



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 05:42 AM UTC

PDB ID : 8EUB / pdb_00008eub
EMDB ID : EMD-28610
Title : Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), eEF2 and GDP, Structure I
Authors : Zhao, Y.; Rai, J.; Li, H.
Deposited on : 2022-10-18
Resolution : 2.52 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

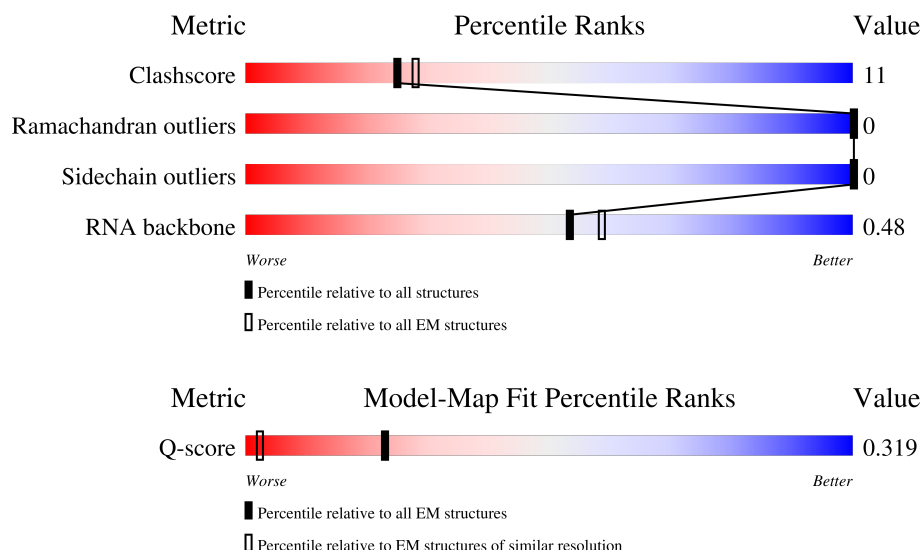
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.52 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.



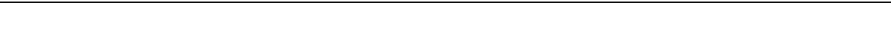
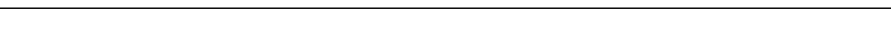
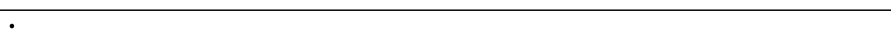
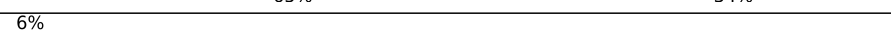
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7226 (2.02 - 3.02)

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	
5	BG	236	
6	BH	190	
7	BI	200	
8	BJ	197	
9	BL	156	
10	BN	151	
11	BO	137	
12	BV	87	
13	BW	130	
14	BX	145	
15	BY	135	
16	Ba	119	
17	Bb	82	
18	Be	63	
19	BD	240	
20	BF	225	
21	BK	105	
22	BP	142	
23	BQ	143	
24	BR	136	
25	BS	146	
26	BT	144	
27	BU	121	
28	BZ	108	

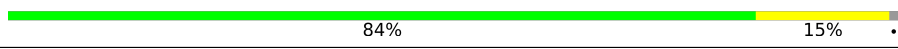
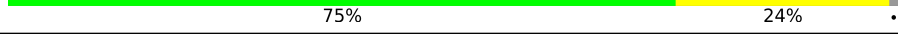
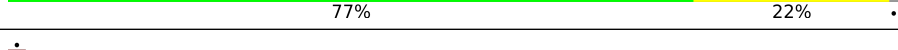
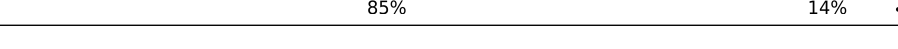
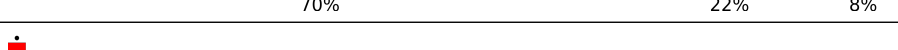
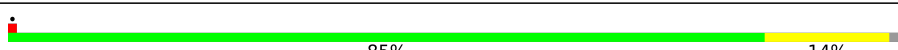
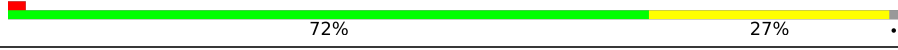
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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	B5	1798	
33	AA	254	
34	AB	387	
35	AC	362	
36	A1	3360	
37	A3	121	
38	A4	158	
39	AD	297	
40	AE	176	
41	AF	244	
42	AG	256	
43	AH	191	
44	AI	221	
45	AJ	174	
46	AL	199	
47	AM	138	
48	AN	204	
49	AO	199	
50	AP	184	
51	AQ	186	
52	AR	189	
53	AS	178	

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Mol	Chain	Length	Quality of chain
54	AT	160	
55	AU	121	
56	AV	137	
57	AW	155	
58	AX	142	
59	AY	127	
60	AZ	136	
61	Aa	149	
62	Ab	59	
63	Ac	105	
64	Ad	113	
65	Ae	130	
66	Af	107	
67	Ag	121	
68	Ah	120	
69	Ai	100	
70	Aj	88	
71	Ak	78	
72	Al	51	
73	Am	128	
74	An	25	
75	Ao	106	
76	Ap	92	
77	E	217	
78	EC	201	

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Mol	Chain	Length	Quality of chain
79	DC	842	
80	Bf	152	
81	BM	143	
82	VA	312	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 214074 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
1	BA	206	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 2 is a protein called RPS1A isoform 1.

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

- Molecule 3 is a protein called RPS2 isoform 1.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 16 is a protein called RPS26B isoform 1.

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

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

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

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

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

- Molecule 19 is a protein called RPS3 isoform 1.

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

- Molecule 20 is a protein called Rps5p.

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

- 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
			442	274	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 RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B5	1782	Total	C	N	O	P	1	0
			38004	17005	6718	12499	1782		

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 33 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L3.

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

- Molecule 35 is a protein called RPL4A isoform 1.

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

- Molecule 36 is a RNA chain called 28S rRNA.

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

- Molecule 37 is a RNA chain called 5S rRNA.

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

- Molecule 38 is a RNA chain called 5.8S rRNA.

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

- Molecule 39 is a protein called RPL5 isoform 1.

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

- Molecule 40 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 41 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 42 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 44 is a protein called RPL10 isoform 1.

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

- Molecule 45 is a protein called RPL11A isoform 1.

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

- Molecule 46 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L20.

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

- Molecule 54 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 57 is a protein called RPL24A isoform 1.

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

- Molecule 58 is a protein called 60S ribosomal protein L25.

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

- Molecule 59 is a protein called 60S ribosomal protein L26-A.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L28.

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

- Molecule 62 is a protein called RPL29 isoform 1.

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

- Molecule 63 is a protein called 60S ribosomal protein L30.

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

- Molecule 64 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 65 is a protein called RPL32 isoform 1.

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

- Molecule 66 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 67 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 68 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 71 is a protein called RPL38 isoform 1.

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

- Molecule 72 is a protein called 60S ribosomal protein L39.

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

- Molecule 73 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 74 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 75 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 76 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 77 is a protein called RPL1A isoform 1.

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

- Molecule 78 is a RNA chain called Taura syndrome virus (TSV) internal ribosome entry site (IRES) RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	EC	195	Total	C	N	O	P	0	0
			4128	1843	731	1359	195		

- Molecule 79 is a protein called Elongation factor 2.

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

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S31.

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

- Molecule 81 is a protein called 40S ribosomal protein S12.

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

- Molecule 82 is a protein called 60S acidic ribosomal protein P0.

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

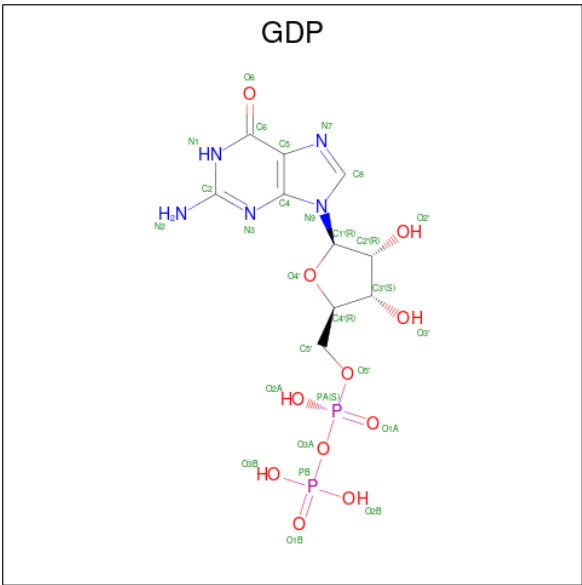
- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	B5	51	Total 51	Mg 51	0
83	AB	1	Total 1	Mg 1	0
83	A1	187	Total 187	Mg 187	0
83	A3	2	Total 2	Mg 2	0
83	A4	5	Total 5	Mg 5	0
83	AG	1	Total 1	Mg 1	0
83	AN	3	Total 3	Mg 3	0
83	AO	2	Total 2	Mg 2	0
83	AP	1	Total 1	Mg 1	0
83	Af	1	Total 1	Mg 1	0
83	Aj	1	Total 1	Mg 1	0

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

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

- Molecule 85 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂) (labeled as "Ligand of Interest" by depositor).

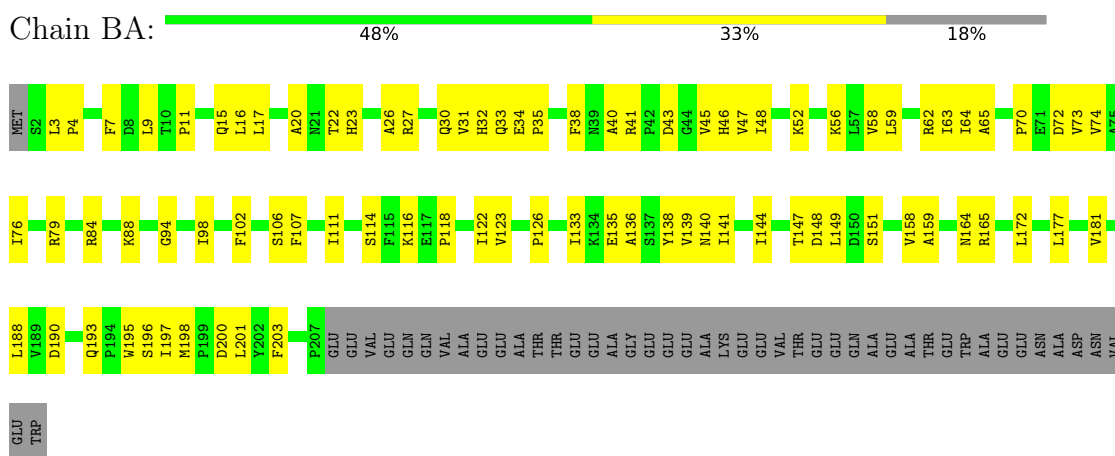


Mol	Chain	Residues	Atoms					AltConf
85	DC	1	Total	C	N	O	P	0
			28	10	5	11	2	

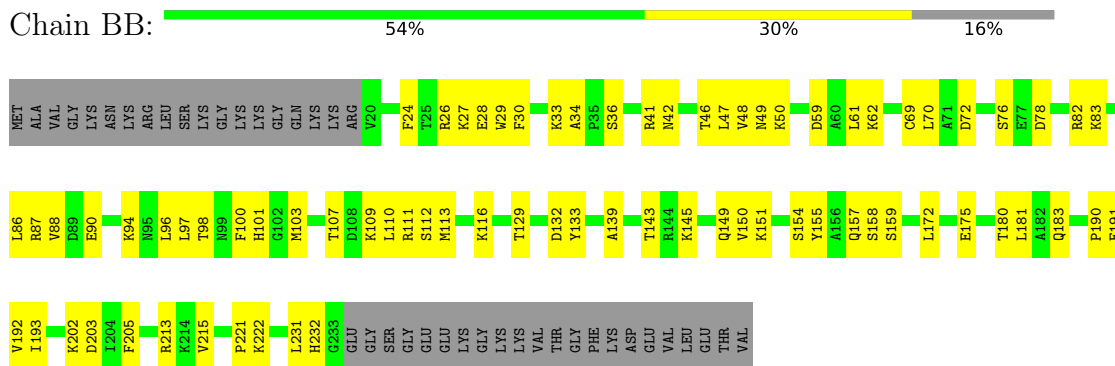
3 Residue-property plots

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

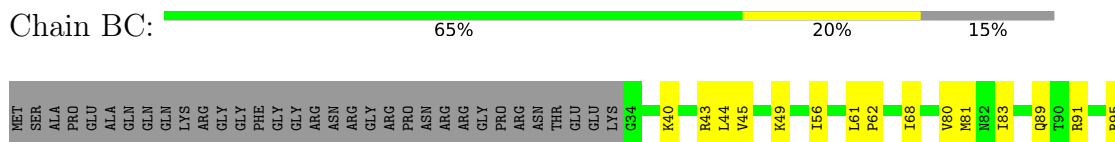
• Molecule 1: 40S ribosomal protein S0-A



• Molecule 2: RPS1A isoform 1



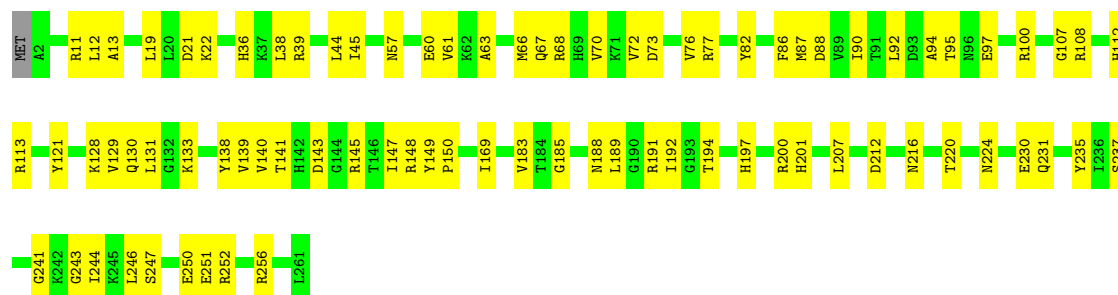
• Molecule 3: RPS2 isoform 1





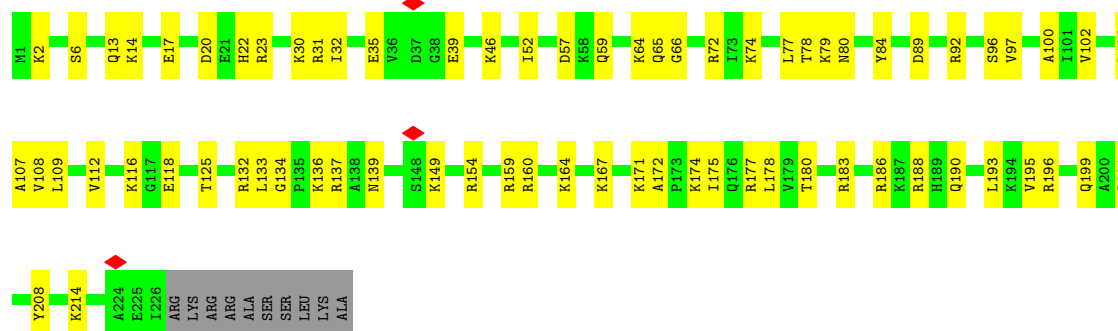
• Molecule 4: 40S ribosomal protein S4-A

Chain BE: 68% 31%



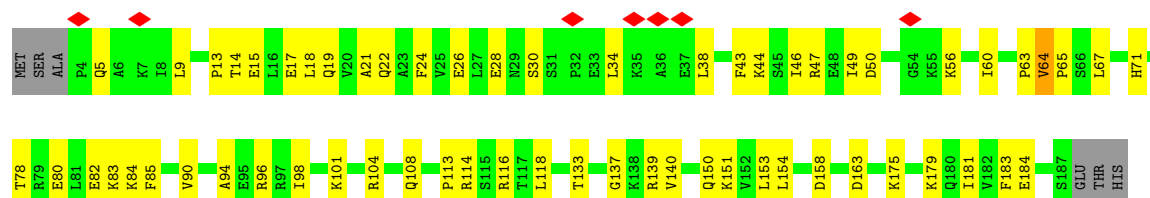
• Molecule 5: 40S ribosomal protein S6-A

Chain BG: 66% 30%



• Molecule 6: 40S ribosomal protein S7-A

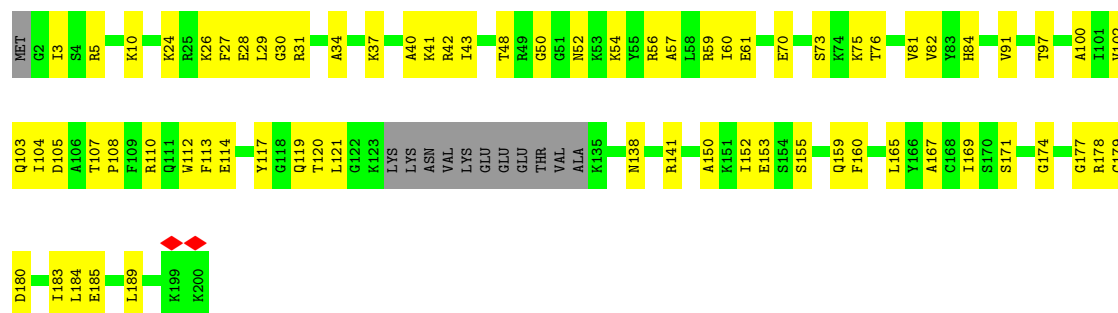
Chain BH: 65% 32%



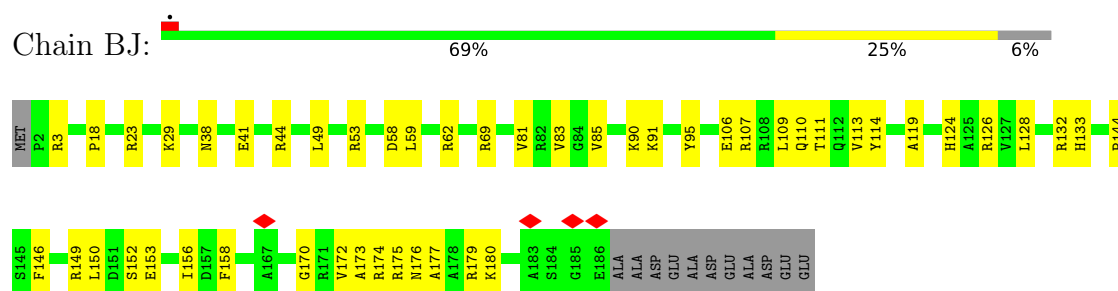
• Molecule 7: 40S ribosomal protein S8-A

Chain BI: 59% 35% 6%

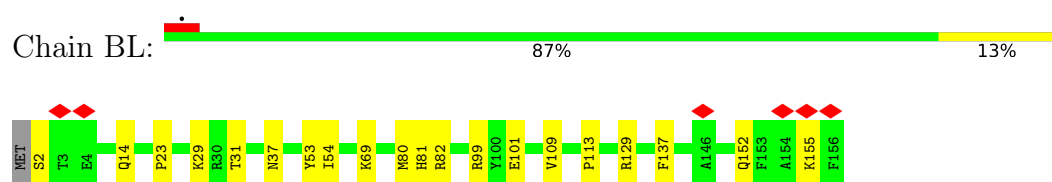




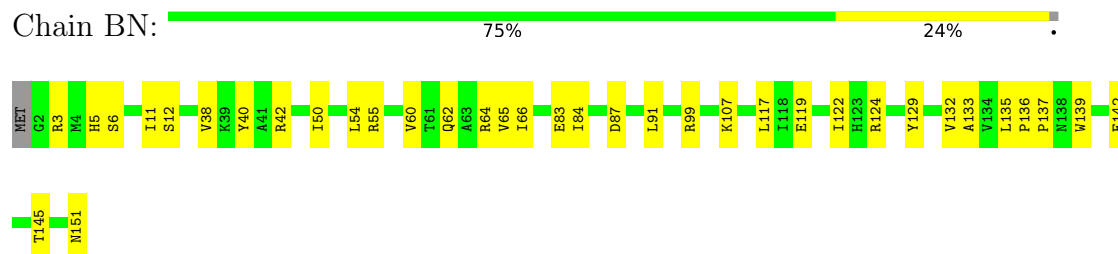
- Molecule 8: 40S ribosomal protein S9-A



- 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

Chain BV:  67% 33%



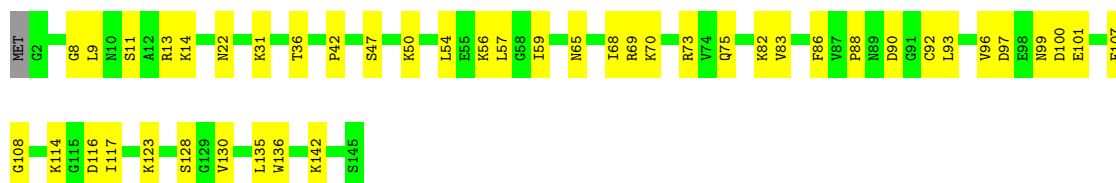
- Molecule 13: RPS22A isoform 1

Chain BW:  68% 31%



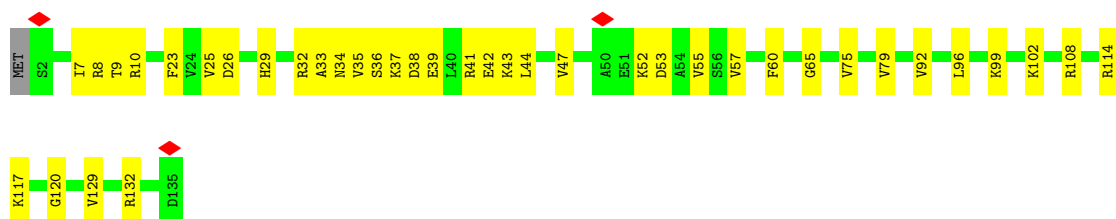
- Molecule 14: 40S ribosomal protein S23-A

Chain BX:  69% 30%



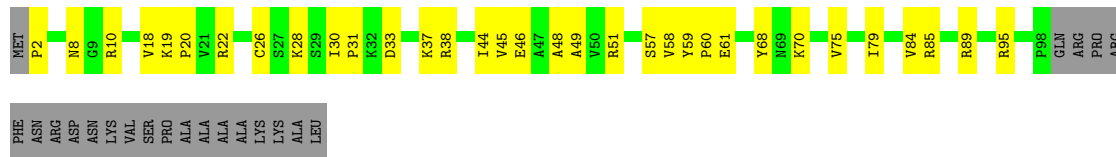
- Molecule 15: 40S ribosomal protein S24-A

Chain BY:  70% 29%



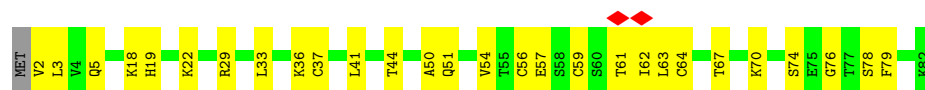
- Molecule 16: RPS26B isoform 1

Chain Ba:  54% 28% 18%



- Molecule 17: 40S ribosomal protein S27-A

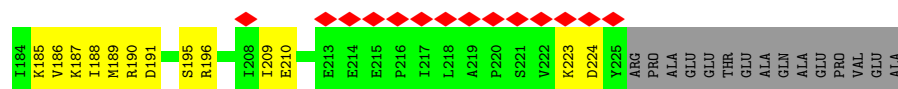
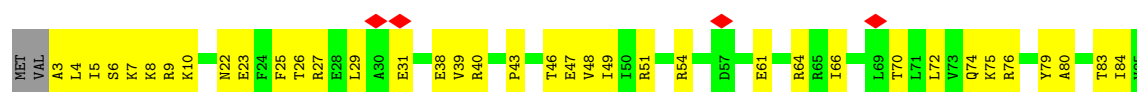
Chain Bb:  65% 34%



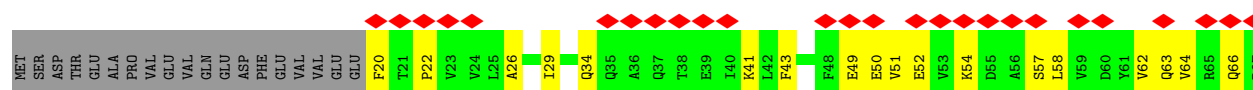
- Molecule 18: 40S ribosomal protein S30-A



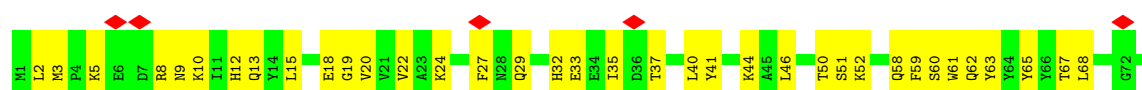
- Molecule 19: RPS3 isoform 1

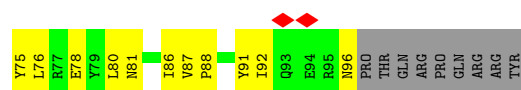


- Molecule 20: Rps5p

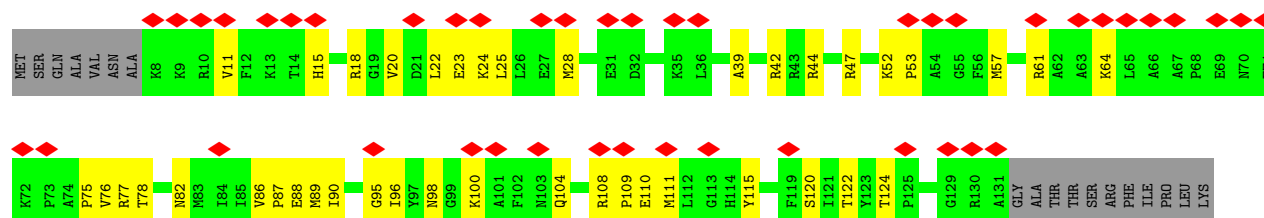


- Molecule 21: 40S ribosomal protein S10-A

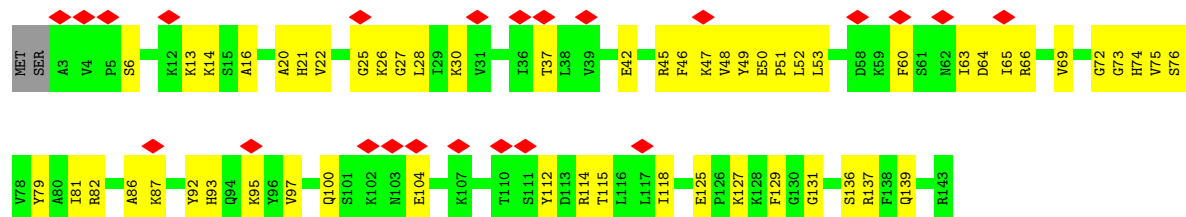




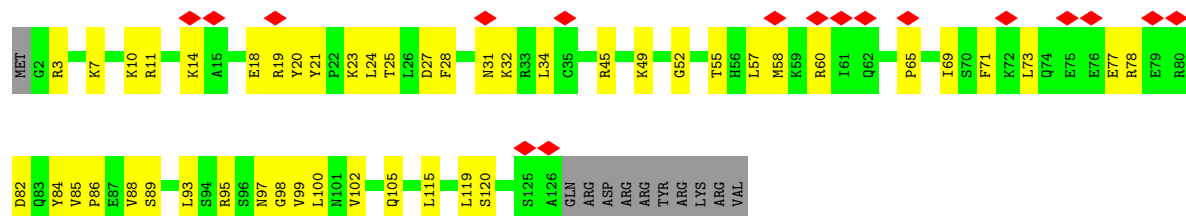
• Molecule 22: RPS15 isoform 1



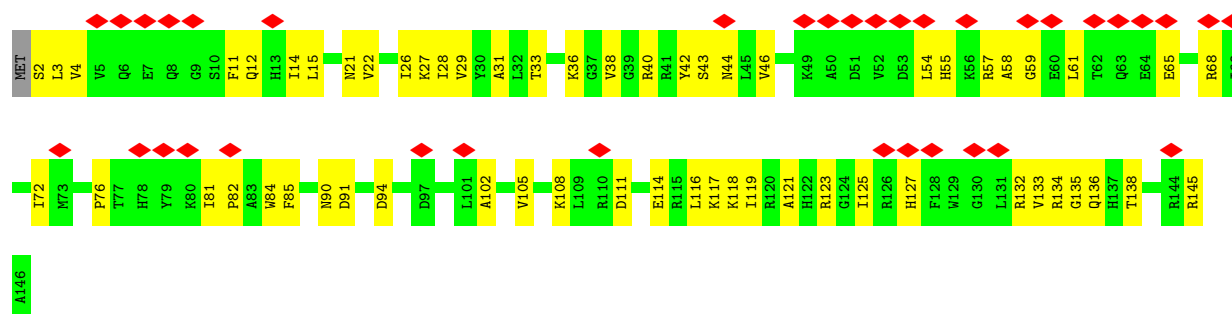
• Molecule 23: 40S ribosomal protein S16-A



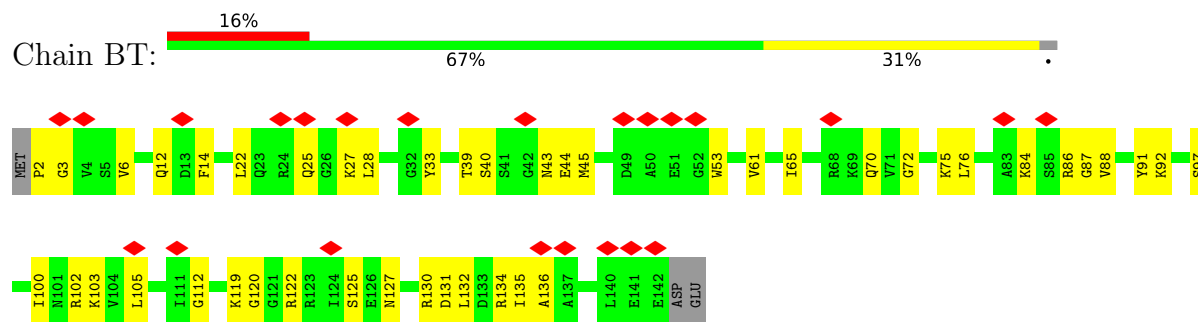
• Molecule 24: 40S ribosomal protein S17-A



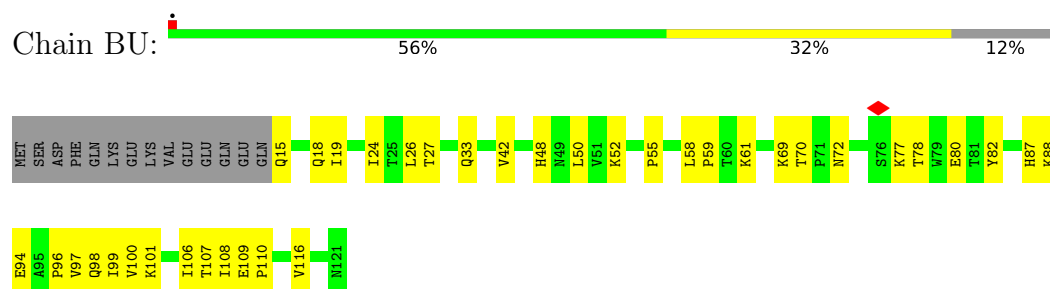
• Molecule 25: 40S ribosomal protein S18-A



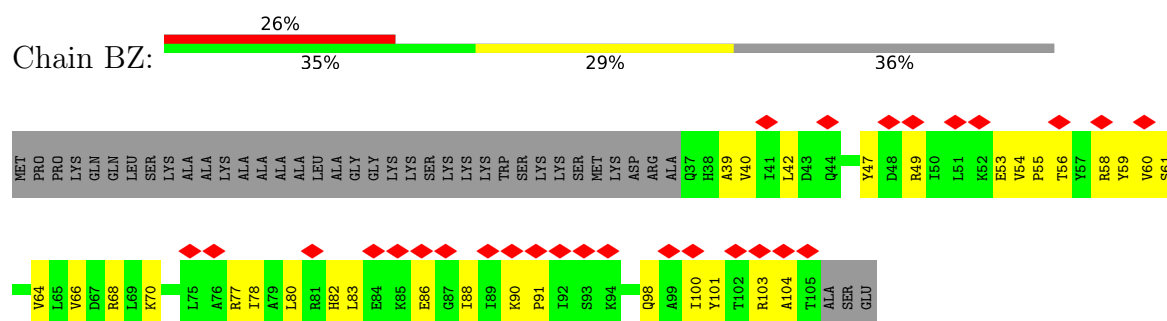
- Molecule 26: 40S ribosomal protein S19-A



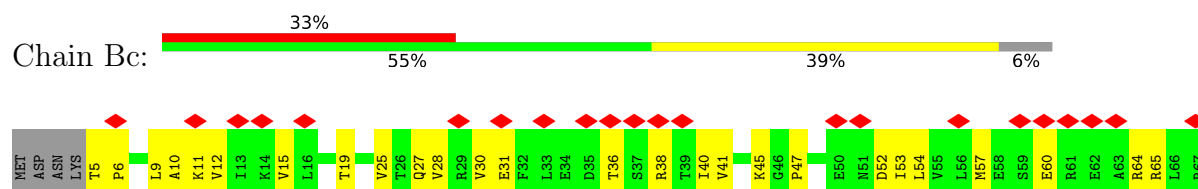
- Molecule 27: RPS20 isoform 1



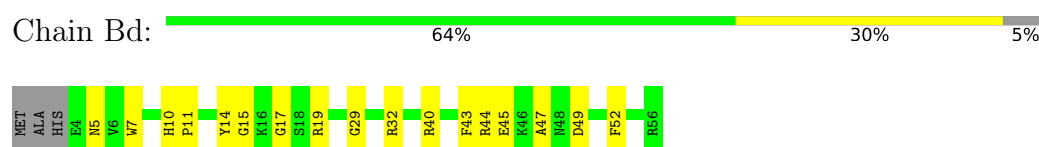
- Molecule 28: RPS25A isoform 1



- Molecule 29: RPS28A isoform 1

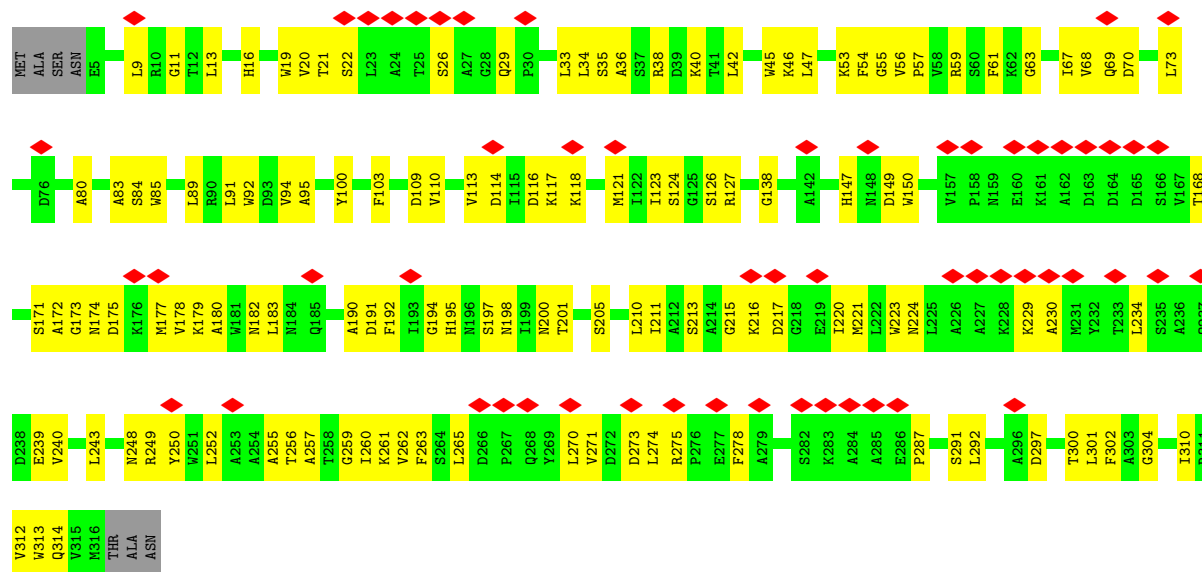


- Molecule 30: RPS29A isoform 1

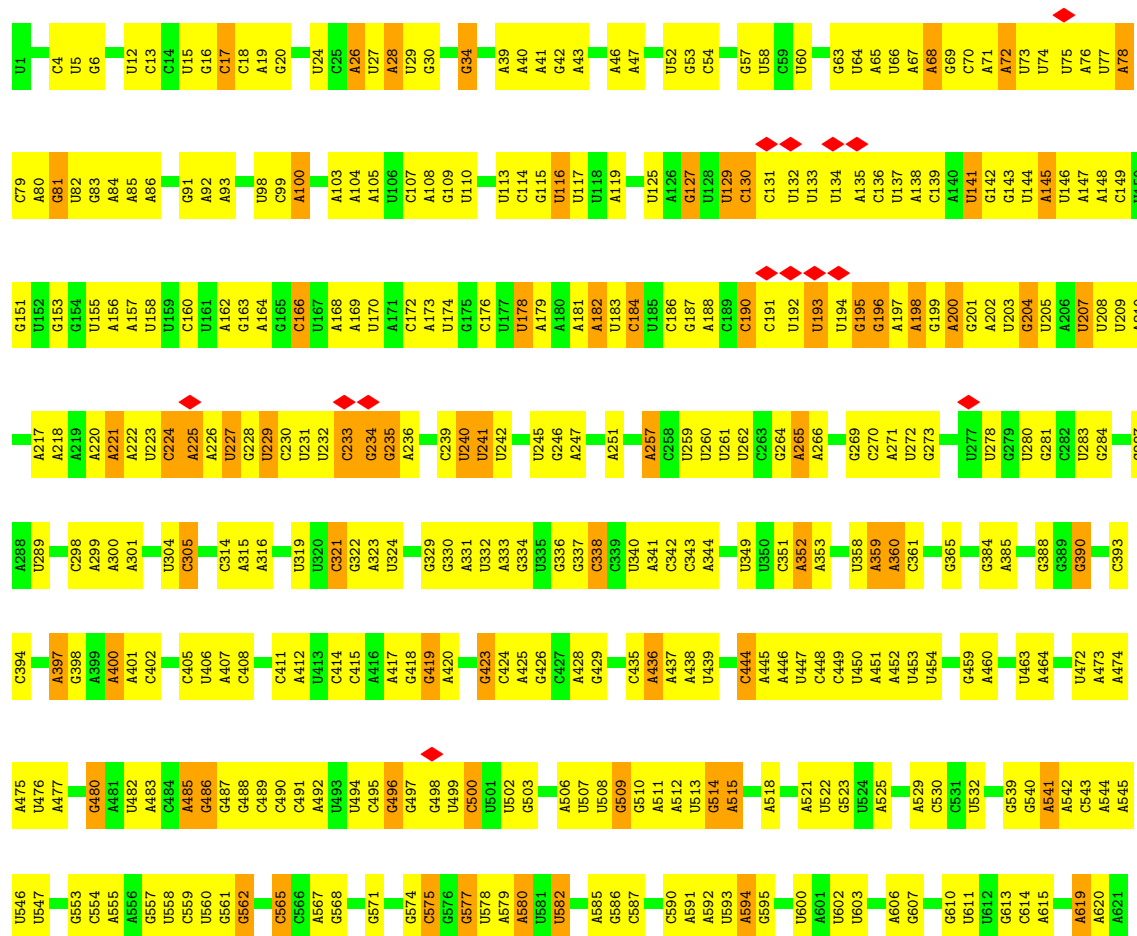


- Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein

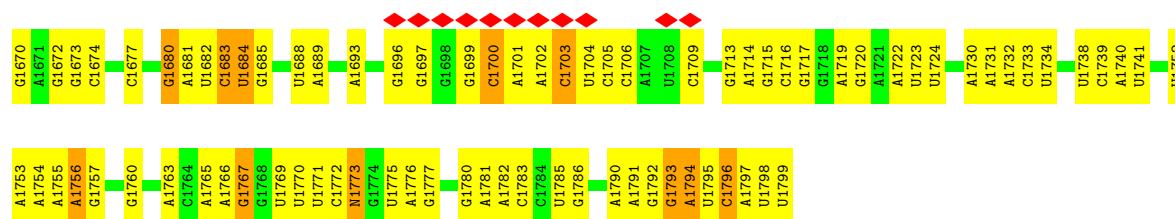




• Molecule 32: 18S rRNA

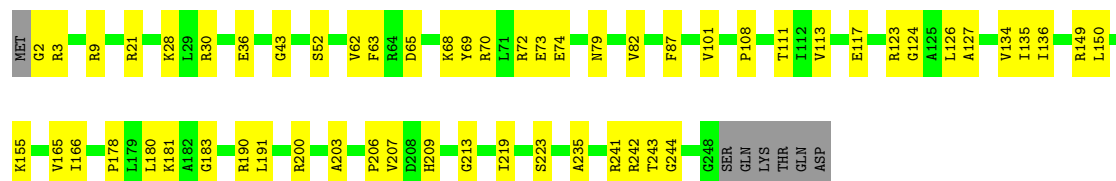






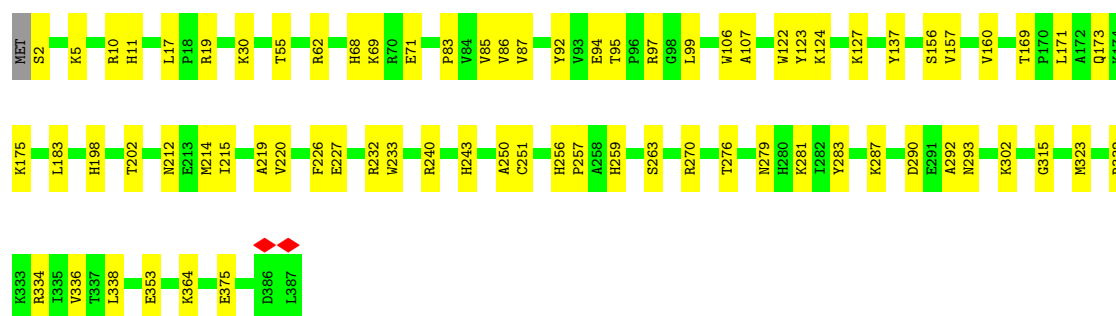
• Molecule 33: 60S ribosomal protein L2-A

Chain AA: 75% 22%



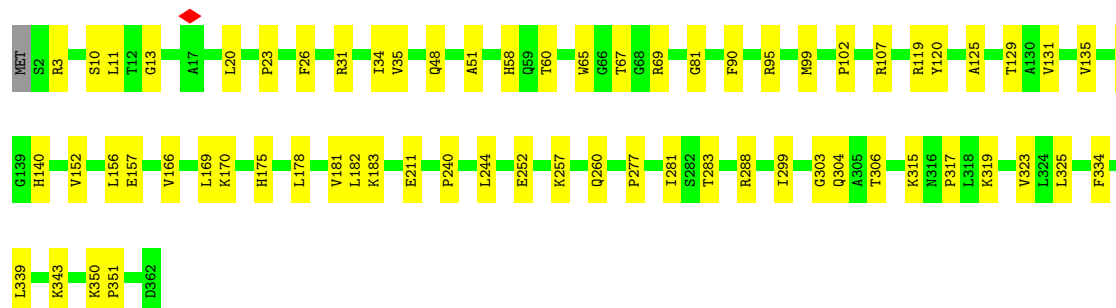
• Molecule 34: 60S ribosomal protein L3

Chain AB: 81% 19%



• Molecule 35: RPL4A isoform 1

Chain AC: 81% 18%

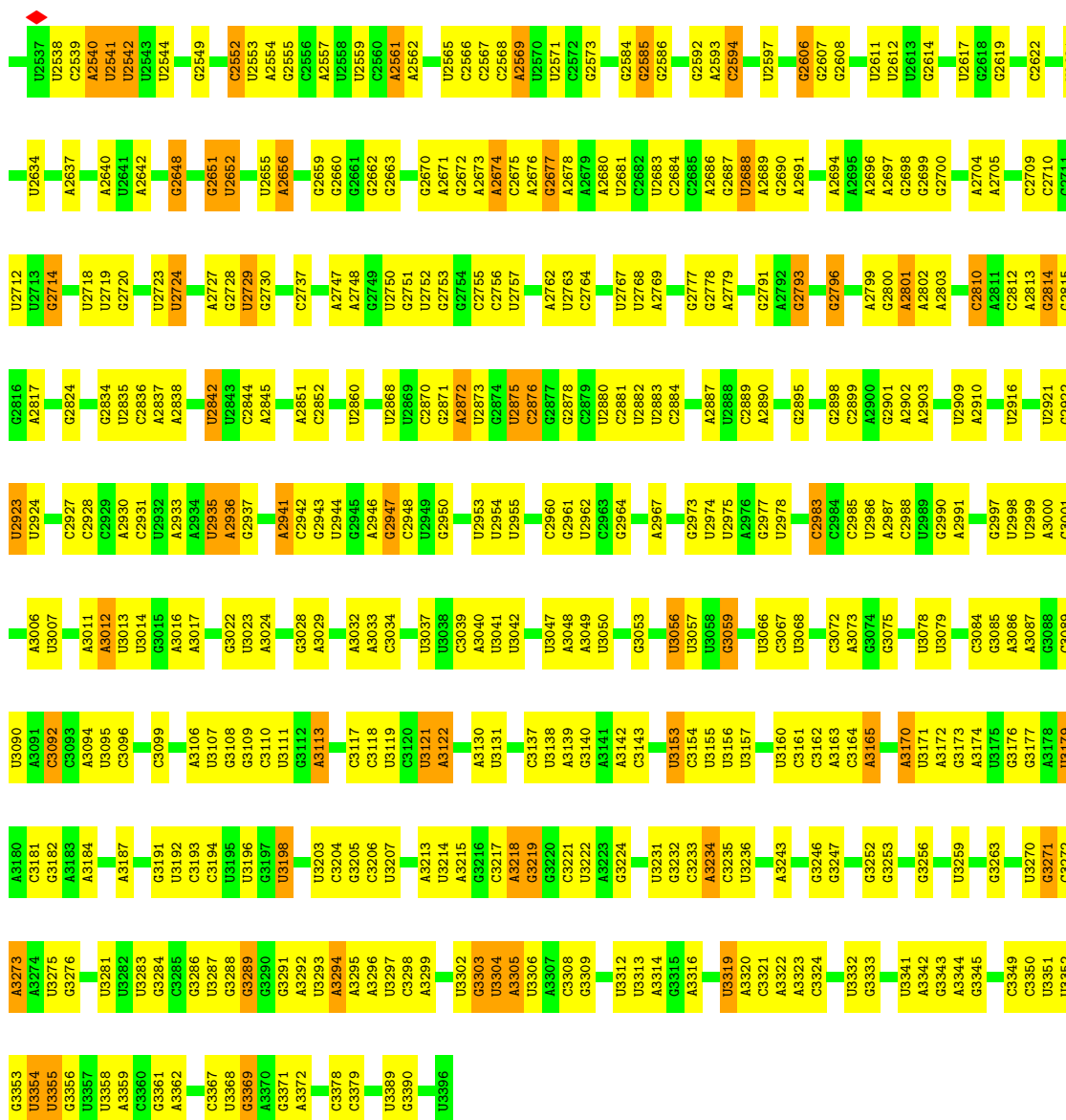


• Molecule 36: 28S rRNA

Chain A1: 49% 38% 7% 5%

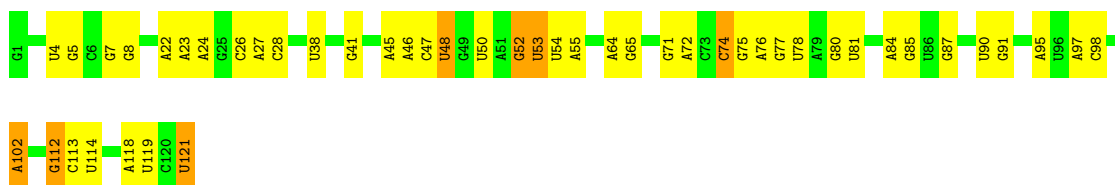
G1249	G1178	G1089	G999	A921	G812	G728	U640	C546	U429	A351	U261	U186	U3
G1250	A1179	C1092	C1000	U922	G813	A735	C641	G547	C435	A352	U262	A187	C7
A1251	A1180	A1093	A1001	C923	G814	A736	U642	G548	A436	A357	C263	U188	C8
U1253	U1181	U1094	A1002	G924	A816	A737	U643	U549	G437	G358	G264	A107	U9
G1255	G1183	U1095	G1010	A925	A817	A738	G644	A550	A438	U359	A265	A108	A10
C1256	A1184	U1096	G1013	G934	A818	A744	A645	A551	C439	G360	A266	A109	A12
C1257	C1185	G1097	U1014	U935	A819	C745	A649	G552	A440	A361	G267	C192	A13
A1259	U1188	A1098	U1015	G937	U825	C746	G651	U553	U	U362	A268	G196	A15
A1260	A1103	G1104	C1016	U938	A828	C747	G652	A557	G	G363	G269	U199	U19
G1261	G1192	G1105	U1017	U939	U829	C748	U646	U558	U	A199	A273	A116	A20
G1262	A1193	G1018	G1018	A830	U830	C749	C655	A559	U	C200	G274	U117	G21
A1263	G1194	C1107	G1019	G941	G831	C752	A656	G567	U	A201	U119	U118	A26
G1264	A1195	U1108	G1020	U942	G832	C753	A657	G568	U	A365	G277	A115	U19
U1265	A1196	U1109	G1021	U943	G833	C754	A658	A569	U	A366	U278	U117	A20
A1197	A1197	U1110	U1022	C944	U834	G755	A660	U569	U	A367	U279	U119	A26
G1268	C1201	U1111	C1023	C945	G835	C756	U673	A569	U	G371	U280	G120	C29
C1272	A1202	U1114	G	U946	G845	C757	G674	C576	U	A373	U281	A122	A34
A1273	A1203	G1117	A	C947	A846	U759	U677	C577	U	A374	G283	C208	A35
C1277	A1205	C1118	A	C948	A847	C760	C663	A578	U	A375	A284	U210	A36
A1278	G1206	A1119	U	U952	A848	A761	U664	G579	U	A376	A285	A211	U37
C1279	G1207	A1120	G1030	U953	A849	C765	A665	A585	U	A377	U286	G212	U38
C1280	U1208	U1121	C1031	U954	C849	U766	U673	C586	U	U380	A289	G214	A39
G1281	G1209	U1122	U1032	U955	G857	C767	G674	C587	U	U381	G290	G215	A40
C1283	U1211	A1130	U1033	U956	G860	C768	A677	A589	U	A385	C291	G216	A43
A1285	A1212	G1131	U1034	C959	C861	C769	G678	G590	U	A386	U292	U217	U44
A1287	G1213	C1132	G1035	C961	U874	C774	U681	A592	U	A387	U294	G218	A45
U1288	U1218	A1133	A1040	C963	A876	C775	A681	C595	U	G392	A296	G219	A49
A1289	C1219	G1134	U1041	U964	A877	C776	U682	C596	U	U393	G297	C226	G59
A1290	U1138	U1139	U1042	U965	A878	C777	U683	G597	U	G394	U298	G227	A60
C1291	G1223	G1140	C1045	U966	A879	C778	U684	A598	U	A397	G301	U228	A61
U1293	C1224	C1141	A1047	U967	A880	C779	U685	C599	U	A398	U302	G229	A62
A1294	G1225	G1142	A1048	C968	A881	C780	U686	A602	U	A399	G303	C233	A63
G1295	C1226	U1143	C1049	C969	A882	C781	C700	G604	U	G400	G304	G234	A64
G1306	U1227	U1144	U1054	G974	U879	C782	C702	A611	U	U401	U305	A235	A65
G1307	G1228	G1152	A1064	C975	G887	C783	U705	U612	U	C403	A307	G236	A66
A1308	A1231	A1153	G1063	U976	A888	C784	U706	U613	U	G406	A308	A238	C68
U1309	C1232	C1154	A1064	C977	A889	C785	U707	U614	U	A407	U313	G239	C69
G1311	G1233	U1155	A1065	U978	U897	C786	U708	G616	U	G412	U314	U240	A71
U1315	A1234	C1156	A1065	U979	U898	C787	U709	G617	U	U413	C315	G241	G74
C1316	G1235	G1157	G1072	U981	G900	C788	U710	C618	U	U417	G171	G242	G75
A1317	U1236	A1158	U1073	C982	G907	C789	U711	A619	U	A418	G172	G243	G76
A1318	C1316	C1159	U1074	C983	G908	C790	U712	U620	U	G419	G173	U244	A77
A1319	U1317	U1160	A1075	G984	G909	C791	U713	A621	U	G420	C175	U245	G86
G1319	G1240	U1170	U1081	U985	G912	C792	U714	U627	U	G421	U328	U246	G87
C1320	U1241	G1171	U1082	U986	G913	C793	U715	U628	U	G422	U329	U247	G91
G1321	G1242	C1174	G1083	U987	A914	C794	U716	U629	U	A423	A336	U248	G92
U1244	A1244	C1175	A1084	U988	A915	C795	U717	A630	U	G424	C339	U249	G93
U1225	U1245	U1226	A1085	G993	A916	C796	U718	U631	U	G425	G340	G251	C93
A1326	G1246	C1327	U1088	U994	A917	C797	U719	C632	U	G426	G341	U252	G94
C1327				U995		C798	U720	C633	U	C427	A349	G256	A95
						C799	U721	C636	U	A428	C350	U257	G98
						C800	U722		U				A99
						C801	U723		U				
						C802	U724		U				
						C803	U725		U				
						C804	U726		U				
						C805	U727		U				
						C806	U728		U				
						C807	U729		U				
						C808	U730		U				
						C809	U731		U				
						C810	U732		U				
						C811	U733		U				
						C812	U734		U				
						C813	U735		U				
						C814	U736		U				
						C815	U737		U				
						C816	U738		U				
						C817	U739		U				
						C818	U740		U				
						C819	U741		U				
						C820	U742		U				
						C821	U743		U				
						C822	U744		U				
						C823	U745		U				
						C824	U746		U				
						C825	U747		U				
						C826	U748		U				
						C827	U749		U				
						C828	U750		U				
						C829	U751		U				
						C830	U752		U				
						C831	U753		U				
						C832	U754		U				
						C833	U755		U				
						C834	U756		U				
						C835	U757		U				
						C836	U758		U				
						C837	U759		U				
						C838	U760		U				
						C839	U761		U				
						C840	U762		U				
						C841	U763		U				
						C842	U764		U				
						C843	U765		U				
						C844	U766		U				
						C845	U767		U				
						C846	U768		U				
						C847	U769		U				
						C848	U770		U				
						C849	U771		U				
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						C857	U779		U				
						C858	U780		U				
						C859	U781		U				
						C860	U782		U				
						C861	U783		U				
						C862	U784		U				
						C863	U785		U				
						C864	U786		U				
						C865	U787		U				
						C866	U788		U				
						C867	U789		U				
						C868	U790		U				
						C869	U791		U				
						C870	U792		U				
						C871	U793		U				
						C872	U794		U				
						C873	U795		U				
						C874	U796		U				
						C875	U797		U				
						C876	U798		U				
						C877	U799		U				
						C878	U800		U				
						C879	U801		U				
						C880	U802		U				
						C881	U803		U				
						C882	U804		U				
						C883	U805		U				
						C884	U806		U				
						C885	U807		U				
						C886	U808						





• Molecule 37: 5S rRNA

Chain A3: 61% 33% 6%



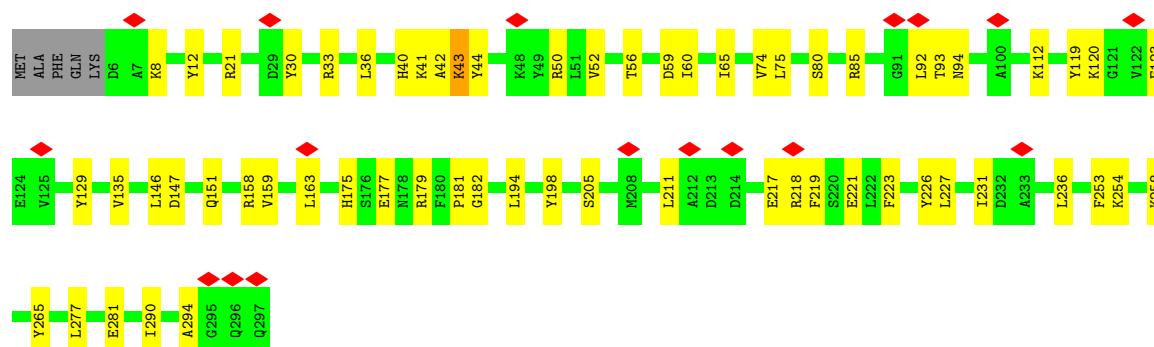
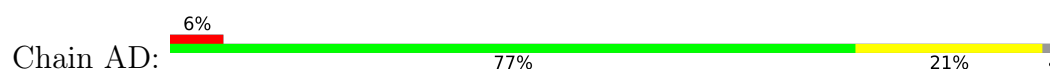
• Molecule 38: 5.8S rRNA

Chain A4: 53% 41% 6%

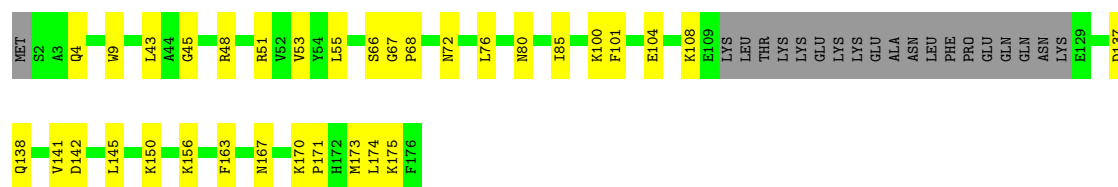




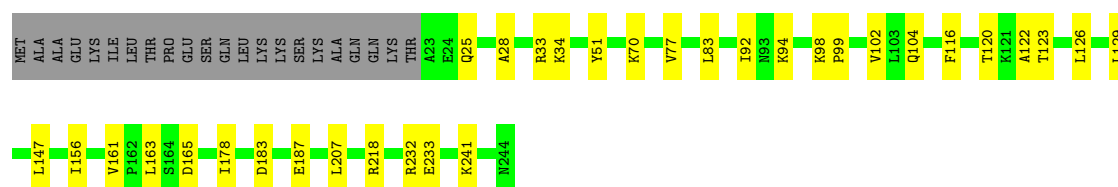
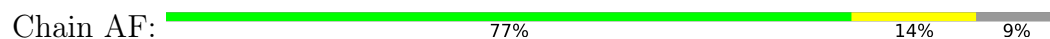
• Molecule 39: RPL5 isoform 1



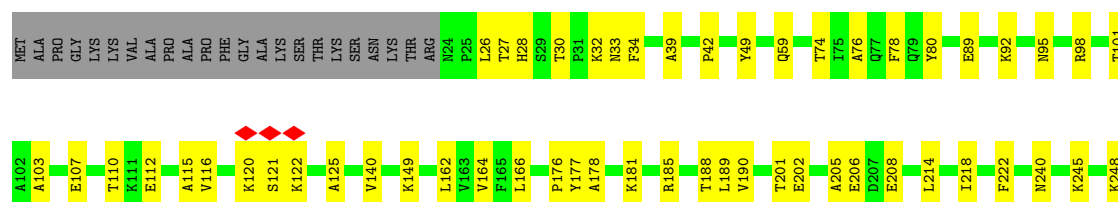
• Molecule 40: 60S ribosomal protein L6-A



• Molecule 41: 60S ribosomal protein L7-A



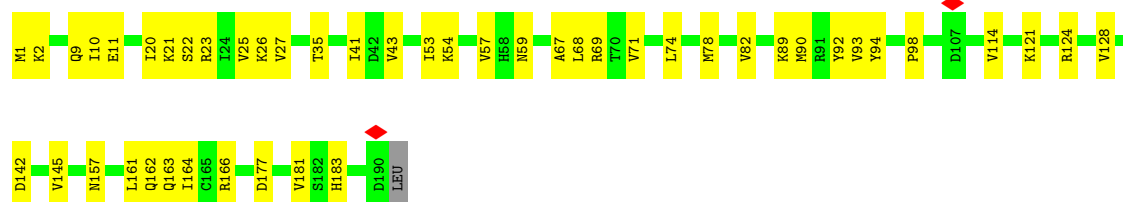
• Molecule 42: 60S ribosomal protein L8-A





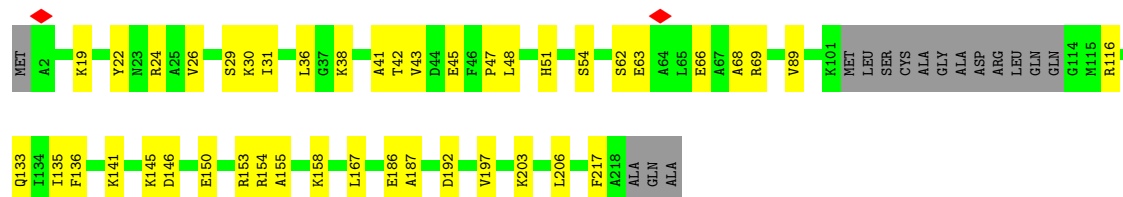
- Molecule 43: 60S ribosomal protein L9-A

Chain AH: 75% 25%



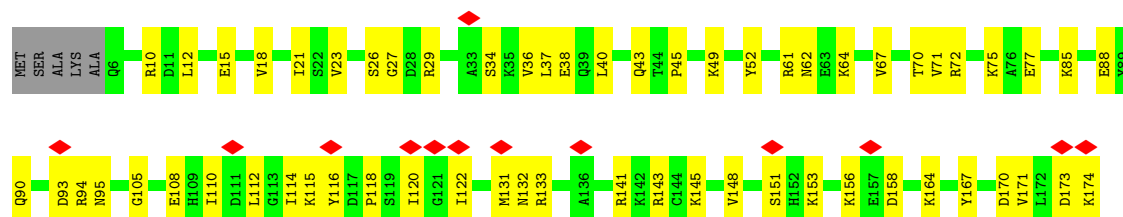
- Molecule 44: RPL10 isoform 1

Chain AI: 73% 19% 7%



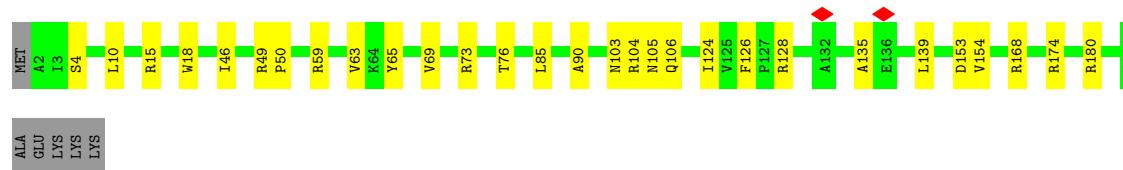
- Molecule 45: RPL11A isoform 1

Chain AJ: 7% 63% 34%



- Molecule 46: 60S ribosomal protein L13-A

Chain AL: 82% 15%



- Molecule 47: 60S ribosomal protein L14-A

Chain AM: 73% 25%



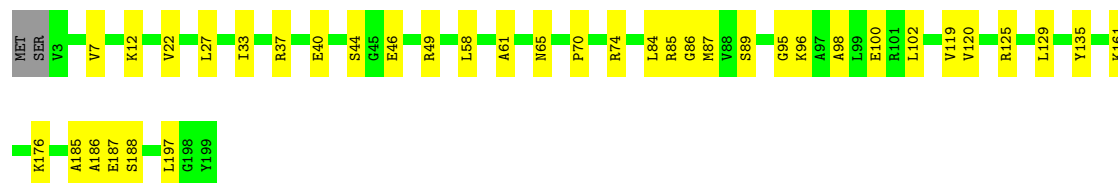
- Molecule 48: 60S ribosomal protein L15-A

Chain AN: 78% 22%



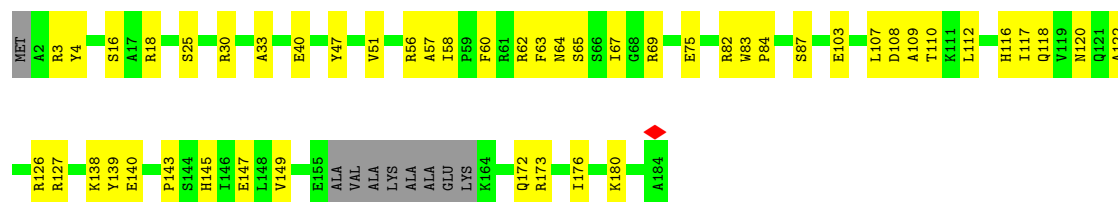
- Molecule 49: 60S ribosomal protein L16-A

Chain AO: 80% 19%



- Molecule 50: 60S ribosomal protein L17-A

Chain AP: 68% 27% 5%



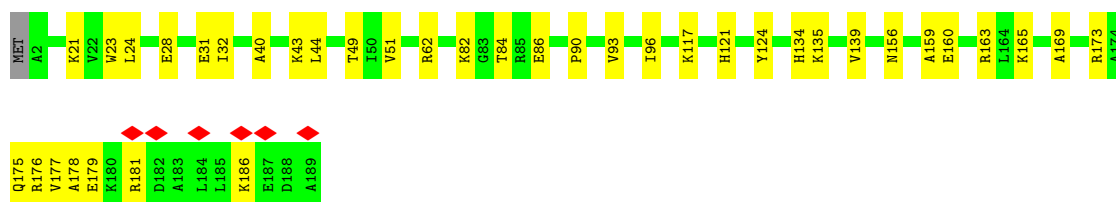
- Molecule 51: 60S ribosomal protein L18-A

Chain AQ: 77% 22%



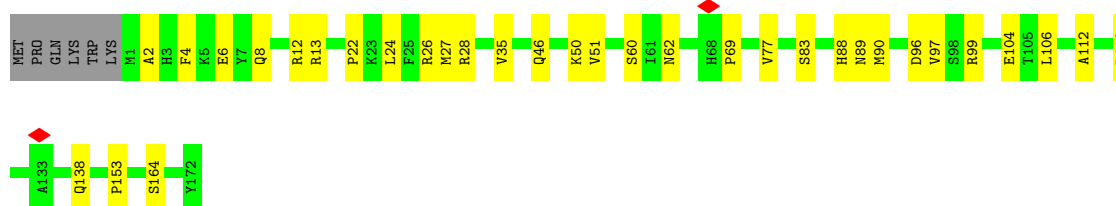
- Molecule 52: 60S ribosomal protein L19-A

Chain AR:  79% 20%



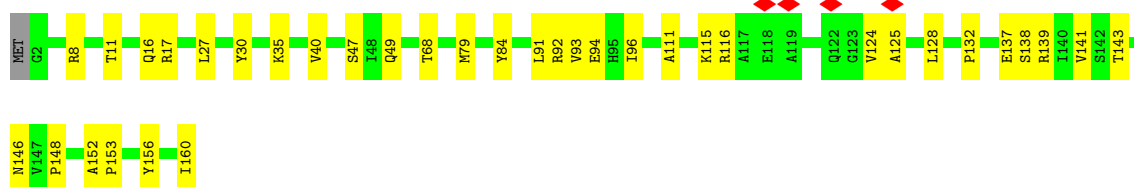
- Molecule 53: 60S ribosomal protein L20

Chain AS:  78% 19%



- Molecule 54: 60S ribosomal protein L21-A

Chain AT:  77% 22%



- Molecule 55: 60S ribosomal protein L22-A

Chain AU:  71% 12% 17%



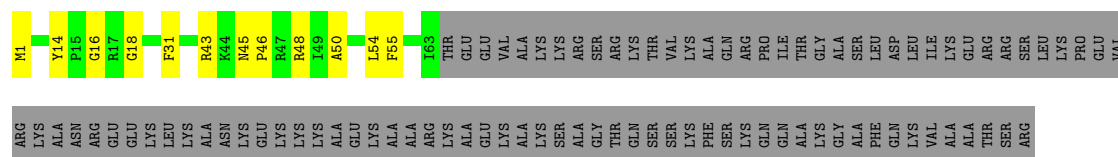
- Molecule 56: 60S ribosomal protein L23-A

Chain AV:  84% 15%



- Molecule 57: RPL24A isoform 1

Chain AW:  33% 8% 59%



- Molecule 58: 60S ribosomal protein L25

Chain AX: 75% 10% 15%



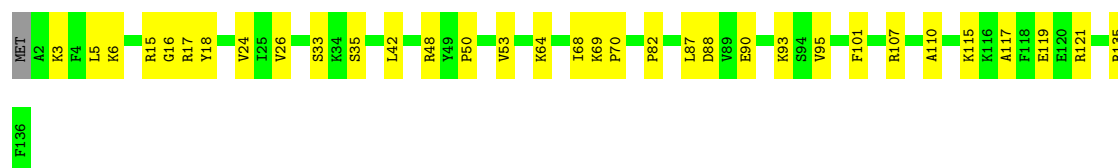
- Molecule 59: 60S ribosomal protein L26-A

Chain AY: 80% 19%



- Molecule 60: 60S ribosomal protein L27-A

Chain AZ: 75% 24%



- Molecule 61: 60S ribosomal protein L28

Chain Aa: 77% 22%



- Molecule 62: RPL29 isoform 1

Chain Ab: 85% 14%



- Molecule 63: 60S ribosomal protein L30

Chain Ac: 70% 22% 8%



- Molecule 64: 60S ribosomal protein L31-A

Chain Ad:  83% 13%



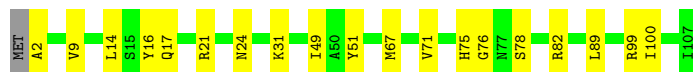
- Molecule 65: RPL32 isoform 1

Chain Ae:  85% 12%



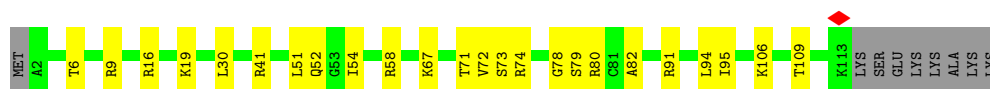
- Molecule 66: 60S ribosomal protein L33-A

Chain Af:  81% 18%



- Molecule 67: 60S ribosomal protein L34-A

Chain Ag:  73% 20% 7%



- Molecule 68: 60S ribosomal protein L35-A

Chain Ah:  79% 20%



- Molecule 69: 60S ribosomal protein L36-A

Chain Ai:  85% 14%



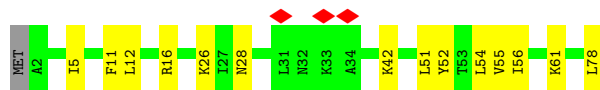
- Molecule 70: 60S ribosomal protein L37-A

Chain Aj:  77% 22%



- Molecule 71: RPL38 isoform 1

Chain Ak:  81% 18%



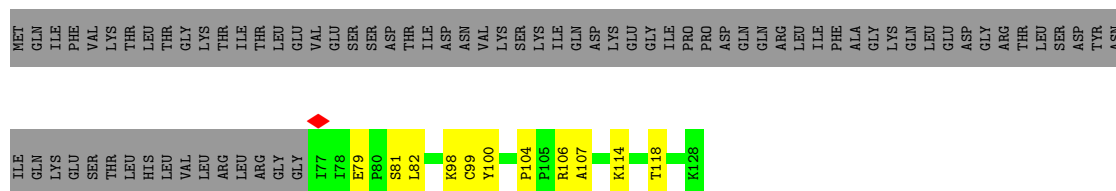
- Molecule 72: 60S ribosomal protein L39

Chain Al:  78% 20%



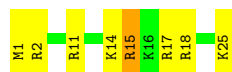
- Molecule 73: Ubiquitin-60S ribosomal protein L40

Chain Am:  32% 9% 59%



- Molecule 74: 60S ribosomal protein L41-A

Chain An:  68% 28%



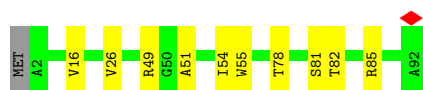
- Molecule 75: 60S ribosomal protein L42-A

Chain Ao:  72% 27%



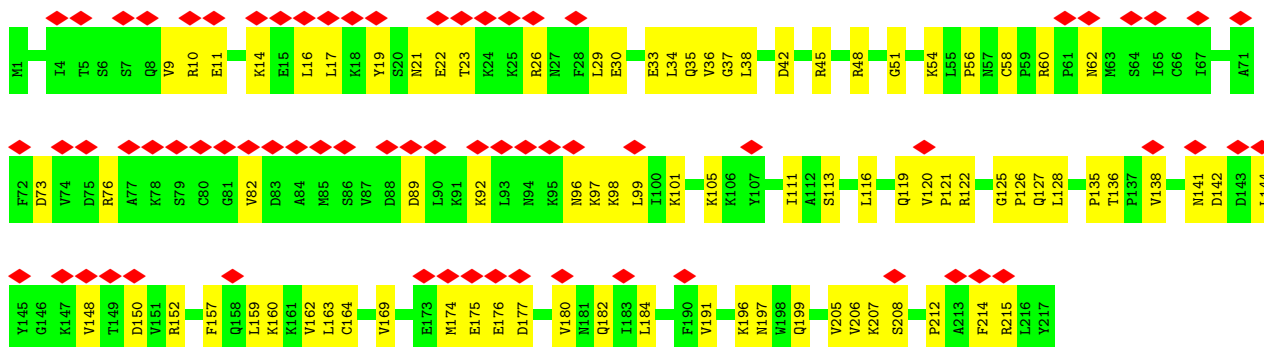
- Molecule 76: 60S ribosomal protein L43-A

Chain Ap:  88% 11%

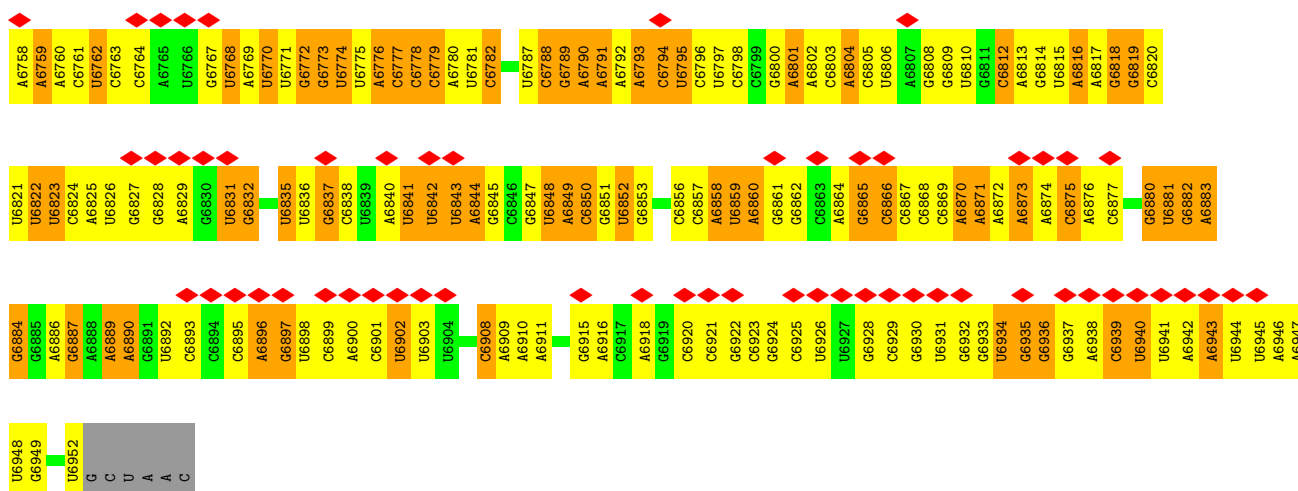
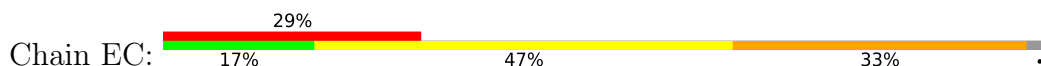


- Molecule 77: RPL1A isoform 1

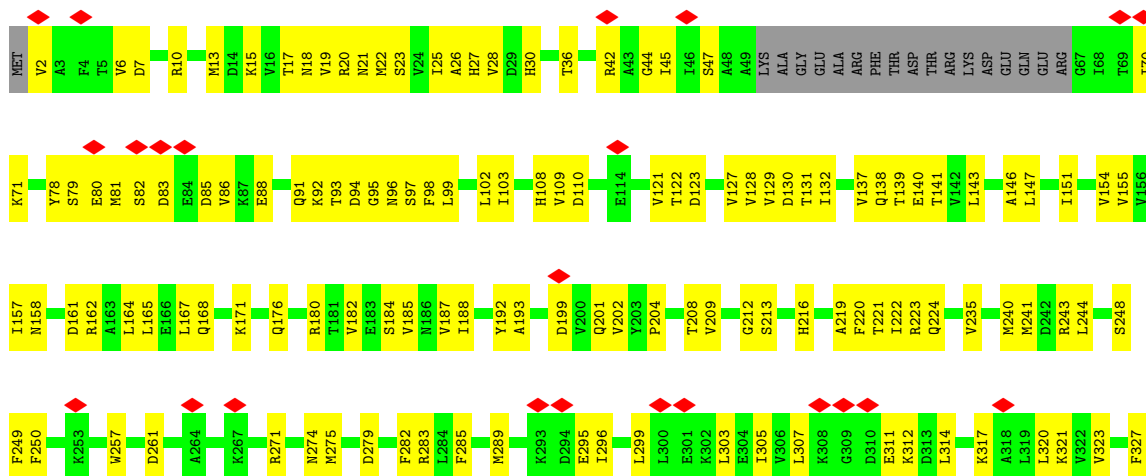
Chain E:  32% 61% 39%

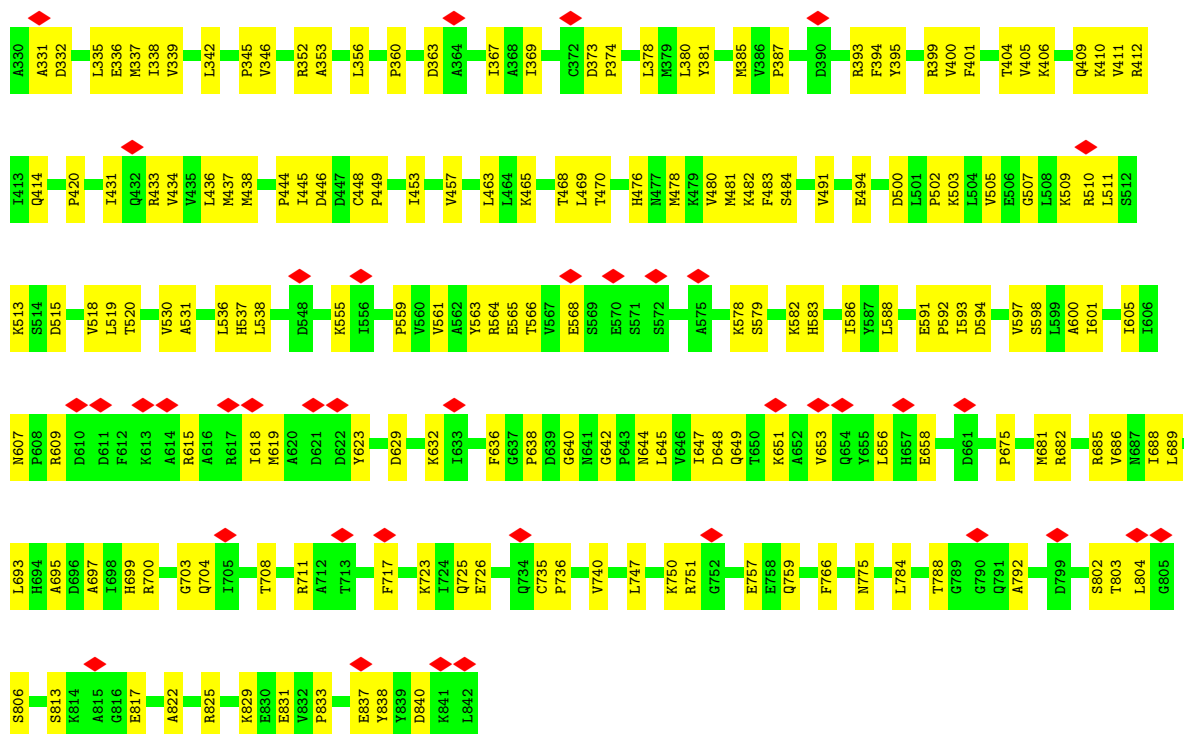


• Molecule 78: Taura syndrome virus (TSV) internal ribosome entry site (IRES) RNA

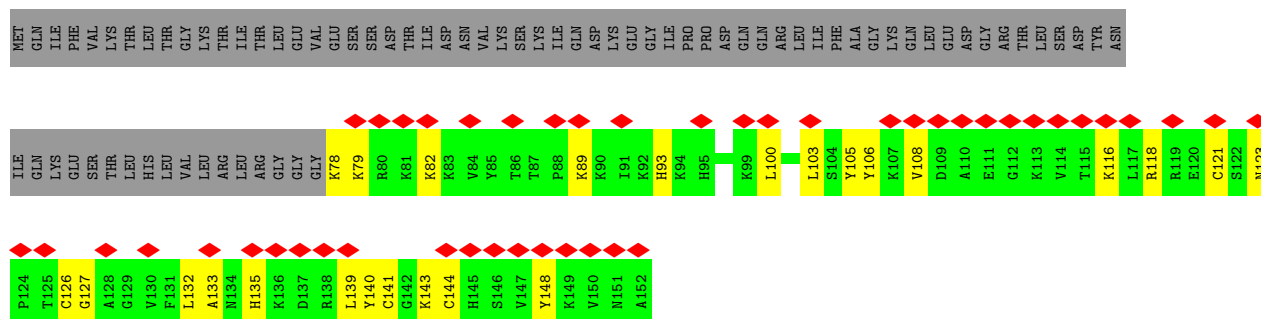
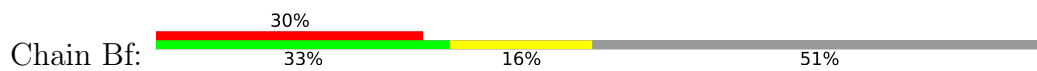


• Molecule 79: Elongation factor 2

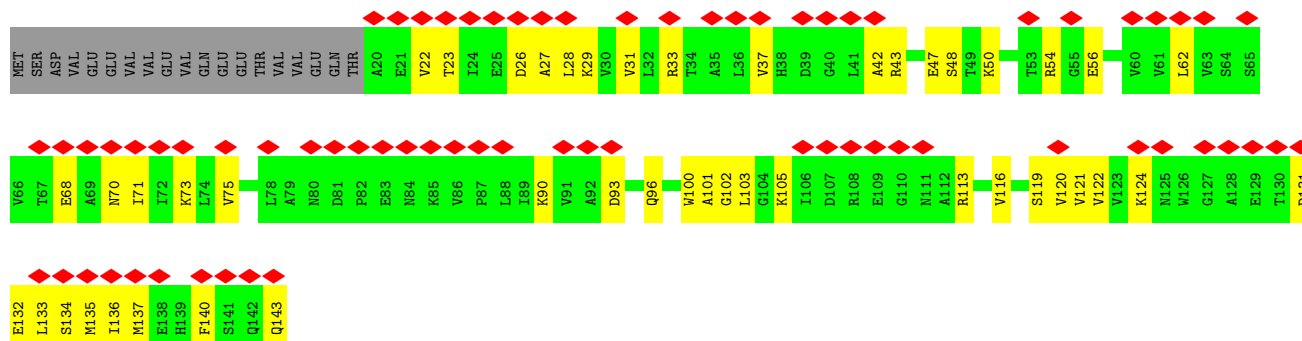




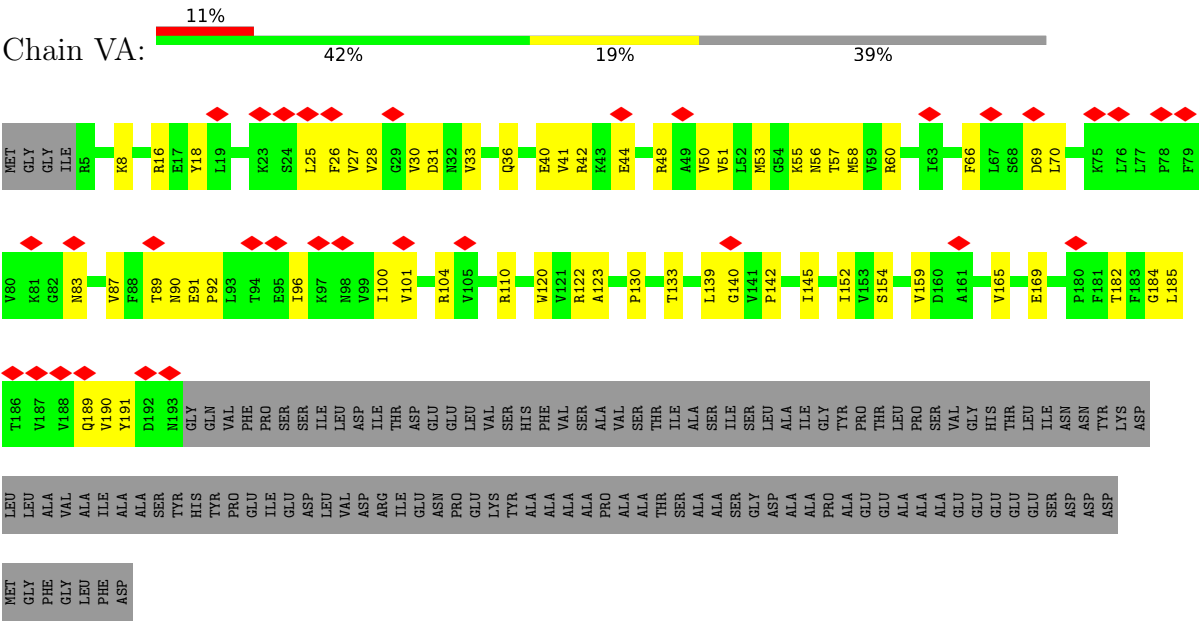
• Molecule 80: Ubiquitin-40S ribosomal protein S31



• Molecule 81: 40S ribosomal protein S12



● Molecule 82: 60S acidic ribosomal protein P0



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	96683	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	4.770	Depositor
Minimum map value	-1.793	Depositor
Average map value	0.035	Depositor
Map value standard deviation	0.202	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

5.1 Standard geometry

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

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	0.38	0/2261
2	BB	0.16	0/1735	0.41	0/2335
3	BC	0.12	0/1665	0.26	0/2263
4	BE	0.12	0/2109	0.33	0/2839
5	BG	0.11	0/1844	0.30	0/2464
6	BH	0.13	0/1506	0.37	0/2028
7	BI	0.13	0/1514	0.35	0/2021
8	BJ	0.11	0/1519	0.28	0/2035
9	BL	0.13	0/1272	0.29	0/1712
10	BN	0.13	0/1215	0.33	0/1638
11	BO	0.18	0/952	0.56	2/1279 (0.2%)
12	BV	0.15	0/693	0.39	0/935
13	BW	0.14	0/1038	0.31	0/1395
14	BX	0.15	0/1139	0.38	0/1518
15	BY	0.12	0/1087	0.34	0/1449
16	Ba	0.17	0/782	0.45	0/1047
17	Bb	0.13	0/620	0.38	0/838
18	Be	0.09	0/483	0.29	0/643
19	BD	0.11	0/1759	0.28	0/2368
20	BF	0.12	0/1629	0.31	0/2202
21	BK	0.11	0/837	0.42	0/1131
22	BP	0.14	0/1012	0.39	0/1356
23	BQ	0.14	0/1125	0.32	0/1510
24	BR	0.14	0/1010	0.38	0/1355
25	BS	0.12	0/1211	0.35	0/1628
26	BT	0.13	0/1113	0.35	0/1494
27	BU	0.13	0/865	0.36	0/1169
28	BZ	0.12	0/566	0.33	0/761
29	Bc	0.14	0/499	0.35	0/670
30	Bd	0.13	0/452	0.34	0/600
31	Bg	0.11	0/2454	0.32	0/3340
32	B5	0.16	1/41880 (0.0%)	0.29	0/65248

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AA	0.20	0/1912	0.36	0/2569
34	AB	0.17	0/3139	0.32	0/4219
35	AC	0.17	0/2800	0.36	0/3790
36	A1	0.21	0/75561	0.32	0/117806
37	A3	0.17	0/2883	0.28	0/4491
38	A4	0.21	0/3746	0.31	0/5832
39	AD	0.14	0/2390	0.31	0/3225
40	AE	0.15	0/1260	0.33	0/1694
41	AF	0.17	0/1821	0.30	0/2451
42	AG	0.16	0/1830	0.34	0/2469
43	AH	0.15	0/1531	0.34	0/2062
44	AI	0.14	0/1708	0.27	0/2290
45	AJ	0.13	0/1374	0.36	0/1842
46	AL	0.16	0/1568	0.30	0/2106
47	AM	0.15	0/1068	0.28	0/1438
48	AN	0.20	0/1757	0.33	0/2354
49	AO	0.17	0/1585	0.29	0/2128
50	AP	0.17	0/1410	0.31	0/1893
51	AQ	0.17	0/1465	0.32	0/1965
52	AR	0.17	0/1538	0.33	0/2050
53	AS	0.17	0/1481	0.34	0/1990
54	AT	0.16	0/1300	0.30	0/1743
55	AU	0.17	0/812	0.45	0/1099
56	AV	0.15	0/1018	0.31	0/1369
57	AW	0.15	0/533	0.28	0/707
58	AX	0.17	0/983	0.30	0/1325
59	AY	0.17	0/1004	0.29	0/1341
60	AZ	0.16	0/1118	0.34	0/1497
61	Aa	0.20	0/1204	0.32	0/1612
62	Ab	0.15	0/473	0.30	0/629
63	Ac	0.17	0/751	0.30	0/1008
64	Ad	0.16	0/904	0.29	0/1213
65	Ae	0.17	0/1041	0.31	0/1394
66	Af	0.19	0/868	0.31	0/1168
67	Ag	0.18	0/890	0.34	0/1189
68	Ah	0.16	0/978	0.28	0/1301
69	Ai	0.16	0/778	0.32	0/1034
70	Aj	0.18	0/696	0.34	0/923
71	Ak	0.15	0/618	0.29	0/826
72	Al	0.17	0/443	0.29	0/588
73	Am	0.15	0/423	0.33	0/562
74	An	0.26	0/234	0.97	4/300 (1.3%)
75	Ao	0.16	0/860	0.31	0/1136

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Ap	0.16	0/701	0.33	0/934
77	E	0.12	0/1745	0.33	0/2342
78	EC	0.13	0/4613	0.32	0/7182
79	DC	0.12	0/6521	0.34	0/8830
80	Bf	0.11	0/616	0.31	0/817
81	BM	0.11	0/943	0.33	0/1274
82	VA	0.15	0/1498	0.42	0/2025
All	All	0.18	1/227631 (0.0%)	0.32	6/333564 (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
14	BX	0	1
39	AD	0	1
41	AF	0	1
42	AG	0	2
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	B5	1575	G7M	O3'-P	5.72	1.61	1.56

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
74	An	15	ARG	CB-CG-CD	-8.89	90.86	111.30
11	BO	125	SER	CA-C-N	6.33	129.70	120.71
11	BO	125	SER	C-N-CA	6.33	129.70	120.71
74	An	15	ARG	CA-CB-CG	6.08	126.26	114.10
74	An	15	ARG	CG-CD-NE	5.59	124.30	112.00

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
39	AD	43	LYS	Peptide
41	AF	232	ARG	Peptide
6	BH	64	VAL	Peptide
11	BO	123	SER	Peptide
14	BX	88	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BA	1612	0	1623	69	0
2	BB	1709	0	1784	64	0
3	BC	1635	0	1723	33	0
4	BE	2068	0	2154	55	0
5	BG	1820	0	1918	69	0
6	BH	1481	0	1572	48	0
7	BI	1489	0	1525	54	0
8	BJ	1494	0	1573	37	0
9	BL	1244	0	1314	17	0
10	BN	1192	0	1255	27	0
11	BO	941	0	979	41	0
12	BV	684	0	672	22	0
13	BW	1021	0	1060	31	0
14	BX	1121	0	1196	39	0
15	BY	1073	0	1132	32	0
16	Ba	769	0	818	33	0
17	Bb	610	0	633	19	0
18	Be	475	0	525	18	0
19	BD	1734	0	1817	64	0
20	BF	1609	0	1675	65	0
21	BK	817	0	804	34	0
22	BP	991	0	1035	37	0
23	BQ	1105	0	1166	48	0
24	BR	1000	0	1063	40	0
25	BS	1192	0	1222	51	0
26	BT	1095	0	1114	40	0
27	BU	855	0	917	32	0
28	BZ	558	0	598	26	0
29	Bc	497	0	535	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Bd	442	0	432	13	0
31	Bg	2401	0	2356	92	0
32	B5	38004	0	19142	811	0
33	AA	1878	0	1946	48	0
34	AB	3081	0	3162	54	0
35	AC	2748	0	2859	51	0
36	A1	68445	0	34455	957	0
37	A3	2579	0	1304	33	0
38	A4	3353	0	1695	46	0
39	AD	2341	0	2290	47	0
40	AE	1239	0	1326	25	0
41	AF	1784	0	1862	24	0
42	AG	1798	0	1894	33	0
43	AH	1510	0	1576	35	0
44	AI	1672	0	1711	32	0
45	AJ	1353	0	1383	40	0
46	AL	1543	0	1608	23	0
47	AM	1053	0	1149	25	0
48	AN	1720	0	1779	34	0
49	AO	1555	0	1659	29	0
50	AP	1388	0	1423	37	0
51	AQ	1441	0	1543	35	0
52	AR	1521	0	1617	31	0
53	AS	1445	0	1487	24	0
54	AT	1276	0	1323	28	0
55	AU	796	0	812	10	0
56	AV	1003	0	1048	14	0
57	AW	521	0	551	8	0
58	AX	968	0	1036	15	0
59	AY	993	0	1081	17	0
60	AZ	1092	0	1155	26	0
61	Aa	1173	0	1215	32	0
62	Ab	462	0	491	7	0
63	Ac	743	0	797	17	0
64	Ad	890	0	938	11	0
65	Ae	1020	0	1089	15	0
66	Af	850	0	880	12	0
67	Ag	880	0	945	21	0
68	Ah	969	0	1078	23	0
69	Ai	771	0	849	12	0
70	Aj	681	0	687	15	0
71	Ak	612	0	682	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	Al	436	0	475	8	0
73	Am	417	0	459	8	0
74	An	233	0	283	10	0
75	Ao	847	0	914	23	0
76	Ap	694	0	738	8	0
77	E	1718	0	1811	83	0
78	EC	4128	0	2082	104	0
79	DC	6419	0	6493	227	0
80	Bf	605	0	654	23	0
81	BM	935	0	975	36	0
82	VA	1473	0	1514	48	0
83	A1	187	0	0	0	0
83	A3	2	0	0	0	0
83	A4	5	0	0	0	0
83	AB	1	0	0	0	0
83	AG	1	0	0	0	0
83	AN	3	0	0	0	0
83	AO	2	0	0	0	0
83	AP	1	0	0	0	0
83	Af	1	0	0	0	0
83	Aj	1	0	0	0	0
83	B5	51	0	0	0	0
84	Ao	1	0	0	0	0
85	DC	28	0	12	1	0
All	All	214074	0	160127	3877	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 3877 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)
32:B5:1697:G:H1	32:B5:1704:U:H3	1.01	1.00
32:B5:1588:G:H1	32:B5:1608:U:H3	1.02	0.94
36:A1:170:G:H5''	68:Ah:109:ILE:HD12	1.51	0.92
32:B5:69:G:H1	32:B5:82:U:H3	1.18	0.92
36:A1:3234:A:H61	36:A1:3253:G:H1	1.11	0.92

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%)	177 (87%)	27 (13%)	0	100	100
2	BB	212/255 (83%)	178 (84%)	34 (16%)	0	100	100
3	BC	215/254 (85%)	206 (96%)	9 (4%)	0	100	100
4	BE	258/261 (99%)	243 (94%)	15 (6%)	0	100	100
5	BG	224/236 (95%)	212 (95%)	12 (5%)	0	100	100
6	BH	182/190 (96%)	168 (92%)	14 (8%)	0	100	100
7	BI	184/200 (92%)	163 (89%)	21 (11%)	0	100	100
8	BJ	183/197 (93%)	172 (94%)	11 (6%)	0	100	100
9	BL	153/156 (98%)	142 (93%)	11 (7%)	0	100	100
10	BN	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
11	BO	125/137 (91%)	114 (91%)	11 (9%)	0	100	100
12	BV	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
13	BW	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
14	BX	142/145 (98%)	123 (87%)	19 (13%)	0	100	100
15	BY	132/135 (98%)	122 (92%)	10 (8%)	0	100	100
16	Ba	95/119 (80%)	78 (82%)	17 (18%)	0	100	100
17	Bb	79/82 (96%)	69 (87%)	10 (13%)	0	100	100
18	Be	58/63 (92%)	50 (86%)	8 (14%)	0	100	100
19	BD	221/240 (92%)	204 (92%)	17 (8%)	0	100	100
20	BF	204/225 (91%)	192 (94%)	12 (6%)	0	100	100
21	BK	94/105 (90%)	85 (90%)	9 (10%)	0	100	100
22	BP	122/142 (86%)	111 (91%)	11 (9%)	0	100	100
23	BQ	139/143 (97%)	133 (96%)	6 (4%)	0	100	100
24	BR	123/136 (90%)	116 (94%)	7 (6%)	0	100	100
25	BS	143/146 (98%)	125 (87%)	18 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	BT	139/144 (96%)	129 (93%)	10 (7%)	0	100	100
27	BU	105/121 (87%)	98 (93%)	7 (7%)	0	100	100
28	BZ	67/108 (62%)	62 (92%)	5 (8%)	0	100	100
29	Bc	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
30	Bd	51/56 (91%)	48 (94%)	3 (6%)	0	100	100
31	Bg	310/319 (97%)	277 (89%)	33 (11%)	0	100	100
33	AA	245/254 (96%)	231 (94%)	14 (6%)	0	100	100
34	AB	383/387 (99%)	365 (95%)	18 (5%)	0	100	100
35	AC	359/362 (99%)	332 (92%)	27 (8%)	0	100	100
39	AD	290/297 (98%)	271 (93%)	19 (7%)	0	100	100
40	AE	152/176 (86%)	139 (91%)	13 (9%)	0	100	100
41	AF	220/244 (90%)	212 (96%)	8 (4%)	0	100	100
42	AG	228/256 (89%)	209 (92%)	19 (8%)	0	100	100
43	AH	188/191 (98%)	174 (93%)	14 (7%)	0	100	100
44	AI	201/221 (91%)	188 (94%)	13 (6%)	0	100	100
45	AJ	167/174 (96%)	150 (90%)	17 (10%)	0	100	100
46	AL	191/199 (96%)	181 (95%)	10 (5%)	0	100	100
47	AM	134/138 (97%)	129 (96%)	5 (4%)	0	100	100
48	AN	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
49	AO	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
50	AP	171/184 (93%)	165 (96%)	6 (4%)	0	100	100
51	AQ	183/186 (98%)	177 (97%)	6 (3%)	0	100	100
52	AR	186/189 (98%)	179 (96%)	7 (4%)	0	100	100
53	AS	170/178 (96%)	162 (95%)	8 (5%)	0	100	100
54	AT	157/160 (98%)	147 (94%)	10 (6%)	0	100	100
55	AU	98/121 (81%)	89 (91%)	9 (9%)	0	100	100
56	AV	134/137 (98%)	131 (98%)	3 (2%)	0	100	100
57	AW	61/155 (39%)	61 (100%)	0	0	100	100
58	AX	119/142 (84%)	116 (98%)	3 (2%)	0	100	100
59	AY	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
60	AZ	133/136 (98%)	129 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	Aa	146/149 (98%)	134 (92%)	12 (8%)	0	100	100
62	Ab	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
63	Ac	95/105 (90%)	95 (100%)	0	0	100	100
64	Ad	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
65	Ae	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
66	Af	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
67	Ag	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
68	Ah	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
69	Ai	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
70	Aj	85/88 (97%)	81 (95%)	4 (5%)	0	100	100
71	Ak	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
72	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
73	Am	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
74	An	23/25 (92%)	23 (100%)	0	0	100	100
75	Ao	103/106 (97%)	92 (89%)	11 (11%)	0	100	100
76	Ap	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
77	E	215/217 (99%)	197 (92%)	18 (8%)	0	100	100
79	DC	819/842 (97%)	754 (92%)	65 (8%)	0	100	100
80	Bf	73/152 (48%)	67 (92%)	6 (8%)	0	100	100
81	BM	122/143 (85%)	110 (90%)	12 (10%)	0	100	100
82	VA	187/312 (60%)	169 (90%)	18 (10%)	0	100	100
All	All	12121/13257 (91%)	11282 (93%)	839 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	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
33	AA	189/196 (96%)	189 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	AB	321/322 (100%)	321 (100%)	0	100	100
35	AC	288/289 (100%)	288 (100%)	0	100	100
39	AD	241/245 (98%)	241 (100%)	0	100	100
40	AE	134/153 (88%)	134 (100%)	0	100	100
41	AF	186/205 (91%)	186 (100%)	0	100	100
42	AG	189/208 (91%)	189 (100%)	0	100	100
43	AH	170/171 (99%)	170 (100%)	0	100	100
44	AI	176/187 (94%)	176 (100%)	0	100	100
45	AJ	147/150 (98%)	147 (100%)	0	100	100
46	AL	154/159 (97%)	154 (100%)	0	100	100
47	AM	107/109 (98%)	107 (100%)	0	100	100
48	AN	175/176 (99%)	175 (100%)	0	100	100
49	AO	160/162 (99%)	160 (100%)	0	100	100
50	AP	141/146 (97%)	141 (100%)	0	100	100
51	AQ	150/151 (99%)	150 (100%)	0	100	100
52	AR	153/154 (99%)	153 (100%)	0	100	100
53	AS	156/162 (96%)	156 (100%)	0	100	100
54	AT	136/137 (99%)	136 (100%)	0	100	100
55	AU	87/107 (81%)	87 (100%)	0	100	100
56	AV	104/105 (99%)	104 (100%)	0	100	100
57	AW	55/129 (43%)	55 (100%)	0	100	100
58	AX	105/118 (89%)	105 (100%)	0	100	100
59	AY	109/110 (99%)	109 (100%)	0	100	100
60	AZ	115/116 (99%)	115 (100%)	0	100	100
61	Aa	118/119 (99%)	118 (100%)	0	100	100
62	Ab	46/47 (98%)	46 (100%)	0	100	100
63	Ac	81/88 (92%)	81 (100%)	0	100	100
64	Ad	96/97 (99%)	96 (100%)	0	100	100
65	Ae	109/111 (98%)	109 (100%)	0	100	100
66	Af	90/91 (99%)	90 (100%)	0	100	100
67	Ag	95/103 (92%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	Ah	104/105 (99%)	104 (100%)	0	100	100
69	Ai	81/82 (99%)	81 (100%)	0	100	100
70	Aj	70/71 (99%)	70 (100%)	0	100	100
71	Ak	68/69 (99%)	68 (100%)	0	100	100
72	Al	45/46 (98%)	45 (100%)	0	100	100
73	Am	47/116 (40%)	47 (100%)	0	100	100
74	An	23/23 (100%)	23 (100%)	0	100	100
75	Ao	90/91 (99%)	90 (100%)	0	100	100
76	Ap	71/72 (99%)	71 (100%)	0	100	100
77	E	198/198 (100%)	198 (100%)	0	100	100
79	DC	699/714 (98%)	699 (100%)	0	100	100
80	Bf	66/135 (49%)	66 (100%)	0	100	100
81	BM	100/119 (84%)	100 (100%)	0	100	100
82	VA	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 164 such sidechains are listed below:

Mol	Chain	Res	Type
52	AR	39	ASN
68	Ah	104	GLN
53	AS	88	HIS
59	AY	42	GLN
73	Am	120	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	B5	1780/1798 (98%)	399 (22%)	11 (0%)
36	A1	3194/3360 (95%)	616 (19%)	26 (0%)
37	A3	120/121 (99%)	12 (10%)	1 (0%)
38	A4	157/158 (99%)	31 (19%)	0
78	EC	191/201 (95%)	109 (57%)	8 (4%)
All	All	5442/5638 (96%)	1167 (21%)	46 (0%)

5 of 1167 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
32	B5	4	C
32	B5	17	C
32	B5	26	A
32	B5	34	G
32	B5	40	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
36	A1	1629	U
36	A1	2875	U
36	A1	2241	U
36	A1	2494	A
37	A3	52	G

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	$\# Z > 2$
36	OMU	A1	2729	36	19,22,23	1.24	3 (15%)	25,31,34	1.79	4 (16%)
36	OMG	A1	1450	36	23,26,27	1.19	3 (13%)	32,38,41	1.92	6 (18%)
36	OMU	A1	2724	36	19,22,23	1.24	3 (15%)	25,31,34	1.83	6 (24%)
36	A2M	A1	2640	36	22,25,26	1.48	4 (18%)	30,36,39	2.04	7 (23%)
32	MA6	B5	1781	32	23,26,27	1.50	4 (17%)	33,38,41	2.07	10 (30%)
36	OMG	A1	2793	36	23,26,27	1.18	3 (13%)	32,38,41	2.01	6 (18%)
32	MA6	B5	1782	32	23,26,27	1.48	5 (21%)	33,38,41	2.11	10 (30%)
36	OMC	A1	2197	36	19,22,23	0.79	0	25,31,34	0.88	0
36	A2M	A1	2280	36	22,25,26	1.47	4 (18%)	30,36,39	2.09	9 (30%)
32	OMU	B5	578	32	19,22,23	1.19	3 (15%)	25,31,34	1.81	5 (20%)
32	OMG	B5	1428	32,83	23,26,27	1.19	3 (13%)	32,38,41	1.97	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	A2M	A1	1133	36	22,25,26	1.46	5 (22%)	30,36,39	2.16	10 (33%)
36	OMC	A1	1437	36,83	19,22,23	0.82	0	25,31,34	1.02	2 (8%)
32	OMG	B5	562	32	23,26,27	1.20	3 (13%)	32,38,41	1.99	5 (15%)
32	4AC	B5	1280	32	21,24,25	1.06	1 (4%)	28,34,37	1.07	2 (7%)
36	OMU	A1	2921	36	19,22,23	1.26	3 (15%)	25,31,34	1.83	4 (16%)
36	OMU	A1	2347	36	19,22,23	1.29	3 (15%)	25,31,34	1.82	5 (20%)
36	OMC	A1	2337	36	19,22,23	0.77	0	25,31,34	0.85	1 (4%)
36	OMG	A1	805	36	23,26,27	1.18	3 (13%)	32,38,41	2.02	7 (21%)
36	OMC	A1	2959	36	19,22,23	0.78	0	25,31,34	0.82	0
32	OMG	B5	1271	32	23,26,27	1.18	3 (13%)	32,38,41	1.95	6 (18%)
36	A2M	A1	2256	36	22,25,26	1.48	4 (18%)	30,36,39	2.09	9 (30%)
36	UR3	A1	2634	36	19,22,23	0.96	0	26,32,35	1.77	2 (7%)
36	A2M	A1	1449	36,83	22,25,26	1.49	3 (13%)	30,36,39	2.04	7 (23%)
32	A2M	B5	420	32	22,25,26	1.50	4 (18%)	30,36,39	2.05	9 (30%)
36	A2M	A1	2281	36	22,25,26	1.43	5 (22%)	30,36,39	2.33	11 (36%)
32	OMC	B5	1007	32	19,22,23	0.77	0	25,31,34	0.81	0
36	OMC	A1	2948	36	19,22,23	0.78	0	25,31,34	0.89	1 (4%)
32	OMG	B5	1572	32	23,26,27	1.18	2 (8%)	32,38,41	2.11	7 (21%)
36	A2M	A1	649	36	22,25,26	1.48	4 (18%)	30,36,39	2.02	8 (26%)
36	A2M	A1	807	36	22,25,26	1.48	5 (22%)	30,36,39	2.09	9 (30%)
32	OMG	B5	1126	32	23,26,27	1.13	2 (8%)	32,38,41	2.08	8 (25%)
36	OMG	A1	2815	36	23,26,27	1.19	3 (13%)	32,38,41	1.94	6 (18%)
36	5MC	A1	2278	36,83	19,22,23	1.54	3 (15%)	26,32,35	1.21	3 (11%)
36	A2M	A1	2946	36,83	22,25,26	1.48	4 (18%)	30,36,39	2.20	10 (33%)
32	OMC	B5	414	32	19,22,23	0.79	0	25,31,34	0.80	1 (4%)
36	1MA	A1	645	36,83	21,25,26	1.35	4 (19%)	30,37,40	1.70	6 (20%)
36	OMU	A1	898	36	19,22,23	1.25	3 (15%)	25,31,34	1.81	4 (16%)
32	OMU	B5	1269	32	19,22,23	1.25	4 (21%)	25,31,34	1.85	5 (20%)
36	OMC	A1	663	36	19,22,23	0.81	0	25,31,34	0.74	0
36	OMG	A1	2288	36	23,26,27	1.21	3 (13%)	32,38,41	1.94	6 (18%)
32	A2M	B5	28	32	22,25,26	1.50	4 (18%)	30,36,39	2.04	7 (23%)
36	OMG	A1	2791	36	23,26,27	1.18	3 (13%)	32,38,41	1.96	6 (18%)
32	G7M	B5	1575	32	23,26,27	2.54	6 (26%)	34,39,42	3.09	14 (41%)
32	A2M	B5	974	32	22,25,26	1.49	4 (18%)	30,36,39	2.03	8 (26%)
36	OMG	A1	867	36,83	23,26,27	1.20	3 (13%)	32,38,41	1.99	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	A2M	B5	796	32	22,25,26	1.51	4 (18%)	30,36,39	2.19	9 (30%)
36	OMU	A1	2421	36	19,22,23	1.26	3 (15%)	25,31,34	1.85	5 (20%)
32	A2M	B5	100	32,83	22,25,26	1.48	4 (18%)	30,36,39	2.08	9 (30%)
36	OMU	A1	1888	36	19,22,23	1.28	3 (15%)	25,31,34	1.87	5 (20%)
36	A2M	A1	876	36	22,25,26	1.47	5 (22%)	30,36,39	2.04	7 (23%)
79	DDE	DC	699	79	18,20,21	1.01	1 (5%)	17,28,30	0.76	1 (5%)
36	A2M	A1	2220	36	22,25,26	1.51	5 (22%)	30,36,39	1.94	9 (30%)
36	5MC	A1	2870	36	19,22,23	1.61	3 (15%)	26,32,35	1.23	3 (11%)
32	A2M	B5	436	32	22,25,26	1.49	4 (18%)	30,36,39	2.07	8 (26%)
36	1MA	A1	2142	36,83	21,25,26	1.33	4 (19%)	30,37,40	1.70	3 (10%)
32	OMC	B5	1639	32	19,22,23	0.76	0	25,31,34	0.71	0
36	OMU	A1	2417	36	19,22,23	1.23	3 (15%)	25,31,34	1.82	5 (20%)
36	OMG	A1	2922	36	23,26,27	1.18	3 (13%)	32,38,41	1.96	6 (18%)
34	HIC	AB	243	34	10,11,12	1.46	1 (10%)	9,14,16	1.23	1 (11%)
36	OMC	A1	650	36,83	19,22,23	0.79	0	25,31,34	0.86	0
32	A2M	B5	619	32,83	22,25,26	1.47	4 (18%)	30,36,39	2.04	9 (30%)
36	OMG	A1	908	36	23,26,27	1.23	3 (13%)	32,38,41	2.03	6 (18%)
36	OMG	A1	2619	36	23,26,27	1.20	3 (13%)	32,38,41	1.95	6 (18%)
36	A2M	A1	817	36,83	22,25,26	1.50	5 (22%)	30,36,39	2.03	8 (26%)
32	XSX	B5	1191	32	24,28,29	1.00	1 (4%)	30,40,43	3.70	5 (16%)
32	A2M	B5	541	32	22,25,26	1.51	4 (18%)	30,36,39	2.09	7 (23%)
32	4AC	B5	1773	32	21,24,25	1.05	2 (9%)	28,34,37	2.58	7 (25%)

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
36	OMU	A1	2729	36	-	3/9/27/28	0/2/2/2
36	OMG	A1	1450	36	-	1/9/27/28	0/3/3/3
36	OMU	A1	2724	36	-	1/9/27/28	0/2/2/2
36	A2M	A1	2640	36	-	0/9/27/28	0/3/3/3
32	MA6	B5	1781	32	-	0/11/29/30	0/3/3/3
36	OMG	A1	2793	36	-	1/9/27/28	0/3/3/3
32	MA6	B5	1782	32	-	2/11/29/30	0/3/3/3
36	OMC	A1	2197	36	-	6/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	A2M	A1	2280	36	-	2/9/27/28	0/3/3/3
32	OMU	B5	578	32	-	0/9/27/28	0/2/2/2
32	OMG	B5	1428	32,83	-	2/9/27/28	0/3/3/3
36	A2M	A1	1133	36	-	0/9/27/28	0/3/3/3
36	OMC	A1	1437	36,83	-	4/9/27/28	0/2/2/2
32	OMG	B5	562	32	-	1/9/27/28	0/3/3/3
32	4AC	B5	1280	32	-	4/11/29/30	0/2/2/2
36	OMU	A1	2921	36	-	0/9/27/28	0/2/2/2
36	OMU	A1	2347	36	-	0/9/27/28	0/2/2/2
36	OMC	A1	2337	36	-	1/9/27/28	0/2/2/2
36	OMG	A1	805	36	-	0/9/27/28	0/3/3/3
36	OMC	A1	2959	36	-	0/9/27/28	0/2/2/2
32	OMG	B5	1271	32	-	1/9/27/28	0/3/3/3
36	A2M	A1	2256	36	-	3/9/27/28	0/3/3/3
36	UR3	A1	2634	36	-	0/7/25/26	0/2/2/2
36	A2M	A1	1449	36,83	-	0/9/27/28	0/3/3/3
32	A2M	B5	420	32	-	1/9/27/28	0/3/3/3
36	A2M	A1	2281	36	-	2/9/27/28	0/3/3/3
32	OMC	B5	1007	32	-	0/9/27/28	0/2/2/2
36	OMC	A1	2948	36	-	0/9/27/28	0/2/2/2
32	OMG	B5	1572	32	-	2/9/27/28	0/3/3/3
36	A2M	A1	649	36	-	0/9/27/28	0/3/3/3
36	A2M	A1	807	36	-	1/9/27/28	0/3/3/3
32	OMG	B5	1126	32	-	1/9/27/28	0/3/3/3
36	OMG	A1	2815	36	-	0/9/27/28	0/3/3/3
36	5MC	A1	2278	36,83	-	1/7/25/26	0/2/2/2
36	A2M	A1	2946	36,83	-	0/9/27/28	0/3/3/3
32	OMC	B5	414	32	-	1/9/27/28	0/2/2/2
36	1MA	A1	645	36,83	-	2/7/25/26	0/3/3/3
36	OMU	A1	898	36	-	0/9/27/28	0/2/2/2
32	OMU	B5	1269	32	-	4/9/27/28	0/2/2/2
36	OMC	A1	663	36	-	1/9/27/28	0/2/2/2
36	OMG	A1	2288	36	-	0/9/27/28	0/3/3/3
32	A2M	B5	28	32	-	0/9/27/28	0/3/3/3
36	OMG	A1	2791	36	-	1/9/27/28	0/3/3/3
32	G7M	B5	1575	32	-	0/7/25/26	0/3/3/3
32	A2M	B5	974	32	-	0/9/27/28	0/3/3/3
36	OMG	A1	867	36,83	-	0/9/27/28	0/3/3/3
32	A2M	B5	796	32	-	0/9/27/28	0/3/3/3
36	OMU	A1	2421	36	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	A2M	B5	100	32,83	-	0/9/27/28	0/3/3/3
36	OMU	A1	1888	36	-	1/9/27/28	0/2/2/2
36	A2M	A1	876	36	-	0/9/27/28	0/3/3/3
79	DDE	DC	699	79	-	7/20/21/23	0/1/1/1
36	A2M	A1	2220	36	-	1/9/27/28	0/3/3/3
36	5MC	A1	2870	36	-	4/7/25/26	0/2/2/2
32	A2M	B5	436	32	-	0/9/27/28	0/3/3/3
36	1MA	A1	2142	36,83	-	0/7/25/26	0/3/3/3
32	OMC	B5	1639	32	-	0/9/27/28	0/2/2/2
36	OMU	A1	2417	36	-	1/9/27/28	0/2/2/2
36	OMG	A1	2922	36	-	1/9/27/28	0/3/3/3
34	HIC	AB	243	34	-	0/5/6/8	0/1/1/1
36	OMC	A1	650	36,83	-	0/9/27/28	0/2/2/2
32	A2M	B5	619	32,83	-	4/9/27/28	0/3/3/3
36	OMG	A1	908	36	-	0/9/27/28	0/3/3/3
36	OMG	A1	2619	36	-	1/9/27/28	0/3/3/3
36	A2M	A1	817	36,83	-	1/9/27/28	0/3/3/3
32	XSX	B5	1191	32	-	6/16/34/35	0/2/2/2
32	A2M	B5	541	32	-	5/9/27/28	0/3/3/3
32	4AC	B5	1773	32	-	4/11/29/30	0/2/2/2

The worst 5 of 194 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	B5	1575	G7M	C8-N7	7.65	1.46	1.33
36	A1	2870	5MC	C5-C4	5.60	1.48	1.44
36	A1	2278	5MC	C5-C4	5.39	1.48	1.44
32	B5	1575	G7M	C5-N7	-4.94	1.33	1.39
32	B5	541	A2M	C5-C4	4.74	1.47	1.39

The worst 5 of 383 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	B5	1191	XSX	C3-C1-N3	18.82	145.05	112.16
32	B5	1773	4AC	N4-C4-N3	9.43	129.18	113.87
32	B5	1575	G7M	CN7-N7-C8	-7.75	113.05	124.79
36	A1	2634	UR3	C4-N3-C2	-7.12	118.85	124.58
36	A1	908	OMG	C5-C4-N3	-6.46	118.11	128.39

There are no chirality outliers.

5 of 86 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	B5	414	OMC	C1'-C2'-O2'-CM2
32	B5	420	A2M	C1'-C2'-O2'-CM'
32	B5	562	OMG	C1'-C2'-O2'-CM2
32	B5	1191	XSX	C3-C1-N3-C2
32	B5	1191	XSX	C3-C1-N3-C4

There are no ring outliers.

29 monomers are involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	A1	2724	OMU	2	0
36	A1	2793	OMG	1	0
36	A1	2197	OMC	2	0
36	A1	1133	A2M	1	0
32	B5	562	OMG	1	0
32	B5	1280	4AC	5	0
36	A1	2256	A2M	1	0
36	A1	1449	A2M	1	0
36	A1	2281	A2M	1	0
32	B5	1572	OMG	1	0
36	A1	649	A2M	2	0
36	A1	807	A2M	1	0
32	B5	1126	OMG	1	0
32	B5	1269	OMU	1	0
36	A1	663	OMC	1	0
32	B5	28	A2M	1	0
32	B5	1575	G7M	3	0
32	B5	974	A2M	1	0
32	B5	796	A2M	1	0
36	A1	2421	OMU	1	0
32	B5	100	A2M	1	0
36	A1	876	A2M	1	0
36	A1	2220	A2M	4	0
32	B5	436	A2M	1	0
32	B5	1639	OMC	2	0
36	A1	2417	OMU	1	0
36	A1	650	OMC	2	0
36	A1	817	A2M	1	0
32	B5	1773	4AC	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 257 ligands modelled in this entry, 256 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	1.14	3 (10%)	45,47,47	1.73	6 (13%)

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	-	-	2/16/32/32	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	3.05	1.47	1.38
85	DC	901	GDP	C6-N1	-2.43	1.34	1.38
85	DC	901	GDP	C5-N7	-2.06	1.34	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	DC	901	GDP	C5-C4-N3	-5.90	119.00	128.39
85	DC	901	GDP	C2-N3-C4	4.89	120.72	112.30
85	DC	901	GDP	N9-C4-N3	4.41	134.76	125.95
85	DC	901	GDP	C6-C5-N7	3.31	136.31	130.29
85	DC	901	GDP	C4-C5-N7	-2.56	106.62	110.67

There are no chirality outliers.

All (2) torsion outliers are listed below:

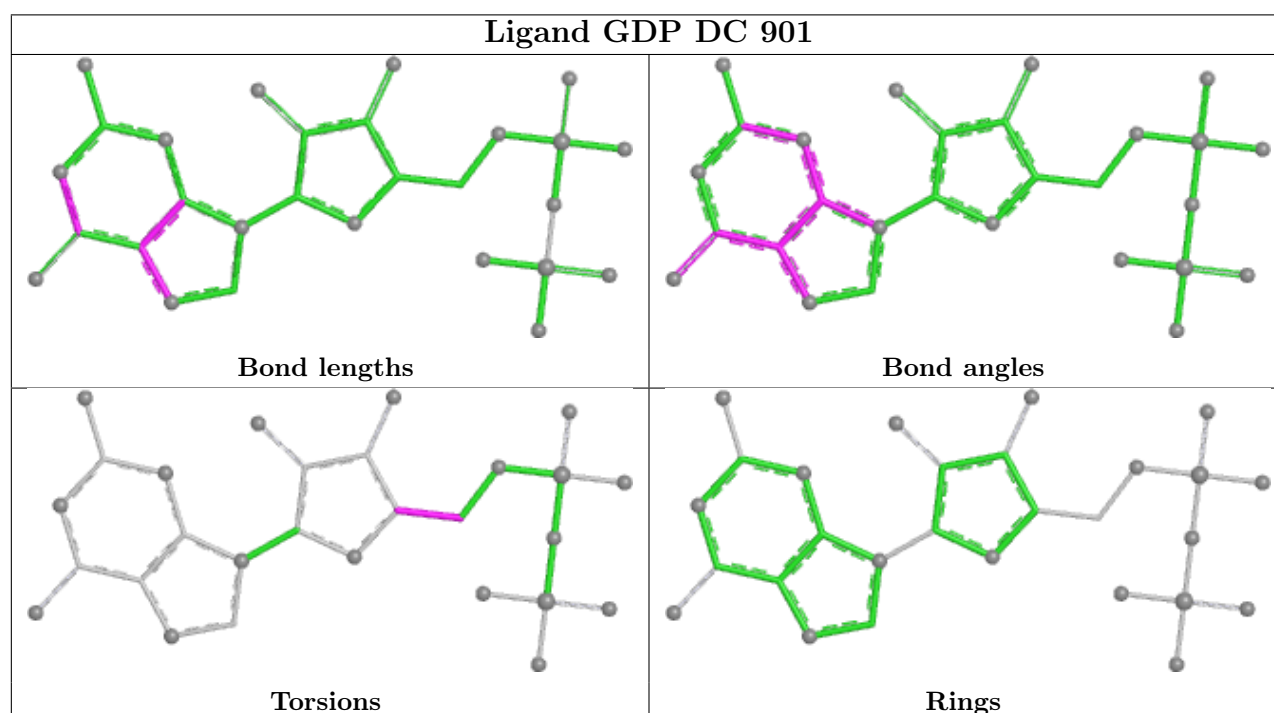
Mol	Chain	Res	Type	Atoms
85	DC	901	GDP	C3'-C4'-C5'-O5'
85	DC	901	GDP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	DC	901	GDP	1	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.

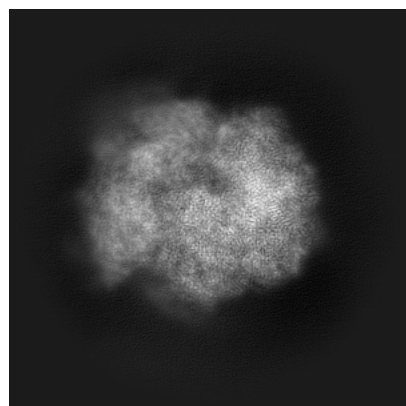
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28610. These allow visual inspection of the internal detail of the map and identification of artifacts.

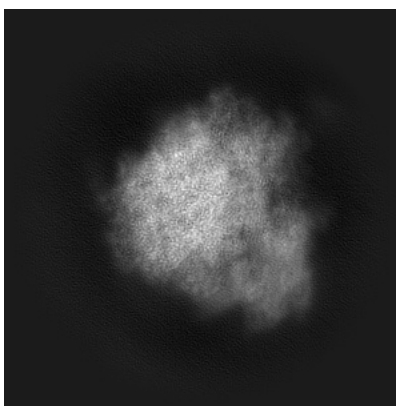
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

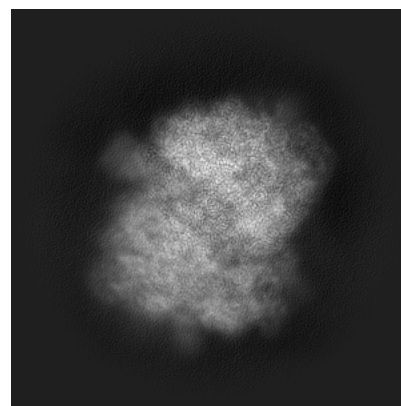
6.1.1 Primary map



X

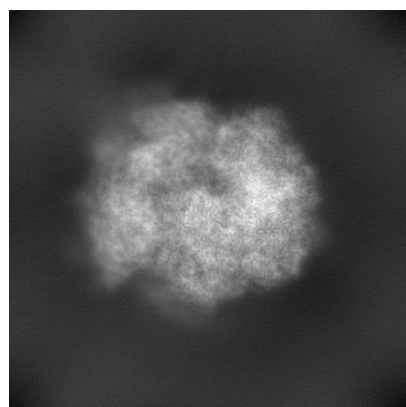


Y

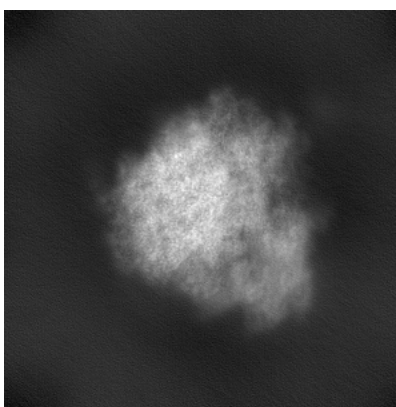


Z

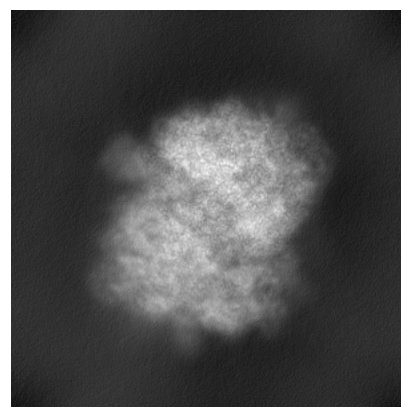
6.1.2 Raw map



X



Y

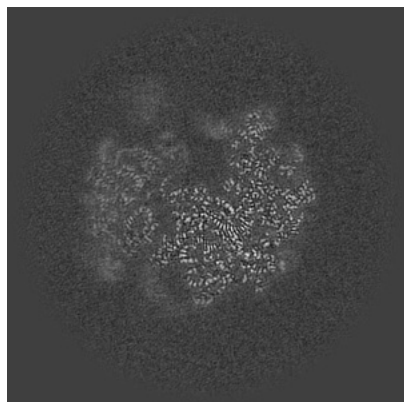


Z

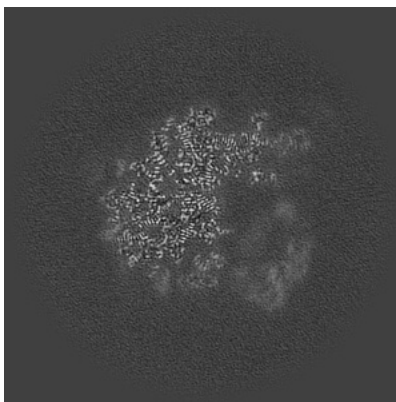
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

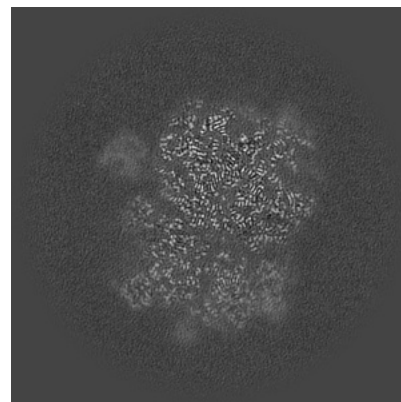
6.2.1 Primary map



X Index: 200

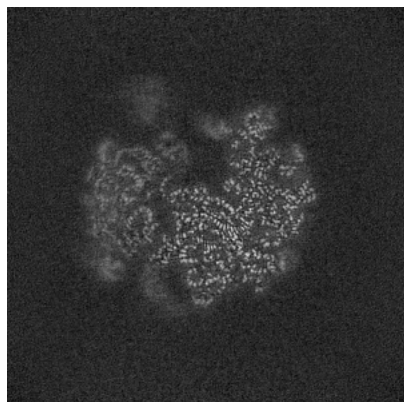


Y Index: 200

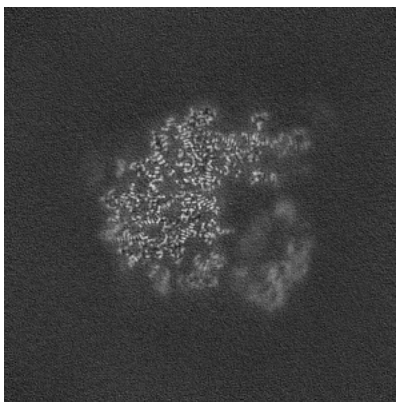


Z Index: 200

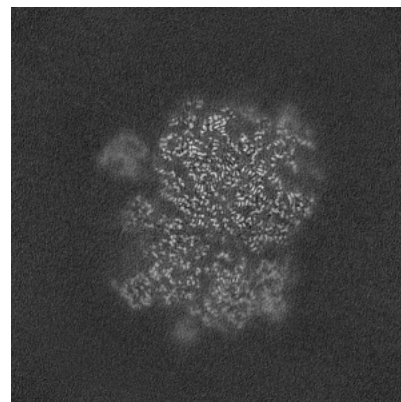
6.2.2 Raw map



X Index: 200



Y Index: 200

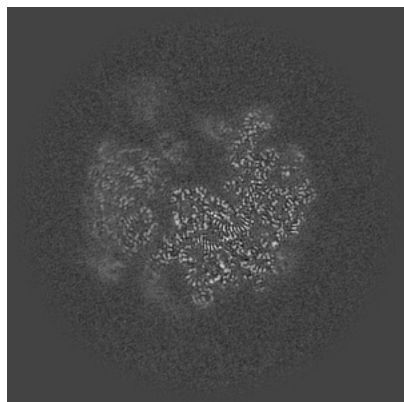


Z Index: 200

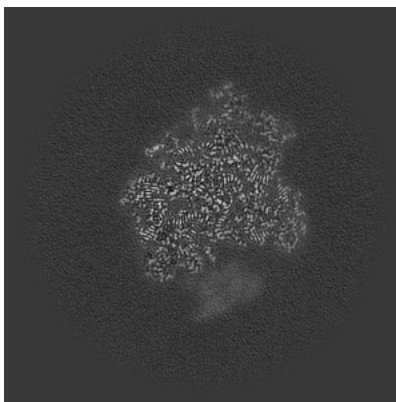
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

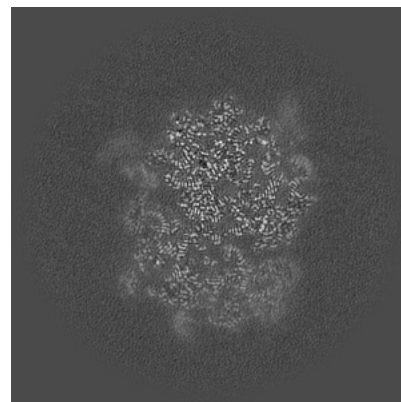
6.3.1 Primary map



X Index: 201

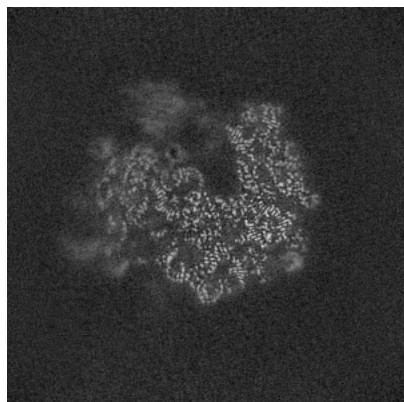


Y Index: 246

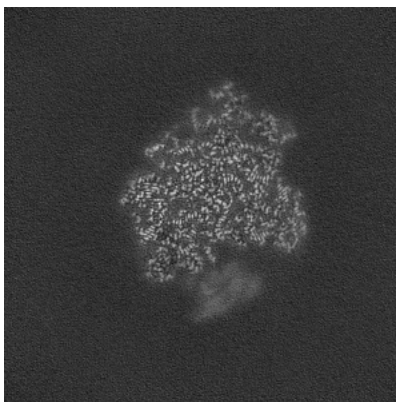


Z Index: 190

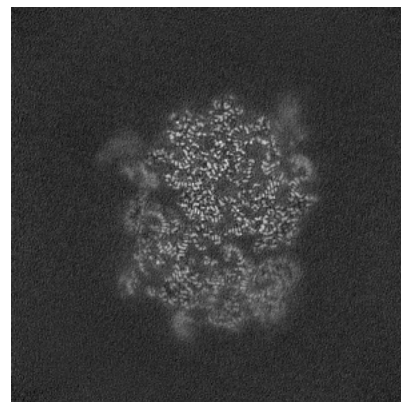
6.3.2 Raw map



X Index: 186



Y Index: 246

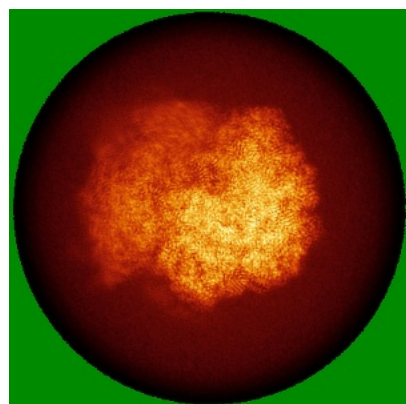


Z Index: 190

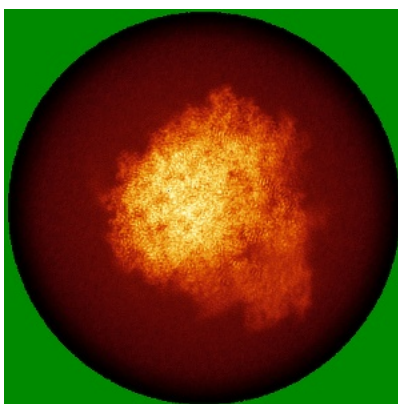
The images above show the largest variance slices of the map in three orthogonal directions.

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

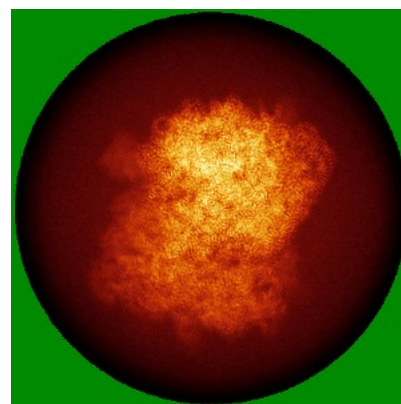
6.4.1 Primary map



X

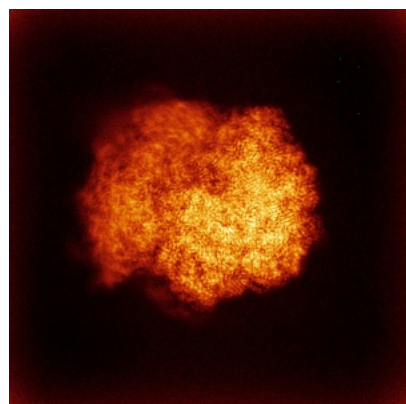


Y

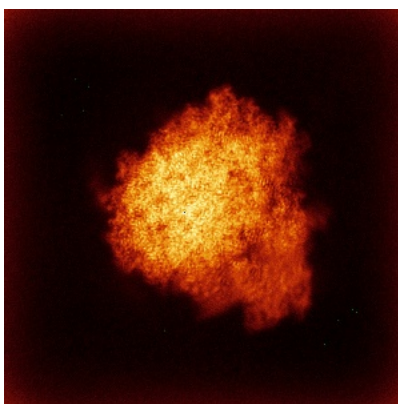


Z

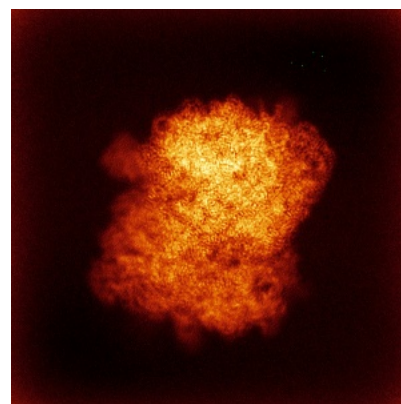
6.4.2 Raw map



X



Y

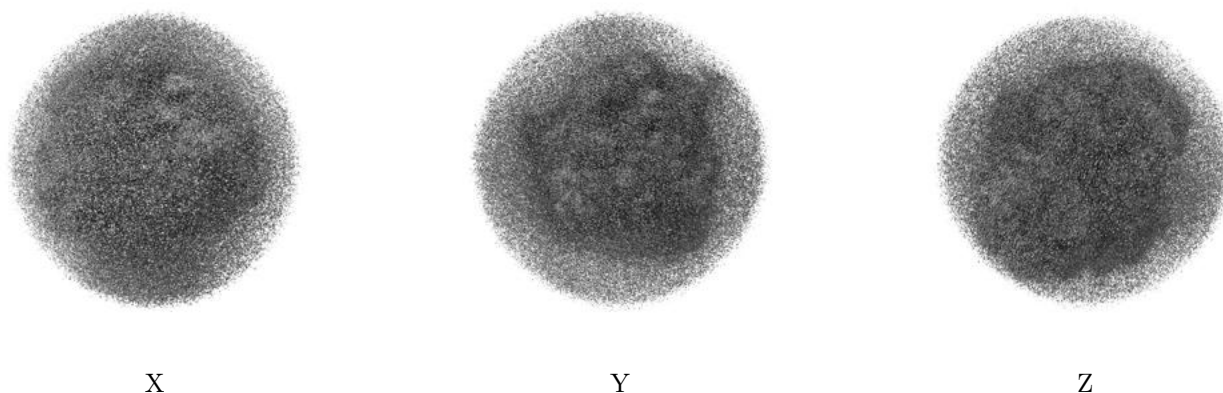


Z

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.

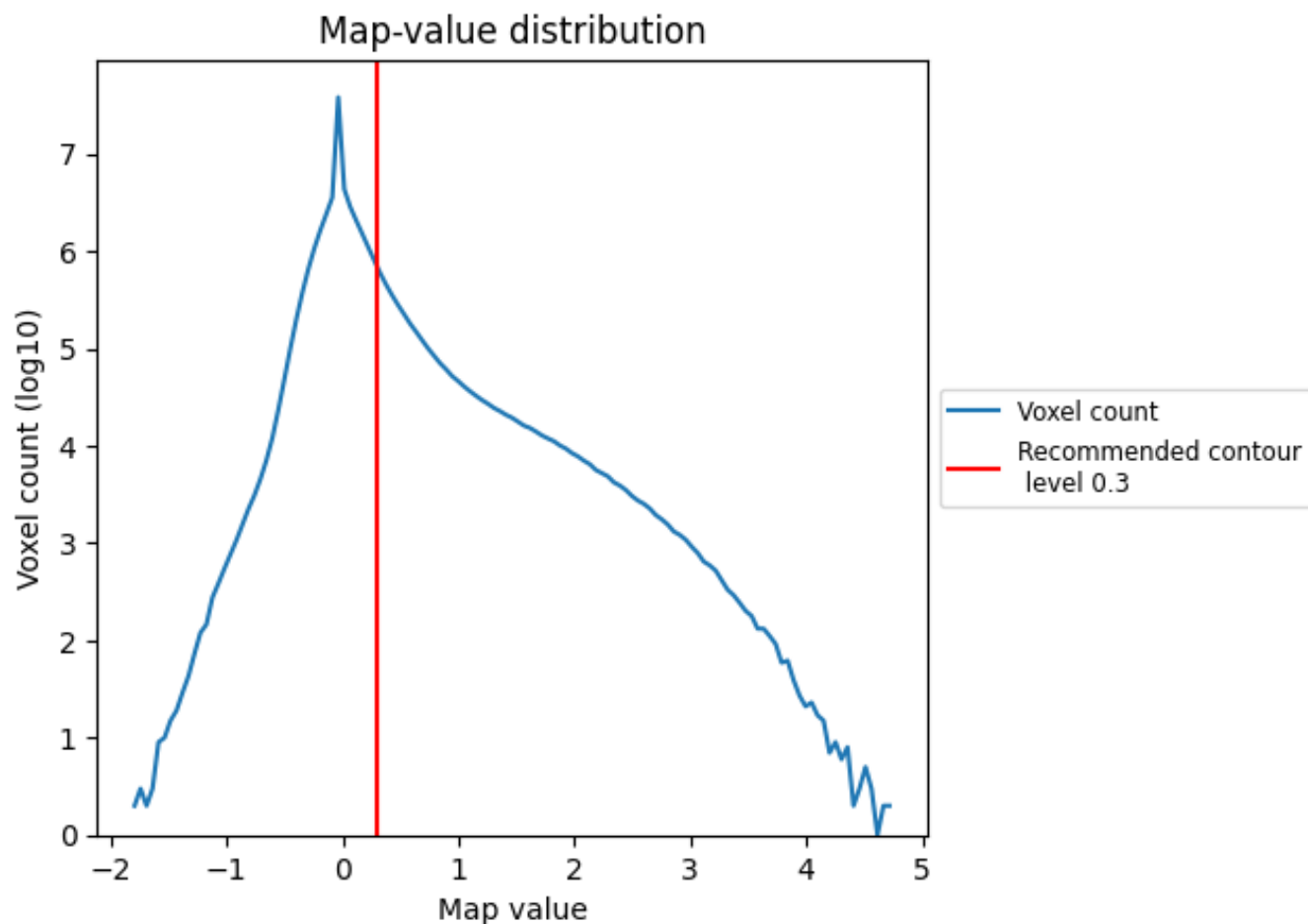
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

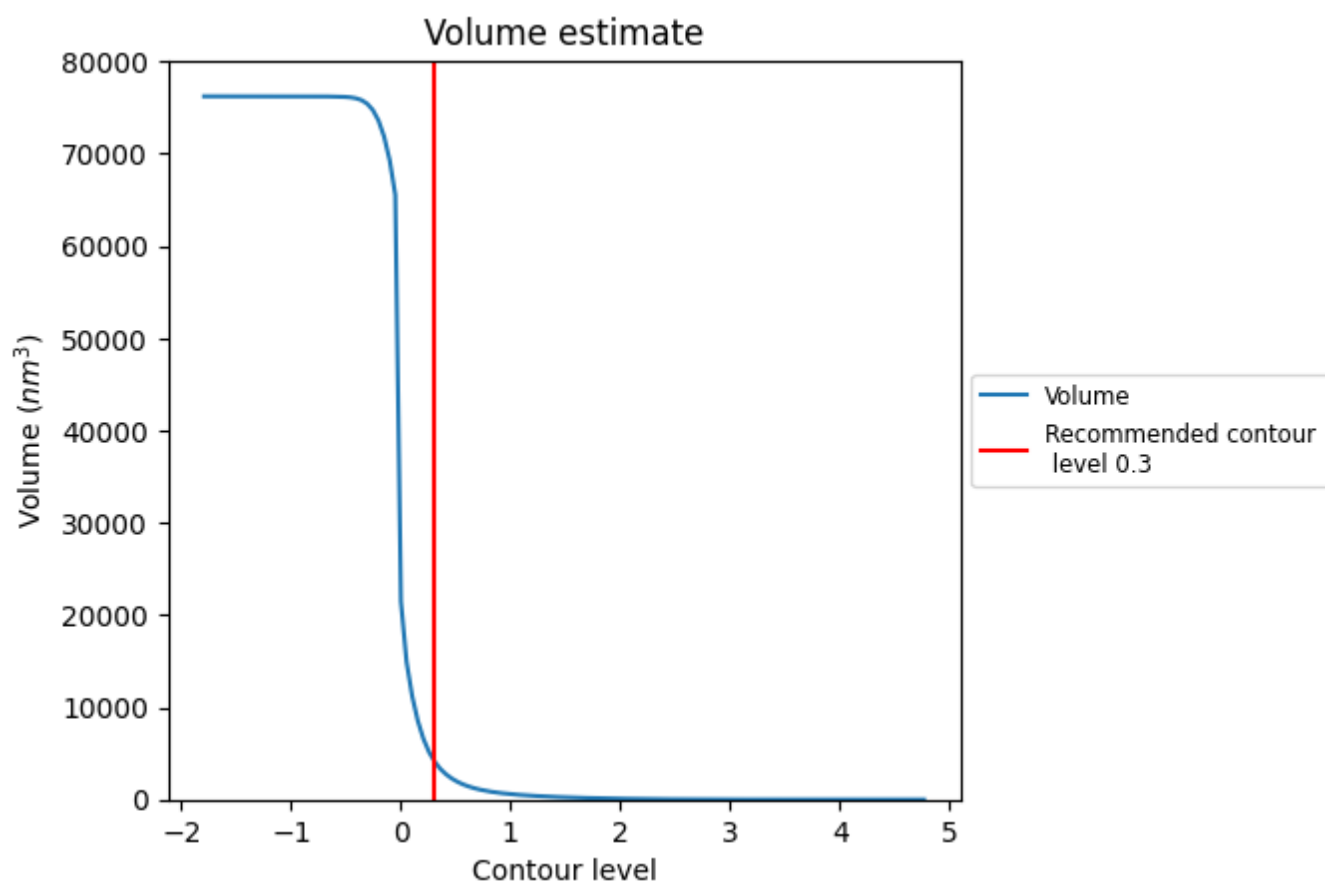
This section contains the results of statistical analysis of the map.

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.

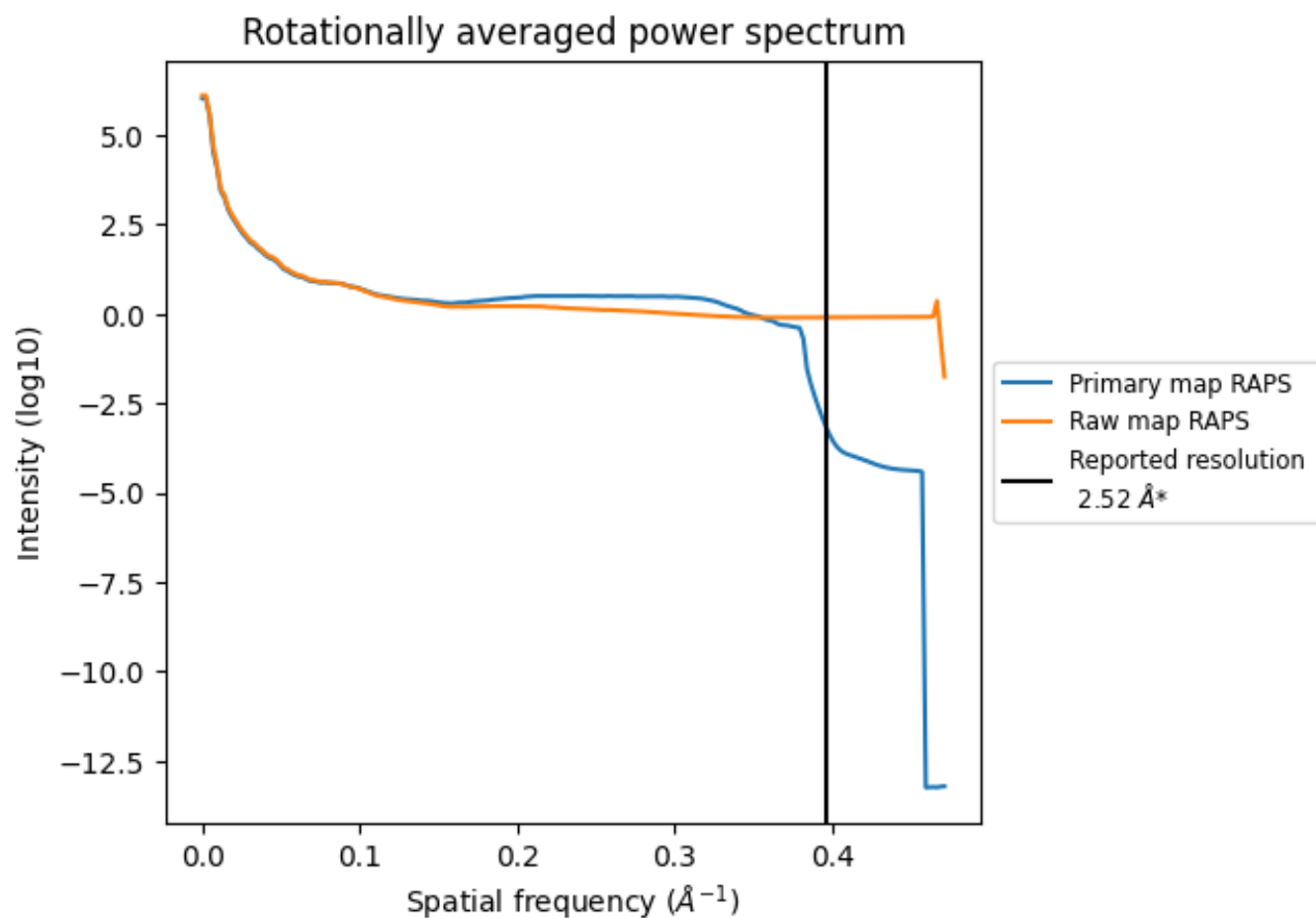
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4289 nm³; this corresponds to an approximate mass of 3874 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

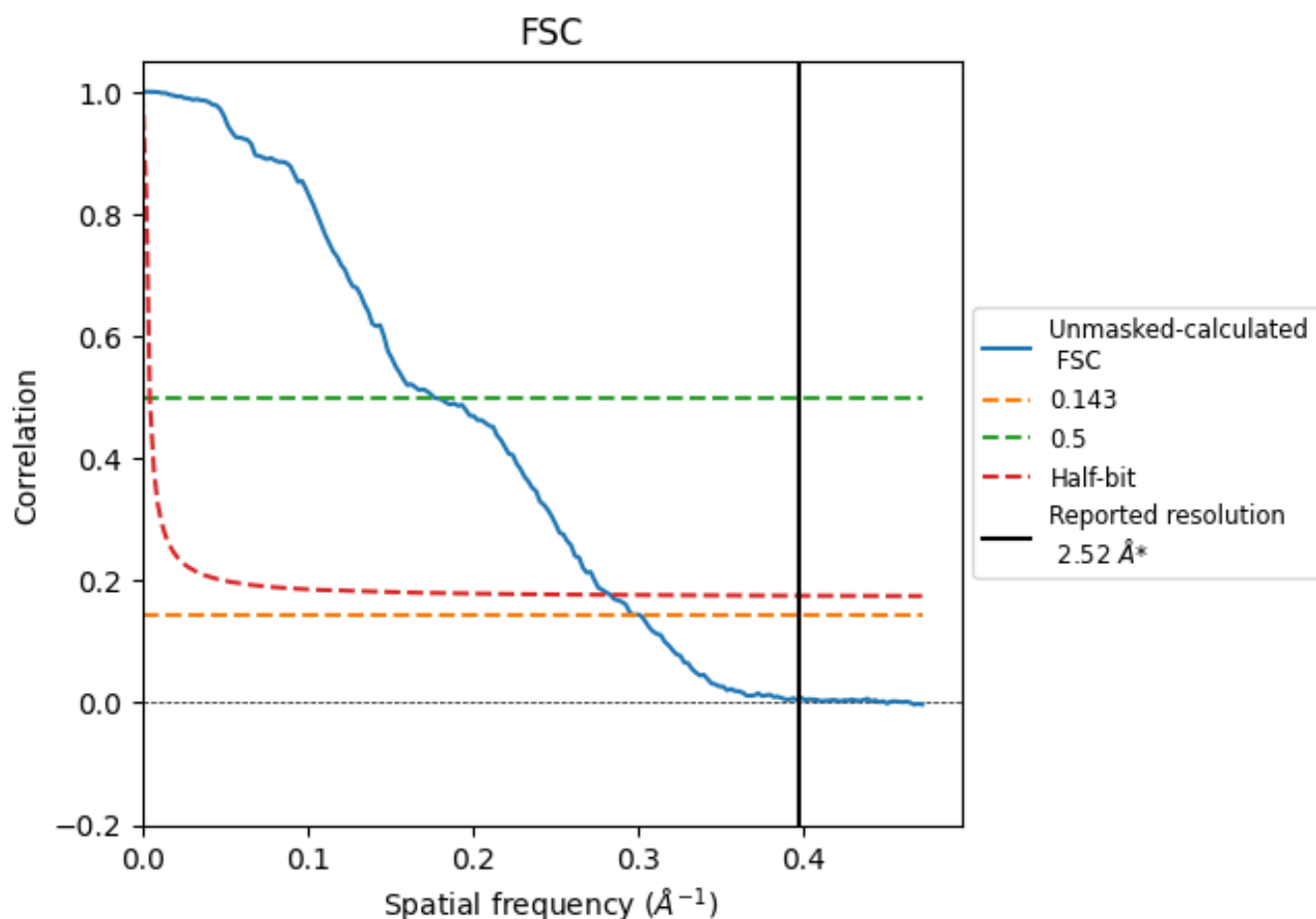


*Reported resolution corresponds to spatial frequency of 0.397 Å⁻¹

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 0.397 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.52	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.37	5.67	3.53

*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 3.37 differs from the reported value 2.52 by more than 10 %

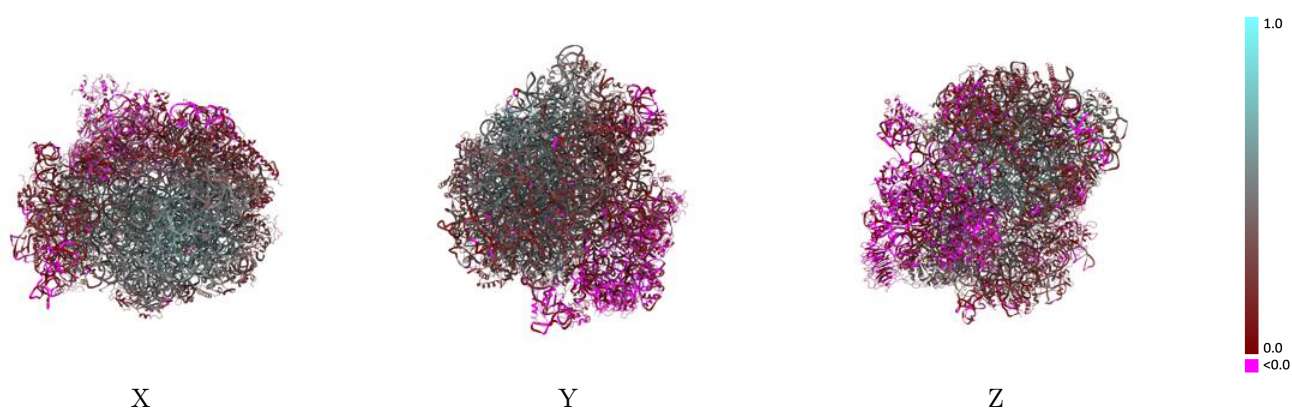
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-28610 and PDB model 8EUB. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

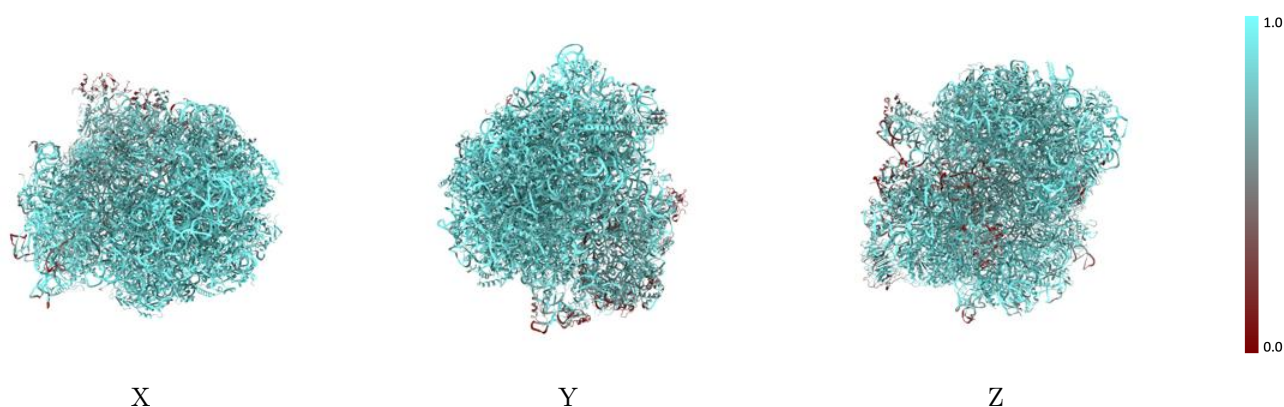
This section was not generated.

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



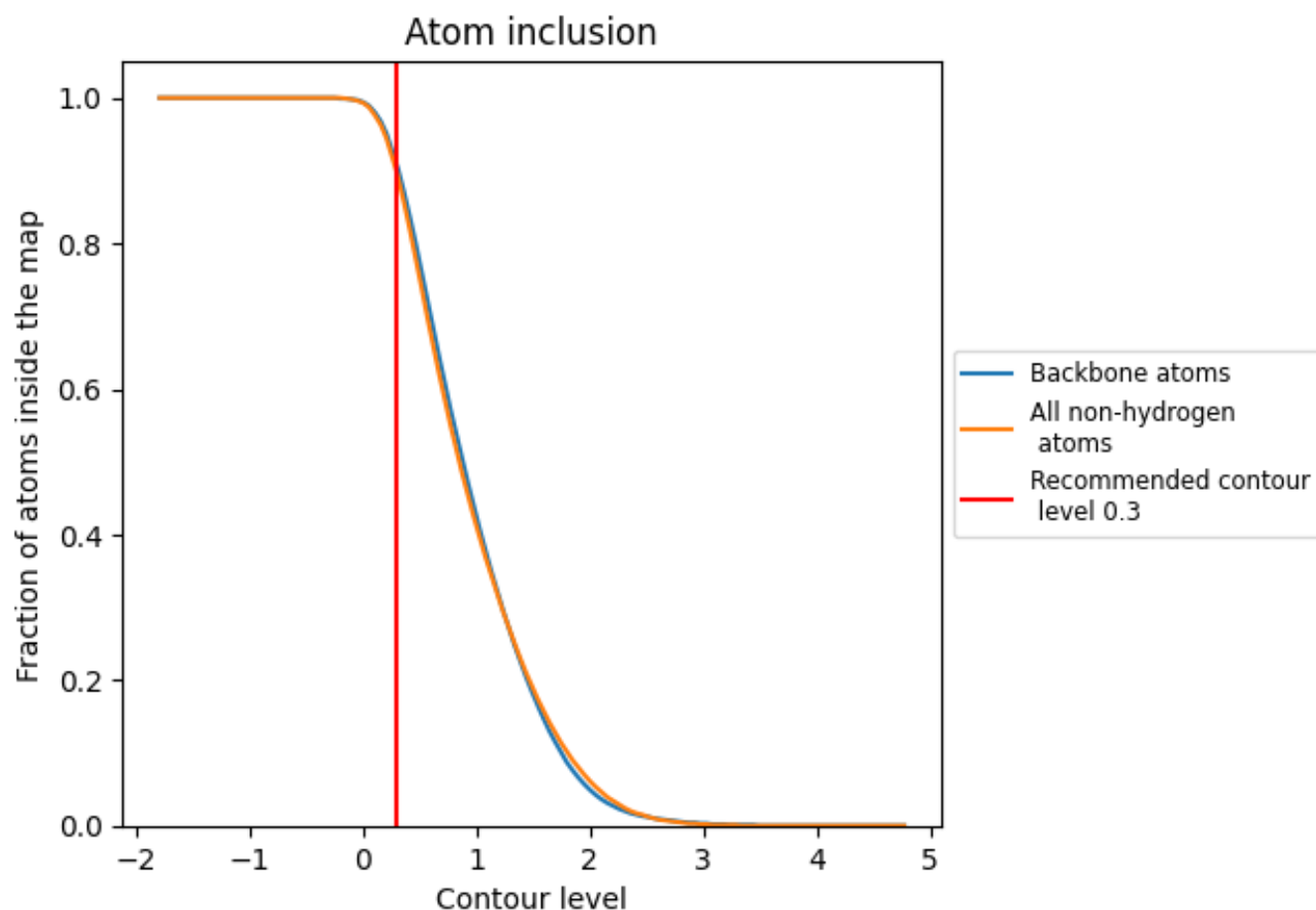
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 91% of all backbone atoms, 90% 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	 0.8960	 0.3190
A1	 0.9640	 0.4260
A3	 0.9010	 0.2260
A4	 0.9740	 0.4720
AA	 0.9870	 0.5900
AB	 0.9600	 0.4810
AC	 0.9080	 0.3380
AD	 0.7540	 0.0920
AE	 0.9300	 0.3710
AF	 0.8930	 0.2610
AG	 0.8840	 0.3370
AH	 0.8490	 0.2560
AI	 0.8640	 0.2530
AJ	 0.7480	 0.1020
AL	 0.8820	 0.2630
AM	 0.8750	 0.2830
AN	 0.9560	 0.4520
AO	 0.9580	 0.4650
AP	 0.9840	 0.5890
AQ	 0.8770	 0.2750
AR	 0.9110	 0.4220
AS	 0.8470	 0.2250
AT	 0.8610	 0.2410
AU	 0.8730	 0.2700
AV	 0.9350	 0.4410
AW	 0.9510	 0.4180
AX	 0.9190	 0.3810
AY	 0.9270	 0.3720
AZ	 0.9190	 0.3610
Aa	 0.8850	 0.3200
Ab	 0.8830	 0.2320
Ac	 0.9450	 0.4620
Ad	 0.9490	 0.4800
Ae	 0.9750	 0.4920
Af	 0.9790	 0.5020



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Chain	Atom inclusion	Q-score
Ag	 0.9580	 0.4780
Ah	 0.8940	 0.3110
Ai	 0.8910	 0.2990
Aj	 0.9800	 0.5260
Ak	 0.8360	 0.2890
Al	 0.9810	 0.5460
Am	 0.8960	 0.3090
An	 0.9670	 0.4900
Ao	 0.8960	 0.3540
Ap	 0.9760	 0.5740
B5	 0.9140	 0.2600
BA	 0.9550	 0.4160
BB	 0.9180	 0.4220
BC	 0.9390	 0.3920
BD	 0.7680	 0.0650
BE	 0.9050	 0.2300
BF	 0.6140	 -0.0070
BG	 0.8730	 0.1930
BH	 0.8650	 0.3080
BI	 0.9050	 0.3060
BJ	 0.8930	 0.2510
BK	 0.7550	 0.0320
BL	 0.8870	 0.3650
BM	 0.3970	 0.0290
BN	 0.9510	 0.4650
BO	 0.9510	 0.4430
BP	 0.5560	 -0.0090
BQ	 0.7070	 -0.0180
BR	 0.7360	 0.1220
BS	 0.5970	 -0.0140
BT	 0.7040	 -0.0060
BU	 0.8440	 0.0780
BV	 0.9410	 0.3980
BW	 0.9640	 0.4410
BX	 0.9300	 0.3930
BY	 0.8640	 0.1710
BZ	 0.5240	 -0.0250
Ba	 0.9490	 0.4860
Bb	 0.9180	 0.4140
Bc	 0.6060	 0.0420
Bd	 0.8940	 0.0820
Be	 0.8500	 0.2190

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Chain	Atom inclusion	Q-score
Bf	 0.3450	 0.0010
Bg	 0.7110	 -0.0050
DC	 0.7690	 0.1330
E	 0.5780	 0.0160
EC	 0.6050	 0.0380
VA	 0.6510	 0.1170