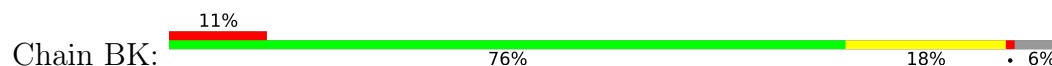
• Molecule 53: 40S ribosomal protein S7-A



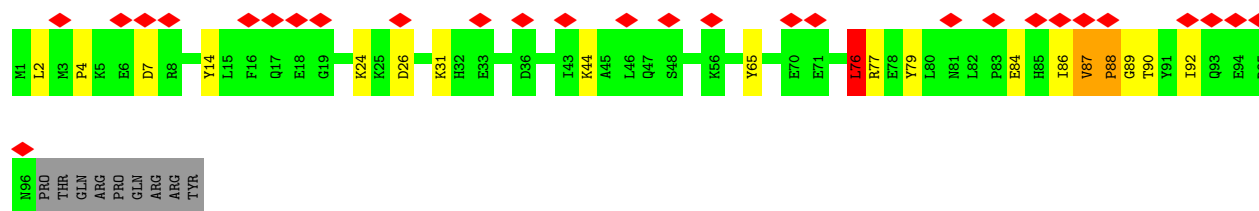
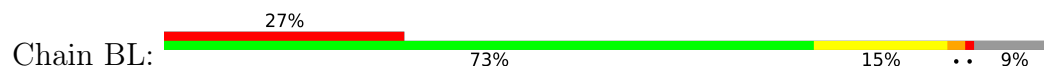
• Molecule 54: 40S ribosomal protein S8-A



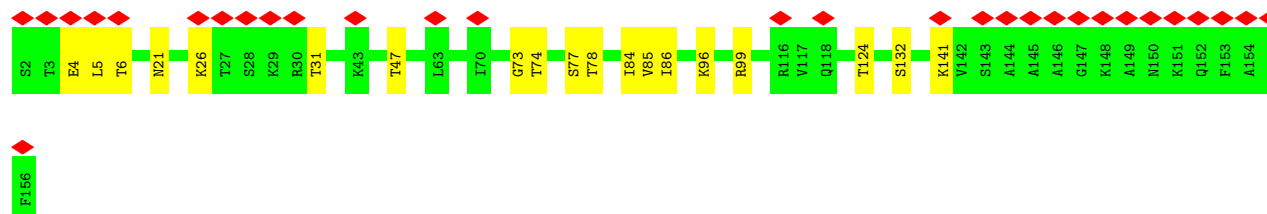
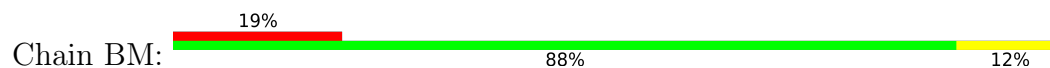
• Molecule 55: 40S ribosomal protein S9-A



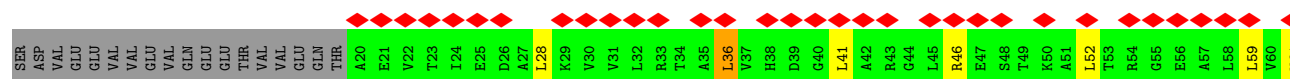
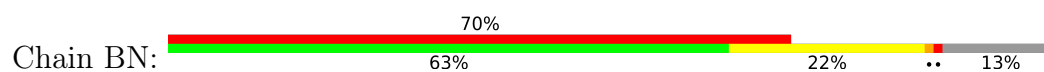
• Molecule 56: 40S ribosomal protein S10-A

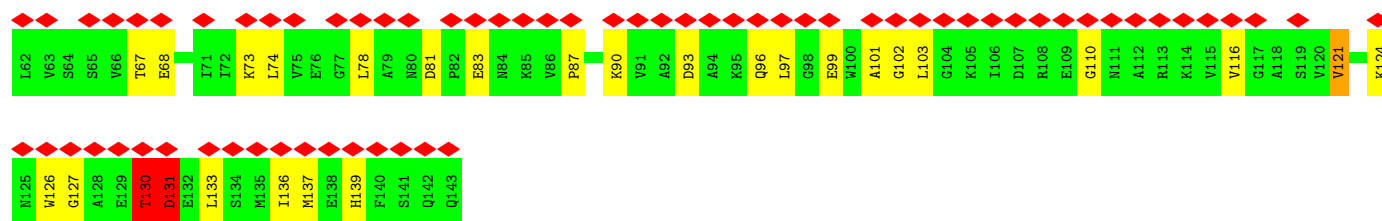


• Molecule 57: 40S ribosomal protein S11-A

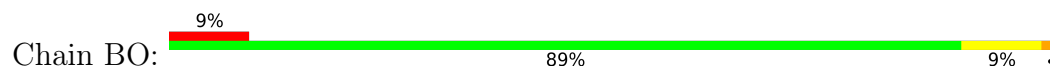


• Molecule 58: 40S ribosomal protein S12

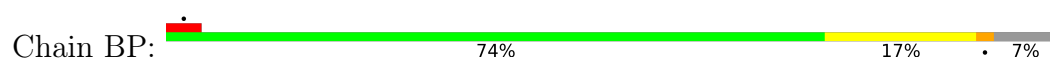




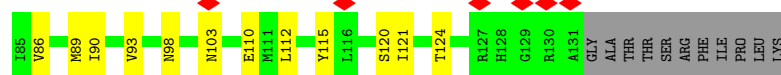
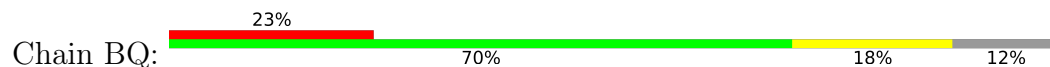
- Molecule 59: 40S ribosomal protein S13



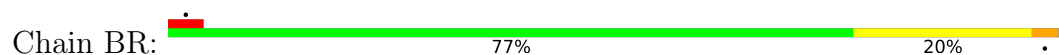
- Molecule 60: 40S ribosomal protein S14-A



- Molecule 61: 40S ribosomal protein S15



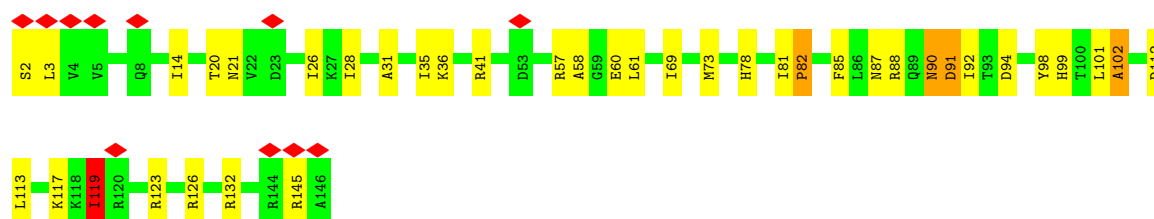
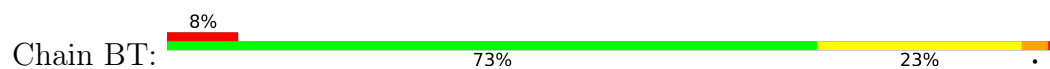
- Molecule 62: 40S ribosomal protein S16-A



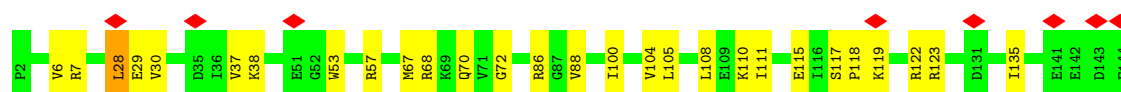
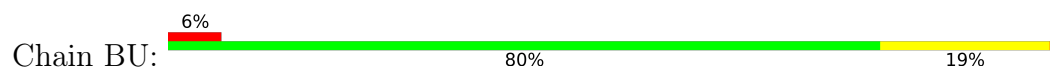
- Molecule 63: 40S ribosomal protein S17-A



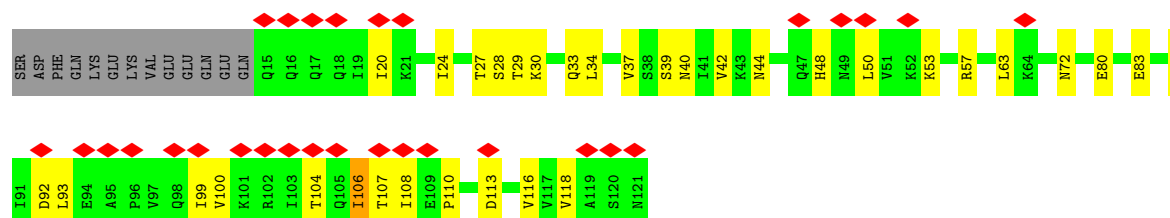
- Molecule 64: 40S ribosomal protein S18-A



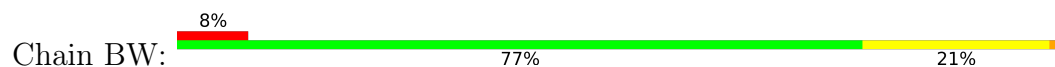
- Molecule 65: 40S ribosomal protein S19-A



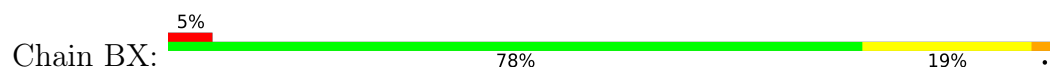
- Molecule 66: 40S ribosomal protein S20



- Molecule 67: 40S ribosomal protein S21-A

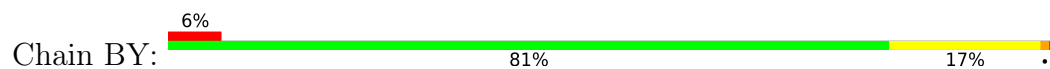


- Molecule 68: 40S ribosomal protein S22-A

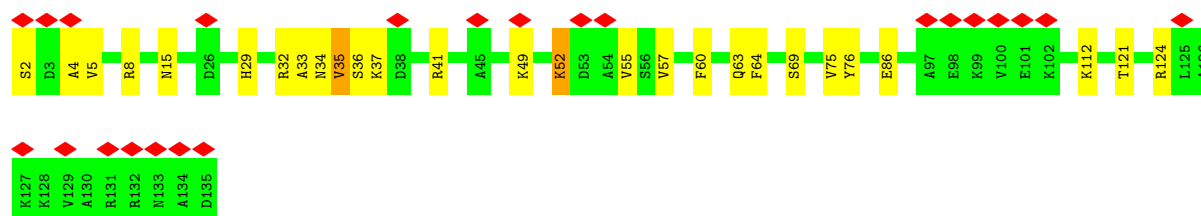
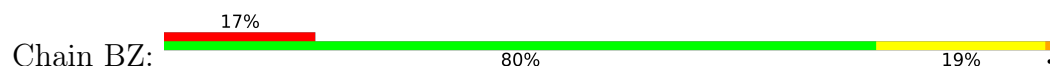




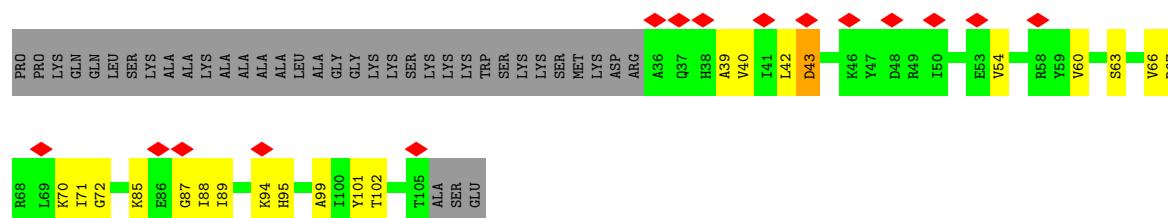
- Molecule 69: 40S ribosomal protein S23-A



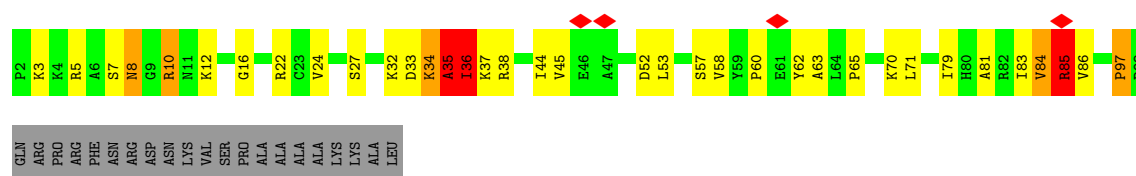
- Molecule 70: 40S ribosomal protein S24-A



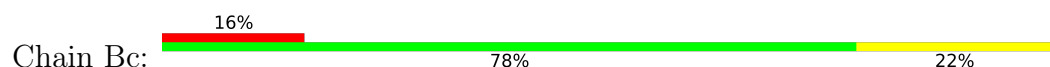
- Molecule 71: 40S ribosomal protein S25-A



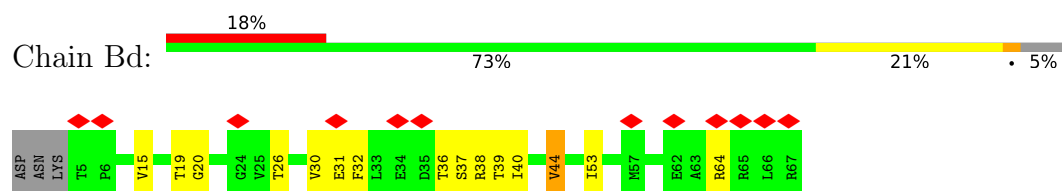
- Molecule 72: 40S ribosomal protein S26-B



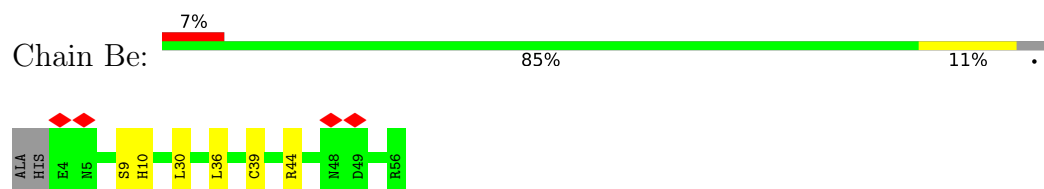
- Molecule 73: 40S ribosomal protein S27-A



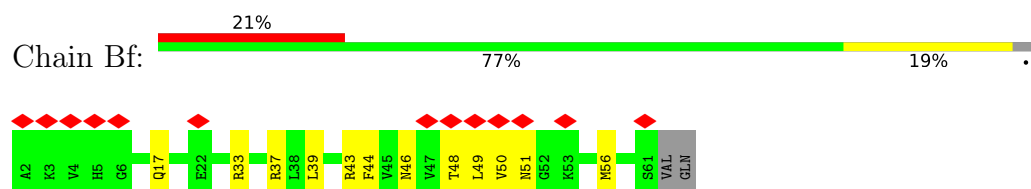
- Molecule 74: 40S ribosomal protein S28-A



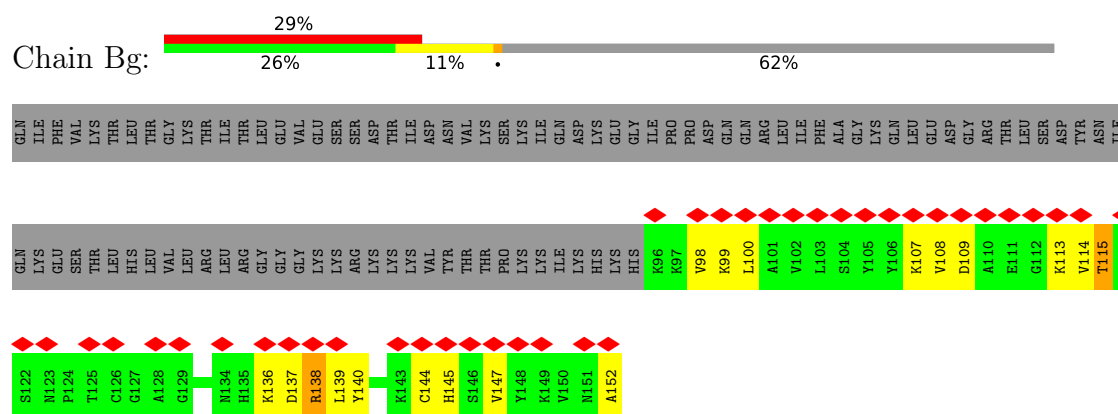
- Molecule 75: 40S ribosomal protein S29-A



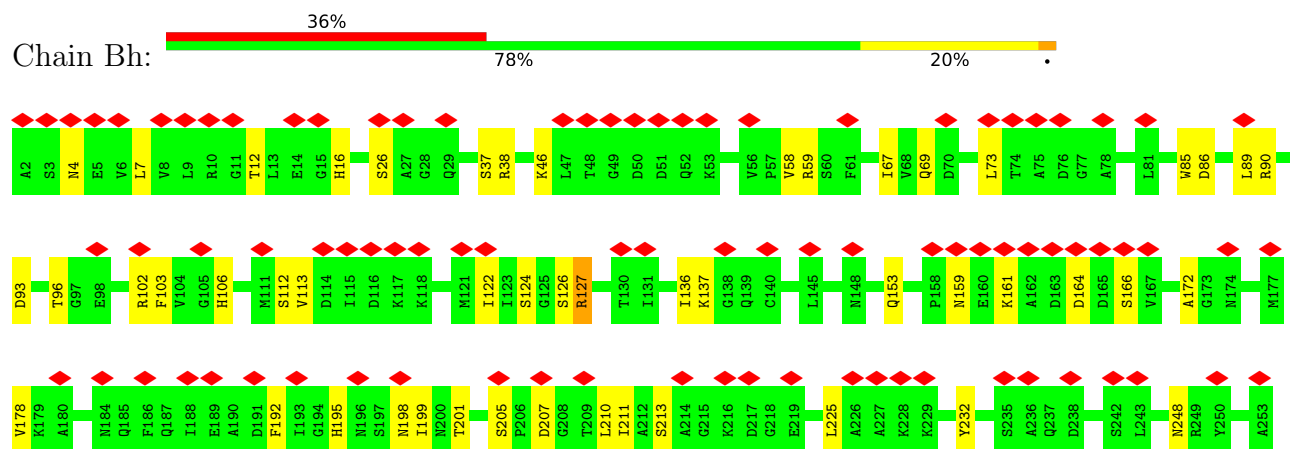
- Molecule 76: 40S ribosomal protein S30-A

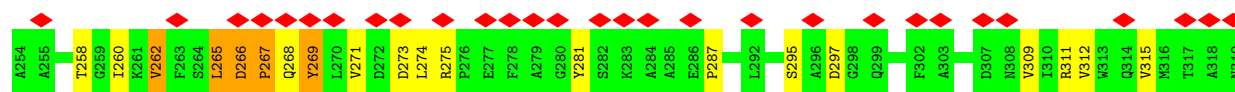


- Molecule 77: Ubiquitin-40S ribosomal protein S31

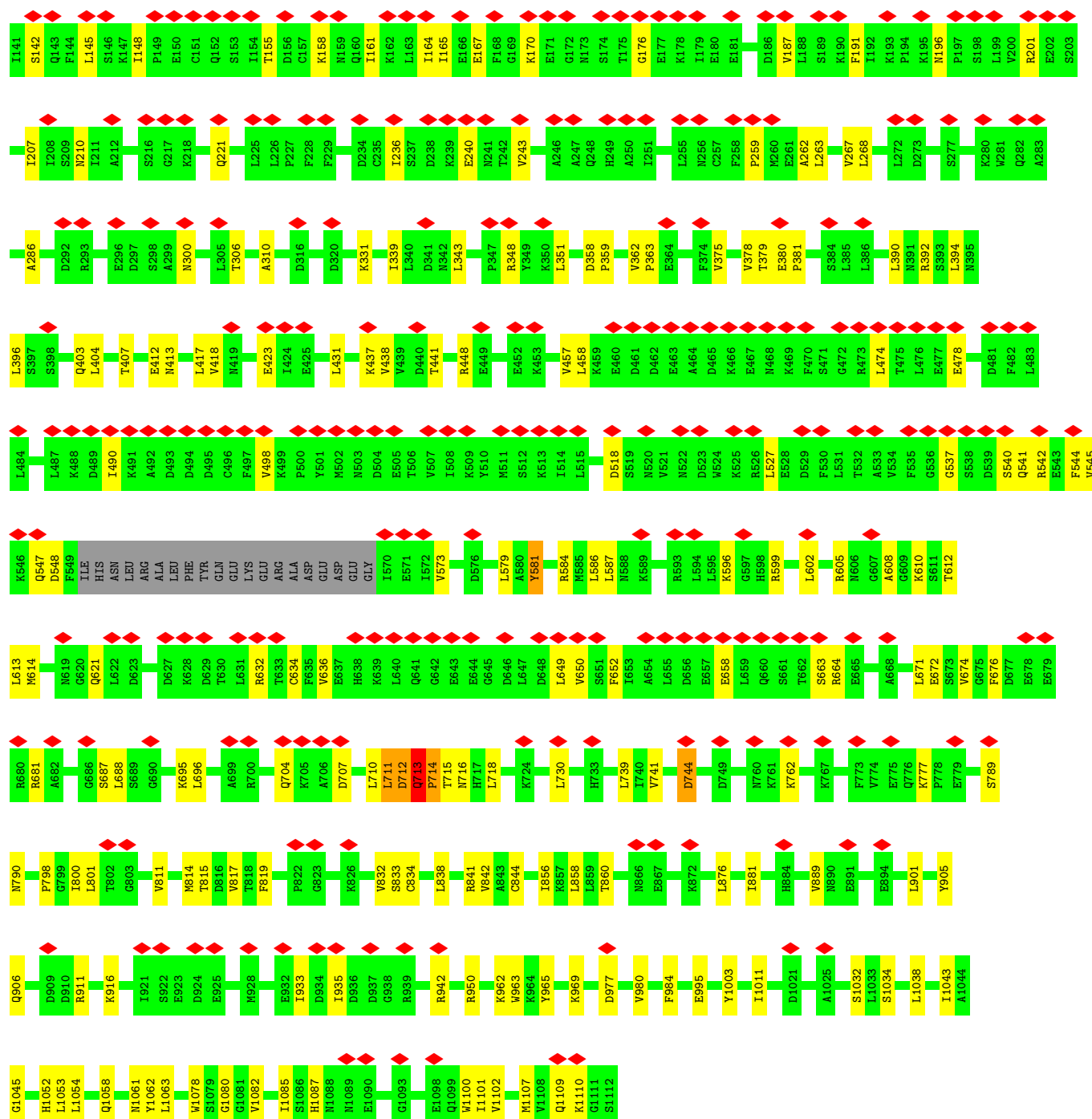
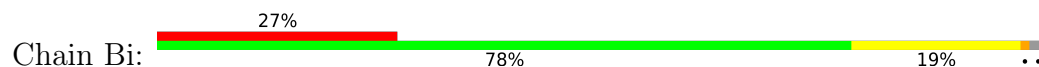


- Molecule 78: Guanine nucleotide-binding protein subunit beta-like protein





• Molecule 79: [NU+] prion formation protein 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	48757	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 ($e^-/\text{\AA}^2$)	45.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.600	Depositor
Minimum map value	-0.343	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	446.46, 446.46, 446.46	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.063, 1.063, 1.063	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP

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	0.42	0/75394	0.45	7/117545 (0.0%)
2	AB	0.40	0/2883	0.39	0/4491
3	AC	0.41	0/3746	0.42	0/5832
4	AD	0.45	0/1948	0.68	0/2617
5	AE	0.52	3/3146 (0.1%)	0.89	8/4228 (0.2%)
6	AF	0.42	0/2800	0.74	3/3790 (0.1%)
7	AG	0.39	0/2425	0.77	4/3271 (0.1%)
8	AH	0.36	0/1260	0.71	4/1694 (0.2%)
9	AI	0.41	0/1821	0.70	0/2451
10	AJ	0.36	0/1836	0.67	0/2481
11	AK	0.37	0/1537	0.63	0/2067
12	AL	0.35	0/1741	0.61	0/2335
13	AM	0.47	2/1374 (0.1%)	0.85	1/1842 (0.1%)
14	AN	0.42	0/1568	0.76	0/2106
15	AO	0.36	0/1068	0.66	0/1438
16	AP	0.44	0/1757	0.68	1/2354 (0.0%)
17	AQ	0.37	0/1585	0.60	0/2128
18	AR	0.40	0/1443	0.74	3/1944 (0.2%)
19	AS	0.39	0/1465	0.62	1/1965 (0.1%)
20	AT	0.36	0/1245	0.61	0/1661
21	AU	0.38	0/1481	0.62	0/1990
22	AV	0.40	0/1300	0.67	0/1743
23	AW	0.33	0/812	0.69	0/1099
24	AX	0.38	0/1018	0.59	0/1369
25	AY	0.37	0/521	0.56	0/691
26	AZ	0.37	0/979	0.60	0/1321
27	Aa	0.37	0/1004	0.60	0/1341
28	Ab	0.36	0/1118	0.70	3/1497 (0.2%)
29	Ac	0.46	0/1204	0.83	3/1612 (0.2%)
30	Ad	0.35	0/473	0.65	0/629
31	Ae	0.40	0/751	0.57	0/1008
32	Af	0.38	0/890	0.64	0/1196

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ag	0.38	0/1041	0.59	0/1394
34	Ah	0.38	0/868	0.54	0/1168
35	Ai	0.41	0/890	0.61	0/1189
36	Aj	0.35	0/978	0.61	0/1301
37	Ak	0.35	0/778	0.71	2/1034 (0.2%)
38	Al	0.42	0/696	0.68	0/923
39	Am	0.33	0/618	0.62	0/826
40	An	0.44	0/443	0.68	0/588
41	Ao	0.36	0/423	0.61	0/562
42	Ap	0.39	0/234	0.67	0/300
43	Aq	0.42	0/860	0.72	0/1136
44	Ar	0.42	0/701	0.66	0/934
45	BA	0.49	0/40685	0.53	14/63392 (0.0%)
46	BB	0.48	0/1617	0.84	2/2215 (0.1%)
47	BC	0.50	0/1735	0.95	0/2335
48	BD	0.54	0/1665	0.73	1/2263 (0.0%)
49	BE	0.58	0/1759	0.80	0/2368
50	BF	0.53	0/2109	0.84	7/2839 (0.2%)
51	BG	0.60	0/1629	0.94	4/2202 (0.2%)
52	BH	0.40	0/1823	0.76	3/2439 (0.1%)
53	BI	0.45	0/1506	0.93	6/2028 (0.3%)
54	BJ	0.52	0/1514	0.82	2/2021 (0.1%)
55	BK	0.48	0/1519	0.78	1/2035 (0.0%)
56	BL	0.62	1/789 (0.1%)	0.90	2/1067 (0.2%)
57	BM	0.50	0/1239	0.74	0/1673
58	BN	0.43	0/898	1.11	5/1220 (0.4%)
59	BO	0.48	0/1215	0.88	5/1638 (0.3%)
60	BP	0.55	0/901	0.97	2/1217 (0.2%)
61	BQ	0.56	0/998	0.87	1/1341 (0.1%)
62	BR	0.63	0/1125	1.23	5/1510 (0.3%)
63	BS	0.49	0/935	0.90	2/1254 (0.2%)
64	BT	0.52	0/1211	0.79	2/1628 (0.1%)
65	BU	0.55	0/1130	0.79	2/1517 (0.1%)
66	BV	0.53	0/865	0.78	2/1169 (0.2%)
67	BW	0.55	0/693	0.85	2/935 (0.2%)
68	BX	0.56	0/1038	0.71	0/1395
69	BY	0.54	0/1139	0.83	0/1518
70	BZ	0.45	0/1087	0.78	0/1449
71	Ba	0.58	0/571	1.12	3/768 (0.4%)
72	Bb	0.54	0/782	0.98	5/1047 (0.5%)
73	Bc	0.51	0/620	0.80	2/838 (0.2%)
74	Bd	0.59	0/499	0.78	0/670
75	Be	0.52	0/452	0.77	0/600

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Bf	0.47	0/483	0.77	0/643
77	Bg	0.40	0/451	1.10	4/603 (0.7%)
78	Bh	0.66	1/2494 (0.0%)	0.81	1/3393 (0.0%)
79	Bi	0.51	10/7649 (0.1%)	0.77	14/10345 (0.1%)
All	All	0.46	17/218948 (0.0%)	0.61	139/320666 (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	AD	0	2
5	AE	0	3
6	AF	0	2
7	AG	0	3
8	AH	0	1
9	AI	0	3
11	AK	0	2
14	AN	0	1
15	AO	0	1
17	AQ	0	1
22	AV	0	1
28	Ab	0	1
35	Ai	0	1
36	Aj	0	2
46	BB	0	4
47	BC	0	2
49	BE	0	1
50	BF	0	2
51	BG	0	10
52	BH	0	3
53	BI	0	1
54	BJ	0	1
55	BK	0	2
56	BL	0	4
57	BM	0	1
58	BN	0	5
60	BP	0	2
62	BR	0	2
63	BS	0	3
64	BT	0	5

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
67	BW	0	2
69	BY	0	3
70	BZ	0	2
71	Ba	0	4
72	Bb	0	9
77	Bg	0	2
79	Bi	0	1
All	All	0	95

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
79	Bi	712	ASP	C-O	-17.79	1.04	1.23
79	Bi	712	ASP	CA-C	14.43	1.69	1.53
79	Bi	712	ASP	N-CA	13.20	1.63	1.46
5	AE	18	PRO	CA-C	12.79	1.70	1.52
79	Bi	711	LEU	C-N	10.50	1.47	1.33

The worst 5 of 139 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	BR	40	GLU	CA-C-N	24.14	143.48	119.82
62	BR	40	GLU	C-N-CA	24.14	143.48	119.82
5	AE	18	PRO	CA-C-O	-22.67	79.33	120.60
79	Bi	711	LEU	CA-C-N	15.39	145.93	122.23
79	Bi	711	LEU	C-N-CA	15.39	145.93	122.23

There are no chirality outliers.

5 of 95 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	AD	143	GLU	Peptide
4	AD	250	GLN	Peptide
5	AE	16	PHE	Mainchain
5	AE	18	PRO	Mainchain,Peptide
6	AF	318	LEU	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	67355	0	33848	402	0
2	AB	2579	0	1304	12	0
3	AC	3353	0	1695	21	0
4	AD	1914	0	1981	61	0
5	AE	3075	0	3142	110	0
6	AF	2748	0	2859	87	0
7	AG	2375	0	2325	30	0
8	AH	1239	0	1326	45	0
9	AI	1784	0	1862	25	0
10	AJ	1804	0	1877	28	0
11	AK	1518	0	1585	18	0
12	AL	1705	0	1736	17	0
13	AM	1353	0	1383	29	0
14	AN	1543	0	1608	30	0
15	AO	1053	0	1149	12	0
16	AP	1720	0	1779	30	0
17	AQ	1555	0	1659	18	0
18	AR	1420	0	1437	16	0
19	AS	1441	0	1543	12	0
20	AT	1228	0	1314	16	0
21	AU	1445	0	1487	29	0
22	AV	1276	0	1323	19	0
23	AW	796	0	812	7	0
24	AX	1003	0	1048	12	0
25	AY	509	0	537	2	0
26	AZ	964	0	1025	9	0
27	Aa	993	0	1081	15	0
28	Ab	1092	0	1155	16	0
29	Ac	1173	0	1215	17	0
30	Ad	462	0	491	2	0
31	Ae	743	0	797	10	0
32	Af	876	0	912	12	0
33	Ag	1020	0	1090	12	0
34	Ah	850	0	880	47	0
35	Ai	880	0	945	14	0
36	Aj	969	0	1078	12	0
37	Ak	771	0	849	12	0
38	Al	681	0	687	25	0
39	Am	612	0	682	6	0
40	An	436	0	475	4	0
41	Ao	417	0	459	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	Ap	233	0	284	5	0
43	Aq	847	0	914	19	0
44	Ar	694	0	738	10	0
45	BA	36375	0	18300	262	0
46	BB	1577	0	1567	28	0
47	BC	1709	0	1784	36	0
48	BD	1635	0	1723	27	0
49	BE	1734	0	1817	21	0
50	BF	2068	0	2154	35	0
51	BG	1609	0	1675	24	0
52	BH	1799	0	1879	32	0
53	BI	1481	0	1572	33	0
54	BJ	1489	0	1525	31	0
55	BK	1494	0	1573	21	0
56	BL	772	0	727	9	0
57	BM	1213	0	1257	11	0
58	BN	890	0	887	19	0
59	BO	1192	0	1254	27	0
60	BP	891	0	883	20	0
61	BQ	977	0	1002	17	0
62	BR	1105	0	1166	23	0
63	BS	926	0	930	17	0
64	BT	1192	0	1222	24	0
65	BU	1112	0	1124	16	0
66	BV	855	0	917	24	0
67	BW	684	0	672	14	0
68	BX	1021	0	1060	45	0
69	BY	1121	0	1196	45	0
70	BZ	1073	0	1132	19	0
71	Ba	563	0	603	10	0
72	Bb	769	0	818	21	0
73	Bc	610	0	633	9	0
74	Bd	497	0	535	12	0
75	Be	442	0	432	4	0
76	Bf	475	0	525	9	0
77	Bg	444	0	463	11	0
78	Bh	2441	0	2397	43	0
79	Bi	7512	0	7546	141	0
80	Bi	62	0	24	10	0
All	All	204313	0	153350	2019	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 2019 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)
59:BO:23:PRO:HG2	59:BO:26:PHE:CB	1.26	1.65
4:AD:186:PHE:HB2	4:AD:196:TRP:CH2	1.15	1.60
4:AD:186:PHE:CD1	4:AD:196:TRP:HZ3	1.21	1.57
5:AE:16:PHE:CE1	5:AE:275:ARG:NH1	1.83	1.47
4:AD:186:PHE:HB2	4:AD:196:TRP:CZ3	1.50	1.44

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AD	250/252 (99%)	233 (93%)	17 (7%)	0	100	100
5	AE	384/386 (100%)	359 (94%)	23 (6%)	2 (0%)	24	55
6	AF	359/361 (99%)	320 (89%)	33 (9%)	6 (2%)	7	30
7	AG	294/296 (99%)	266 (90%)	26 (9%)	2 (1%)	18	48
8	AH	152/175 (87%)	142 (93%)	9 (6%)	1 (1%)	18	48
9	AI	220/243 (90%)	204 (93%)	13 (6%)	3 (1%)	9	34
10	AJ	231/233 (99%)	214 (93%)	17 (7%)	0	100	100
11	AK	186/191 (97%)	173 (93%)	13 (7%)	0	100	100
12	AL	207/220 (94%)	194 (94%)	13 (6%)	0	100	100
13	AM	167/169 (99%)	144 (86%)	21 (13%)	2 (1%)	10	37
14	AN	191/198 (96%)	169 (88%)	19 (10%)	3 (2%)	7	31
15	AO	134/137 (98%)	123 (92%)	11 (8%)	0	100	100
16	AP	201/203 (99%)	188 (94%)	11 (6%)	2 (1%)	12	40
17	AQ	195/198 (98%)	185 (95%)	8 (4%)	2 (1%)	12	40

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	AR	181/183 (99%)	165 (91%)	16 (9%)	0	100	100
19	AS	183/185 (99%)	177 (97%)	6 (3%)	0	100	100
20	AT	150/188 (80%)	145 (97%)	5 (3%)	0	100	100
21	AU	170/172 (99%)	161 (95%)	9 (5%)	0	100	100
22	AV	157/159 (99%)	146 (93%)	10 (6%)	1 (1%)	21	51
23	AW	98/120 (82%)	90 (92%)	8 (8%)	0	100	100
24	AX	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
25	AY	59/155 (38%)	59 (100%)	0	0	100	100
26	AZ	119/141 (84%)	114 (96%)	5 (4%)	0	100	100
27	Aa	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
28	Ab	133/135 (98%)	121 (91%)	11 (8%)	1 (1%)	16	44
29	Ac	146/148 (99%)	129 (88%)	16 (11%)	1 (1%)	18	48
30	Ad	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
31	Ae	95/104 (91%)	93 (98%)	2 (2%)	0	100	100
32	Af	107/112 (96%)	100 (94%)	7 (6%)	0	100	100
33	Ag	125/129 (97%)	122 (98%)	3 (2%)	0	100	100
34	Ah	104/106 (98%)	94 (90%)	9 (9%)	1 (1%)	12	40
35	Ai	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
36	Aj	117/119 (98%)	110 (94%)	7 (6%)	0	100	100
37	Ak	97/99 (98%)	88 (91%)	7 (7%)	2 (2%)	5	26
38	Al	85/87 (98%)	74 (87%)	9 (11%)	2 (2%)	4	24
39	Am	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
40	An	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
41	Ao	50/127 (39%)	48 (96%)	2 (4%)	0	100	100
42	Ap	23/25 (92%)	23 (100%)	0	0	100	100
43	Aq	103/105 (98%)	98 (95%)	5 (5%)	0	100	100
44	Ar	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
46	BB	204/251 (81%)	171 (84%)	31 (15%)	2 (1%)	12	40
47	BC	212/254 (84%)	180 (85%)	32 (15%)	0	100	100
48	BD	215/253 (85%)	196 (91%)	18 (8%)	1 (0%)	24	55
49	BE	221/239 (92%)	207 (94%)	14 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	BF	258/260 (99%)	229 (89%)	28 (11%)	1 (0%)	30	60
51	BG	204/224 (91%)	178 (87%)	22 (11%)	4 (2%)	6	27
52	BH	224/236 (95%)	207 (92%)	13 (6%)	4 (2%)	6	30
53	BI	182/189 (96%)	157 (86%)	18 (10%)	7 (4%)	2	16
54	BJ	184/199 (92%)	157 (85%)	26 (14%)	1 (0%)	24	55
55	BK	183/196 (93%)	156 (85%)	24 (13%)	3 (2%)	7	31
56	BL	94/105 (90%)	76 (81%)	16 (17%)	2 (2%)	5	26
57	BM	153/155 (99%)	140 (92%)	12 (8%)	1 (1%)	18	48
58	BN	122/142 (86%)	90 (74%)	29 (24%)	3 (2%)	4	23
59	BO	148/150 (99%)	138 (93%)	8 (5%)	2 (1%)	9	34
60	BP	125/136 (92%)	109 (87%)	16 (13%)	0	100	100
61	BQ	122/141 (86%)	104 (85%)	17 (14%)	1 (1%)	16	44
62	BR	139/142 (98%)	124 (89%)	14 (10%)	1 (1%)	18	48
63	BS	116/135 (86%)	103 (89%)	9 (8%)	4 (3%)	3	18
64	BT	143/145 (99%)	123 (86%)	16 (11%)	4 (3%)	4	21
65	BU	141/143 (99%)	131 (93%)	9 (6%)	1 (1%)	18	48
66	BV	105/120 (88%)	92 (88%)	13 (12%)	0	100	100
67	BW	85/87 (98%)	71 (84%)	11 (13%)	3 (4%)	3	17
68	BX	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
69	BY	142/144 (99%)	120 (84%)	20 (14%)	2 (1%)	9	34
70	BZ	132/134 (98%)	117 (89%)	12 (9%)	3 (2%)	5	25
71	Ba	68/107 (64%)	56 (82%)	12 (18%)	0	100	100
72	Bb	95/118 (80%)	77 (81%)	12 (13%)	6 (6%)	1	7
73	Bc	79/81 (98%)	67 (85%)	12 (15%)	0	100	100
74	Bd	61/66 (92%)	54 (88%)	7 (12%)	0	100	100
75	Be	51/55 (93%)	48 (94%)	3 (6%)	0	100	100
76	Bf	58/62 (94%)	48 (83%)	10 (17%)	0	100	100
77	Bg	55/151 (36%)	38 (69%)	15 (27%)	2 (4%)	2	17
78	Bh	316/318 (99%)	288 (91%)	27 (8%)	1 (0%)	36	66
79	Bi	948/972 (98%)	857 (90%)	90 (10%)	1 (0%)	48	76
All	All	11821/12759 (93%)	10708 (91%)	1022 (9%)	91 (1%)	18	44

5 of 91 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	AE	19	ARG
6	AF	152	VAL
6	AF	339	LEU
14	AN	63	VAL
17	AQ	111	PRO

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	AD	193/194 (100%)	190 (98%)	3 (2%)	55	72
5	AE	319/322 (99%)	309 (97%)	10 (3%)	35	61
6	AF	288/288 (100%)	283 (98%)	5 (2%)	53	71
7	AG	244/244 (100%)	242 (99%)	2 (1%)	73	79
8	AH	134/152 (88%)	133 (99%)	1 (1%)	76	80
9	AI	186/204 (91%)	183 (98%)	3 (2%)	55	72
10	AJ	187/191 (98%)	184 (98%)	3 (2%)	55	72
11	AK	171/171 (100%)	168 (98%)	3 (2%)	51	70
12	AL	177/186 (95%)	177 (100%)	0	100	100
13	AM	147/147 (100%)	145 (99%)	2 (1%)	59	74
14	AN	154/158 (98%)	153 (99%)	1 (1%)	78	82
15	AO	107/108 (99%)	103 (96%)	4 (4%)	30	57
16	AP	175/175 (100%)	175 (100%)	0	100	100
17	AQ	160/161 (99%)	159 (99%)	1 (1%)	78	82
18	AR	140/145 (97%)	137 (98%)	3 (2%)	47	67
19	AS	150/150 (100%)	148 (99%)	2 (1%)	61	75
20	AT	126/153 (82%)	126 (100%)	0	100	100
21	AU	156/156 (100%)	155 (99%)	1 (1%)	78	82
22	AV	136/136 (100%)	133 (98%)	3 (2%)	45	66

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	AW	87/106 (82%)	87 (100%)	0	100	100
24	AX	104/104 (100%)	104 (100%)	0	100	100
25	AY	54/129 (42%)	53 (98%)	1 (2%)	50	69
26	AZ	104/117 (89%)	104 (100%)	0	100	100
27	Aa	109/109 (100%)	108 (99%)	1 (1%)	70	78
28	Ab	115/115 (100%)	114 (99%)	1 (1%)	70	78
29	Ac	118/118 (100%)	117 (99%)	1 (1%)	73	79
30	Ad	46/46 (100%)	46 (100%)	0	100	100
31	Ae	81/87 (93%)	80 (99%)	1 (1%)	63	75
32	Af	92/96 (96%)	91 (99%)	1 (1%)	65	76
33	Ag	109/110 (99%)	109 (100%)	0	100	100
34	Ah	90/90 (100%)	86 (96%)	4 (4%)	25	54
35	Ai	95/103 (92%)	95 (100%)	0	100	100
36	Aj	104/104 (100%)	104 (100%)	0	100	100
37	Ak	81/81 (100%)	81 (100%)	0	100	100
38	Al	70/70 (100%)	69 (99%)	1 (1%)	59	74
39	Am	68/68 (100%)	68 (100%)	0	100	100
40	An	45/45 (100%)	45 (100%)	0	100	100
41	Ao	47/115 (41%)	47 (100%)	0	100	100
42	Ap	23/23 (100%)	23 (100%)	0	100	100
43	Aq	90/90 (100%)	90 (100%)	0	100	100
44	Ar	71/71 (100%)	71 (100%)	0	100	100
46	BB	164/209 (78%)	161 (98%)	3 (2%)	51	70
47	BC	191/223 (86%)	187 (98%)	4 (2%)	47	67
48	BD	176/204 (86%)	174 (99%)	2 (1%)	65	76
49	BE	182/194 (94%)	177 (97%)	5 (3%)	39	63
50	BF	221/221 (100%)	216 (98%)	5 (2%)	44	66
51	BG	173/190 (91%)	167 (96%)	6 (4%)	32	58
52	BH	188/201 (94%)	187 (100%)	1 (0%)	81	83
53	BI	165/169 (98%)	164 (99%)	1 (1%)	78	82
54	BJ	150/160 (94%)	149 (99%)	1 (1%)	76	80

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	BK	158/165 (96%)	158 (100%)	0	100	100
56	BL	77/98 (79%)	76 (99%)	1 (1%)	61	75
57	BM	129/136 (95%)	127 (98%)	2 (2%)	55	72
58	BN	88/118 (75%)	86 (98%)	2 (2%)	44	66
59	BO	127/127 (100%)	127 (100%)	0	100	100
60	BP	81/104 (78%)	77 (95%)	4 (5%)	22	51
61	BQ	101/117 (86%)	101 (100%)	0	100	100
62	BR	117/118 (99%)	115 (98%)	2 (2%)	53	71
63	BS	94/123 (76%)	93 (99%)	1 (1%)	65	76
64	BT	128/128 (100%)	126 (98%)	2 (2%)	55	72
65	BU	115/115 (100%)	112 (97%)	3 (3%)	40	64
66	BV	100/113 (88%)	99 (99%)	1 (1%)	68	77
67	BW	74/74 (100%)	73 (99%)	1 (1%)	59	74
68	BX	110/110 (100%)	105 (96%)	5 (4%)	24	53
69	BY	119/119 (100%)	115 (97%)	4 (3%)	32	59
70	BZ	112/112 (100%)	112 (100%)	0	100	100
71	Ba	61/88 (69%)	59 (97%)	2 (3%)	33	59
72	Bb	83/99 (84%)	81 (98%)	2 (2%)	43	65
73	Bc	70/70 (100%)	69 (99%)	1 (1%)	59	74
74	Bd	56/59 (95%)	54 (96%)	2 (4%)	31	58
75	Be	47/48 (98%)	46 (98%)	1 (2%)	47	67
76	Bf	51/53 (96%)	49 (96%)	2 (4%)	28	56
77	Bg	48/134 (36%)	47 (98%)	1 (2%)	47	67
78	Bh	260/261 (100%)	252 (97%)	8 (3%)	35	61
79	Bi	840/857 (98%)	830 (99%)	10 (1%)	63	75
All	All	10009/10755 (93%)	9866 (99%)	143 (1%)	57	74

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
71	Ba	102	THR
74	Bd	15	VAL
78	Bh	266	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	Aa	59	VAL
25	AY	19	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 165 such sidechains are listed below:

Mol	Chain	Res	Type
61	BQ	103	ASN
79	Bi	210	ASN
63	BS	62	GLN
69	BY	65	ASN
79	Bi	522	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	3145/3149 (99%)	649 (20%)	42 (1%)
2	AB	120/121 (99%)	16 (13%)	0
3	AC	157/158 (99%)	31 (19%)	1 (0%)
45	BA	1703/1707 (99%)	437 (25%)	37 (2%)
All	All	5125/5135 (99%)	1133 (22%)	80 (1%)

5 of 1133 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	A
1	AA	18	G
1	AA	26	A
1	AA	40	A
1	AA	43	A

5 of 80 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	BA	512	A
45	BA	1250	U
45	BA	558	U
45	BA	855	A
45	BA	1568	C

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](#)

2 ligands 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	$\# Z > 2$
80	ATP	Bi	1201	-	32,33,33	1.37	5 (15%)	48,52,52	1.72	9 (18%)
80	ATP	Bi	1202	-	32,33,33	1.44	6 (18%)	48,52,52	1.75	9 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
80	ATP	Bi	1201	-	-	2/22/38/38	0/3/3/3
80	ATP	Bi	1202	-	-	3/22/38/38	0/3/3/3

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
80	Bi	1202	ATP	C5-C4	4.64	1.47	1.39
80	Bi	1201	ATP	C5-C4	4.60	1.47	1.39
80	Bi	1202	ATP	C5-C6	2.71	1.48	1.41
80	Bi	1201	ATP	C5-C6	2.61	1.48	1.41
80	Bi	1202	ATP	PA-O3A	2.38	1.62	1.59

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	Bi	1202	ATP	C5-C4-N3	-5.78	118.76	126.72
80	Bi	1201	ATP	C5-C4-N3	-5.59	119.03	126.72
80	Bi	1202	ATP	N3-C4-N9	4.57	134.94	127.17
80	Bi	1201	ATP	N3-C4-N9	4.51	134.84	127.17
80	Bi	1202	ATP	C2-N3-C4	3.69	120.83	111.83

There are no chirality outliers.

All (5) torsion outliers are listed below:

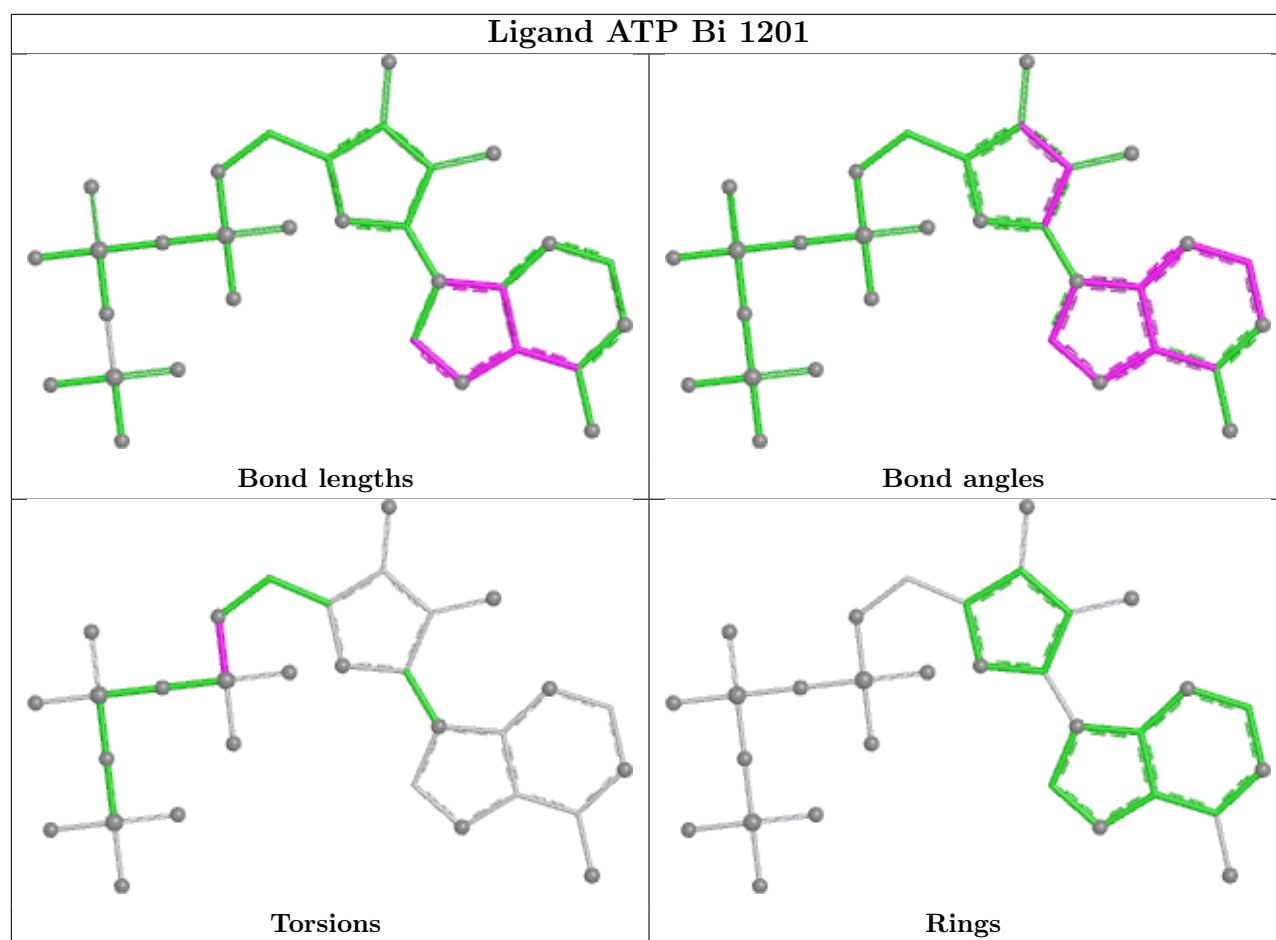
Mol	Chain	Res	Type	Atoms
80	Bi	1201	ATP	C5'-O5'-PA-O3A
80	Bi	1202	ATP	PB-O3A-PA-O5'
80	Bi	1201	ATP	C5'-O5'-PA-O1A
80	Bi	1202	ATP	C3'-C4'-C5'-O5'
80	Bi	1202	ATP	O4'-C4'-C5'-O5'

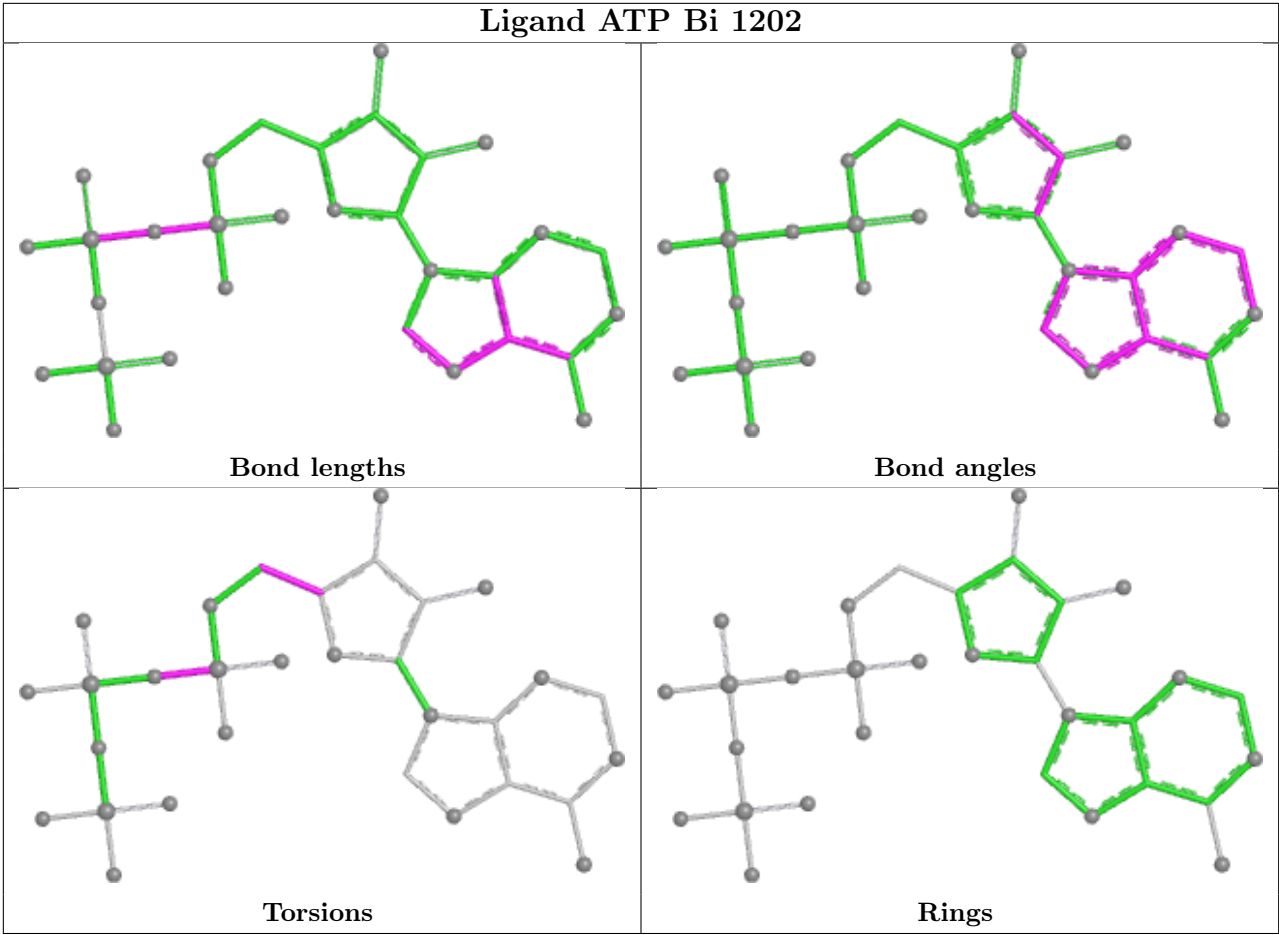
There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
80	Bi	1201	ATP	1	0
80	Bi	1202	ATP	9	0

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





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	3
45	BA	3
11	AK	2

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	1955:U	O3'	2093:A	P	24.80
1	BA	652:G	O3'	682:C	P	17.82
1	BA	703:G	O3'	735:C	P	16.09

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BA	1685:G	O3'	1717:G	P	15.70
1	AA	2445:A	O3'	2501:U	P	15.05

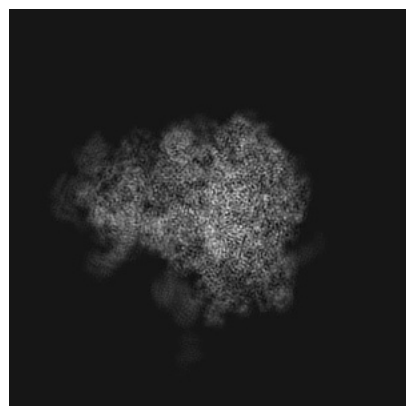
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10098. These allow visual inspection of the internal detail of the map and identification of artifacts.

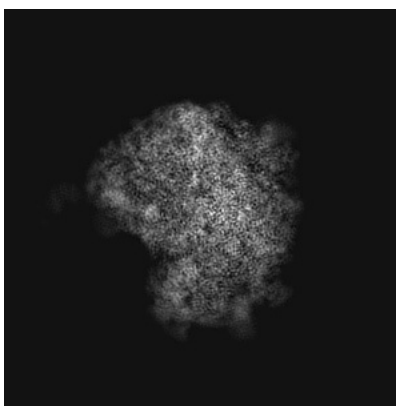
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

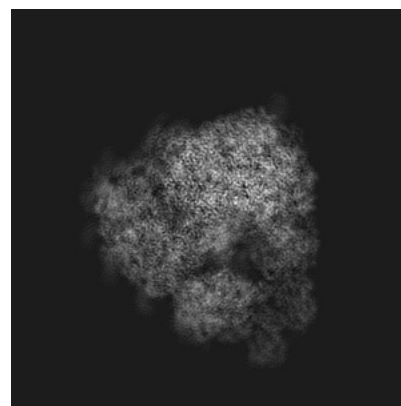
6.1.1 Primary map



X

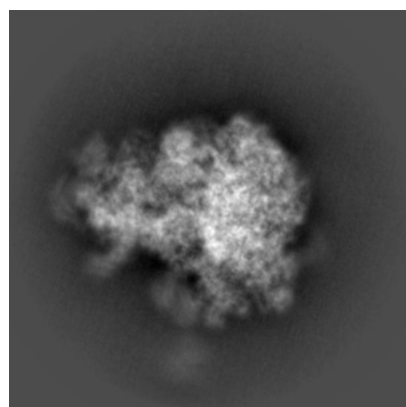


Y

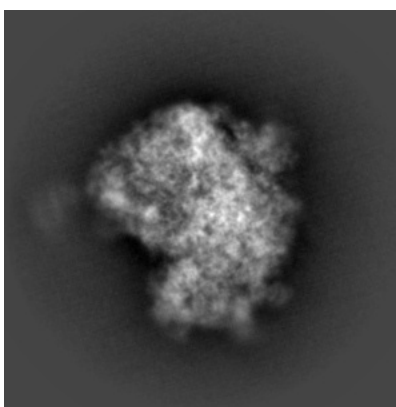


Z

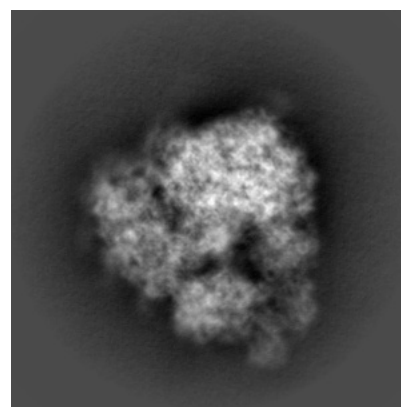
6.1.2 Raw map



X



Y

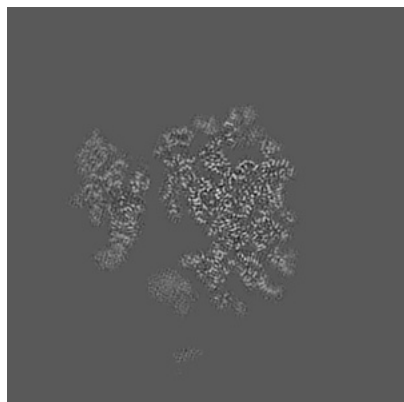


Z

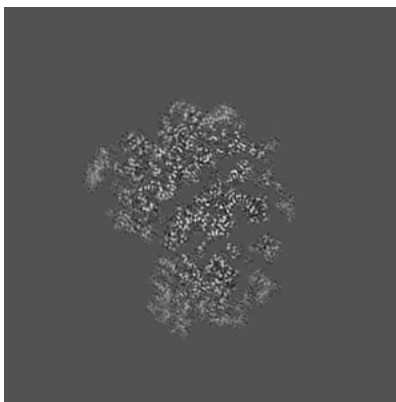
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

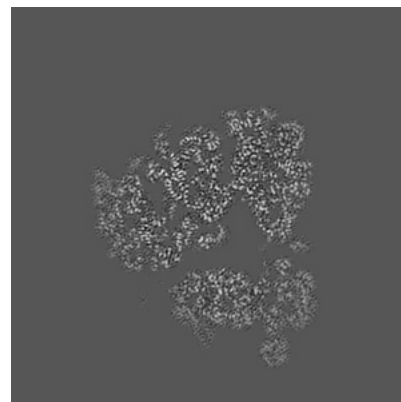
6.2.1 Primary map



X Index: 210

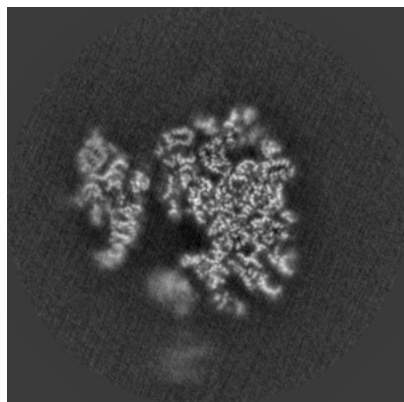


Y Index: 210

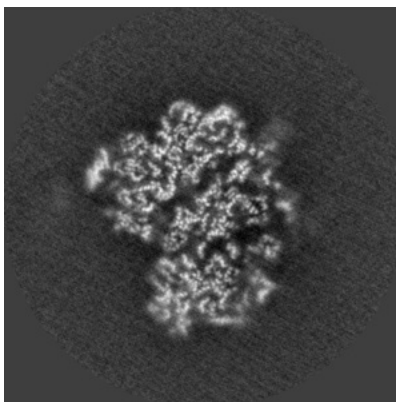


Z Index: 210

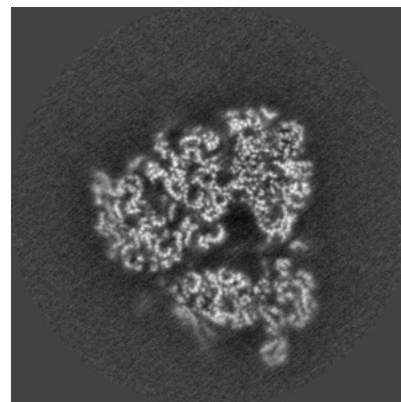
6.2.2 Raw map



X Index: 210



Y Index: 210

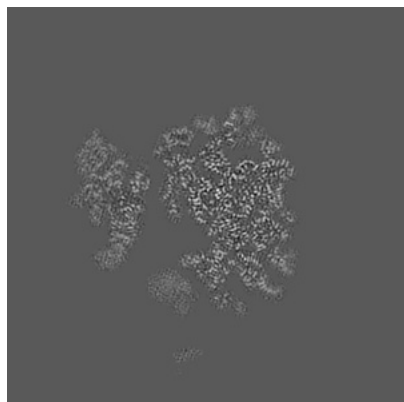


Z Index: 210

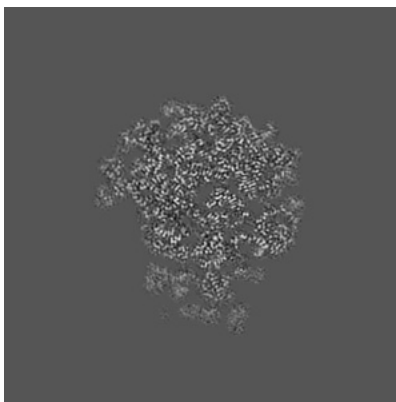
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

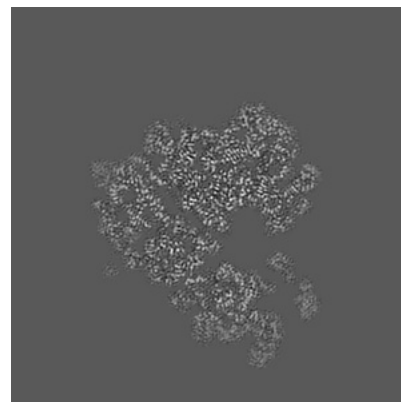
6.3.1 Primary map



X Index: 210

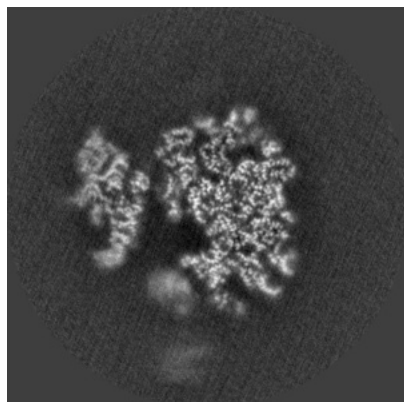


Y Index: 240

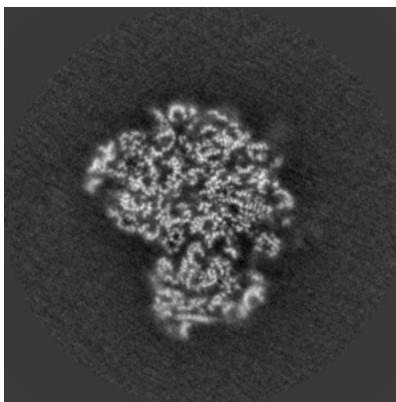


Z Index: 222

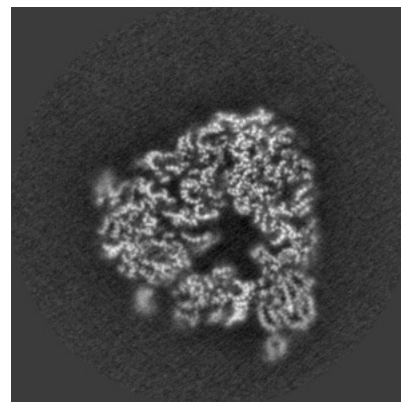
6.3.2 Raw map



X Index: 209



Y Index: 216

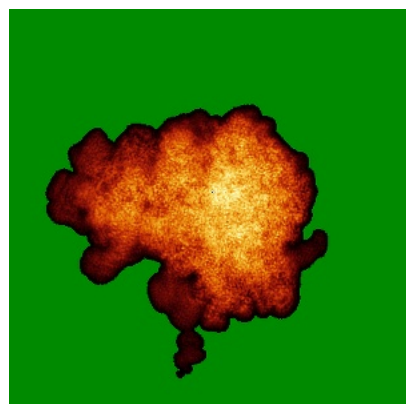


Z Index: 200

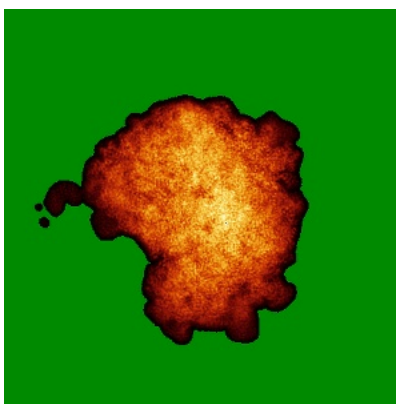
The images above show the largest variance slices of the map in three orthogonal directions.

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

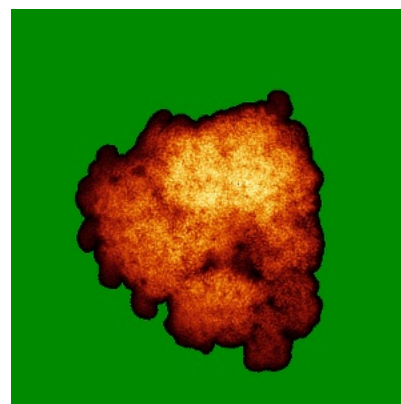
6.4.1 Primary map



X

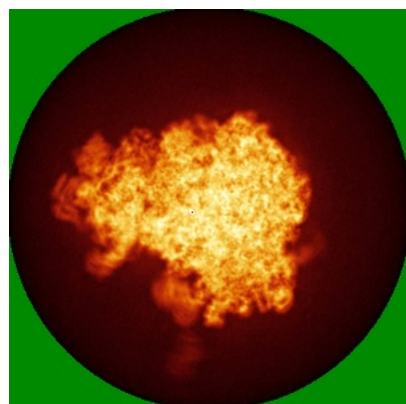


Y

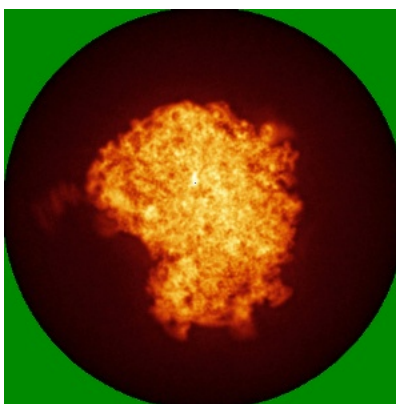


Z

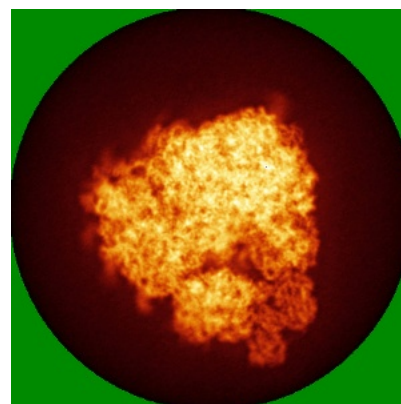
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

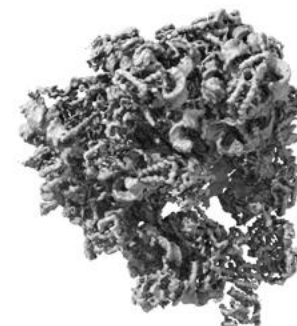
6.5.2 Raw map



X



Y



Z

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.

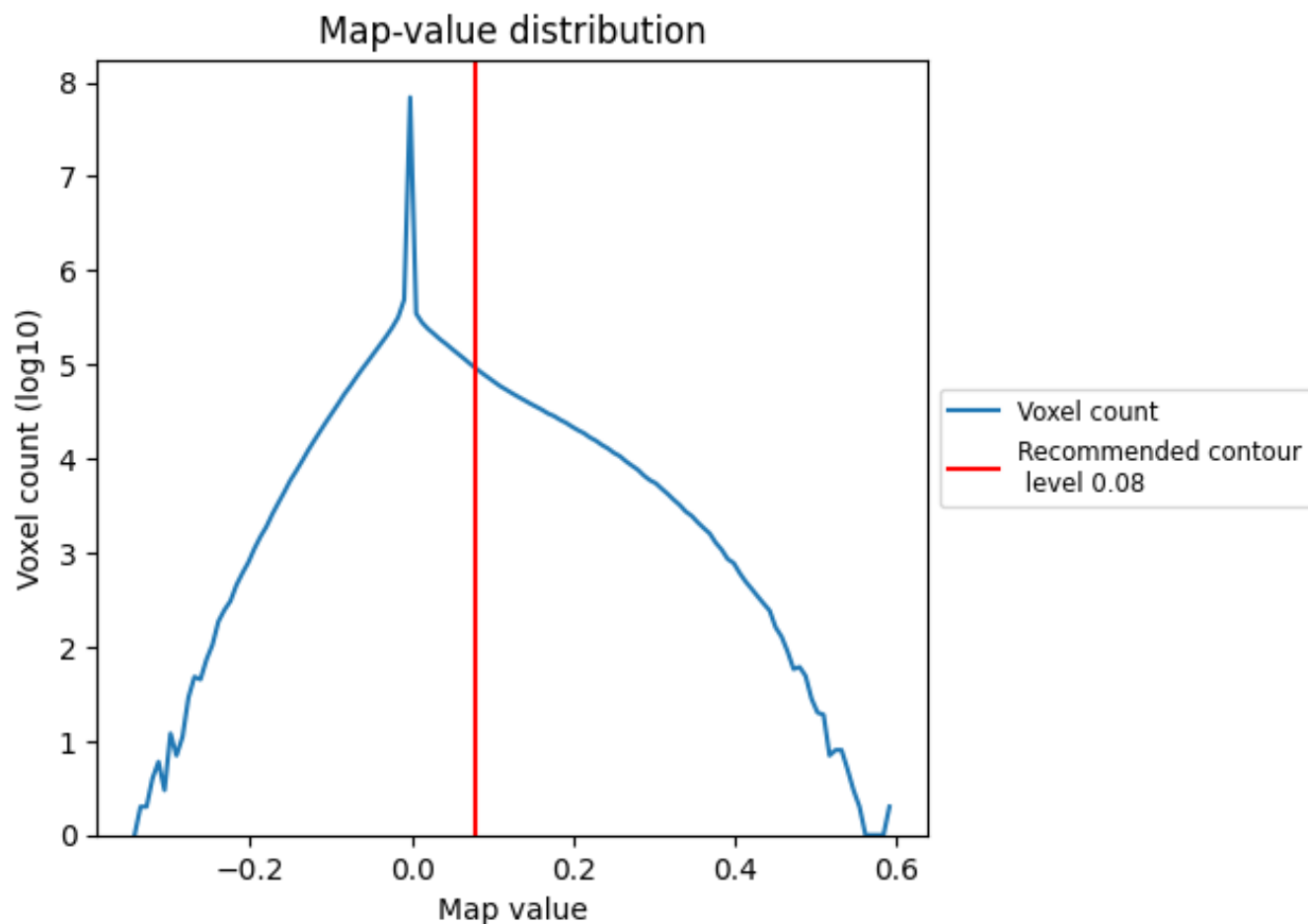
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

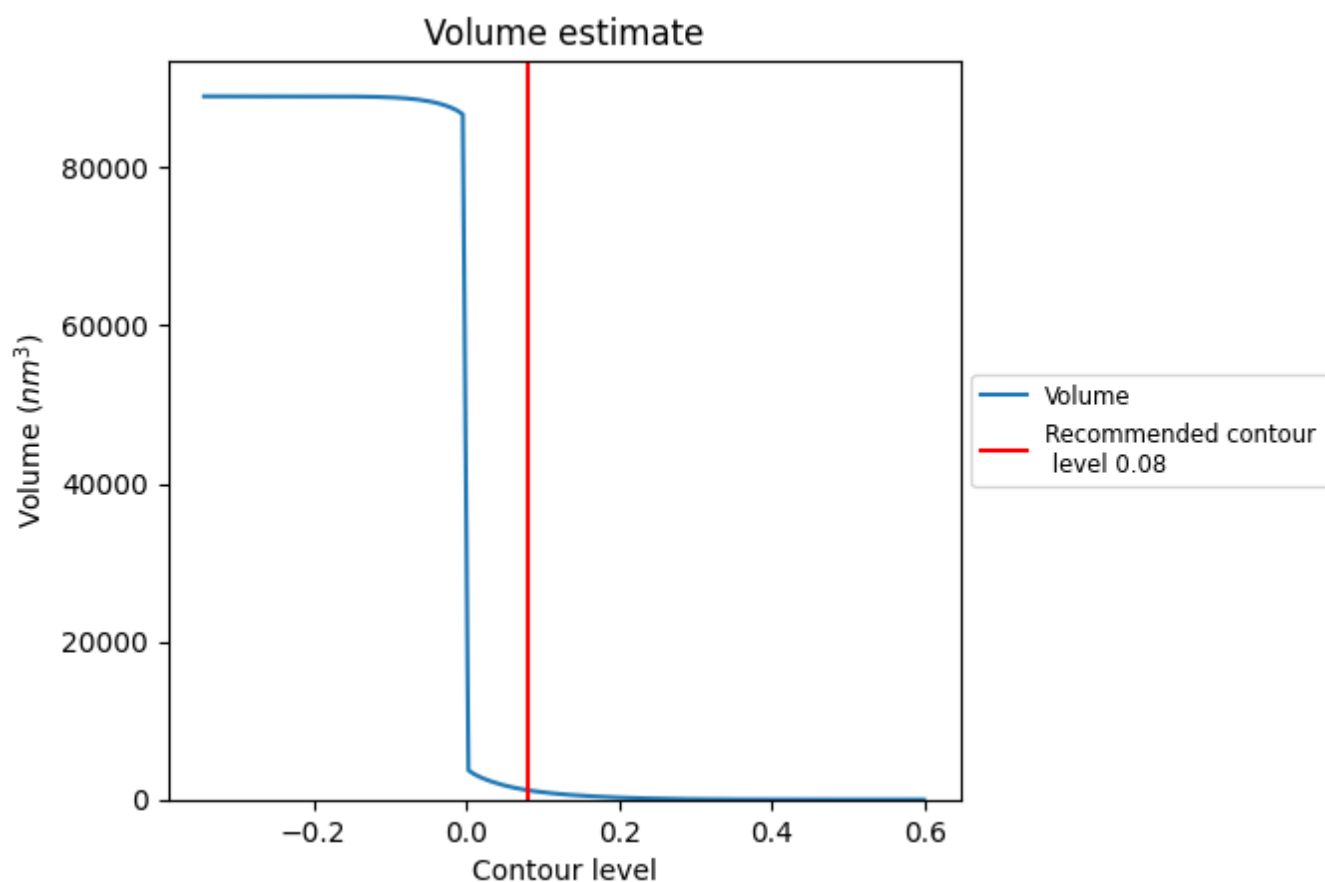
This section contains the results of statistical analysis of the map.

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.

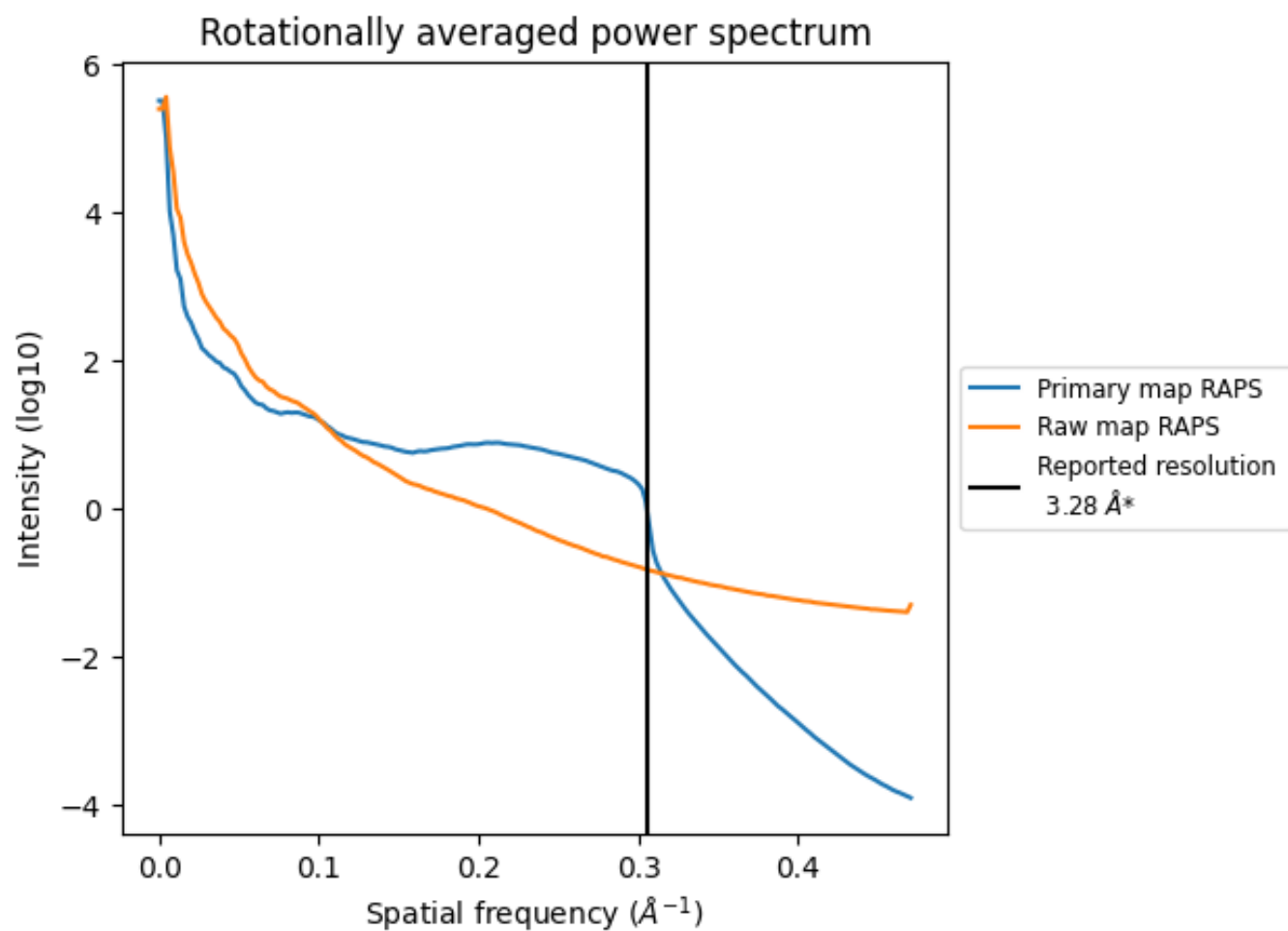
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1193 nm³; this corresponds to an approximate mass of 1078 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 ⓘ

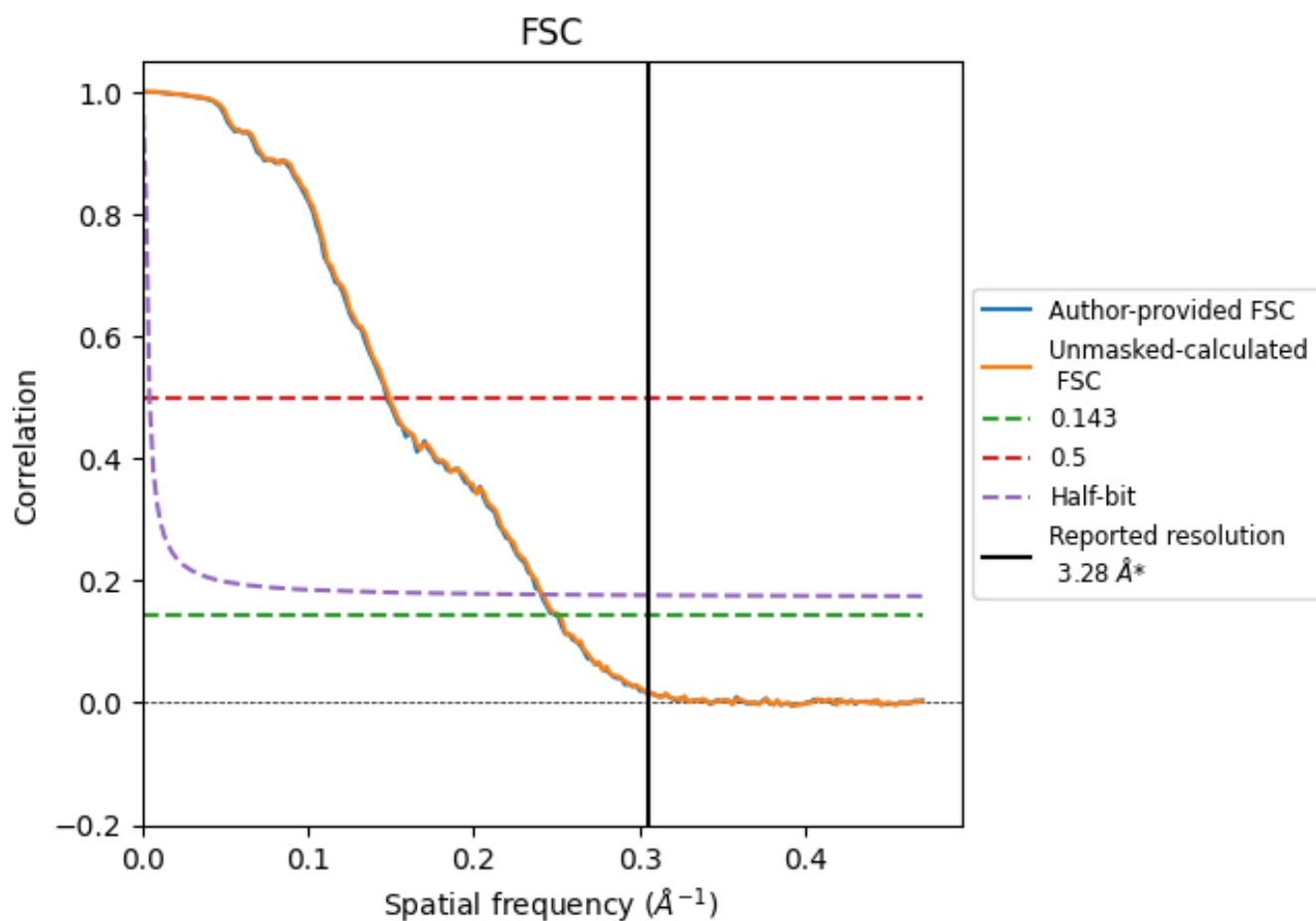


*Reported resolution corresponds to spatial frequency of $0.305 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.305 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.28	-	-
Author-provided FSC curve	4.00	6.78	4.15
Unmasked-calculated*	3.98	6.71	4.14

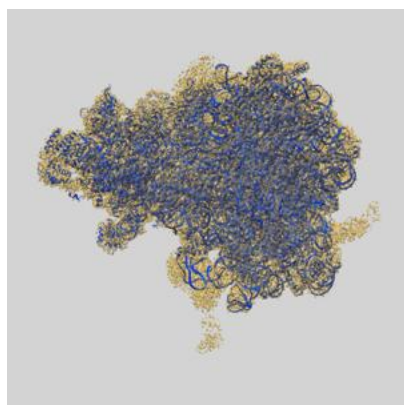
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.00 differs from the reported value 3.28 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.98 differs from the reported value 3.28 by more than 10 %

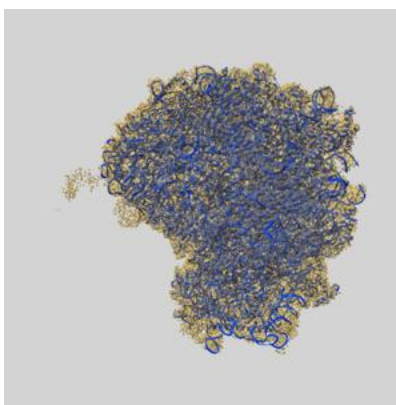
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10098 and PDB model 6S47. Per-residue inclusion information can be found in section [3](#) on page [20](#).

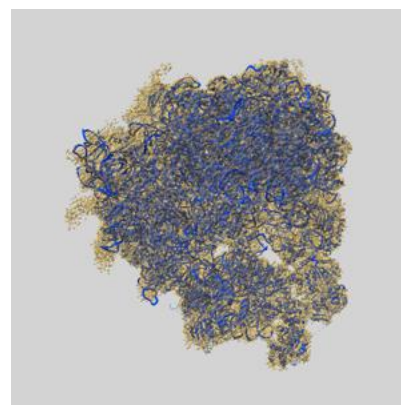
9.1 Map-model overlay [i](#)



X



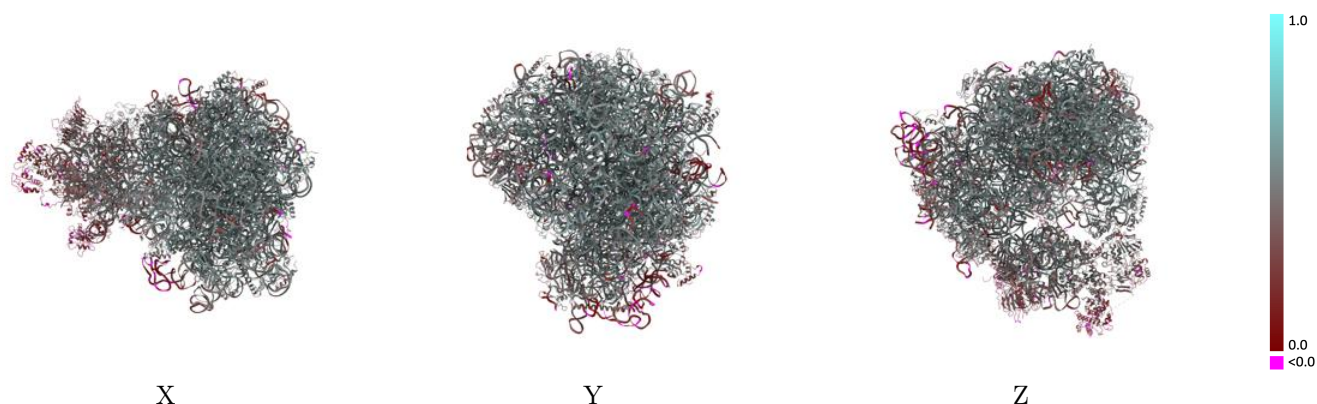
Y



Z

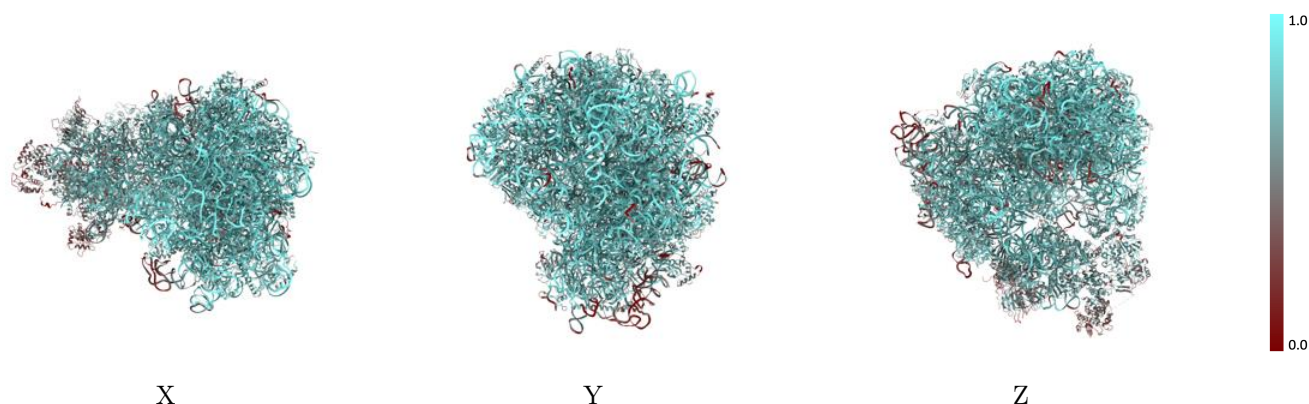
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



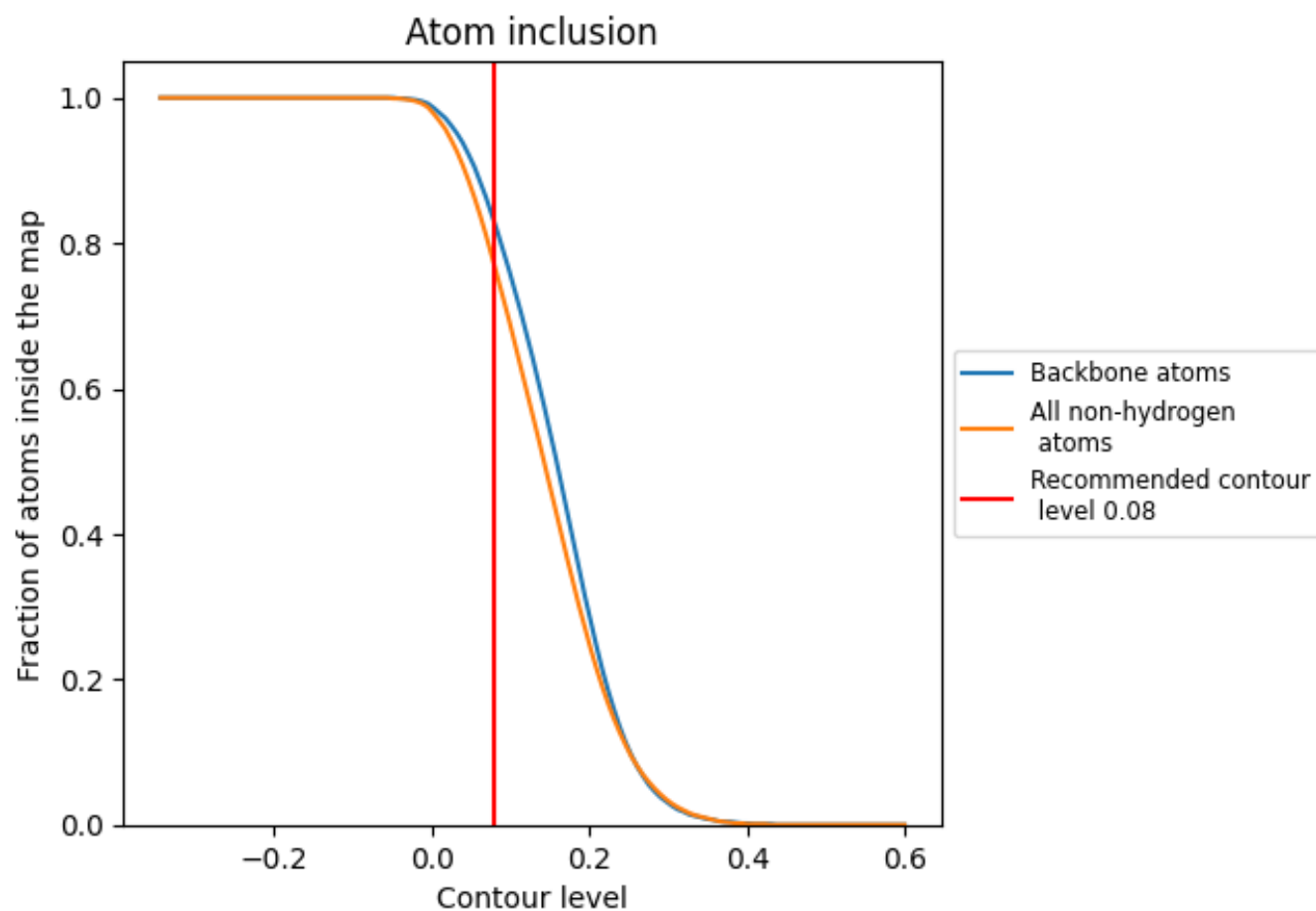
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion ⓘ



At the recommended contour level, 83% of all backbone atoms, 77% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7690	 0.4720
AA	 0.8610	 0.5000
AB	 0.9050	 0.5110
AC	 0.8880	 0.5190
AD	 0.7740	 0.5370
AE	 0.7640	 0.5160
AF	 0.7650	 0.5130
AG	 0.7260	 0.4730
AH	 0.6940	 0.4770
AI	 0.7420	 0.5110
AJ	 0.6990	 0.4720
AK	 0.6970	 0.4690
AL	 0.7310	 0.5030
AM	 0.6910	 0.4680
AN	 0.7360	 0.5100
AO	 0.7370	 0.4910
AP	 0.7900	 0.5500
AQ	 0.7540	 0.5100
AR	 0.7400	 0.5050
AS	 0.7390	 0.5270
AT	 0.7780	 0.5280
AU	 0.7460	 0.5130
AV	 0.7460	 0.5160
AW	 0.6830	 0.4400
AX	 0.7300	 0.5130
AY	 0.7650	 0.5180
AZ	 0.7470	 0.5130
Aa	 0.7590	 0.5160
Ab	 0.7560	 0.4940
Ac	 0.7810	 0.5340
Ad	 0.6900	 0.4940
Ae	 0.7210	 0.4940
Af	 0.7190	 0.4950
Ag	 0.7150	 0.5300
Ah	 0.7700	 0.5280



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Ai	 0.7320	 0.5170
Aj	 0.7550	 0.5150
Ak	 0.7170	 0.4850
Al	 0.7980	 0.5390
Am	 0.6660	 0.4390
An	 0.7450	 0.5330
Ao	 0.7300	 0.4800
Ap	 0.4950	 0.4850
Aq	 0.7070	 0.5040
Ar	 0.7130	 0.5240
BA	 0.8040	 0.4520
BB	 0.7110	 0.4680
BC	 0.6920	 0.4680
BD	 0.7300	 0.4980
BE	 0.5510	 0.3770
BF	 0.7010	 0.4750
BG	 0.6230	 0.4210
BH	 0.5950	 0.3870
BI	 0.5980	 0.3940
BJ	 0.6890	 0.4720
BK	 0.6680	 0.4420
BL	 0.5130	 0.3060
BM	 0.6740	 0.4720
BN	 0.2410	 0.1620
BO	 0.7130	 0.4830
BP	 0.7520	 0.4880
BQ	 0.5670	 0.3520
BR	 0.6890	 0.4470
BS	 0.6320	 0.4070
BT	 0.6780	 0.4290
BU	 0.7090	 0.4500
BV	 0.5390	 0.3590
BW	 0.7110	 0.4770
BX	 0.7510	 0.5260
BY	 0.7150	 0.5010
BZ	 0.6240	 0.4210
Ba	 0.5580	 0.3470
Bb	 0.7500	 0.4760
Bc	 0.6510	 0.4590
Bd	 0.5810	 0.4000
Be	 0.7310	 0.4490
Bf	 0.5770	 0.4060

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bg	 0.2860	 0.1360
Bh	 0.4970	 0.3120
Bi	 0.5360	 0.3310