



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 02:52 PM UTC

PDB ID : 8EWB / pdb_00008ewb
EMDB ID : EMD-28642
Title : Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), eEF2 and GDP, Structure III
Authors : Zhao, Y.; Rai, J.; Li, H.
Deposited on : 2022-10-22
Resolution : 2.87 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

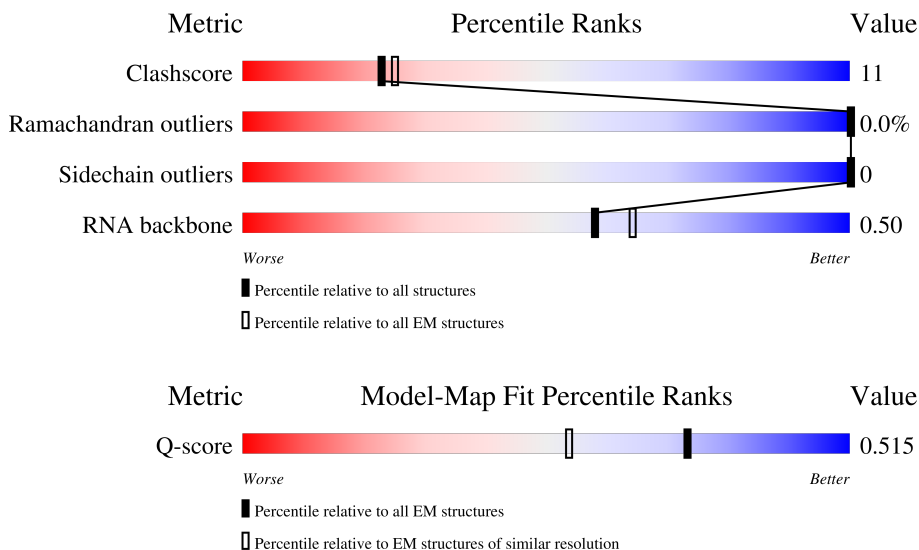
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.87 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	12062 (2.37 - 3.37)

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	BA	252	
2	BB	255	
3	BC	254	






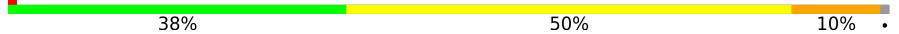



















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Mol	Chain	Length	Quality of chain
4	BE	261	69% 31%
5	BG	236	61% 34% .
6	BH	190	63% 33% ..
7	BI	200	70% 24% 6%
8	BJ	197	65% 28% 6%
9	BL	156	81% 18% .
10	BN	151	72% 28% .
11	BO	137	55% 36% . 7%
12	BV	87	70% 30%
13	BW	130	68% 31% .
14	BX	145	68% 32% .
15	BY	135	70% 30% .
16	Ba	119	53% 29% 18%
17	Bb	82	76% 23% .
18	Be	63	60% 35% 5%
19	BD	240	66% 27% 7%
20	BF	225	57% 35% 8%
21	BK	105	60% 31% 9%
22	BP	142	57% 30% 13% 5%
23	BQ	143	70% 29%
24	BR	136	56% 36% 8%
25	BS	146	55% 45% .
26	BT	144	56% 42% .
27	BU	121	54% 35% 12%
28	BZ	108	32% 31% 36%







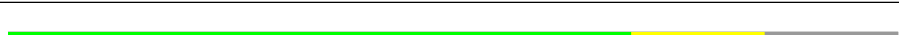
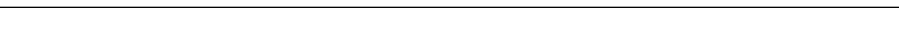
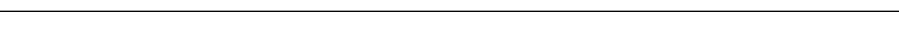
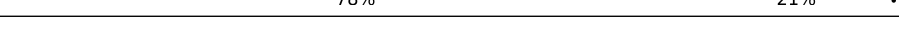
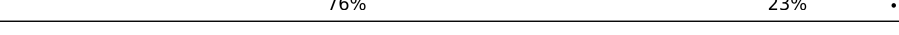
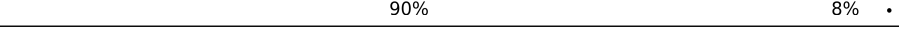













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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	
34	B5	1798	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3360	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	221	
47	AJ	174	
48	AL	199	
49	AM	138	
50	AN	204	
51	AO	199	
52	AP	184	
53	AQ	186	

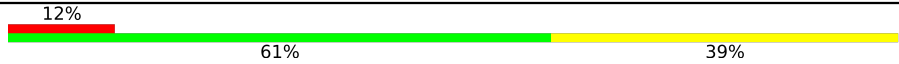
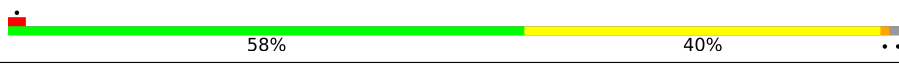
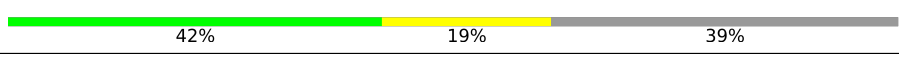

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Mol	Chain	Length	Quality of chain
54	AR	189	 83% 16%
55	AS	178	 70% 26%
56	AT	160	 73% 26%
57	AU	121	 56% 26% 17%
58	AV	137	 81% 18%
59	AW	155	 32% 8% 59%
60	AX	142	 70% 15% 15%
61	AY	127	 74% 25%
62	AZ	136	 78% 21%
63	Aa	149	 76% 23%
64	Ab	59	 90% 8%
65	Ac	105	 66% 27% 8%
66	Ad	113	 81% 16%
67	Ae	130	 82% 16%
68	Af	107	 84% 15%
69	Ag	121	 74% 18% 7%
70	Ah	120	 84% 15%
71	Ai	100	 79% 20%
72	Aj	88	 73% 26%
73	Ak	78	 68% 31%
74	Al	51	 69% 29%
75	Am	128	 34% 6% 59%
76	An	25	 56% 40%
77	Ao	106	 78% 21%
78	Ap	92	 77% 22%

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Mol	Chain	Length	Quality of chain
79	E	217	
80	DC	842	
81	V	312	
82	EC	202	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 213196 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	BA	206	1612	1034	285	291	2	0	0

- Molecule 2 is a protein called RPS1A isoform 1.

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

- Molecule 3 is a protein called RPS2 isoform 1.

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

- Molecule 4 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 5 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	BG	226	1820	1142	350	325	3	0	0

- Molecule 6 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	BH	184	1481	951	265	265	0	0

- Molecule 7 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	BL	155	Total	C	N	O	S	0	0
			1244	798	235	208	3		

- Molecule 10 is a protein called 40S ribosomal protein S13.

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

- Molecule 11 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	BO	127	Total	C	N	O	S	0	0
			941	578	186	174	3		

- Molecule 12 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 13 is a protein called RPS22A isoform 1.

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

- Molecule 14 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	BY	134	1073	676	208	189		0	0

- Molecule 16 is a protein called RPS26B isoform 1.

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

- Molecule 17 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 19 is a protein called RPS3 isoform 1.

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

- Molecule 20 is a protein called Rps5p.

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

- Molecule 21 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BK	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 22 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BP	124	Total	C	N	O	S	0	0
			991	631	187	166	7		

- Molecule 23 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BR	125	Total	C	N	O	S	0	0
			1000	625	188	185	2		

- Molecule 25 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BT	141	Total	C	N	O	S	0	0
			1095	685	206	202	2		

- Molecule 27 is a protein called RPS20 isoform 1.

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

- Molecule 28 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	BZ	69	Total	C	N	O	0	0
			558	357	103	98		

- Molecule 29 is a protein called RPS28A isoform 1.

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

- Molecule 30 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Bd	53	Total	C	N	O	S	0	0
			443	275	92	72	4		

- Molecule 31 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bg	312	Total	C	N	O	S	0	0
			2401	1522	410	461	8		

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bf	75	Total	C	N	O	S	0	0
			605	386	116	99	4		

- Molecule 33 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BM	124	Total	C	N	O	S	0	0
			935	587	165	181	2		

- Molecule 34 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B5	1782	Total	C	N	O	P	1	0
			38005	17006	6718	12499	1782		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B5	1191	B8N	U	conflict	GB 1329886537
B5	1280	4AC	C	conflict	GB 1329886537
B5	1773	4AC	C	conflict	GB 1329886537

- Molecule 35 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AA	247	Total	C	N	O	S	0	0
			1878	1170	381	326	1		

- Molecule 36 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 37 is a protein called RPL4A isoform 1.

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

- Molecule 38 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	3198	Total	C	N	O	P	0	0
			68445	30596	12331	22320	3198		

- Molecule 39 is a RNA chain called 5s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 40 is a RNA chain called 5.8 S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 41 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AD	292	Total	C	N	O	S	0	0
			2341	1478	408	453	2		

- Molecule 42 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AG	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 45 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AH	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 46 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AI	205	Total	C	N	O	S	0	0
			1672	1063	316	288	5		

- Molecule 47 is a protein called RPL11A isoform 1.

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

- Molecule 48 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	AP	175	Total	C	N	O	0	0
			1388	862	277	249		

- Molecule 53 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	AR	188	Total	C	N	O	0	0
			1521	935	326	260		

- Molecule 55 is a protein called 60S ribosomal protein L20.

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

- Molecule 56 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
57	AU	100	796	516	131	149	0	0

- Molecule 58 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 59 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	AW	63	521	336	102	82	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	AX	121	968	623	170	173	2	0	0

- Molecule 61 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
61	AY	126	993	625	192	176	0	0

- Molecule 62 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L28.

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

- Molecule 64 is a protein called RPL29 isoform 1.

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

- Molecule 65 is a protein called 60S ribosomal protein L30.

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

- Molecule 66 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Ad	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 67 is a protein called RPL32 isoform 1.

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

- Molecule 68 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 73 is a protein called RPL38 isoform 1.

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

- Molecule 74 is a protein called 60S ribosomal protein L39.

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

- Molecule 75 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 76 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 78 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 79 is a protein called RPL1A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	E	217	Total	C	N	O	S	0	0
			1718	1097	299	312	10		

- Molecule 80 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	DC	824	Total	C	N	O	S	0	0
			6419	4085	1096	1208	30		

- Molecule 81 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	V	189	Total	C	N	O	S	0	0
			1473	942	257	270	4		

- Molecule 82 is a RNA chain called Taura syndrome virus (TSV) internal ribosome entry site (IRES) RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	EC	153	Total	C	N	O	P	0	0
			3261	1457	580	1071	153		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EC	6953	U	-	expression tag	GB 14701764
EC	6954	A	-	expression tag	GB 14701764
EC	6955	A	-	expression tag	GB 14701764
EC	6956	A	-	expression tag	GB 14701764
EC	6957	A	-	expression tag	GB 14701764
EC	6958	C	-	expression tag	GB 14701764
EC	6959	C	-	expression tag	GB 14701764

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

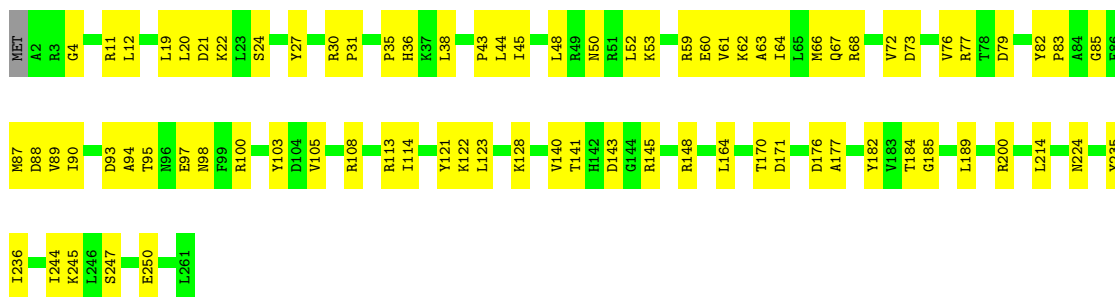
Mol	Chain	Residues	Atoms	AltConf
83	Ba	1	Total Mg 1 1	0
83	B5	63	Total Mg 63 63	0
83	AB	1	Total Mg 1 1	0
83	A1	173	Total Mg 173 173	0
83	A3	1	Total Mg 1 1	0
83	A4	1	Total Mg 1 1	0
83	AP	1	Total Mg 1 1	0
83	Aj	1	Total Mg 1 1	0

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
84	Ao	1	Total Zn 1 1	0

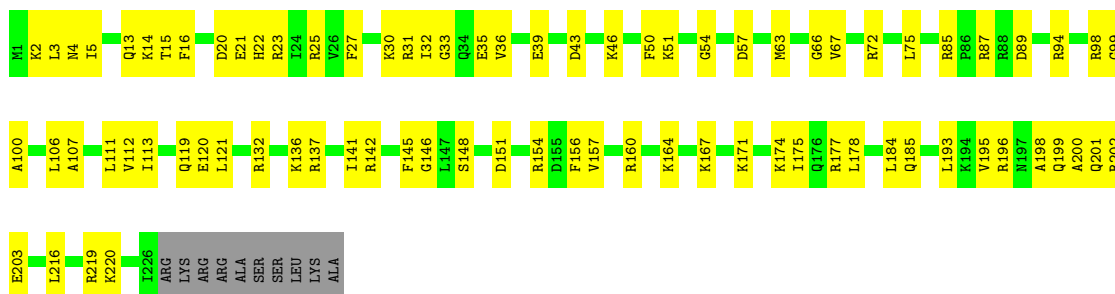
- Molecule 85 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

Chain BE: 69% 31%



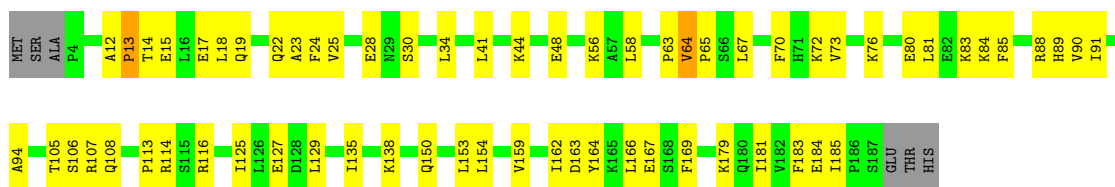
• Molecule 5: 40S ribosomal protein S6-A

Chain BG: 61% 34%



• Molecule 6: 40S ribosomal protein S7-A

Chain BH: 63% 33%



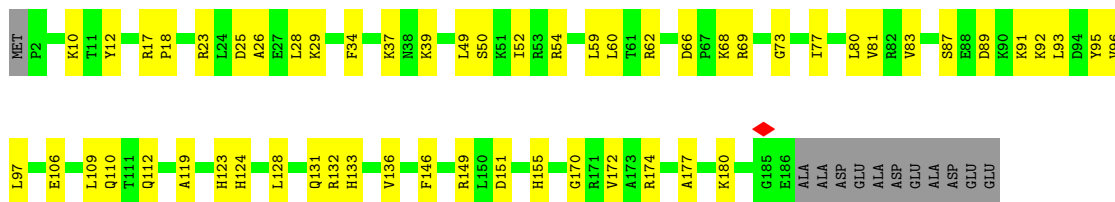
• Molecule 7: 40S ribosomal protein S8-A

Chain BI: 70% 24% 6%

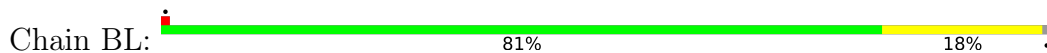


• Molecule 8: 40S ribosomal protein S9-A

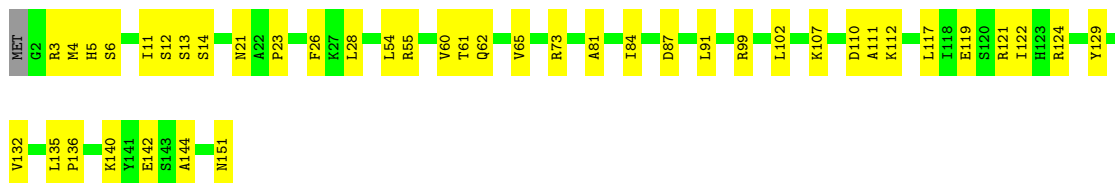
Chain BJ: 65% 28% 6%



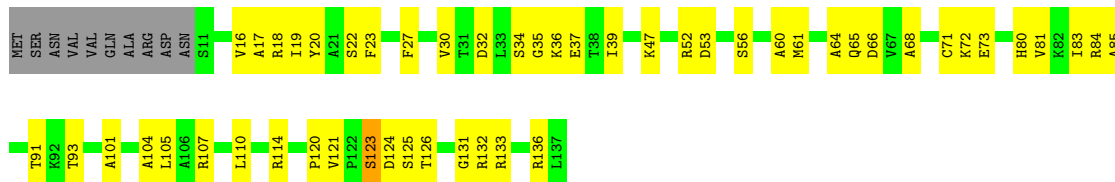
• Molecule 9: 40S ribosomal protein S11-A



• Molecule 10: 40S ribosomal protein S13



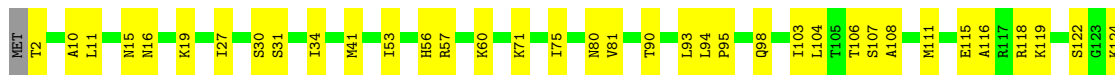
• Molecule 11: 40S ribosomal protein S14-A



• Molecule 12: 40S ribosomal protein S21-A



• Molecule 13: RPS22A isoform 1



L125
L126
G127
F128
V129
Y130

- Molecule 14: 40S ribosomal protein S23-A

Chain BX: 68% 32%

MET G2 G8 L9 N10 S11 H18 N22 A25 E26 Y29 S40 S41 F42 F43 S46 S47 G51 L54 E55 E56 I59 N65 R69 K70 G71 V72 Q75 L76 I77 K78 N79 G80 T84 A85 F86 D90 G91 C92 L93 V96 E101 V102

F107 G108 R109 K110 N115 D116 L117 P118 V120 K123 V124 V130 V136 K140 R144 S145

- Molecule 15: 40S ribosomal protein S24-A

Chain BY: 70% 30%

MET S2 I13 N14 S15 P16 L17 L18 A19 Q22 D26 H29 R32 A33 N34 V35 E36 K37 L40 L44 V47 V55 S56 V57 F60 R61 T62 S69 V70 G71 V75 E81 P87 T88 Y89 E98 K102 R105 R108 K109 K112

N113 K116 T121 G122 K123 R124 K128 R132 D135

- Molecule 16: RPS26B isoform 1

Chain Ba: 53% 29% 18%

MET P2 K3 K4 R5 R8 G9 R10 K11 K12 R15 R22 S29 K37 I41 I44 V45 E46 A47 A48 R51 D52 L53 E54 E55 S57 V58 Y59 L64 P65 K66 T67 Y68 N69 K70 V75 I79 V84 R87 D91 P97 G98 GLN ARG

PRO ARG PHE ASN ARG ASP ASN LYS VAL SER PRO ALA ALA ALA LYS LYS ALA LEU

- Molecule 17: 40S ribosomal protein S27-A

Chain Bb: 76% 23%

MET Y2 H19 K20 L21 Q26 Y31 F32 L33 C37 L41 A50 Q51 C56 E57 S58 C59 S60 T61 P66 T67 K70 S74 E75 G76 F79 R82

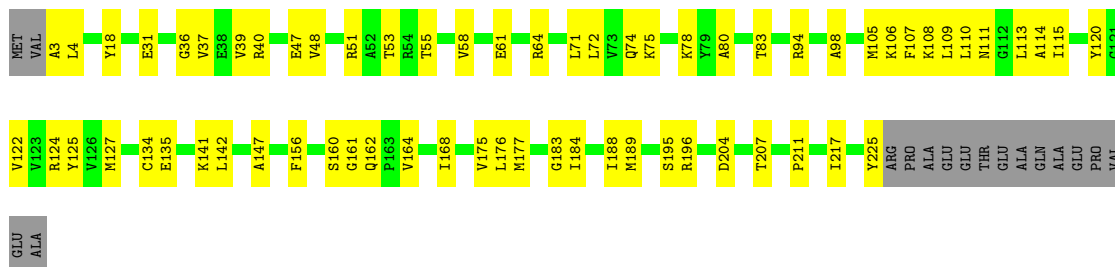
- Molecule 18: 40S ribosomal protein S30-A

Chain Be: 60% 35% 5%

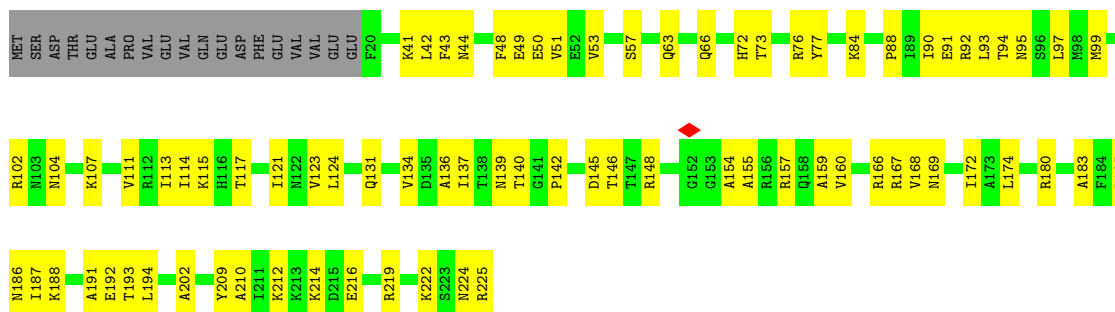
MET A2 R10 V14 K15 S16 Q17 K23 T24 E25 K26 P27 K28 K29 F30 K31 G32 R33 L38 L39 Y40 T41 R42 R43 F44 V45 V50 K53 R54 R55 R56 P58 S61 VAL GLN

- Molecule 19: RPS3 isoform 1

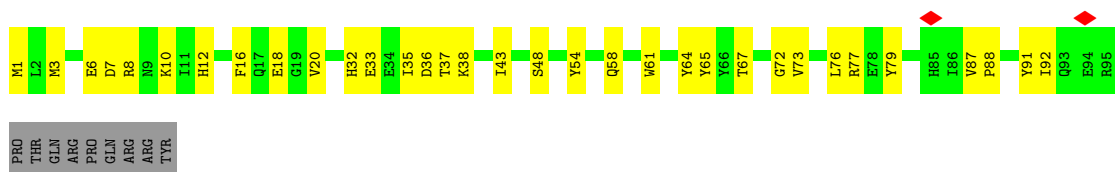
Chain BD: 66% 27% 7%



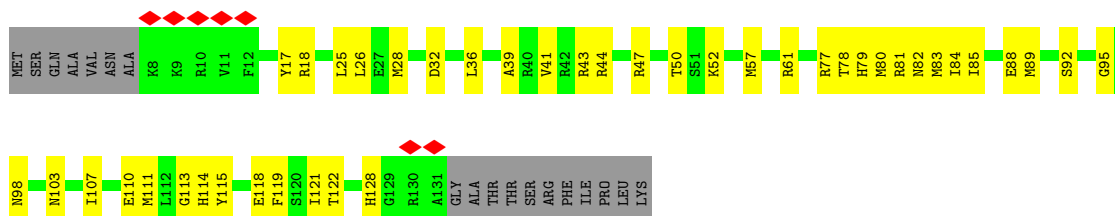
• Molecule 20: Rps5p



• Molecule 21: 40S ribosomal protein S10-A

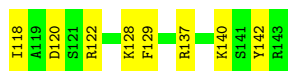


• Molecule 22: RPS15 isoform 1

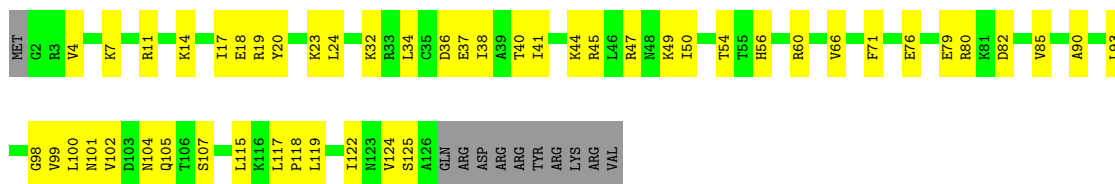


• Molecule 23: 40S ribosomal protein S16-A

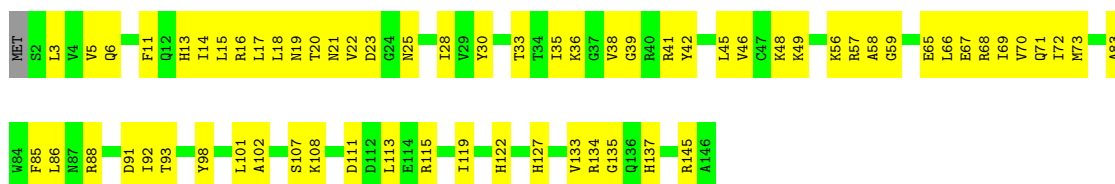




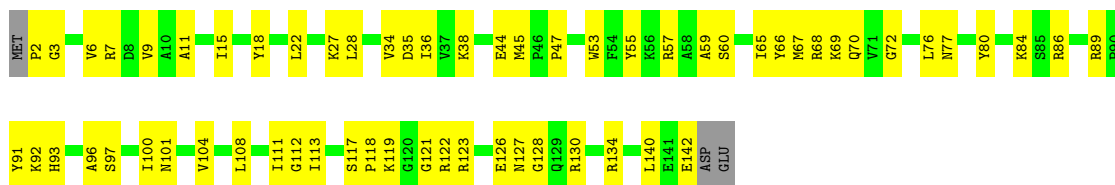
• Molecule 24: 40S ribosomal protein S17-A



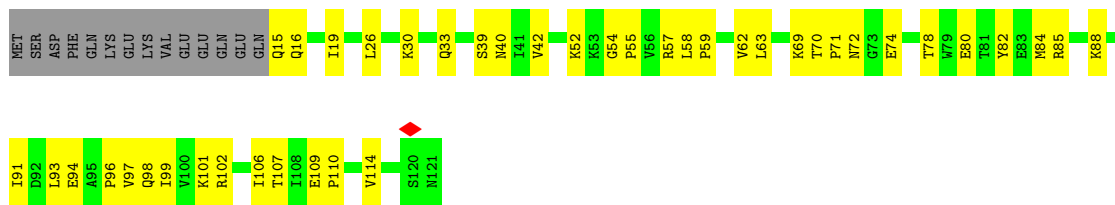
• Molecule 25: 40S ribosomal protein S18-A



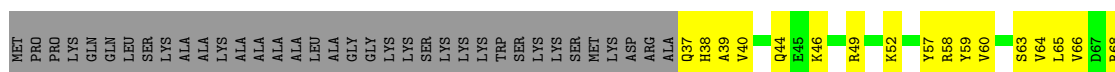
• Molecule 26: 40S ribosomal protein S19-A



• Molecule 27: RPS20 isoform 1



• Molecule 28: RPS25A isoform 1





• Molecule 29: RPS28A isoform 1



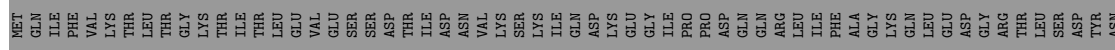
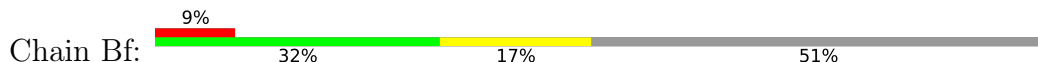
• Molecule 30: RPS29A isoform 1



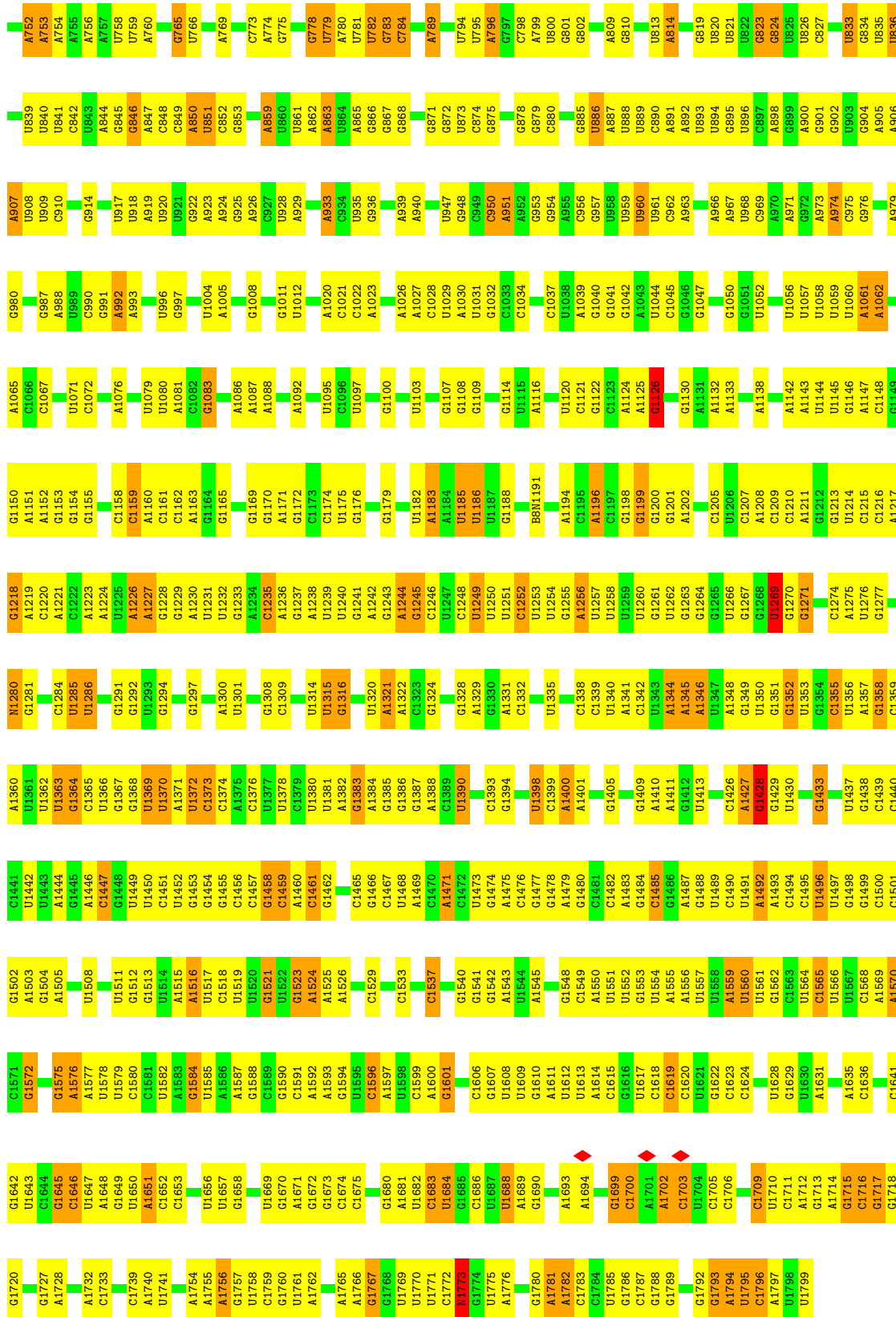
• Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein




• Molecule 32: Ubiquitin-40S ribosomal protein S31

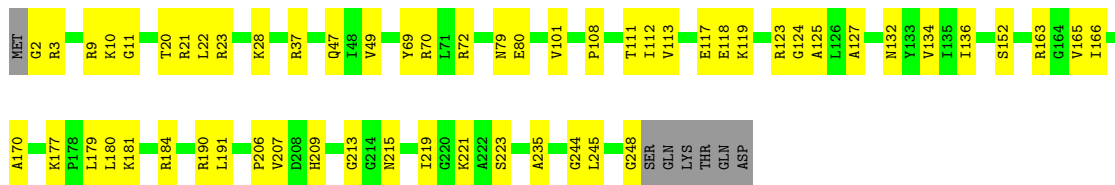


• Molecule 33: 40S ribosomal protein S12




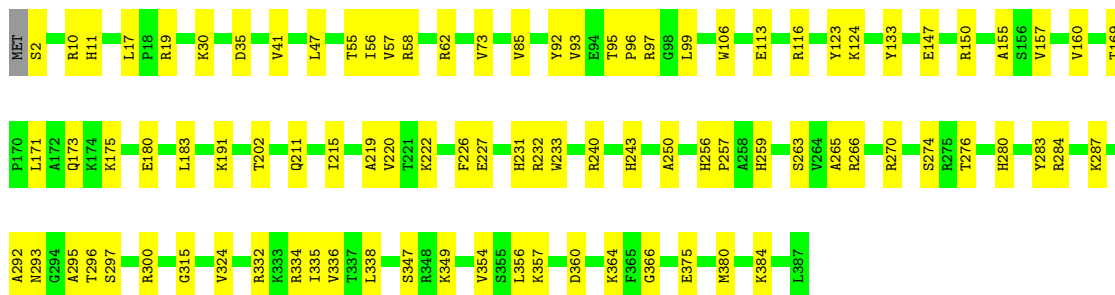
• Molecule 35: 60S ribosomal protein L2-A

Chain AA:  75% 22%




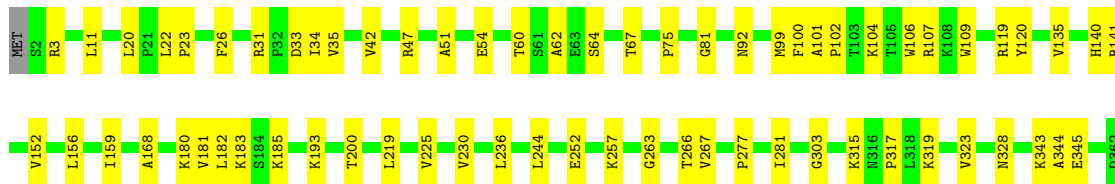
• Molecule 36: 60S ribosomal protein L3

Chain AB:  76% 24%



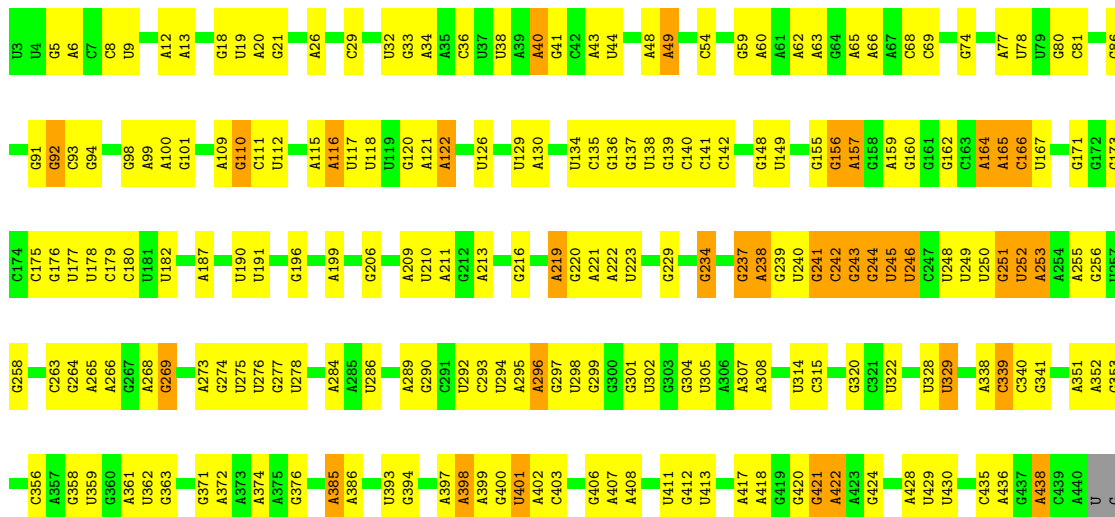
• Molecule 37: RPL4A isoform 1

Chain AC:  81% 18%



• Molecule 38: 25S rRNA

Chain A1:  48% 39% 8% 5%



U1689	C1596	G1507	U1415	G1237	C1156	G1072	G993	G910	G809	U719	G632	A557
C1597	C1598	C1508	A1418	C1238	G1157	G1073	G994	C911	A810	G727	C636	U558
U1695	U1601	U1522	A1419	A1240	A1158	U1074	U995	A912	U811	G728	U640	A559
A1696	A1602	U1523	C1420	U1241	A1159	A1075	A996	A913	G812	C729	C641	G560
C1698	A1603	A1524	G1421	G1242	U1167	U1081	A997	A914	G813	U642	U643	C561
A1699	G1604	G1525	G1422	G1243	U1168	U1082	G999	G916	U814	A735	U644	C562
G1700	C1613	A1534	G1431	A1244	A1169	G1083	C1000	A917	A816	A736	G644	U665
U1717	C1614	A1535	G1434	G1245	A1170	A1084	A1002	A921	A817	A737	G645	G666
G1718	C1615	A1539	G1435	G1246	G1174	A1085	U1008	U922	U821	A738	A645	G667
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A1723	G1618	G1544	C1437	A1253	G1179	C1092	A1011	A929	U825	C749	C655	A572
U1724	A1621	G1544	A1446	U1254	U1179	U1108	G1012	A944	U826	U749	C656	C576
C1725	U1622	G1547	G1447	C1254	A1180	U1109	G1013	U946	A827	C753	C657	C577
C1726	G1623	G1547	U1448	U1255	U1181	U1110	U1014	G947	G831	U662	C663	G584
G1727	G1624	U1449	U1449	G1256	A1182	U1111	U1015	C948	U834	U759	U664	A500
A1729	G1625	C1551	A1450	C1257	A1183	U1114	C1016	C949	G845	A761	U665	A501
U1737	U1626	U1555	U1455	U1258	U1184	U1114	G1018	G950	G846	U762	A666	U502
C1738	C1628	A1556	A1456	A1260	G1186	U1114	G1019	A951	G847	C765	C667	U506
U1740	U1629	A1557	A1456	G1261	G1186	U1114	G1020	A952	A848	U766	U671	U507
A1741	U1630	A1558	A1460	A1262	C1192	U1117	G1021	C944	A848	U767	A672	C515
G1742	C1631	A1559	A1461	A1263	A1193	G1117	U1022	C945	C849	U772	U673	A516
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A1749	G1634	C1562	A1465	A1271	C1196	U1110	A	C948	G860	A772	A676	A521
A1750	C1639	U1564	G1466	C1272	A1197	U1111	A	C949	G861	U773	A677	A522
G1751	G1640	G1564	A1467	A1273	C1201	U1114	U	G950	G862	U774	A678	A523
A1752	U1641	A1566	A1468	U1274	A1202	U1114	G	A951	A866	G775	G679	U601
G1757	U1642	A1566	C1469	C1277	A1203	G1117	A1030	U955	A867	A775	U680	A602
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C1759	C1644	U1568	G1473	C1279	A1205	G1119	C1032	U956	U872	U777	U682	A604
U1760	U1645	U1570	A1474	G1282	G1206	A1120	U1033	U956	C873	A780	U683	U605
C1761	G1646	A1571	A1474	C1283	G1207	U1121	U1034	C959	C874	G781	U684	U606
U1762	U1650	G1572	A1477	U1286	U1211	U1128	G1035	G964	U874	A780	U685	U607
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U1764	A1654	A1574	A1481	U1288	A1213	A1131	C1038	U966	A691	G785	A692	A609
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G1769	G1658	C1578	G1493	A1292	G1222	G1134	U1042	C975	A884	C788	U698	U612
U1770	U1659	A1580	G1486	U1293	A1223	U1138	C1043	U976	A888	A791	A699	G616
C1771	C1660	C1581	G1487	G1294	C1224	G1139	U1044	C977	A888	G792	G701	G617
G1772	G1661	A1582	G1492	G1295	C1224	C1142	U1046	U979	A885	C793	A705	G618
G1775	G1662	A1583	G1493	G1306	C1227	G1144	A1047	A980	A895	A705	A619	U620
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U1785	G1668	U1589	U1497	U1309	G1230	U1144	A1055	A983	U898	A711	A627	U627
G1786	U1682	A1592	C1498	G1311	C1232	A1150	A1062	U987	U899	G800	A628	A628
A1787	U1687	A1593	G1499	A1317	G1233	A1153	G1063	U988	G900	G805	A629	U629
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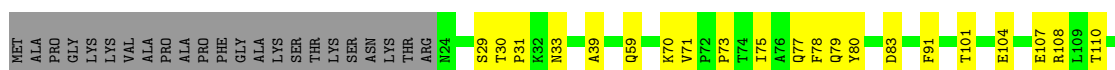
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A1797	A1880	C	A	C2156	A2242	U2426	C2490	C2567	G2648	C2741	G2828	U2922
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A1799	A1884	C	A	U2159	A2244	U2428	C2492	C2569	U2652	G2745	A2834	C2928
A1800	A1885	C	A	G2160	A2245	G2429	U2493	C2570	U2653	U2746	C2835	C2929
C1805	U1886	C	U	G2161	A2246	A2430	A2494	C2571	U2654	A2748	C2836	A2930
A1806	A1887	C	U	U2162	A2247	C2431	C2495	C2572	U2655	G2749	A2838	C2931
G1807	U1888	C	A	C2163	U2248	A2432	U2497	G2573	A2656	G2752	U2839	U2932
G1808	G1889	C	A	G2164	A2249	U2433	U2498	G2574	G2661	U2753	U2842	A2933
A1809	U1890	C	C	A2167	A2250	U2434	U2499	G2575	G2662	G2754	U2843	A2934
A1810	U1891	C	C	A2168	A2251	G2435	A2500	A2580	G2663	G2755	A2844	U2935
G1811	U1894	C	C	U2170	U2252	A2436	U2501	A2581	A2664	U2756	A2845	U2936
G1812	U1895	C	C	G2171	A2253	A2437	A2502	G2582	A2665	C2757	C2852	G2937
A1813	G1897	C	C	U2176	U2254	G2440	G2503	G2583	A2666	U2758	C2853	G2938
A1814	G1898	C	C	G2177	A2255	A2441	G2504	G2584	A2667	A2674	U2855	A2941
U1815	G1899	C	C	A2178	A2256	G2442	U2505	G2585	U2668	A2675	G2856	C2942
G1816	G1906	C	G	U2179	U2257	U2443	U2506	G2586	G2669	G2676	G2857	G2943
G1817	C1907	C	G	A2180	U2258	U2444	C2507	U2587	A2670	A2677	U2858	U2944
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U1821	A1909	C	U	C2185	U2260	A2449	U2509	A2590	A2672	A2679	U2860	A2946
C1827	A1910	C	U	G2186	U2261	G2450	U2510	A2591	U2673	G2700	U2861	G2947
A1828	A1911	C	A	A2188	U2262	G2451	A2511	A2592	A2674	A2696	U2862	C2948
G1829	U1912	C	A	A2189	U2263	G2452	U2512	A2593	A2675	A2697	C2863	U2953
G1830	A1913	C	U	G2189	U2264	A2453	U2513	U2594	A2676	G2698	U2864	U2954
U1831	G1914	C	U	A2190	U2265	U2454	U2514	U2595	A2677	G2699	G2865	
C1832	U1921	C	C	G2191	U2266	G2455	U2515	C2600	A2678	G2700	A2866	
A1835	A1922	C	C	A2192	U2267	U2456	U2516	G2601	A2679	A2704	A2867	U2974
C1836	U1925	C	U	G2193	U2268	A2457	U2517	G2602	A2680	G2800	C2868	U2975
U1837	C1926	C	U	C2201	U2269	U2458	U2518	G2603	A2681	A2801	A2889	A2976
G1838	G1927	C	C	G2202	U2270	A2459	C2526	A2604	A2682	A2802	C2894	G2977
U1839	U1932	C	U	U2203	U2271	U2460	G2527	G2605	A2683	A2803	C2895	U2980
A1841	G1940	C	U	C2204	U2272	A2461	U2528	G2606	U2684	U2806	A2896	
A1842	U1942	C	U	G2205	U2273	A2462	U2529	G2607	A2685	U2807	A2897	C2983
C1846	C1943	C	U	U2206	U2274	G2463	U2530	A2608	U2686	C2810	G2898	C2984
C1849	G1947	C	G	A2213	U2275	U2464	G2531	G2609	A2687	A2811	C2901	C2985
A1850	G1948	C	U	G2207	U2276	U2465	G2532	A2610	A2688	G2713	G2902	U2986
C1856	G1949	C	C	A2208	U2277	G2466	G2533	G2611	A2689	G2714	A2903	A2987
C1857	U1950	C	U	U2209	U2278	G2467	G2534	G2612	A2690	A2812	C2904	C2988
G1863	U1951	C	U	A2210	U2279	A2468	U2540	U2613	A2691	U2813	A2905	U2989
A1864	G1952	C	G	G2218	U2280	U2471	U2541	U2614	A2692	G2715	U2906	G2990
A1865	G1953	C	C	A2219	U2281	G2472	U2542	U2615	A2693	G2716	A2907	A2991
G1954	G1954	C	A	A2220	U2282	C2473	U2543	U2616	A2694	U2717	U2908	
U1955	G1955	C	C	G2221	U2283	U2474	U2544	U2617	A2695	U2718	U2909	
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					U2296	U2487	U2557	U2630	A2708	U2829	U2922	
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					U2326	U2517	U2587	U2660	A2738	U2859	U2952	
					U2327	U2518	U2588	U2661	A2739	U2860	U2953	
					U2328	U2519	U2589	U2662	A2740	U2861	U2954	
					U2329	U2520	U2590	U2663	A2741	U2862	U2955	
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					U2331	U2522	U2592	U2665	A2743	U2864	U2957	
					U2332	U2523	U2593	U2666	A2744	U2865	U2958	
					U2333	U2524	U2594	U2667	A2745	U2866	U2959	
					U2334	U2525	U2595	U2668	A2746	U2867	U2960	
					U2335	U2526	U2596	U2669	A2747	U2868	U2961	
					U2336	U2527	U2597	U2670	A2748	U2869	U2962	
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					U2340	U2531	U2601	U2674	A2752	U2873	U2966	
					U2341	U2532	U2602	U2675	A2753	U2874	U2967	
					U2342	U2533	U2603	U2676	A2754	U2875	U2968	
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					U2344	U2535	U2605	U2678	A2756	U2877	U2970	
					U2345	U2536	U2606	U2679	A2757	U2878	U2971	
					U2346	U2537	U2607	U2680	A2758	U2879	U2972	
					U2347	U2538	U2608	U2681	A2759	U2880	U2973	
					U2348	U2539	U2609	U2682	A2760	U2881	U2974	
					U2349	U2540	U2610	U2683	A2761	U2882	U2975	
					U2350	U2541	U2611	U2684	A2762	U2883	U2976	
					U2351	U2542	U2612	U2685	A2763	U2884	U2977	
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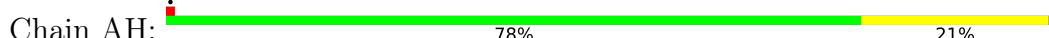
• Molecule 43: 60S ribosomal protein L7-A



• Molecule 44: 60S ribosomal protein L8-A



• Molecule 45: 60S ribosomal protein L9-A

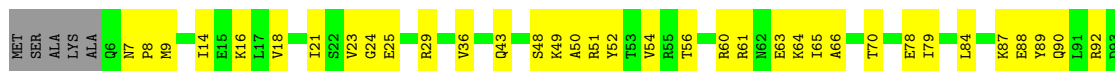


• Molecule 46: RPL10 isoform 1

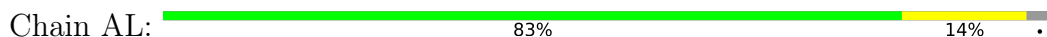


• Molecule 47: RPL11A isoform 1

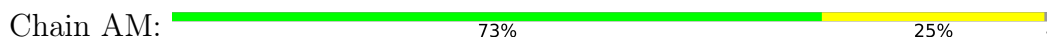




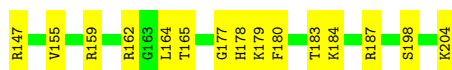
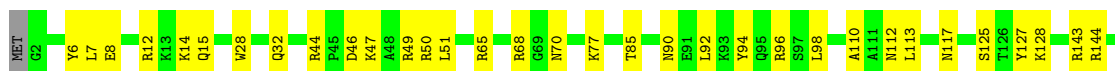
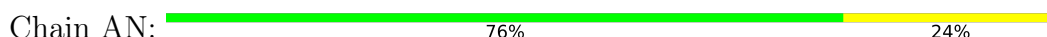
• Molecule 48: 60S ribosomal protein L13-A



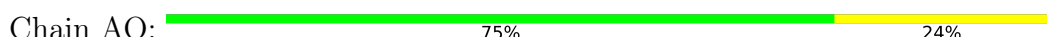
• Molecule 49: 60S ribosomal protein L14-A



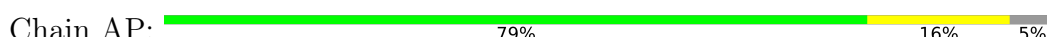
• Molecule 50: 60S ribosomal protein L15-A



• Molecule 51: 60S ribosomal protein L16-A

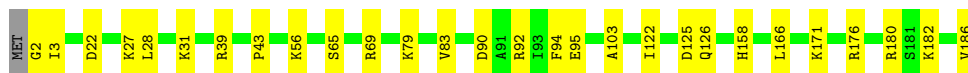
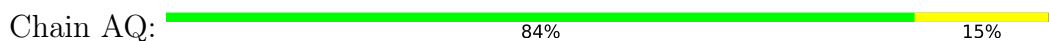


• Molecule 52: 60S ribosomal protein L17-A

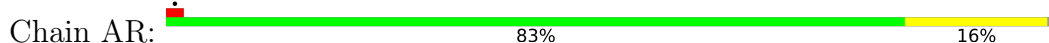




• Molecule 53: 60S ribosomal protein L18-A



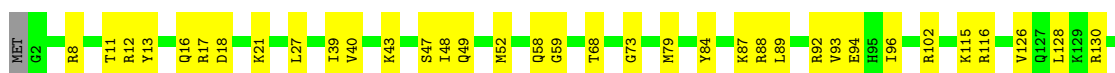
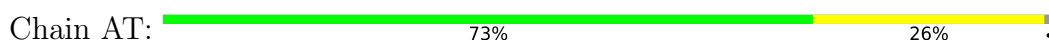
• Molecule 54: 60S ribosomal protein L19-A



• Molecule 55: 60S ribosomal protein L20

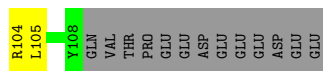


• Molecule 56: 60S ribosomal protein L21-A

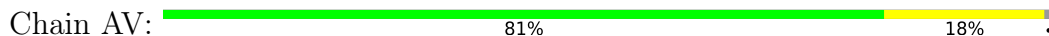


• Molecule 57: 60S ribosomal protein L22-A

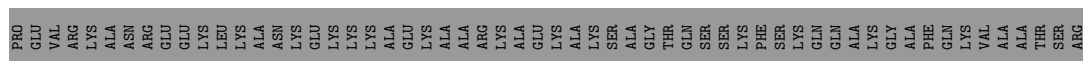
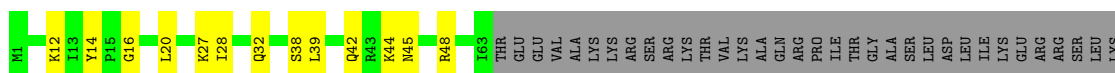




• Molecule 58: 60S ribosomal protein L23-A



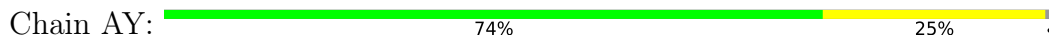
• Molecule 59: RPL24A isoform 1



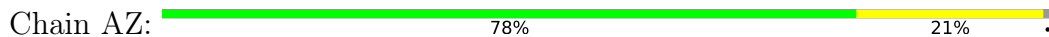
• Molecule 60: 60S ribosomal protein L25



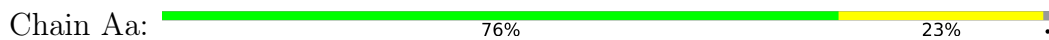
• Molecule 61: 60S ribosomal protein L26-A



• Molecule 62: 60S ribosomal protein L27-A



• Molecule 63: 60S ribosomal protein L28





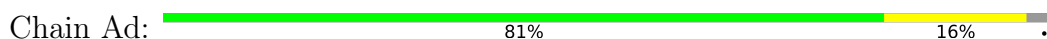
• Molecule 64: RPL29 isoform 1



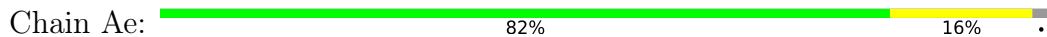
• Molecule 65: 60S ribosomal protein L30



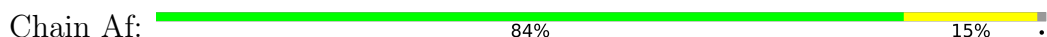
• Molecule 66: 60S ribosomal protein L31-A



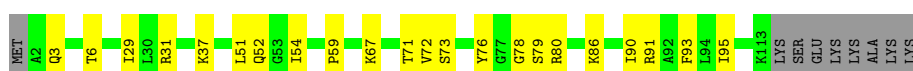
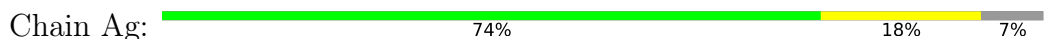
• Molecule 67: RPL32 isoform 1



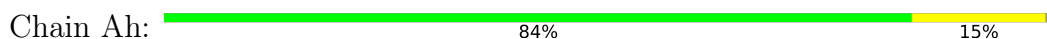
• Molecule 68: 60S ribosomal protein L33-A



• Molecule 69: 60S ribosomal protein L34-A

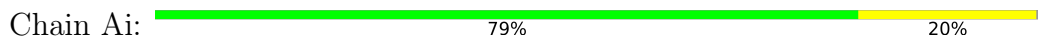


• Molecule 70: 60S ribosomal protein L35-A





- Molecule 71: 60S ribosomal protein L36-A



- Molecule 72: 60S ribosomal protein L37-A



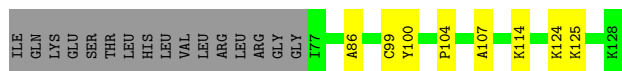
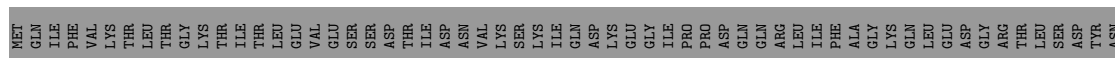
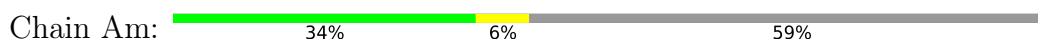
- Molecule 73: RPL38 isoform 1



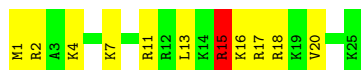
- Molecule 74: 60S ribosomal protein L39



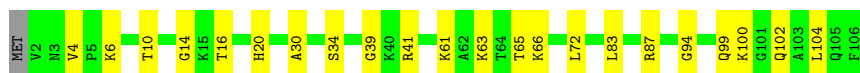
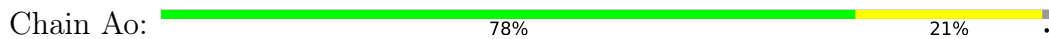
- Molecule 75: Ubiquitin-60S ribosomal protein L40



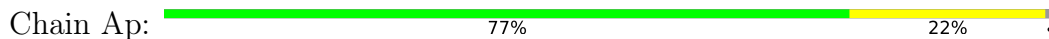
- Molecule 76: 60S ribosomal protein L41-A



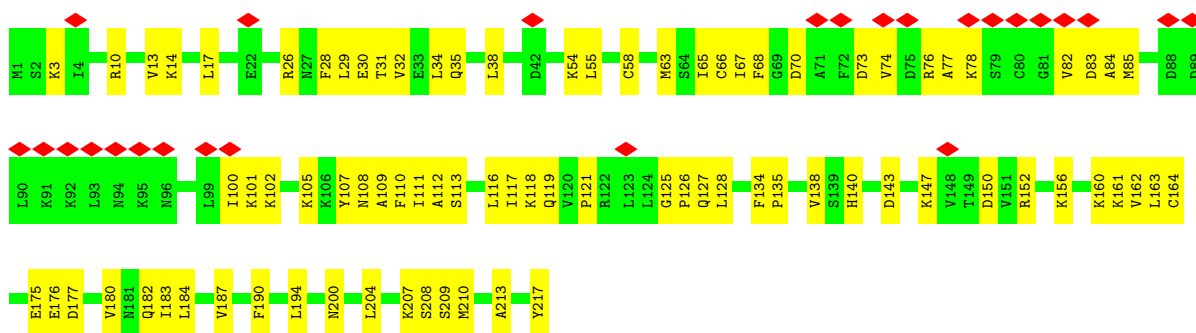
- Molecule 77: 60S ribosomal protein L42-A



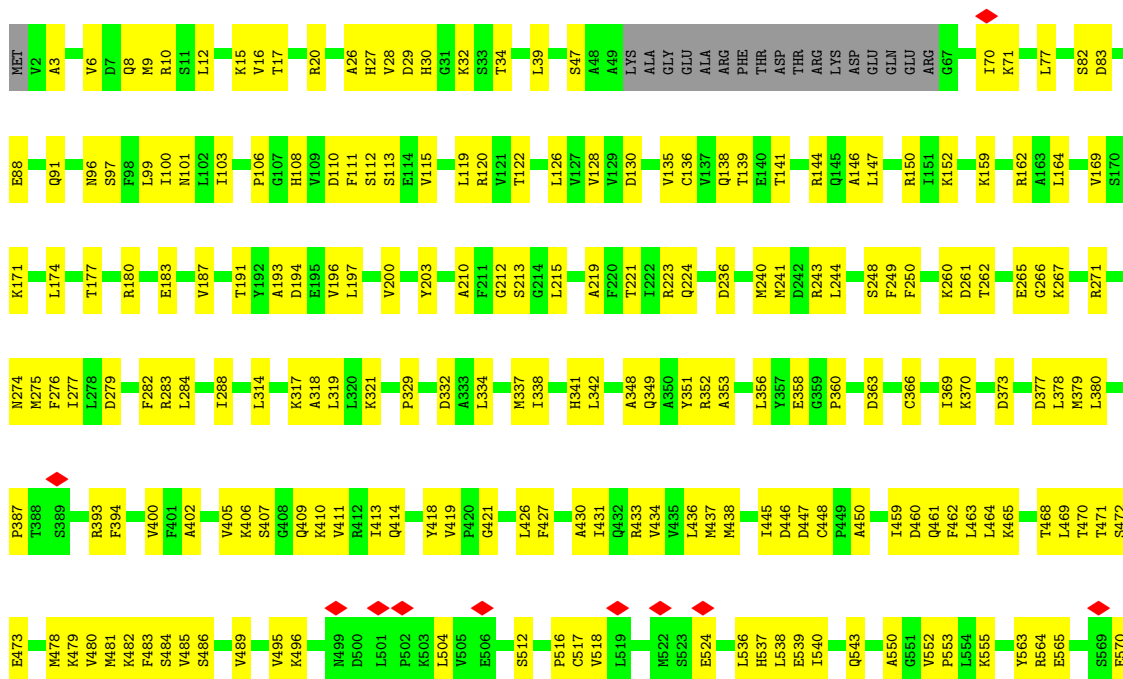
• Molecule 78: 60S ribosomal protein L43-A



• Molecule 79: RPL1A isoform 1



• Molecule 80: Elongation factor 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20205	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.399	Depositor
Minimum map value	-1.080	Depositor
Average map value	0.037	Depositor
Map value standard deviation	0.185	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 1MA, HIC, MA6, UR3, OMG, B8N, 5MC, G7M, DDE, 4AC, OMC, OMU, MG, GDP, ZN, A2M

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	BA	0.15	0/1653	0.29	0/2261
2	BB	0.18	0/1735	0.39	0/2335
3	BC	0.16	0/1665	0.27	0/2263
4	BE	0.16	0/2109	0.32	0/2839
5	BG	0.12	0/1844	0.27	0/2464
6	BH	0.66	4/1506 (0.3%)	0.84	8/2028 (0.4%)
7	BI	0.17	0/1514	0.37	0/2021
8	BJ	0.15	0/1519	0.29	0/2035
9	BL	0.17	0/1272	0.31	0/1712
10	BN	0.18	0/1215	0.32	0/1638
11	BO	0.19	0/952	0.38	0/1279
12	BV	0.16	0/693	0.36	0/935
13	BW	0.17	0/1038	0.30	0/1395
14	BX	0.17	0/1139	0.33	0/1518
15	BY	0.13	0/1087	0.29	0/1449
16	Ba	0.19	0/782	0.40	0/1047
17	Bb	0.15	0/620	0.35	0/838
18	Be	0.14	0/483	0.34	0/643
19	BD	0.13	0/1759	0.30	0/2368
20	BF	0.13	0/1629	0.33	0/2202
21	BK	0.12	0/837	0.37	0/1131
22	BP	0.12	0/1012	0.36	0/1356
23	BQ	0.12	0/1125	0.28	0/1510
24	BR	0.17	0/1010	0.48	0/1355
25	BS	0.12	0/1211	0.35	0/1628
26	BT	0.13	0/1113	0.32	0/1494
27	BU	0.15	0/865	0.33	0/1169
28	BZ	0.13	0/566	0.35	0/761
29	Bc	0.11	0/499	0.28	0/670
30	Bd	0.13	0/453	0.27	0/602
31	Bg	0.12	0/2454	0.33	0/3340
32	Bf	0.10	0/616	0.31	0/817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.12	0/943	0.35	0/1274
34	B5	0.19	0/41880	0.28	0/65248
35	AA	0.21	0/1912	0.33	0/2569
36	AB	0.18	0/3139	0.28	0/4219
37	AC	0.19	0/2800	0.32	0/3790
38	A1	0.22	0/75561	0.30	0/117806
39	A3	0.18	0/2883	0.25	0/4491
40	A4	0.23	0/3746	0.29	0/5832
41	AD	0.16	0/2390	0.28	0/3225
42	AE	0.16	0/1260	0.30	0/1694
43	AF	0.18	0/1821	0.28	0/2451
44	AG	0.19	0/1830	0.38	0/2469
45	AH	0.16	0/1531	0.30	0/2062
46	AI	0.16	0/1708	0.27	0/2290
47	AJ	0.14	0/1374	0.35	0/1842
48	AL	0.19	0/1568	0.30	0/2106
49	AM	0.18	0/1068	0.30	0/1438
50	AN	0.22	0/1757	0.29	0/2354
51	AO	0.18	0/1585	0.28	0/2128
52	AP	0.18	0/1410	0.28	0/1893
53	AQ	0.19	0/1465	0.29	0/1965
54	AR	0.17	0/1538	0.26	0/2050
55	AS	0.19	0/1481	0.35	0/1990
56	AT	0.18	0/1300	0.28	0/1743
57	AU	0.16	0/812	0.36	0/1099
58	AV	0.18	0/1018	0.30	0/1369
59	AW	0.17	0/533	0.26	0/707
60	AX	0.19	0/983	0.29	0/1325
61	AY	0.18	0/1004	0.28	0/1341
62	AZ	0.19	0/1118	0.30	0/1497
63	Aa	0.21	0/1204	0.30	0/1612
64	Ab	0.17	0/473	0.30	0/629
65	Ac	0.20	0/751	0.27	0/1008
66	Ad	0.17	0/904	0.28	0/1213
67	Ae	0.19	0/1041	0.28	0/1394
68	Af	0.20	0/868	0.31	0/1168
69	Ag	0.21	0/890	0.34	0/1189
70	Ah	0.19	0/978	0.30	0/1301
71	Ai	0.18	0/778	0.33	0/1034
72	Aj	0.21	0/696	0.30	0/923
73	Ak	0.17	0/618	0.30	0/826
74	Al	0.21	0/443	0.38	0/588
75	Am	0.16	0/423	0.29	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.26	0/234	0.77	1/300 (0.3%)
77	Ao	0.19	0/860	0.35	0/1136
78	Ap	0.19	0/701	0.30	0/934
79	E	0.14	0/1745	0.40	0/2342
80	DC	0.22	1/6521 (0.0%)	0.43	3/8830 (0.0%)
81	V	0.13	0/1498	0.32	0/2025
82	EC	0.13	0/3643	0.31	0/5666
All	All	0.20	5/226662 (0.0%)	0.31	12/332050 (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
6	BH	0	1
11	BO	0	1
43	AF	0	1
44	AG	0	1
76	An	0	1
All	All	0	5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	BH	13	PRO	CG-CD	-19.03	0.86	1.50
6	BH	13	PRO	CB-CG	13.20	2.15	1.49
80	DC	833	PRO	CG-CD	-7.15	1.26	1.50
6	BH	13	PRO	CA-CB	-6.86	1.44	1.54
6	BH	13	PRO	N-CD	5.98	1.56	1.47

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	BH	13	PRO	N-CD-CG	-19.50	73.94	103.20
6	BH	13	PRO	CA-CB-CG	-14.48	76.98	104.50
6	BH	13	PRO	CB-CG-CD	-14.25	60.49	106.10
6	BH	13	PRO	N-CA-CB	-13.90	87.14	102.85
80	DC	702	GLY	N-CA-C	-13.56	99.75	114.67

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
43	AF	232	ARG	Peptide
44	AG	30	THR	Peptide
76	An	15	ARG	Sidechain
6	BH	64	VAL	Peptide
11	BO	123	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	BA	1612	0	1623	56	0
2	BB	1709	0	1784	57	0
3	BC	1635	0	1723	31	0
4	BE	2068	0	2154	55	0
5	BG	1820	0	1918	61	0
6	BH	1481	0	1572	44	0
7	BI	1489	0	1525	38	0
8	BJ	1494	0	1573	38	0
9	BL	1244	0	1314	19	0
10	BN	1192	0	1255	34	0
11	BO	941	0	979	41	0
12	BV	684	0	672	25	0
13	BW	1021	0	1060	30	0
14	BX	1121	0	1196	36	0
15	BY	1073	0	1132	36	0
16	Ba	769	0	818	35	0
17	Bb	610	0	633	15	0
18	Be	475	0	525	25	0
19	BD	1734	0	1817	55	0
20	BF	1609	0	1675	61	0
21	BK	817	0	804	27	0
22	BP	991	0	1035	44	0
23	BQ	1105	0	1166	29	0
24	BR	1000	0	1063	44	0
25	BS	1192	0	1222	60	0
26	BT	1095	0	1114	52	0
27	BU	855	0	917	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	BZ	558	0	598	27	0
29	Bc	497	0	535	21	0
30	Bd	443	0	436	18	0
31	Bg	2401	0	2356	91	0
32	Bf	605	0	654	27	0
33	BM	935	0	975	37	0
34	B5	38005	0	19140	852	0
35	AA	1878	0	1946	48	0
36	AB	3081	0	3162	70	0
37	AC	2748	0	2859	51	0
38	A1	68445	0	34456	1073	0
39	A3	2579	0	1304	48	0
40	A4	3353	0	1695	51	0
41	AD	2341	0	2290	52	0
42	AE	1239	0	1326	31	0
43	AF	1784	0	1862	31	0
44	AG	1798	0	1894	32	0
45	AH	1510	0	1576	32	0
46	AI	1672	0	1711	34	0
47	AJ	1353	0	1383	45	0
48	AL	1543	0	1608	26	0
49	AM	1053	0	1149	30	0
50	AN	1720	0	1779	41	0
51	AO	1555	0	1659	36	0
52	AP	1388	0	1423	28	0
53	AQ	1441	0	1543	24	0
54	AR	1521	0	1617	31	0
55	AS	1445	0	1487	35	0
56	AT	1276	0	1323	32	0
57	AU	796	0	812	21	0
58	AV	1003	0	1048	16	0
59	AW	521	0	551	9	0
60	AX	968	0	1036	16	0
61	AY	993	0	1081	24	0
62	AZ	1092	0	1155	21	0
63	Aa	1173	0	1215	34	0
64	Ab	462	0	491	4	0
65	Ac	743	0	797	22	0
66	Ad	890	0	938	11	0
67	Ae	1020	0	1090	18	0
68	Af	850	0	880	13	0
69	Ag	880	0	945	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	Ah	969	0	1078	17	0
71	Ai	771	0	849	15	0
72	Aj	681	0	687	20	0
73	Ak	612	0	682	19	0
74	Al	436	0	475	11	0
75	Am	417	0	459	8	0
76	An	233	0	281	15	0
77	Ao	847	0	914	19	0
78	Ap	694	0	738	17	0
79	E	1718	0	1811	69	0
80	DC	6419	0	6493	264	0
81	V	1473	0	1514	53	0
82	EC	3261	0	1648	80	0
83	A1	173	0	0	0	0
83	A3	1	0	0	0	0
83	A4	1	0	0	0	0
83	AB	1	0	0	0	0
83	AP	1	0	0	0	0
83	Aj	1	0	0	0	0
83	B5	63	0	0	0	0
83	Ba	1	0	0	0	0
84	Ao	1	0	0	0	0
85	DC	28	0	11	7	0
All	All	213196	0	159694	4100	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 11.

The worst 5 of 4100 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)
38:A1:237:G:HO2'	38:A1:238:A:H8	1.02	0.98
34:B5:1356:U:H3	34:B5:1367:G:H1	1.03	0.98
34:B5:1756[A]:A:H3'	38:A1:2256:A2M:H61	1.27	0.98
38:A1:3234:A:N6	38:A1:3253:G:H1	1.62	0.97
34:B5:1756[A]:A:H1'	80:DC:703:GLY:HA2	1.46	0.96

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	189 (93%)	15 (7%)	0	100	100
2	BB	212/255 (83%)	182 (86%)	30 (14%)	0	100	100
3	BC	215/254 (85%)	204 (95%)	11 (5%)	0	100	100
4	BE	258/261 (99%)	237 (92%)	21 (8%)	0	100	100
5	BG	224/236 (95%)	210 (94%)	14 (6%)	0	100	100
6	BH	182/190 (96%)	167 (92%)	15 (8%)	0	100	100
7	BI	184/200 (92%)	163 (89%)	21 (11%)	0	100	100
8	BJ	183/197 (93%)	169 (92%)	14 (8%)	0	100	100
9	BL	153/156 (98%)	141 (92%)	12 (8%)	0	100	100
10	BN	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
11	BO	125/137 (91%)	112 (90%)	13 (10%)	0	100	100
12	BV	85/87 (98%)	73 (86%)	12 (14%)	0	100	100
13	BW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
14	BX	142/145 (98%)	127 (89%)	15 (11%)	0	100	100
15	BY	132/135 (98%)	119 (90%)	13 (10%)	0	100	100
16	Ba	95/119 (80%)	83 (87%)	12 (13%)	0	100	100
17	Bb	79/82 (96%)	69 (87%)	10 (13%)	0	100	100
18	Be	58/63 (92%)	49 (84%)	9 (16%)	0	100	100
19	BD	221/240 (92%)	204 (92%)	17 (8%)	0	100	100
20	BF	204/225 (91%)	184 (90%)	20 (10%)	0	100	100
21	BK	94/105 (90%)	81 (86%)	13 (14%)	0	100	100
22	BP	122/142 (86%)	112 (92%)	10 (8%)	0	100	100
23	BQ	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
24	BR	123/136 (90%)	113 (92%)	10 (8%)	0	100	100
25	BS	143/146 (98%)	129 (90%)	14 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	BT	139/144 (96%)	122 (88%)	17 (12%)	0	100	100
27	BU	105/121 (87%)	93 (89%)	12 (11%)	0	100	100
28	BZ	67/108 (62%)	62 (92%)	5 (8%)	0	100	100
29	Bc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
30	Bd	51/56 (91%)	48 (94%)	3 (6%)	0	100	100
31	Bg	310/319 (97%)	276 (89%)	34 (11%)	0	100	100
32	Bf	73/152 (48%)	64 (88%)	9 (12%)	0	100	100
33	BM	122/143 (85%)	110 (90%)	12 (10%)	0	100	100
35	AA	245/254 (96%)	228 (93%)	17 (7%)	0	100	100
36	AB	383/387 (99%)	362 (94%)	21 (6%)	0	100	100
37	AC	359/362 (99%)	334 (93%)	25 (7%)	0	100	100
41	AD	290/297 (98%)	275 (95%)	15 (5%)	0	100	100
42	AE	152/176 (86%)	141 (93%)	11 (7%)	0	100	100
43	AF	220/244 (90%)	208 (94%)	12 (6%)	0	100	100
44	AG	228/256 (89%)	209 (92%)	19 (8%)	0	100	100
45	AH	188/191 (98%)	174 (93%)	14 (7%)	0	100	100
46	AI	201/221 (91%)	190 (94%)	11 (6%)	0	100	100
47	AJ	167/174 (96%)	143 (86%)	24 (14%)	0	100	100
48	AL	191/199 (96%)	177 (93%)	14 (7%)	0	100	100
49	AM	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
50	AN	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
51	AO	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
52	AP	171/184 (93%)	165 (96%)	6 (4%)	0	100	100
53	AQ	183/186 (98%)	178 (97%)	5 (3%)	0	100	100
54	AR	186/189 (98%)	175 (94%)	11 (6%)	0	100	100
55	AS	170/178 (96%)	159 (94%)	11 (6%)	0	100	100
56	AT	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
57	AU	98/121 (81%)	88 (90%)	10 (10%)	0	100	100
58	AV	134/137 (98%)	131 (98%)	3 (2%)	0	100	100
59	AW	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
60	AX	119/142 (84%)	113 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	AY	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
62	AZ	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
63	Aa	146/149 (98%)	135 (92%)	11 (8%)	0	100	100
64	Ab	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
65	Ac	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
66	Ad	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
67	Ae	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
68	Af	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
69	Ag	110/121 (91%)	104 (94%)	6 (6%)	0	100	100
70	Ah	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
71	Ai	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
72	Aj	85/88 (97%)	82 (96%)	3 (4%)	0	100	100
73	Ak	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
74	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
75	Am	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	103/106 (97%)	90 (87%)	13 (13%)	0	100	100
78	Ap	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
79	E	215/217 (99%)	197 (92%)	18 (8%)	0	100	100
80	DC	819/842 (97%)	755 (92%)	63 (8%)	1 (0%)	48	74
81	V	187/312 (60%)	174 (93%)	13 (7%)	0	100	100
All	All	12121/13257 (91%)	11233 (93%)	887 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
80	DC	700	ARG

5.3.2 Protein sidechains [i](#)

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	BA	173/210 (82%)	173 (100%)	0	100	100
2	BB	191/224 (85%)	191 (100%)	0	100	100
3	BC	176/205 (86%)	176 (100%)	0	100	100
4	BE	221/222 (100%)	221 (100%)	0	100	100
5	BG	193/201 (96%)	193 (100%)	0	100	100
6	BH	165/170 (97%)	165 (100%)	0	100	100
7	BI	150/161 (93%)	150 (100%)	0	100	100
8	BJ	158/166 (95%)	158 (100%)	0	100	100
9	BL	136/137 (99%)	136 (100%)	0	100	100
10	BN	127/128 (99%)	127 (100%)	0	100	100
11	BO	96/105 (91%)	96 (100%)	0	100	100
12	BV	74/74 (100%)	74 (100%)	0	100	100
13	BW	110/111 (99%)	110 (100%)	0	100	100
14	BX	119/120 (99%)	119 (100%)	0	100	100
15	BY	112/113 (99%)	112 (100%)	0	100	100
16	Ba	83/100 (83%)	83 (100%)	0	100	100
17	Bb	70/71 (99%)	70 (100%)	0	100	100
18	Be	51/54 (94%)	51 (100%)	0	100	100
19	BD	182/195 (93%)	182 (100%)	0	100	100
20	BF	173/191 (91%)	173 (100%)	0	100	100
21	BK	89/98 (91%)	89 (100%)	0	100	100
22	BP	104/118 (88%)	104 (100%)	0	100	100
23	BQ	117/119 (98%)	117 (100%)	0	100	100
24	BR	113/124 (91%)	113 (100%)	0	100	100
25	BS	128/129 (99%)	128 (100%)	0	100	100
26	BT	113/116 (97%)	113 (100%)	0	100	100
27	BU	100/114 (88%)	100 (100%)	0	100	100
28	BZ	61/89 (68%)	61 (100%)	0	100	100
29	Bc	56/60 (93%)	56 (100%)	0	100	100
30	Bd	47/49 (96%)	47 (100%)	0	100	100
31	Bg	256/262 (98%)	256 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	Bf	66/135 (49%)	66 (100%)	0	100	100
33	BM	100/119 (84%)	100 (100%)	0	100	100
35	AA	189/196 (96%)	189 (100%)	0	100	100
36	AB	321/322 (100%)	321 (100%)	0	100	100
37	AC	288/289 (100%)	288 (100%)	0	100	100
41	AD	241/245 (98%)	241 (100%)	0	100	100
42	AE	134/153 (88%)	134 (100%)	0	100	100
43	AF	186/205 (91%)	186 (100%)	0	100	100
44	AG	189/208 (91%)	189 (100%)	0	100	100
45	AH	170/171 (99%)	170 (100%)	0	100	100
46	AI	176/187 (94%)	176 (100%)	0	100	100
47	AJ	147/150 (98%)	147 (100%)	0	100	100
48	AL	154/159 (97%)	154 (100%)	0	100	100
49	AM	107/109 (98%)	107 (100%)	0	100	100
50	AN	175/176 (99%)	175 (100%)	0	100	100
51	AO	160/162 (99%)	160 (100%)	0	100	100
52	AP	141/146 (97%)	141 (100%)	0	100	100
53	AQ	150/151 (99%)	150 (100%)	0	100	100
54	AR	153/154 (99%)	153 (100%)	0	100	100
55	AS	156/162 (96%)	156 (100%)	0	100	100
56	AT	136/137 (99%)	136 (100%)	0	100	100
57	AU	87/107 (81%)	87 (100%)	0	100	100
58	AV	104/105 (99%)	104 (100%)	0	100	100
59	AW	55/129 (43%)	55 (100%)	0	100	100
60	AX	105/118 (89%)	105 (100%)	0	100	100
61	AY	109/110 (99%)	109 (100%)	0	100	100
62	AZ	115/116 (99%)	115 (100%)	0	100	100
63	Aa	118/119 (99%)	118 (100%)	0	100	100
64	Ab	46/47 (98%)	46 (100%)	0	100	100
65	Ac	81/88 (92%)	81 (100%)	0	100	100
66	Ad	96/97 (99%)	96 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	Ae	109/111 (98%)	109 (100%)	0	100	100
68	Af	90/91 (99%)	90 (100%)	0	100	100
69	Ag	95/103 (92%)	95 (100%)	0	100	100
70	Ah	104/105 (99%)	104 (100%)	0	100	100
71	Ai	81/82 (99%)	81 (100%)	0	100	100
72	Aj	70/71 (99%)	70 (100%)	0	100	100
73	Ak	68/69 (99%)	68 (100%)	0	100	100
74	Al	45/46 (98%)	45 (100%)	0	100	100
75	Am	47/116 (40%)	47 (100%)	0	100	100
76	An	23/23 (100%)	23 (100%)	0	100	100
77	Ao	90/91 (99%)	90 (100%)	0	100	100
78	Ap	71/72 (99%)	71 (100%)	0	100	100
79	E	198/198 (100%)	198 (100%)	0	100	100
80	DC	699/714 (98%)	699 (100%)	0	100	100
81	V	160/254 (63%)	160 (100%)	0	100	100
All	All	10349/11154 (93%)	10349 (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 135 such sidechains are listed below:

Mol	Chain	Res	Type
73	Ak	57	ASN
74	Al	43	ASN
80	DC	654	GLN
31	Bg	153	GLN
31	Bg	139	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1780/1798 (98%)	396 (22%)	12 (0%)
38	A1	3194/3360 (95%)	568 (17%)	22 (0%)
39	A3	120/121 (99%)	18 (15%)	1 (0%)
40	A4	157/158 (99%)	32 (20%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
82	EC	149/202 (73%)	78 (52%)	5 (3%)
All	All	5400/5639 (95%)	1092 (20%)	40 (0%)

5 of 1092 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	2	A
34	B5	4	C
34	B5	17	C
34	B5	25	C
34	B5	26	A

5 of 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A1	2496	C
82	EC	6789	G
38	A1	2497	U
38	A1	3121	U
82	EC	6911	A

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

68 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
38	1MA	A1	2142	38,83	21,25,26	1.34	4 (19%)	30,37,40	1.70	5 (16%)
38	A2M	A1	2220	38	22,25,26	1.50	4 (18%)	30,36,39	1.98	9 (30%)
38	OMG	A1	2793	38	23,26,27	1.18	3 (13%)	32,38,41	1.99	6 (18%)
38	OMU	A1	2729	38	19,22,23	1.25	3 (15%)	25,31,34	1.78	4 (16%)
34	A2M	B5	974	34	22,25,26	1.45	4 (18%)	30,36,39	2.12	10 (33%)
38	A2M	A1	1449	38,83	22,25,26	1.50	3 (13%)	30,36,39	2.06	7 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	OMC	A1	650	38,83	19,22,23	0.82	0	25,31,34	0.83	0
34	OMU	B5	578	34	19,22,23	1.20	3 (15%)	25,31,34	1.79	5 (20%)
38	A2M	A1	807	38	22,25,26	1.46	5 (22%)	30,36,39	2.16	10 (33%)
34	OMG	B5	1428	34	23,26,27	1.17	3 (13%)	32,38,41	1.96	6 (18%)
34	A2M	B5	100	34,83	22,25,26	1.50	5 (22%)	30,36,39	2.03	7 (23%)
34	OMG	B5	1271	34	23,26,27	1.18	3 (13%)	32,38,41	1.98	6 (18%)
36	HIC	AB	243	36	10,11,12	1.47	1 (10%)	9,14,16	1.31	2 (22%)
34	OMG	B5	1572	34	23,26,27	1.18	2 (8%)	32,38,41	1.96	6 (18%)
38	OMG	A1	2619	38	23,26,27	1.19	3 (13%)	32,38,41	1.94	6 (18%)
38	OMG	A1	2288	38	23,26,27	1.22	3 (13%)	32,38,41	2.02	5 (15%)
38	OMG	A1	867	38	23,26,27	1.18	3 (13%)	32,38,41	1.96	6 (18%)
38	OMC	A1	2197	38	19,22,23	0.80	0	25,31,34	0.84	0
38	OMU	A1	1888	38	19,22,23	1.29	3 (15%)	25,31,34	1.92	5 (20%)
34	A2M	B5	619	34,83	22,25,26	1.48	5 (22%)	30,36,39	2.10	9 (30%)
38	OMC	A1	663	38	19,22,23	0.80	0	25,31,34	0.75	0
38	A2M	A1	2280	38	22,25,26	1.50	4 (18%)	30,36,39	2.06	9 (30%)
38	OMC	A1	2948	38	19,22,23	0.78	0	25,31,34	0.84	1 (4%)
38	OMC	A1	1437	38,83	19,22,23	0.80	0	25,31,34	0.94	2 (8%)
34	A2M	B5	436	34	22,25,26	1.49	4 (18%)	30,36,39	2.06	8 (26%)
34	A2M	B5	796	34	22,25,26	1.48	4 (18%)	30,36,39	2.25	10 (33%)
38	1MA	A1	645	38,83	21,25,26	1.35	4 (19%)	30,37,40	1.71	5 (16%)
34	MA6	B5	1782	34	23,26,27	1.48	5 (21%)	33,38,41	2.08	11 (33%)
34	A2M	B5	541	34	22,25,26	1.49	4 (18%)	30,36,39	2.13	7 (23%)
38	OMG	A1	2815	38	23,26,27	1.19	3 (13%)	32,38,41	2.01	7 (21%)
38	5MC	A1	2278	38,83	19,22,23	1.46	3 (15%)	26,32,35	1.16	3 (11%)
38	OMG	A1	2922	38	23,26,27	1.20	3 (13%)	32,38,41	1.97	6 (18%)
38	OMU	A1	2347	38	19,22,23	1.29	3 (15%)	25,31,34	1.85	5 (20%)
38	OMU	A1	2921	38	19,22,23	1.25	3 (15%)	25,31,34	1.80	5 (20%)
38	A2M	A1	2946	38,83	22,25,26	1.46	5 (22%)	30,36,39	2.20	10 (33%)
34	4AC	B5	1773	34	21,24,25	1.06	1 (4%)	28,34,37	1.16	3 (10%)
38	OMU	A1	2724	38	19,22,23	1.27	3 (15%)	25,31,34	1.81	5 (20%)
34	A2M	B5	28	34,83	22,25,26	1.47	4 (18%)	30,36,39	2.06	10 (33%)
34	G7M	B5	1575	34,82	23,26,27	2.57	6 (26%)	34,39,42	3.06	15 (44%)
34	A2M	B5	420	34	22,25,26	1.50	4 (18%)	30,36,39	2.05	8 (26%)
80	DDE	DC	699	80	18,20,21	1.05	1 (5%)	17,28,30	0.92	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	A2M	A1	1133	38	22,25,26	1.49	5 (22%)	30,36,39	2.13	9 (30%)
34	B8N	B5	1191	34	25,29,30	1.38	3 (12%)	28,42,45	2.61	6 (21%)
38	UR3	A1	2634	38	19,22,23	0.98	0	26,32,35	1.72	4 (15%)
38	A2M	A1	2256	38	22,25,26	1.48	4 (18%)	30,36,39	2.13	9 (30%)
38	A2M	A1	817	38,83	22,25,26	1.49	5 (22%)	30,36,39	2.05	8 (26%)
34	MA6	B5	1781	34	23,26,27	1.49	5 (21%)	33,38,41	2.08	11 (33%)
38	OMG	A1	805	38	23,26,27	1.18	4 (17%)	32,38,41	2.02	6 (18%)
38	OMU	A1	898	38	19,22,23	1.26	3 (15%)	25,31,34	1.80	5 (20%)
34	OMG	B5	1126	34	23,26,27	1.17	3 (13%)	32,38,41	2.05	6 (18%)
38	OMC	A1	2337	38	19,22,23	0.78	0	25,31,34	0.77	0
34	OMC	B5	1639	34	19,22,23	0.78	0	25,31,34	0.70	0
38	A2M	A1	649	38,83	22,25,26	1.46	5 (22%)	30,36,39	2.09	9 (30%)
34	OMC	B5	414	34	19,22,23	0.78	0	25,31,34	0.81	0
34	OMC	B5	1007	34	19,22,23	0.81	0	25,31,34	0.86	0
38	OMC	A1	2959	38	19,22,23	0.80	0	25,31,34	0.79	0
38	A2M	A1	876	38	22,25,26	1.48	4 (18%)	30,36,39	2.02	7 (23%)
38	OMU	A1	2417	38	19,22,23	1.25	3 (15%)	25,31,34	1.77	5 (20%)
38	OMG	A1	2791	38	23,26,27	1.20	3 (13%)	32,38,41	1.98	5 (15%)
38	5MC	A1	2870	38	19,22,23	1.51	3 (15%)	26,32,35	1.26	3 (11%)
34	OMG	B5	562	34	23,26,27	1.20	3 (13%)	32,38,41	1.95	5 (15%)
38	OMG	A1	908	38	23,26,27	1.23	3 (13%)	32,38,41	2.10	6 (18%)
34	OMU	B5	1269	34,83	19,22,23	1.29	4 (21%)	25,31,34	1.81	5 (20%)
38	A2M	A1	2281	38	22,25,26	1.44	5 (22%)	30,36,39	2.16	11 (36%)
38	OMU	A1	2421	38	19,22,23	1.25	3 (15%)	25,31,34	1.83	5 (20%)
34	4AC	B5	1280	34	21,24,25	1.06	1 (4%)	28,34,37	1.02	2 (7%)
38	A2M	A1	2640	38	22,25,26	1.47	4 (18%)	30,36,39	2.03	7 (23%)
38	OMG	A1	1450	38	23,26,27	1.19	3 (13%)	32,38,41	1.98	6 (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
38	1MA	A1	2142	38,83	-	0/7/25/26	0/3/3/3
38	A2M	A1	2220	38	-	1/9/27/28	0/3/3/3
38	OMG	A1	2793	38	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	OMU	A1	2729	38	-	4/9/27/28	0/2/2/2
34	A2M	B5	974	34	-	1/9/27/28	0/3/3/3
38	A2M	A1	1449	38,83	-	0/9/27/28	0/3/3/3
38	OMC	A1	650	38,83	-	0/9/27/28	0/2/2/2
34	OMU	B5	578	34	-	0/9/27/28	0/2/2/2
38	A2M	A1	807	38	-	1/9/27/28	0/3/3/3
34	OMG	B5	1428	34	-	4/9/27/28	0/3/3/3
34	A2M	B5	100	34,83	-	1/9/27/28	0/3/3/3
34	OMG	B5	1271	34	-	1/9/27/28	0/3/3/3
36	HIC	AB	243	36	-	0/5/6/8	0/1/1/1
34	OMG	B5	1572	34	-	2/9/27/28	0/3/3/3
38	OMG	A1	2619	38	-	1/9/27/28	0/3/3/3
38	OMG	A1	2288	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	867	38	-	1/9/27/28	0/3/3/3
38	OMC	A1	2197	38	-	6/9/27/28	0/2/2/2
38	OMU	A1	1888	38	-	0/9/27/28	0/2/2/2
34	A2M	B5	619	34,83	-	3/9/27/28	0/3/3/3
38	OMC	A1	663	38	-	1/9/27/28	0/2/2/2
38	A2M	A1	2280	38	-	0/9/27/28	0/3/3/3
38	OMC	A1	2948	38	-	0/9/27/28	0/2/2/2
38	OMC	A1	1437	38,83	-	4/9/27/28	0/2/2/2
34	A2M	B5	436	34	-	1/9/27/28	0/3/3/3
34	A2M	B5	796	34	-	0/9/27/28	0/3/3/3
38	1MA	A1	645	38,83	-	2/7/25/26	0/3/3/3
34	MA6	B5	1782	34	-	5/11/29/30	0/3/3/3
34	A2M	B5	541	34	-	6/9/27/28	0/3/3/3
38	OMG	A1	2815	38	-	0/9/27/28	0/3/3/3
38	5MC	A1	2278	38,83	-	0/7/25/26	0/2/2/2
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2347	38	-	0/9/27/28	0/2/2/2
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	2946	38,83	-	1/9/27/28	0/3/3/3
34	4AC	B5	1773	34	-	7/11/29/30	0/2/2/2
38	OMU	A1	2724	38	-	1/9/27/28	0/2/2/2
34	A2M	B5	28	34,83	-	1/9/27/28	0/3/3/3
34	G7M	B5	1575	34,82	-	0/7/25/26	0/3/3/3
34	A2M	B5	420	34	-	0/9/27/28	0/3/3/3
80	DDE	DC	699	80	-	8/20/21/23	0/1/1/1
38	A2M	A1	1133	38	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	B8N	B5	1191	34	-	6/16/34/35	0/2/2/2
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
38	A2M	A1	2256	38	-	1/9/27/28	0/3/3/3
38	A2M	A1	817	38,83	-	2/9/27/28	0/3/3/3
34	MA6	B5	1781	34	-	3/11/29/30	0/3/3/3
38	OMG	A1	805	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	898	38	-	0/9/27/28	0/2/2/2
34	OMG	B5	1126	34	-	2/9/27/28	0/3/3/3
38	OMC	A1	2337	38	-	1/9/27/28	0/2/2/2
34	OMC	B5	1639	34	-	1/9/27/28	0/2/2/2
38	A2M	A1	649	38,83	-	1/9/27/28	0/3/3/3
34	OMC	B5	414	34	-	0/9/27/28	0/2/2/2
34	OMC	B5	1007	34	-	1/9/27/28	0/2/2/2
38	OMC	A1	2959	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	876	38	-	1/9/27/28	0/3/3/3
38	OMU	A1	2417	38	-	1/9/27/28	0/2/2/2
38	OMG	A1	2791	38	-	1/9/27/28	0/3/3/3
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
34	OMG	B5	562	34	-	1/9/27/28	0/3/3/3
38	OMG	A1	908	38	-	0/9/27/28	0/3/3/3
34	OMU	B5	1269	34,83	-	5/9/27/28	0/2/2/2
38	A2M	A1	2281	38	-	2/9/27/28	0/3/3/3
38	OMU	A1	2421	38	-	1/9/27/28	0/2/2/2
34	4AC	B5	1280	34	-	2/11/29/30	0/2/2/2
38	A2M	A1	2640	38	-	1/9/27/28	0/3/3/3
38	OMG	A1	1450	38	-	1/9/27/28	0/3/3/3

The worst 5 of 200 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	C8-N7	7.70	1.46	1.33
34	B5	1575	G7M	C5-N7	-5.13	1.33	1.39
38	A1	2278	5MC	C5-C4	5.06	1.47	1.44
38	A1	2870	5MC	C5-C4	5.03	1.47	1.44
34	B5	1781	MA6	C5-C4	4.68	1.47	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1191	B8N	C32-C31-N3	10.82	131.06	112.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1575	G7M	CN7-N7-C8	-7.64	113.22	124.79
38	A1	2634	UR3	C4-N3-C2	-6.76	119.14	124.58
38	A1	908	OMG	C5-C4-N3	-6.67	117.77	128.39
34	B5	1575	G7M	N9-C8-N7	-6.58	96.51	112.48

There are no chirality outliers.

5 of 101 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B5	28	A2M	C1'-C2'-O2'-CM'
34	B5	100	A2M	C1'-C2'-O2'-CM'
34	B5	562	OMG	C1'-C2'-O2'-CM2
34	B5	974	A2M	C1'-C2'-O2'-CM'
34	B5	1271	OMG	C1'-C2'-O2'-CM2

There are no ring outliers.

35 monomers are involved in 54 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	2220	A2M	3	0
38	A1	2793	OMG	1	0
34	B5	974	A2M	1	0
38	A1	1449	A2M	2	0
38	A1	650	OMC	3	0
34	B5	1428	OMG	1	0
34	B5	100	A2M	1	0
34	B5	1271	OMG	1	0
34	B5	1572	OMG	1	0
38	A1	867	OMG	1	0
38	A1	2197	OMC	2	0
34	B5	619	A2M	1	0
38	A1	663	OMC	1	0
34	B5	436	A2M	1	0
34	B5	796	A2M	1	0
38	A1	2347	OMU	1	0
34	B5	1773	4AC	4	0
38	A1	2724	OMU	1	0
34	B5	28	A2M	1	0
34	B5	1575	G7M	4	0
80	DC	699	DDE	1	0
38	A1	1133	A2M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	2256	A2M	7	0
38	A1	817	A2M	1	0
34	B5	1781	MA6	1	0
38	A1	898	OMU	1	0
34	B5	1126	OMG	1	0
38	A1	649	A2M	3	0
38	A1	876	A2M	1	0
38	A1	2417	OMU	1	0
34	B5	1269	OMU	2	0
38	A1	2281	A2M	1	0
34	B5	1280	4AC	2	0
38	A1	2640	A2M	1	0
38	A1	1450	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 244 ligands modelled in this entry, 243 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
85	GDP	DC	901	-	29,30,30	1.12	3 (10%)	45,47,47	1.92	9 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
85	GDP	DC	901	-	-	5/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	DC	901	GDP	C5-C4	3.06	1.47	1.38
85	DC	901	GDP	C6-N1	-2.14	1.34	1.38
85	DC	901	GDP	C5-N7	-2.13	1.34	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	DC	901	GDP	C5-C4-N3	-6.76	117.63	128.39
85	DC	901	GDP	C2-N3-C4	5.33	121.48	112.30
85	DC	901	GDP	N9-C4-N3	4.78	135.52	125.95
85	DC	901	GDP	C6-C5-N7	3.20	136.11	130.29
85	DC	901	GDP	C2-N1-C6	-2.89	119.86	125.11

There are no chirality outliers.

All (5) torsion outliers are listed below:

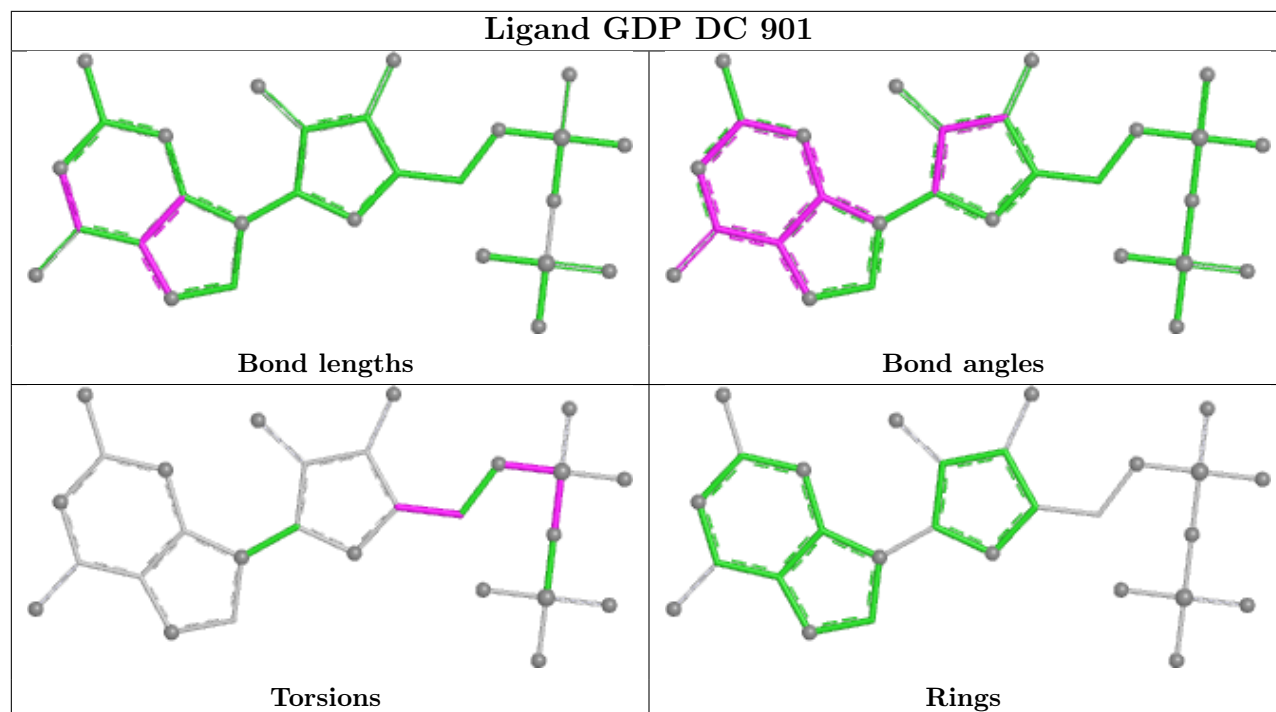
Mol	Chain	Res	Type	Atoms
85	DC	901	GDP	C5'-O5'-PA-O3A
85	DC	901	GDP	C5'-O5'-PA-O2A
85	DC	901	GDP	O4'-C4'-C5'-O5'
85	DC	901	GDP	C3'-C4'-C5'-O5'
85	DC	901	GDP	PB-O3A-PA-O1A

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	DC	901	GDP	7	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

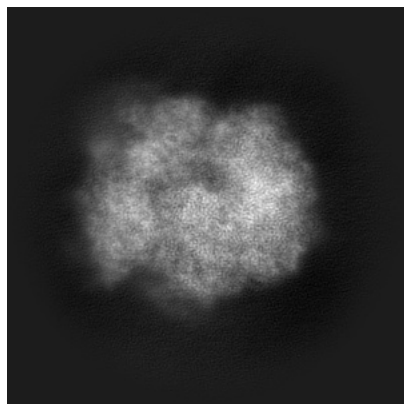
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28642. These allow visual inspection of the internal detail of the map and identification of artifacts.

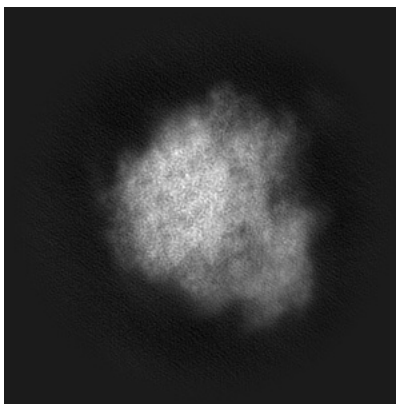
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

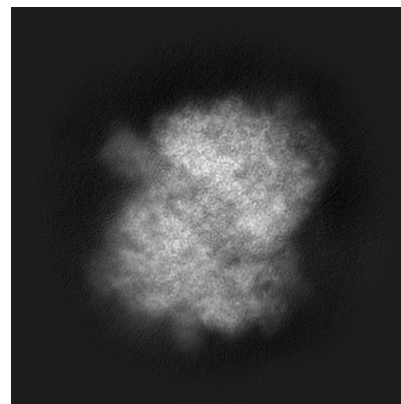
6.1.1 Primary map



X

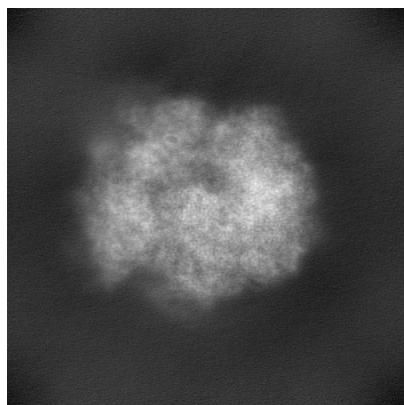


Y

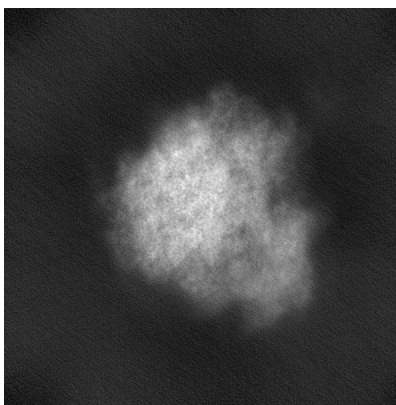


Z

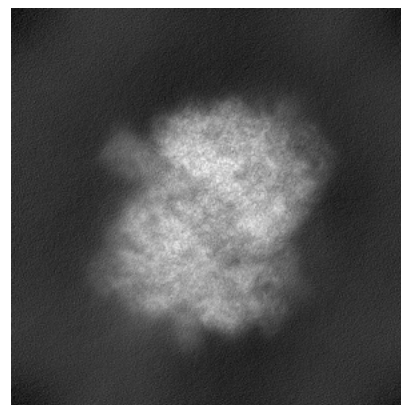
6.1.2 Raw map



X



Y

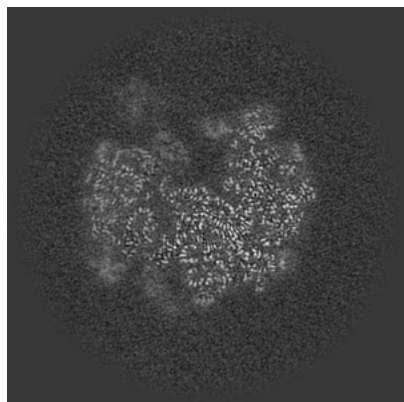


Z

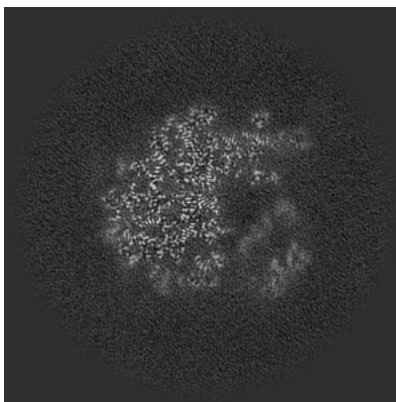
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

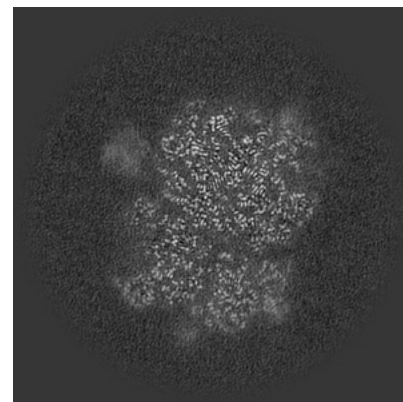
6.2.1 Primary map



X Index: 200

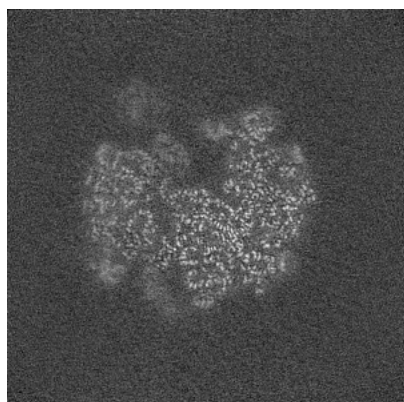


Y Index: 200

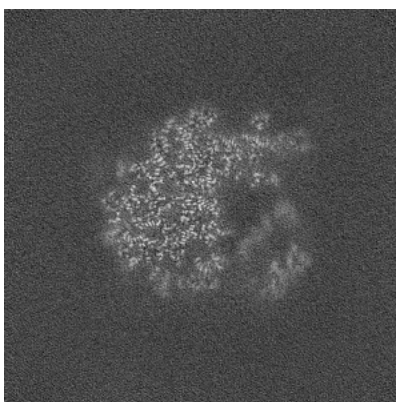


Z Index: 200

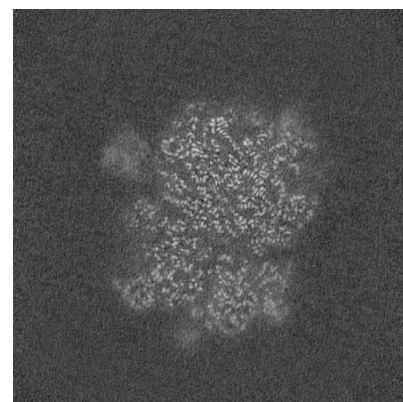
6.2.2 Raw map



X Index: 200



Y Index: 200

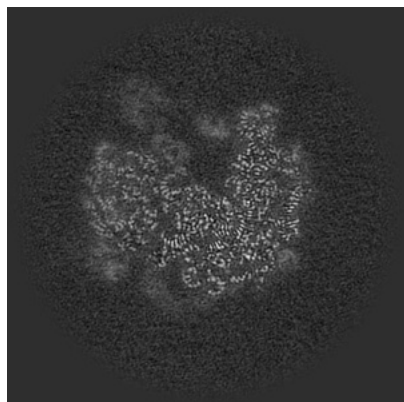


Z Index: 200

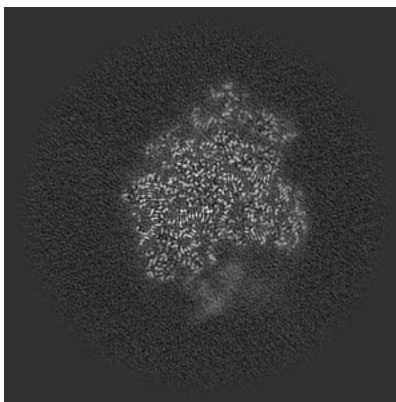
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

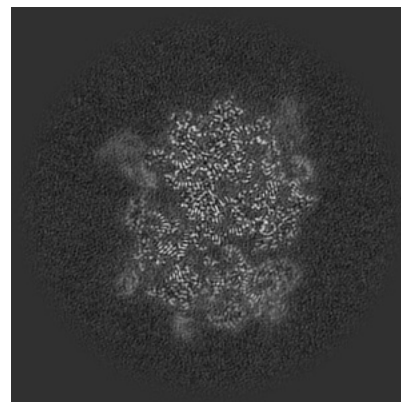
6.3.1 Primary map



X Index: 197

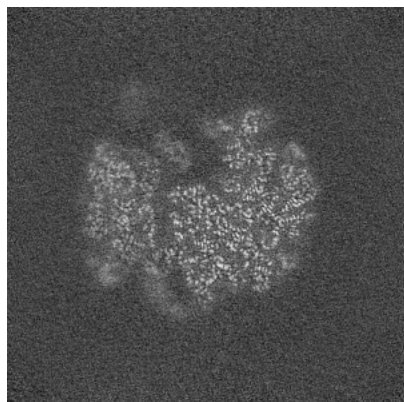


Y Index: 245

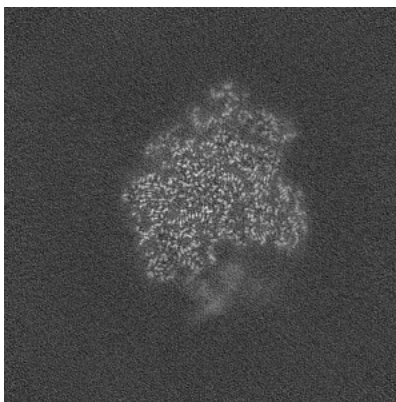


Z Index: 190

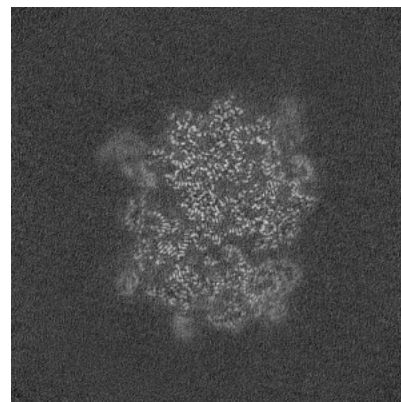
6.3.2 Raw map



X Index: 204



Y Index: 245

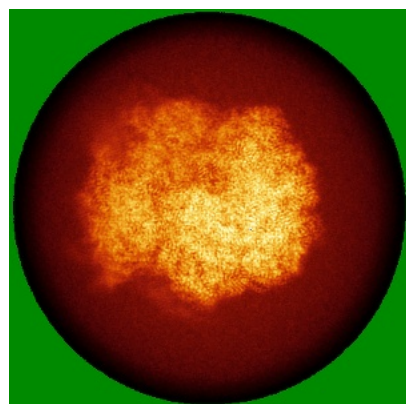


Z Index: 190

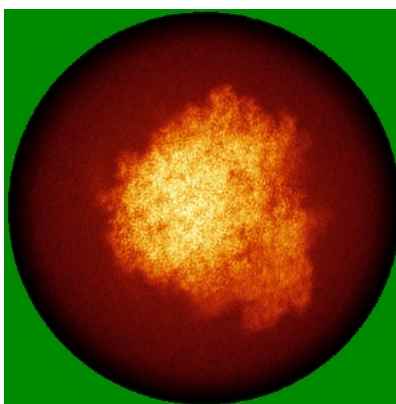
The images above show the largest variance slices of the map in three orthogonal directions.

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

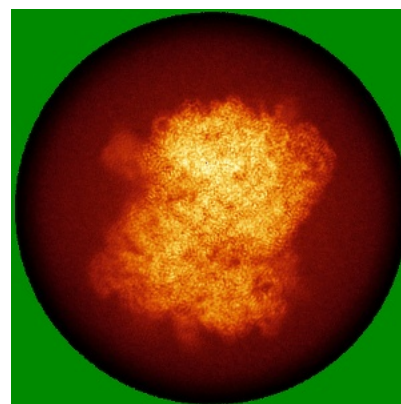
6.4.1 Primary map



X

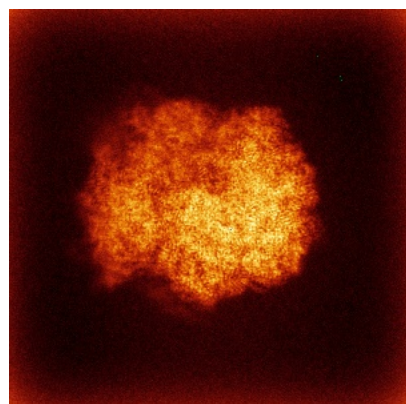


Y

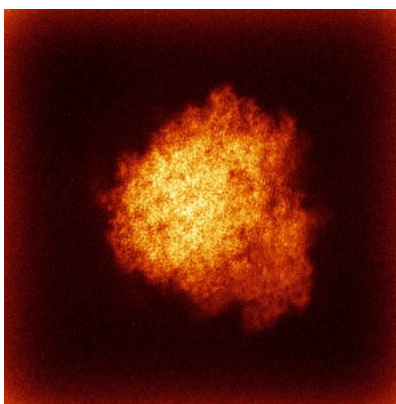


Z

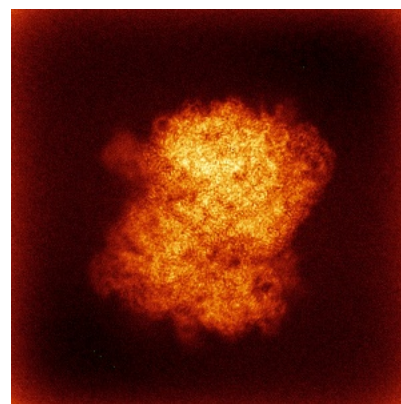
6.4.2 Raw map



X



Y

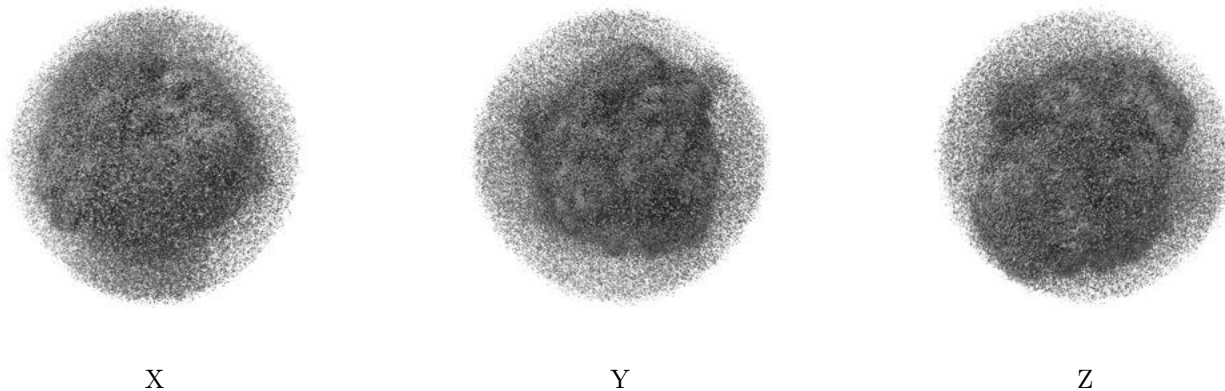


Z

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.

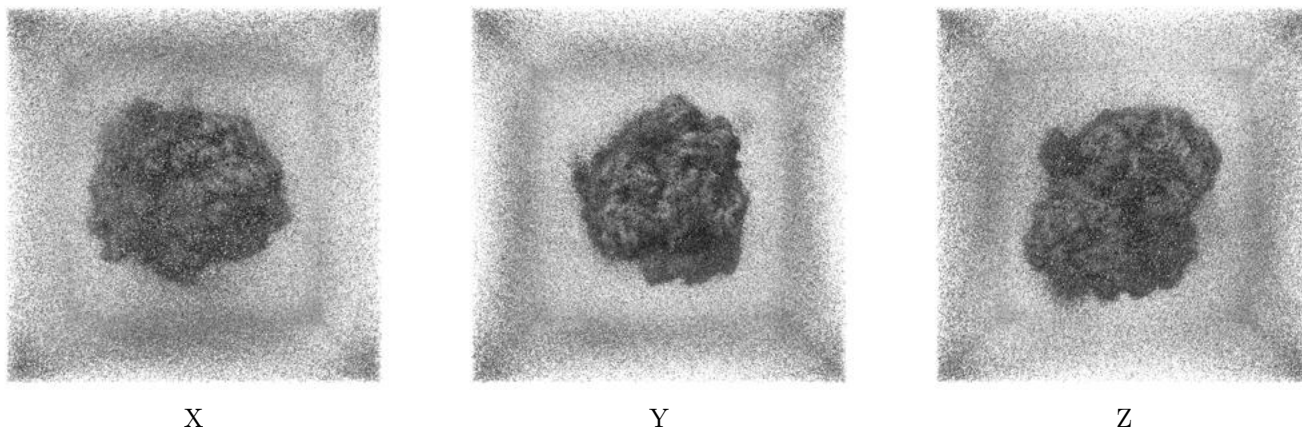
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

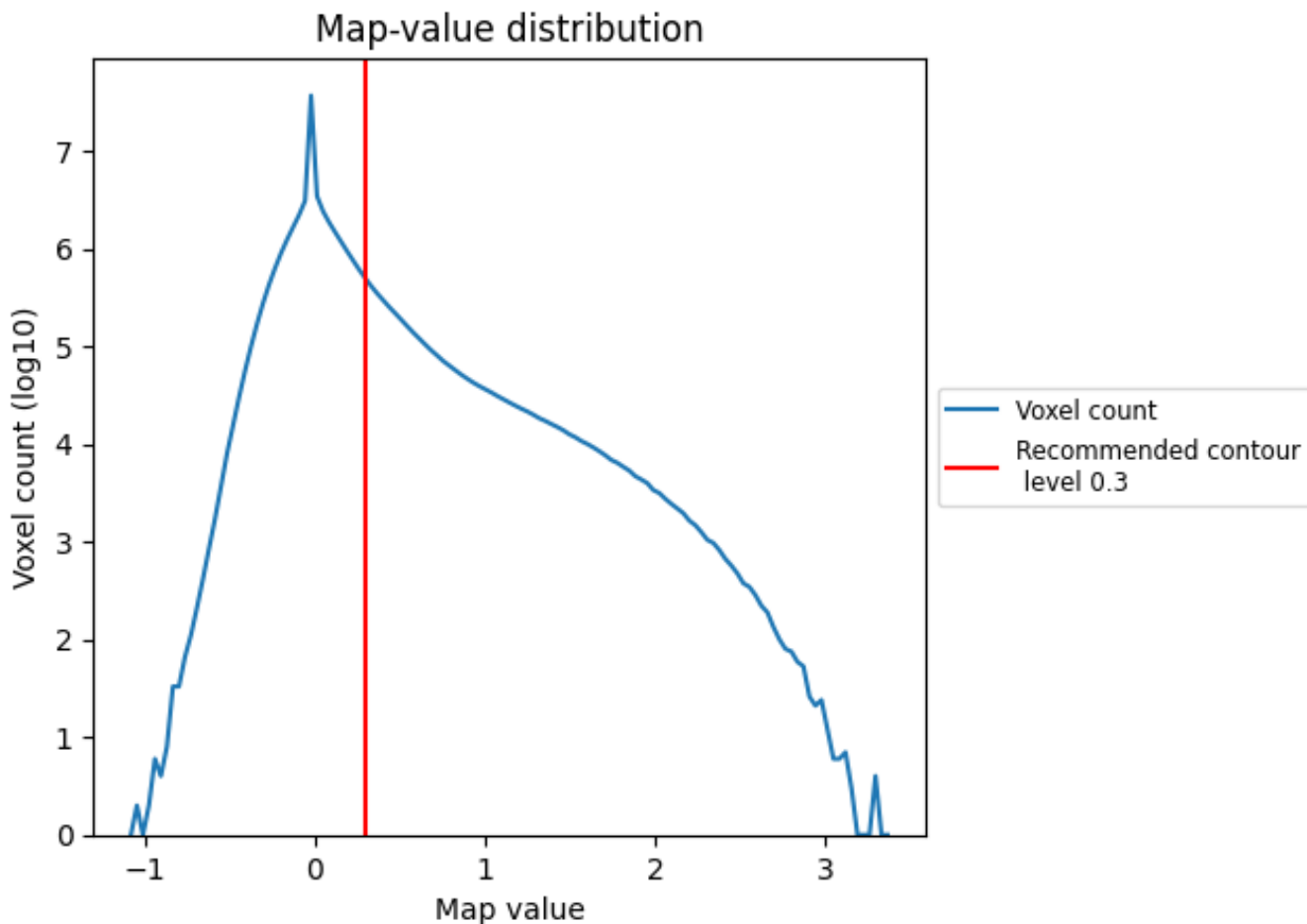
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

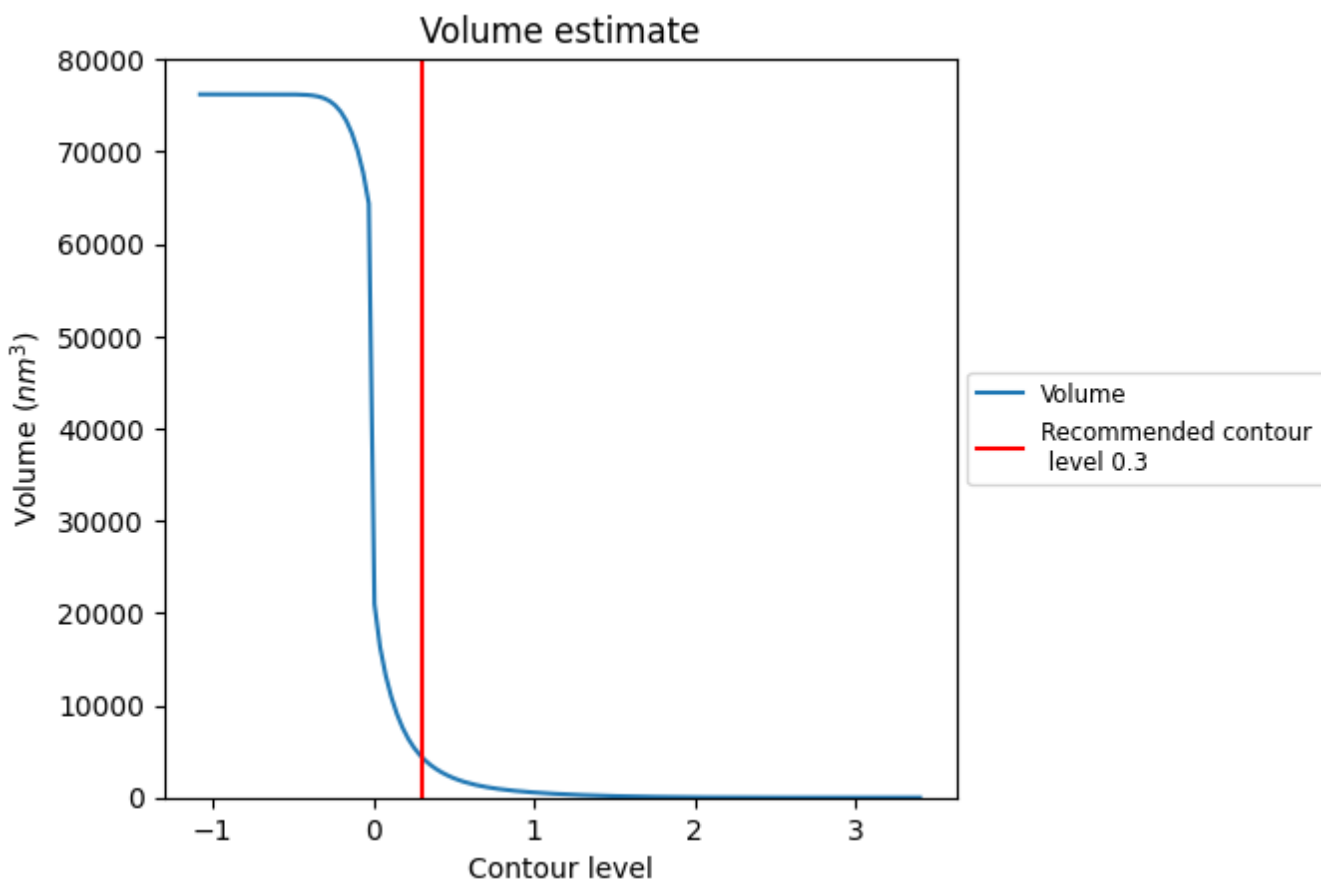
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

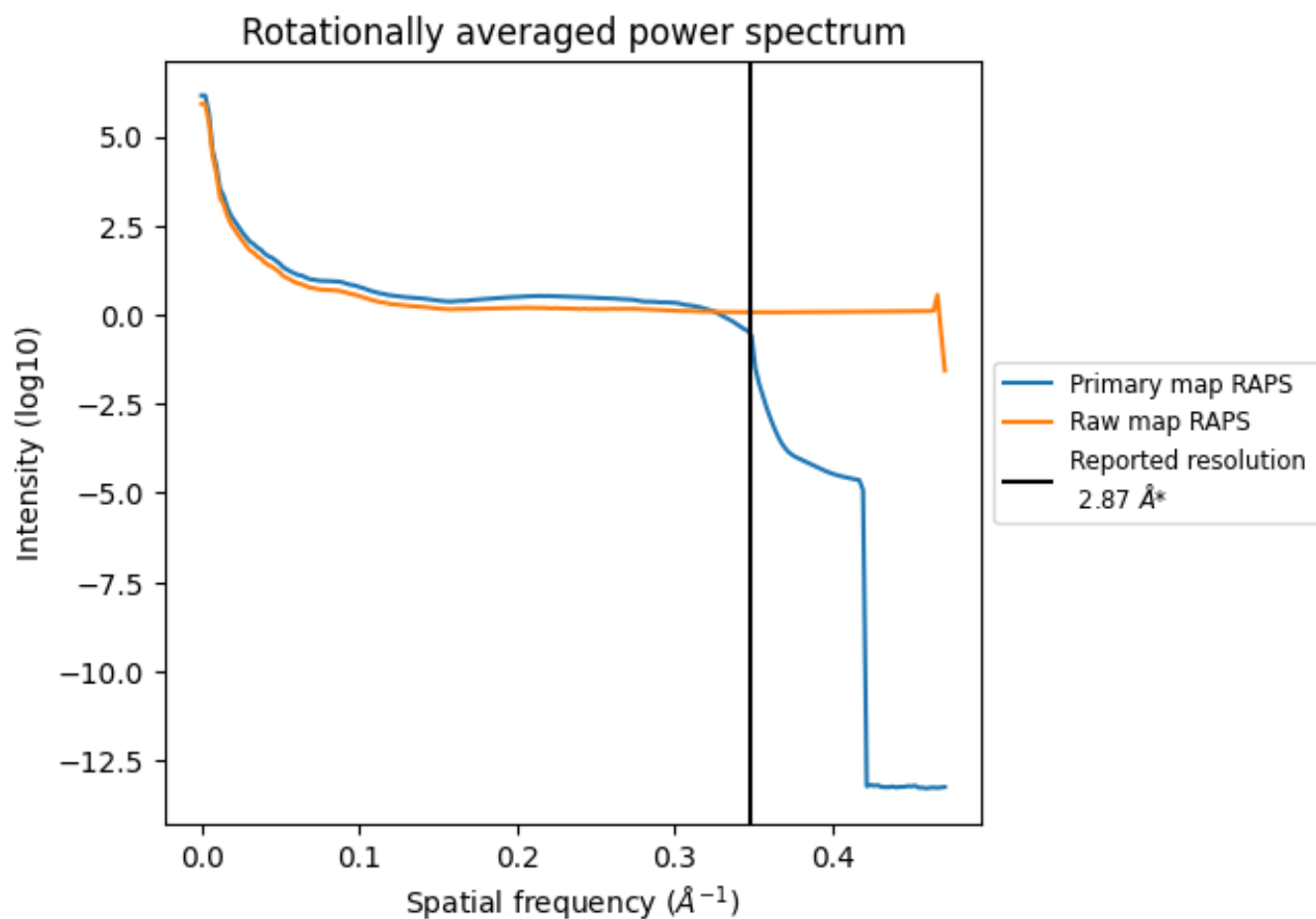
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 4390 nm³; this corresponds to an approximate mass of 3966 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 [i](#)

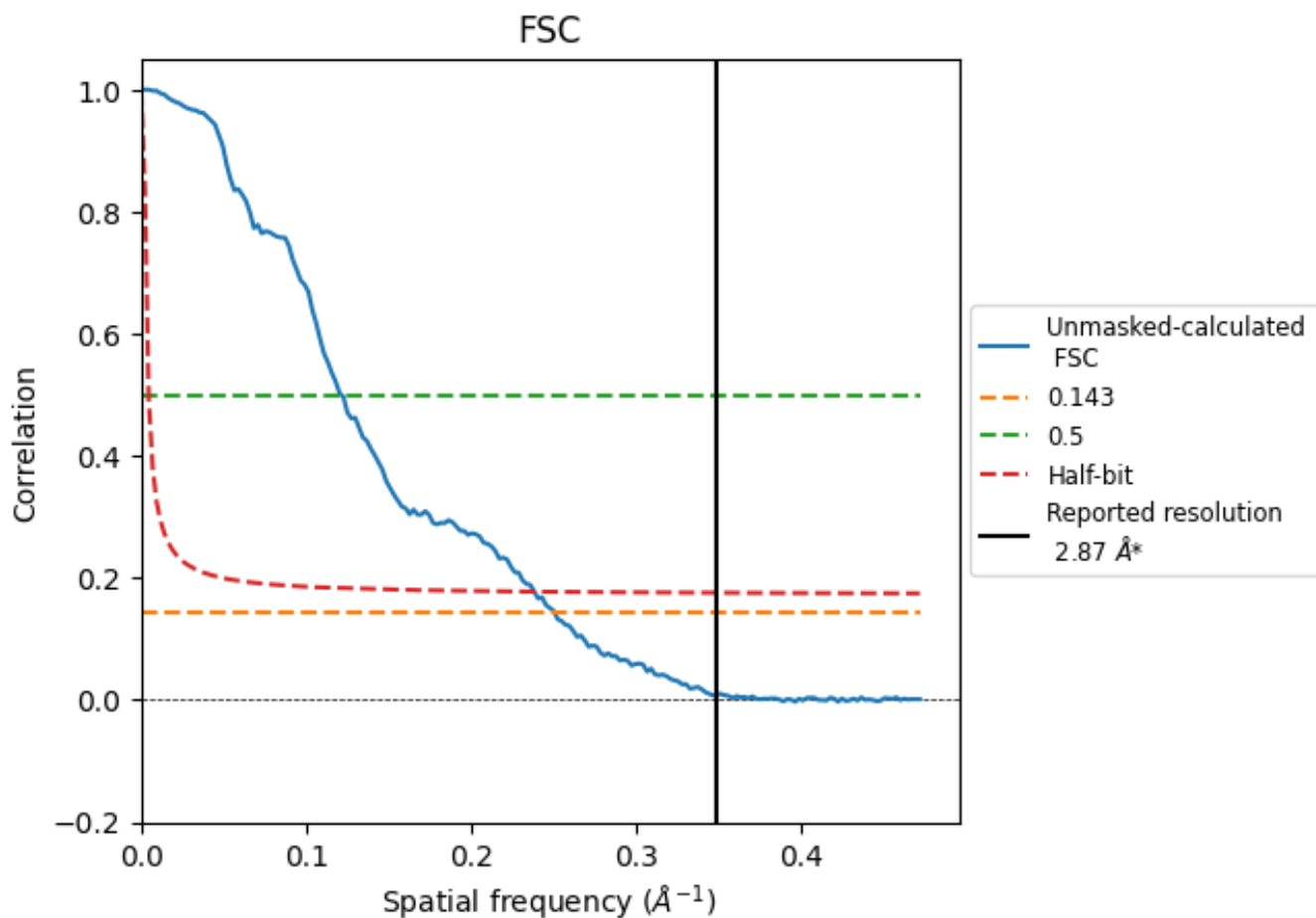


*Reported resolution corresponds to spatial frequency of 0.348 Å⁻¹

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 0.348 Å⁻¹

8.2 Resolution estimates [i](#)

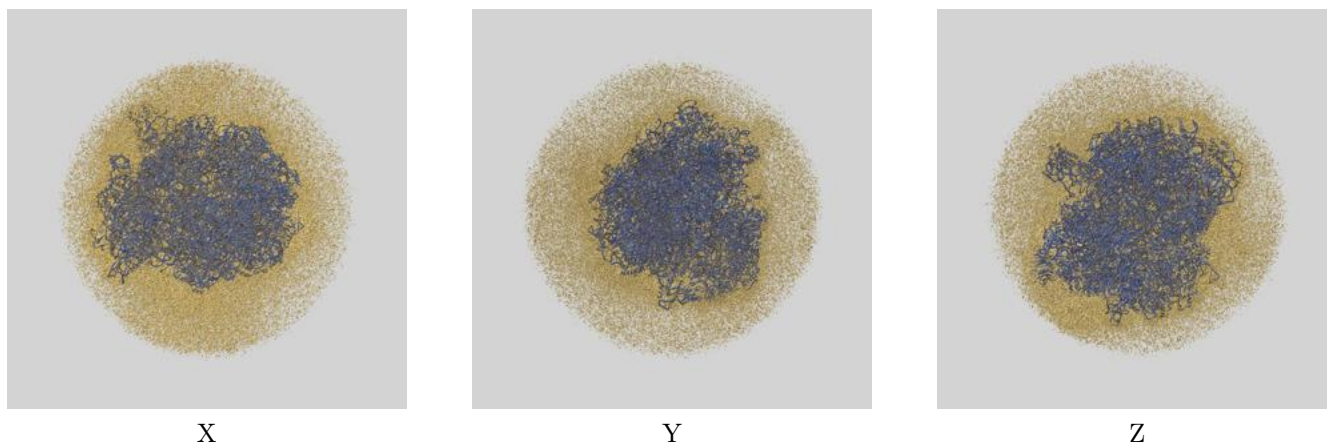
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.87	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.99	8.25	4.20

*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 3.99 differs from the reported value 2.87 by more than 10 %

9 Map-model fit [i](#)

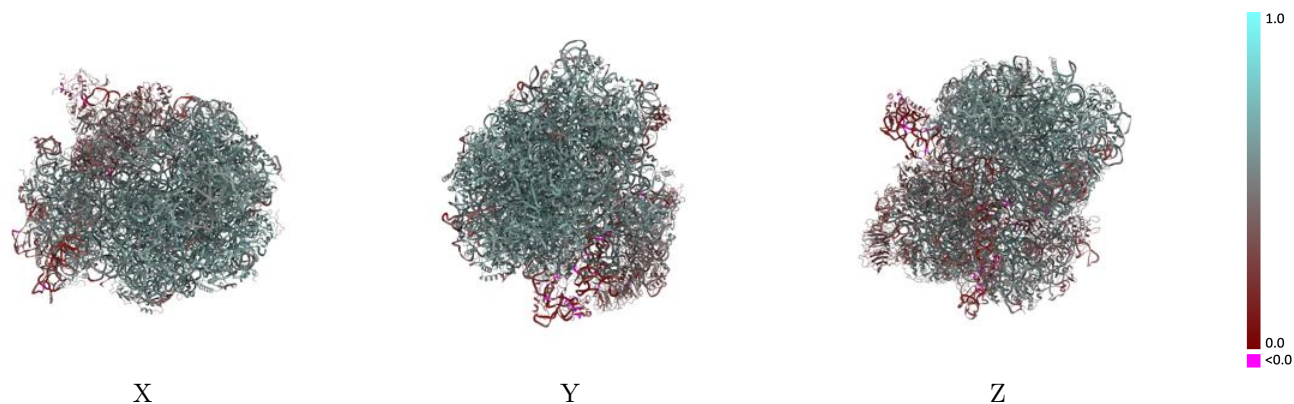
This section contains information regarding the fit between EMDB map EMD-28642 and PDB model 8EWB. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



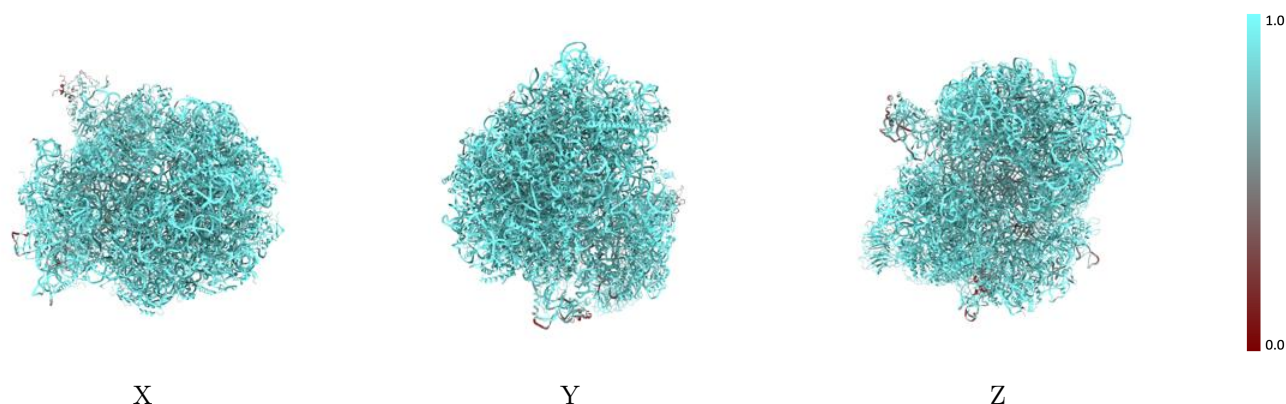
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



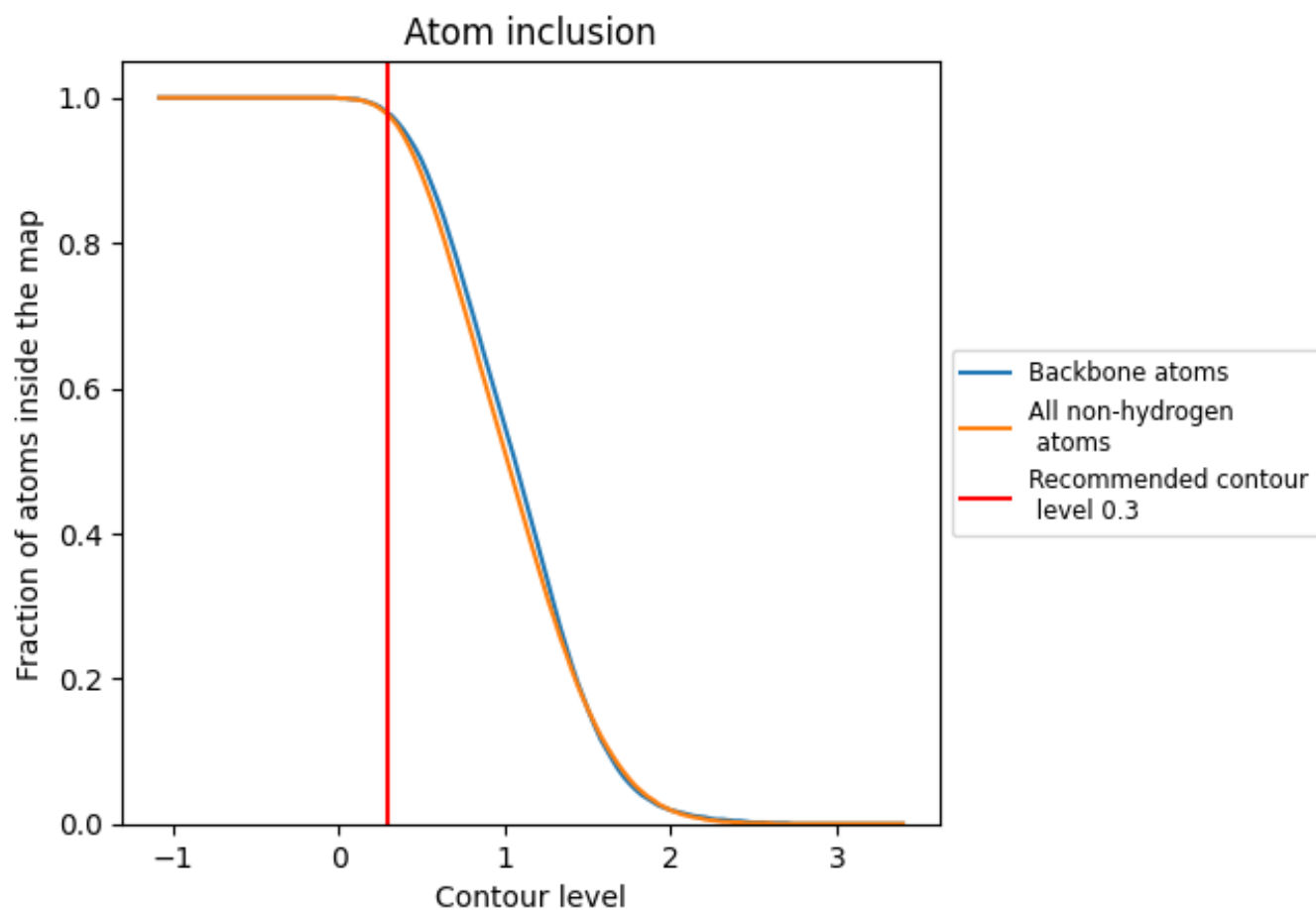
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9760	 0.5150
A1	 0.9920	 0.5620
A3	 1.0000	 0.5630
A4	 0.9980	 0.5870
AA	 0.9950	 0.6070
AB	 0.9970	 0.5820
AC	 0.9970	 0.5840
AD	 0.9880	 0.5280
AE	 0.9910	 0.5430
AF	 0.9970	 0.5790
AG	 0.9900	 0.5540
AH	 0.9820	 0.5450
AI	 0.9900	 0.5510
AJ	 0.9610	 0.4650
AL	 0.9950	 0.5750
AM	 0.9950	 0.5580
AN	 0.9990	 0.6090
AO	 0.9970	 0.5820
AP	 0.9940	 0.5880
AQ	 1.0000	 0.5980
AR	 0.9600	 0.5420
AS	 0.9960	 0.5690
AT	 0.9910	 0.5660
AU	 0.9830	 0.5190
AV	 0.9930	 0.5790
AW	 0.9960	 0.5880
AX	 0.9930	 0.5770
AY	 0.9950	 0.5920
AZ	 0.9950	 0.5670
Aa	 0.9980	 0.5990
Ab	 0.9890	 0.5470
Ac	 0.9890	 0.5710
Ad	 0.9720	 0.5610
Ae	 1.0000	 0.5990
Af	 0.9960	 0.5950















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Chain	Atom inclusion	Q-score
Ag	 0.9920	 0.5810
Ah	 0.9930	 0.5690
Ai	 0.9870	 0.5490
Aj	 0.9970	 0.6070
Ak	 0.9730	 0.5240
Al	 0.9980	 0.5900
Am	 0.9800	 0.5570
An	 0.9670	 0.5270
Ao	 0.9860	 0.5640
Ap	 0.9930	 0.5890
B5	 0.9760	 0.4790
BA	 0.9910	 0.5170
BB	 0.9850	 0.5300
BC	 0.9930	 0.5430
BD	 0.9730	 0.4230
BE	 0.9920	 0.5250
BF	 0.9690	 0.4220
BG	 0.9860	 0.4420
BH	 0.9680	 0.4740
BI	 0.9850	 0.5470
BJ	 0.9810	 0.5130
BK	 0.9390	 0.3340
BL	 0.9570	 0.5380
BM	 0.4890	 0.2250
BN	 0.9940	 0.5540
BO	 0.9910	 0.5420
BP	 0.8730	 0.3310
BQ	 0.9880	 0.4330
BR	 0.9820	 0.4500
BS	 0.9550	 0.3620
BT	 0.9770	 0.3940
BU	 0.9580	 0.4020
BV	 0.9850	 0.5220
BW	 0.9980	 0.5810
BX	 0.9880	 0.5450
BY	 0.9800	 0.4760
BZ	 0.9690	 0.3680
Ba	 0.9930	 0.5540
Bb	 0.9750	 0.5280
Bc	 0.9750	 0.4660
Bd	 0.9810	 0.4780
Be	 0.9700	 0.4770

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Chain	Atom inclusion	Q-score
Bf	 0.6790	 0.2920
Bg	 0.9590	 0.3420
DC	 0.9120	 0.3480
E	 0.7660	 0.2020
EC	 0.8160	 0.2150
V	 0.8950	 0.3570