



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:20 AM UTC

PDB ID : 8T3F / pdb_00008t3f
EMDB ID : EMD-41002
Title : Hypomethylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), eEF2, GDP, and sordarin, Structure V
Authors : Zhao, Y.; Li, H.
Deposited on : 2023-06-07
Resolution : 3.09 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

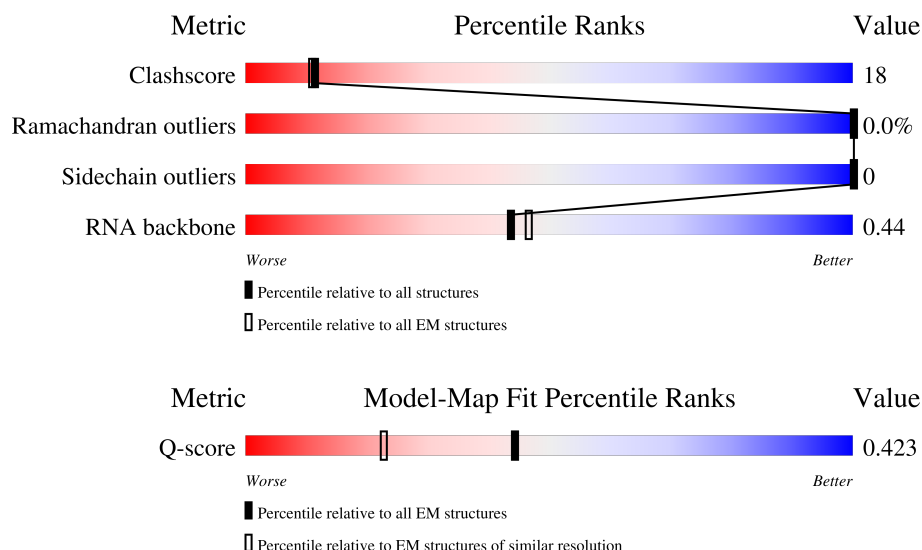
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.09 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	14003 (2.59 - 3.59)

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	

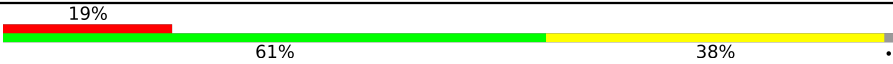
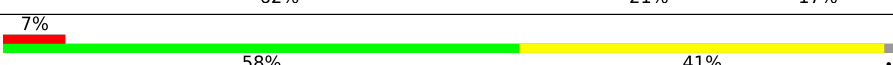
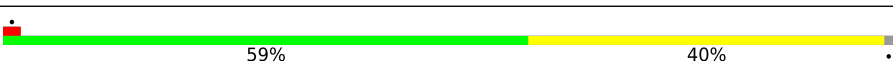
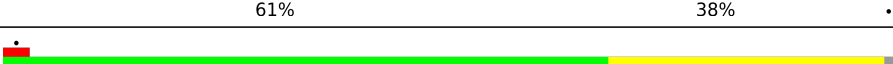
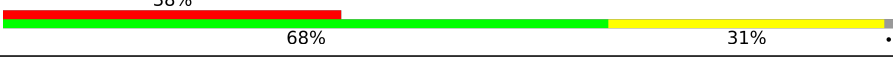
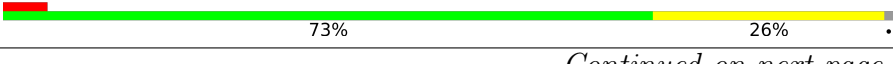
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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	
34	B5	1798	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3393	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	222	
47	AJ	174	
48	AL	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	
55	AS	178	
56	AT	160	
57	AU	121	
58	AV	137	
59	AW	155	
60	AX	142	
61	AY	127	
62	AZ	136	
63	Aa	149	
64	Ab	59	
65	Ac	105	
66	Ad	113	
67	Ae	130	
68	Af	107	
69	Ag	121	
70	Ah	120	
71	Ai	100	
72	Aj	88	
73	Ak	78	
74	Al	51	
75	Am	128	
76	An	25	
77	Ao	106	
78	Ap	92	

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

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
34	MA6	B5	1782	-	-	X	-
38	PSU	A1	2266	-	-	X	-
85	SO1	DC	903	X	-	-	-

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 211022 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	121	Total	C	N	O	S	0	0
			948	596	179	171	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	71	Total	C	N	O	0	0
			574	366	108	100		

- 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 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	1757	Total	C	N	O	P	1	0
			37463	16754	6635	12317	1757		

- 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	3216	Total	C	N	O	P	0	0
			68786	30729	12387	22454	3216		

- 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	167	Total	C	N	O	S	0	0
			1303	840	234	228	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	120	LYS	ASN	conflict	UNP Q02326

- 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 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AI	222	Total	C	N	O	S	0	0
			1804	1147	339	310	8		

- 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
55	AS	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

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

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

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

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

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

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

- Molecule 59 is a protein called RPL24A isoform 1.

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

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

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

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

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

- 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		

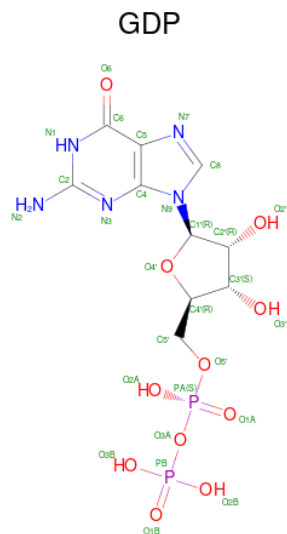
- Molecule 81 is a RNA chain called TSV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	EC	133	Total	C	N	O	P	0	0
			2808	1254	499	922	133		

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 83 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



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

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
84	DC	1	Total Mg 1 1	0

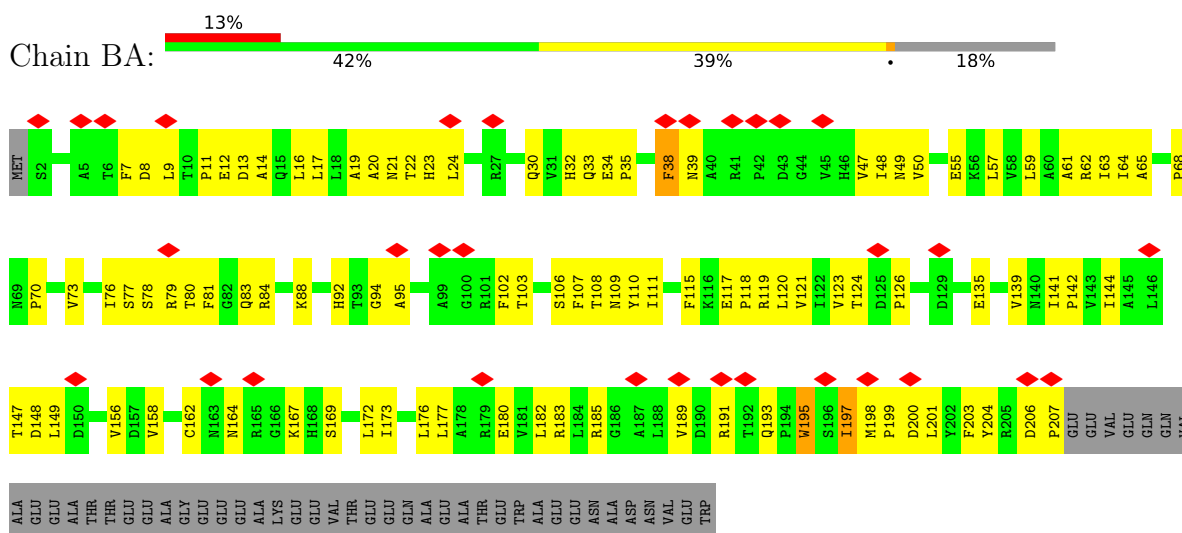
- Molecule 85 is [1R-(1.ALPHA.,3A.BETA.,4.BETA.,4A.BETA.,7.BETA.,7A.ALPHA.,8A.BETA.)]8A-[(6-DEOXY-4-O-METHYL-BETA-D-ALTROPYRANOSYLOXY)METHYL]-4-FORMYL-4,4A,5,6,7,7A,8,8A-OCTAHYDRO-7-METHYL-3-(1-METHYLETHYL)-1,4-METHANO-S-INDACENE-3A(1H)-CARBOXYLIC ACID (CCD ID: SO1) (formula: C₂₇H₄₂O₈).



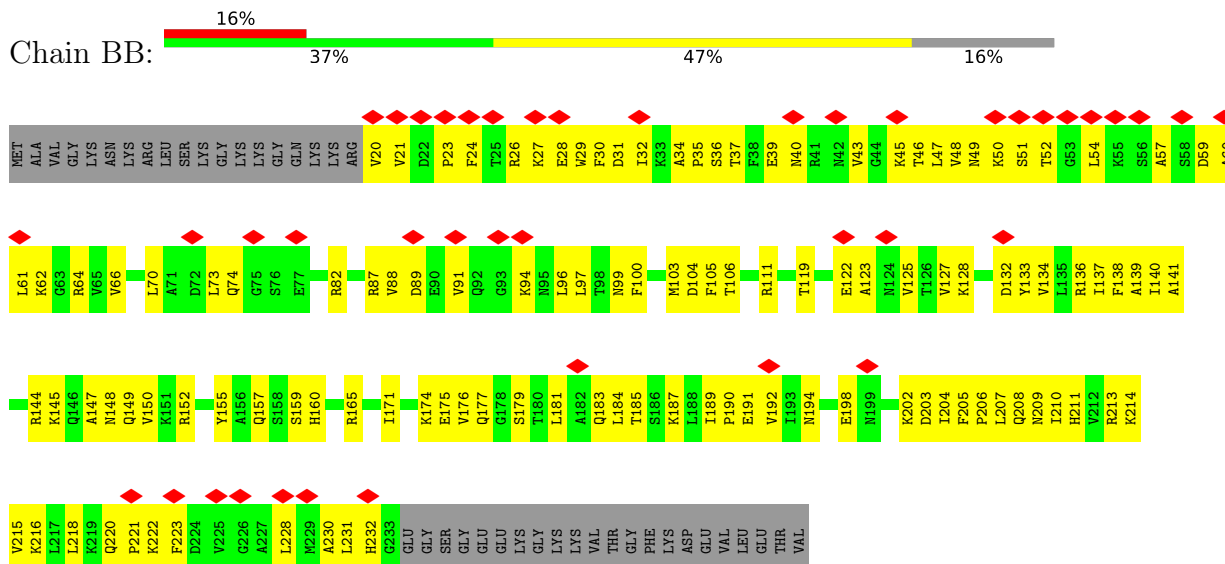
3 Residue-property plots [i](#)

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

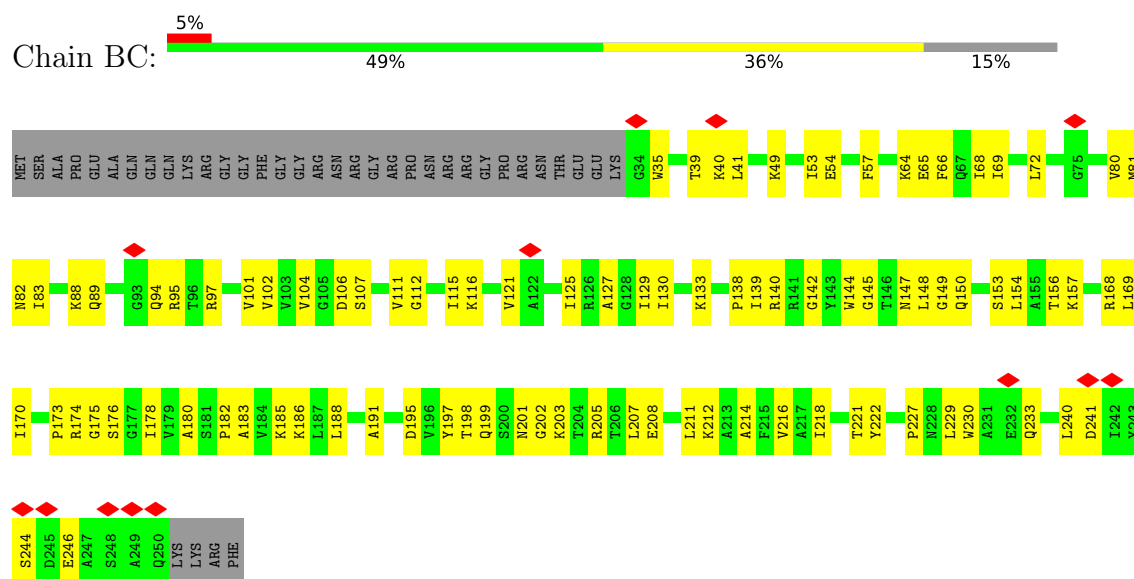
• Molecule 1: 40S ribosomal protein S0-A



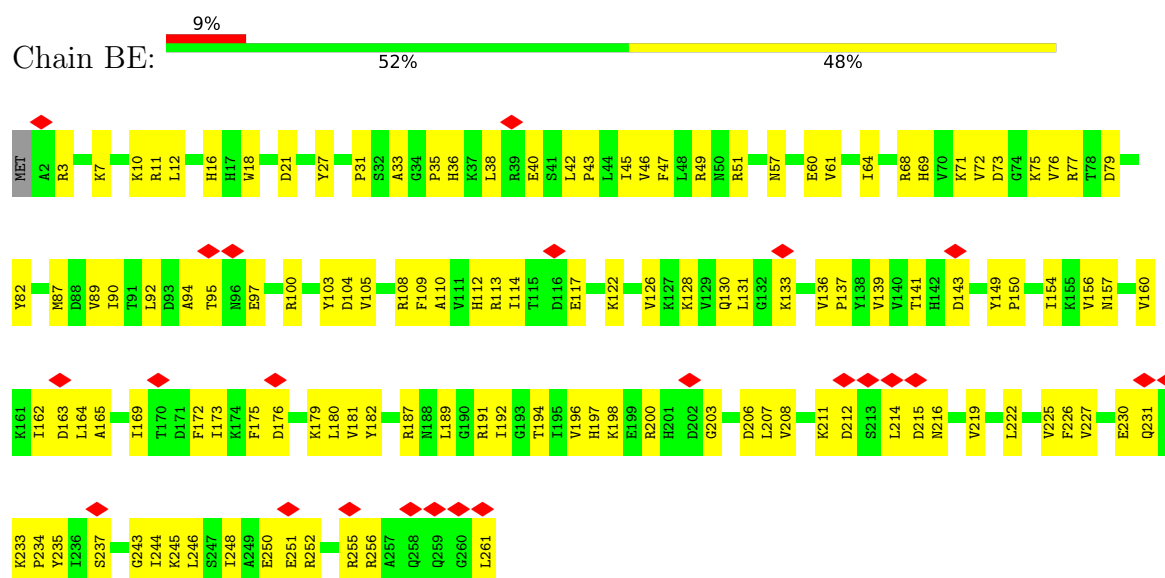
• Molecule 2: RPS1A isoform 1



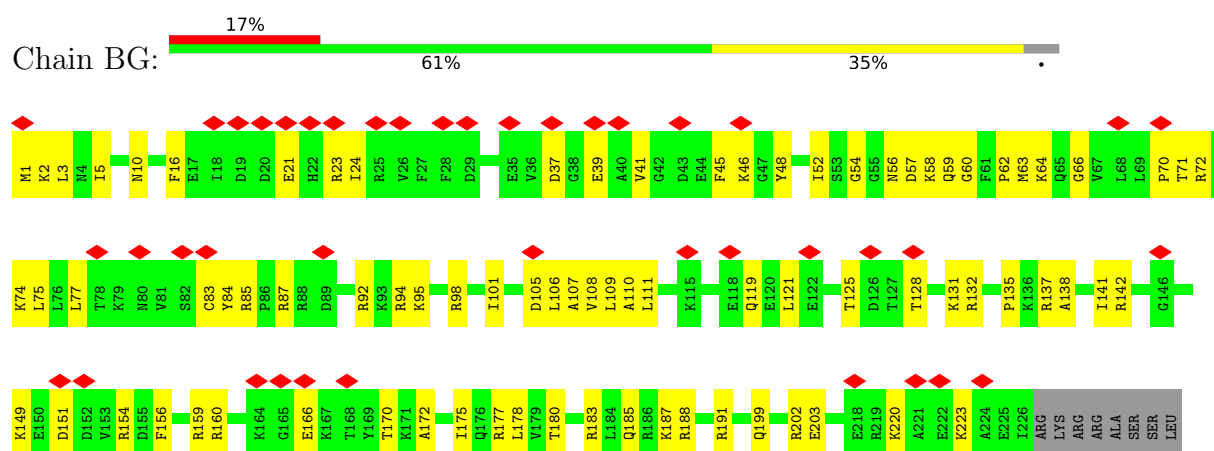
• Molecule 3: RPS2 isoform 1



• Molecule 4: 40S ribosomal protein S4-A

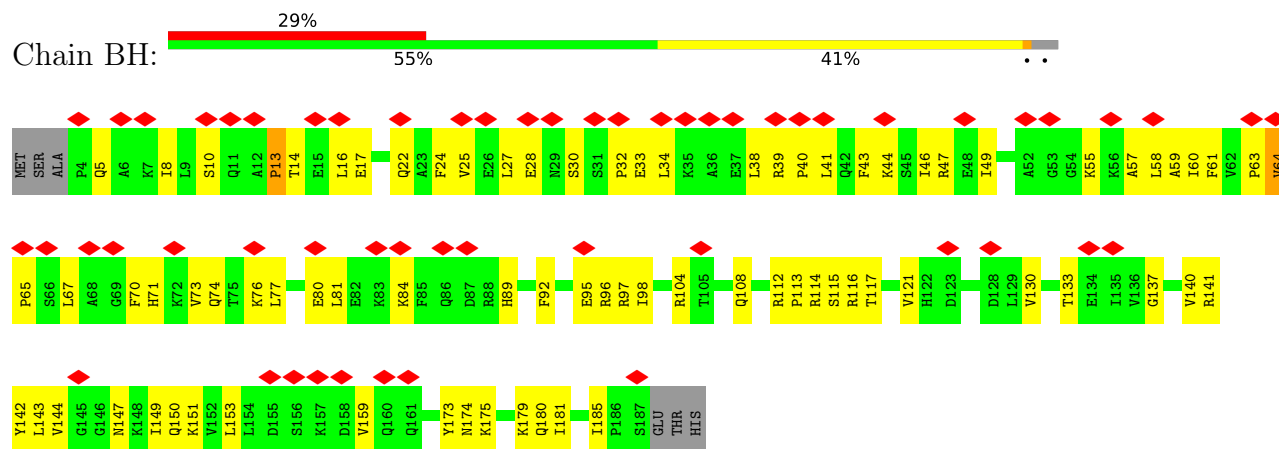


• Molecule 5: 40S ribosomal protein S6-A

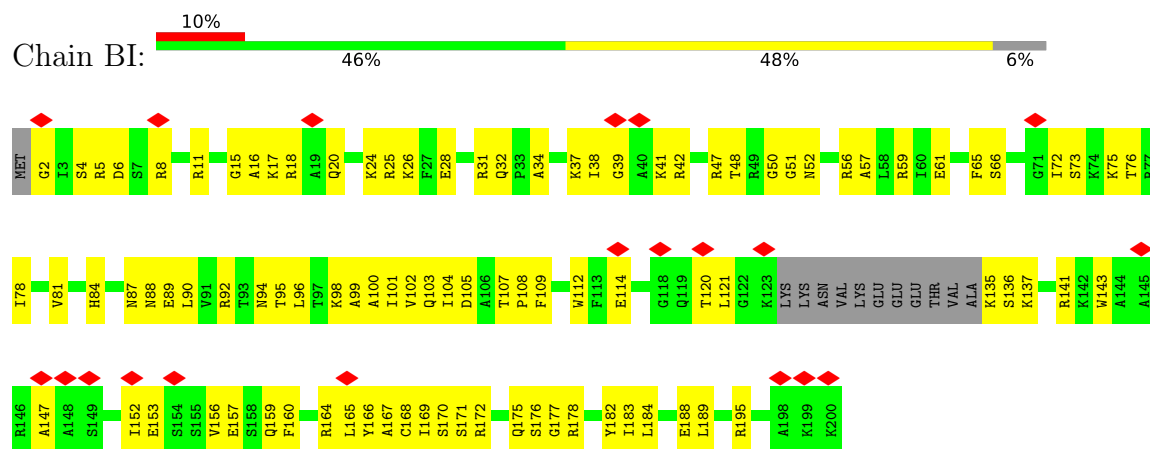


LYS
ALA

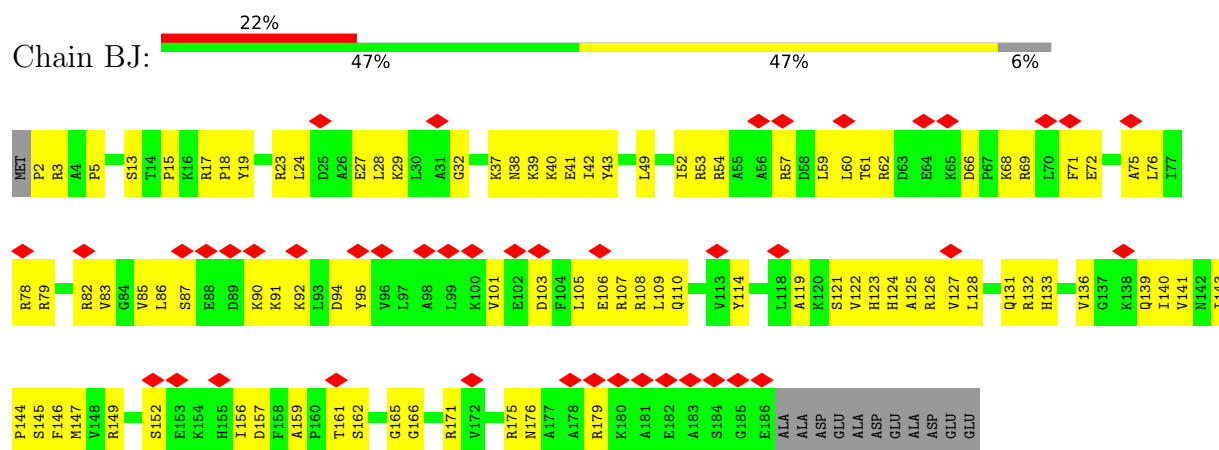
• Molecule 6: 40S ribosomal protein S7-A



• Molecule 7: 40S ribosomal protein S8-A

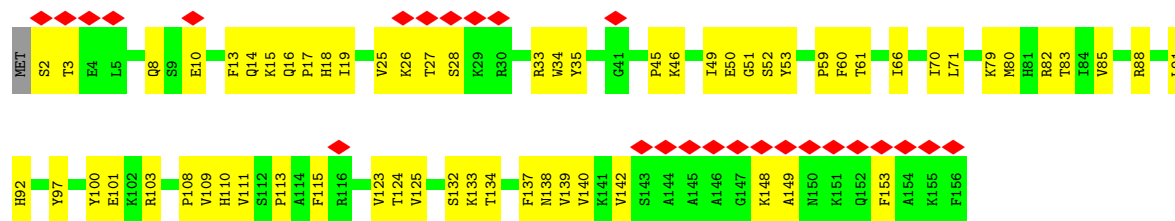


• Molecule 8: 40S ribosomal protein S9-A

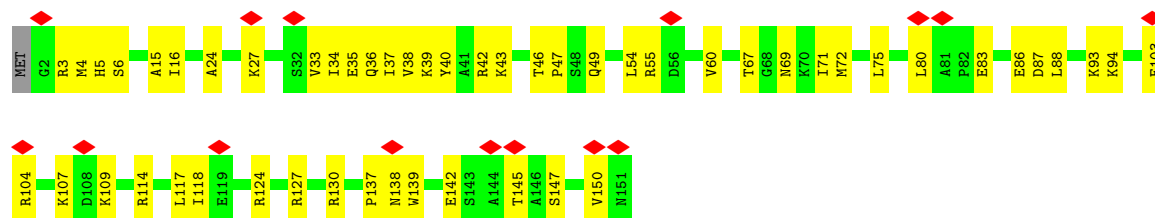


• Molecule 9: 40S ribosomal protein S11-A

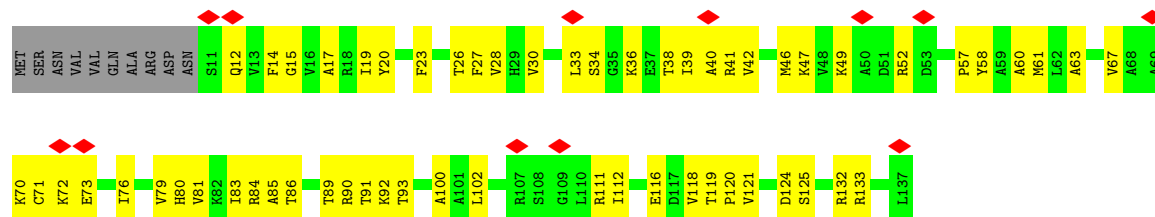




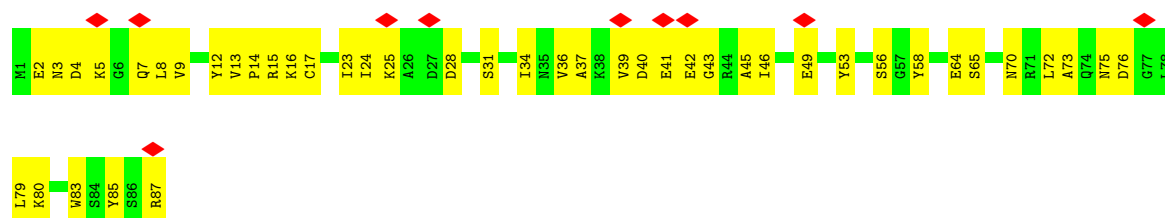
• Molecule 10: 40S ribosomal protein S13



• Molecule 11: 40S ribosomal protein S14-A



• Molecule 12: 40S ribosomal protein S21-A

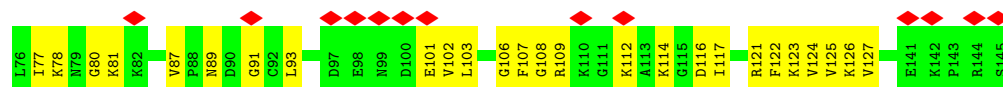
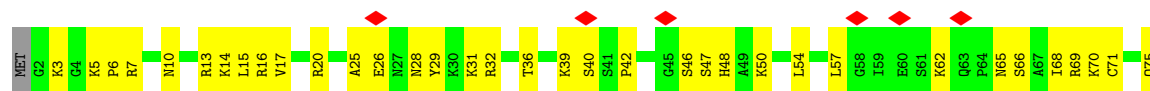


• Molecule 13: RPS22A isoform 1

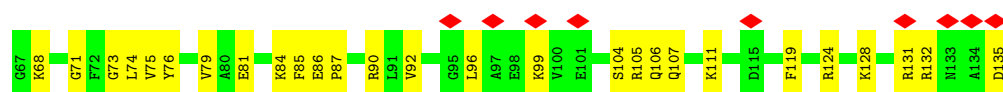




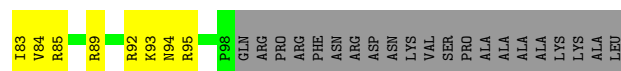
• Molecule 14: 40S ribosomal protein S23-A



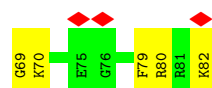
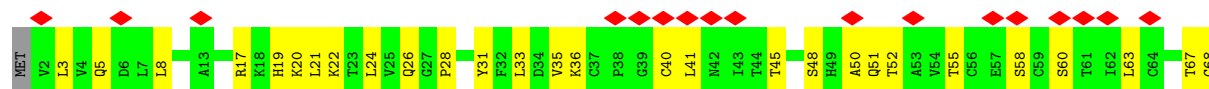
• Molecule 15: 40S ribosomal protein S24-A



• Molecule 16: RPS26B isoform 1



• Molecule 17: 40S ribosomal protein S27-A



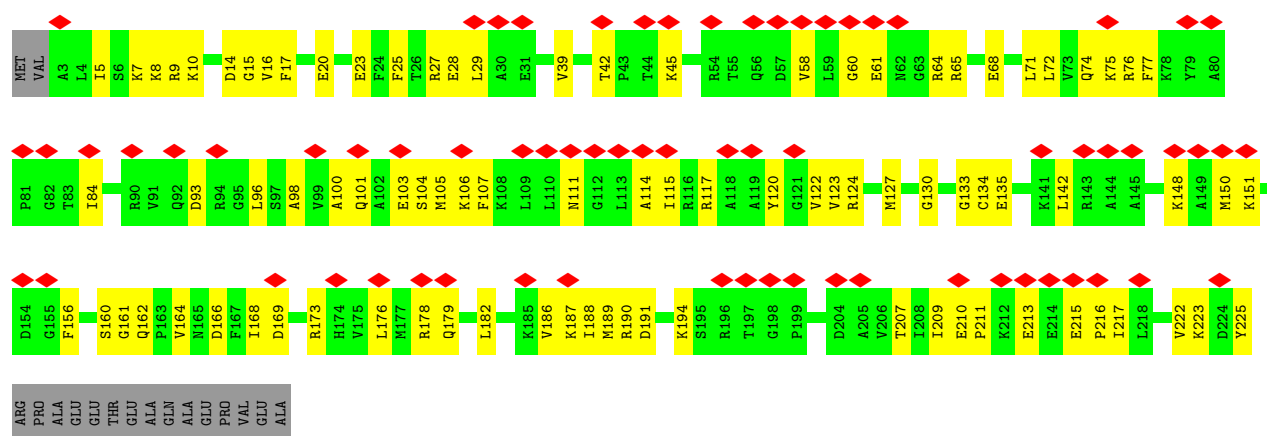
• Molecule 18: 40S ribosomal protein S30-A

Chain Be: 



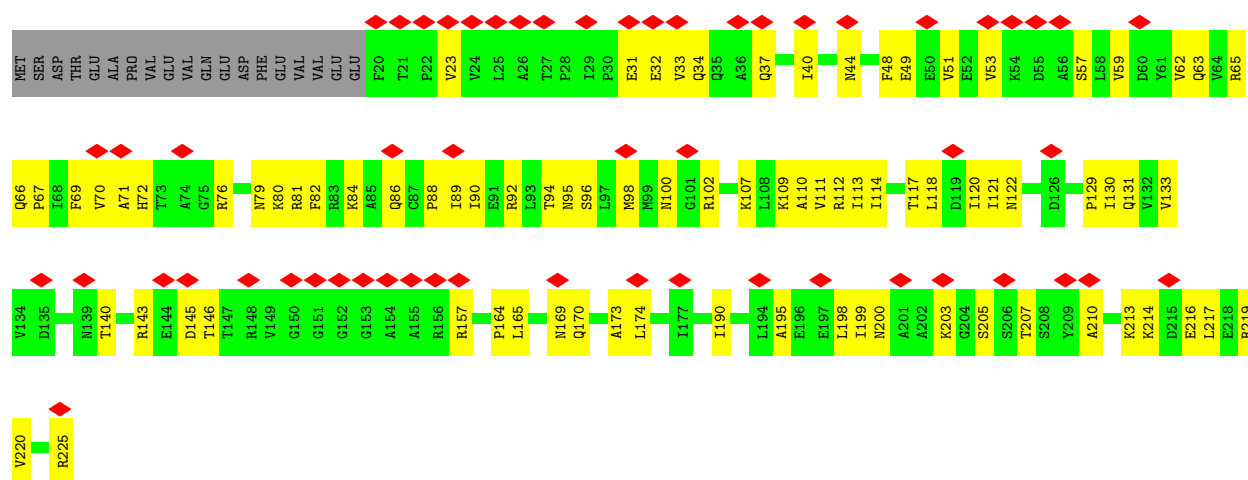
• Molecule 19: RPS3 isoform 1

Chain BD: 



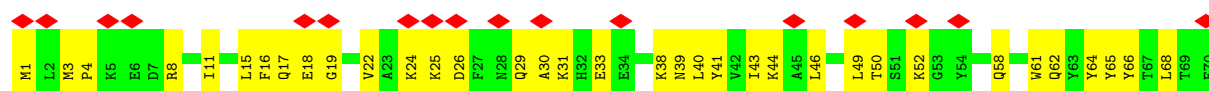
• Molecule 20: Rps5p

Chain BF: 



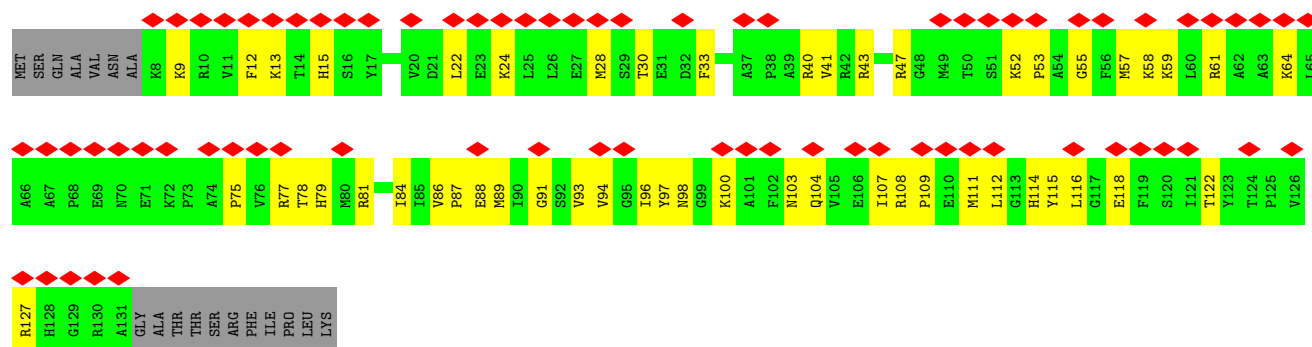
• Molecule 21: 40S ribosomal protein S10-A

Chain BK: 

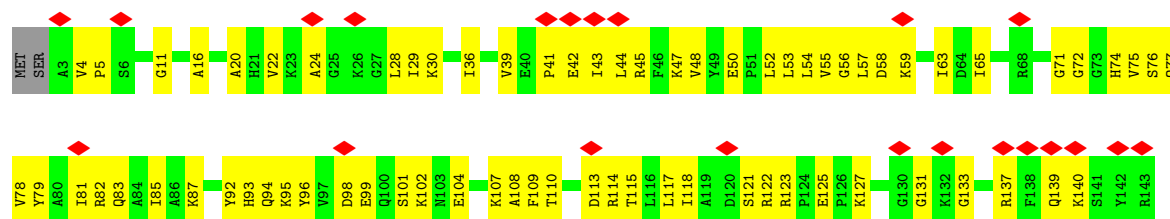




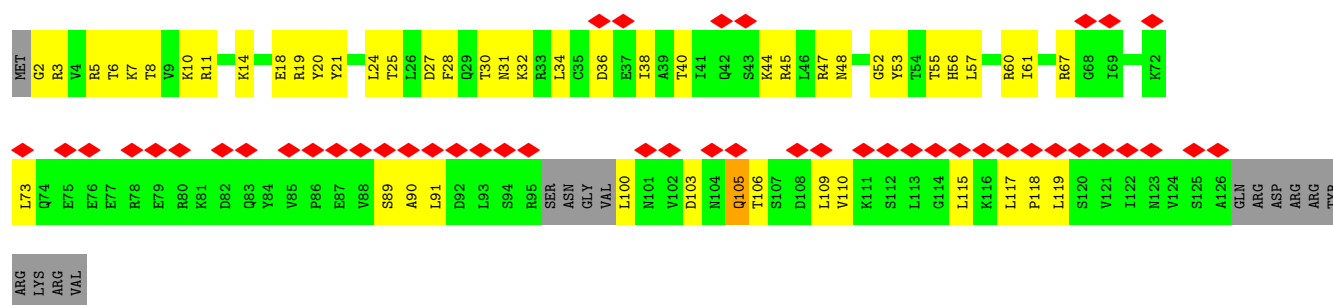
• Molecule 22: RPS15 isoform 1



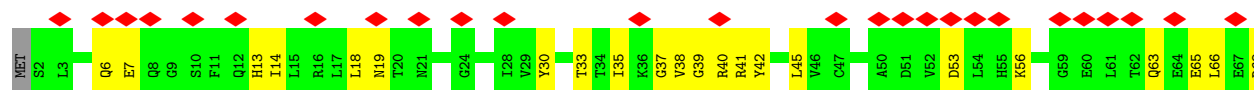
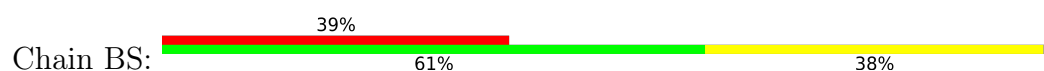
• Molecule 23: 40S ribosomal protein S16-A

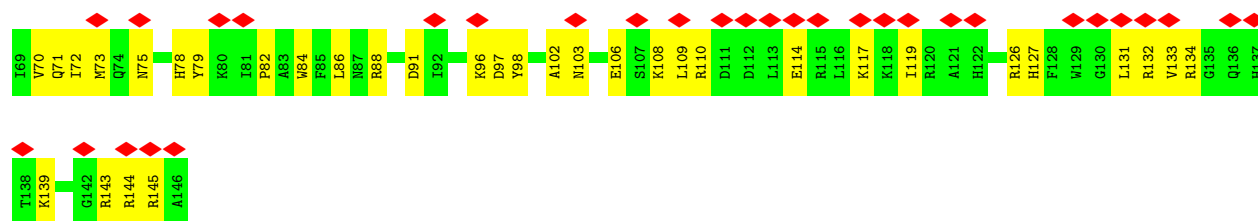


• Molecule 24: 40S ribosomal protein S17-A

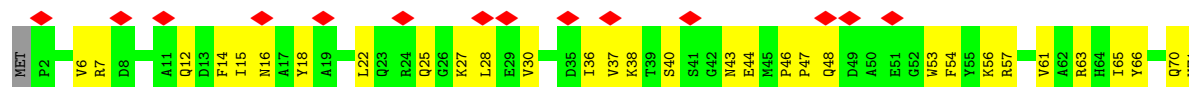


• Molecule 25: 40S ribosomal protein S18-A

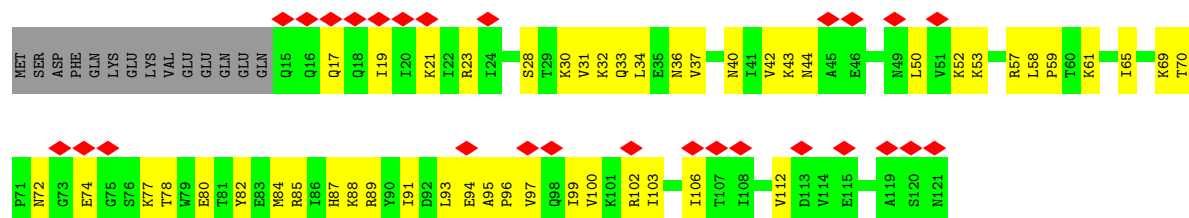




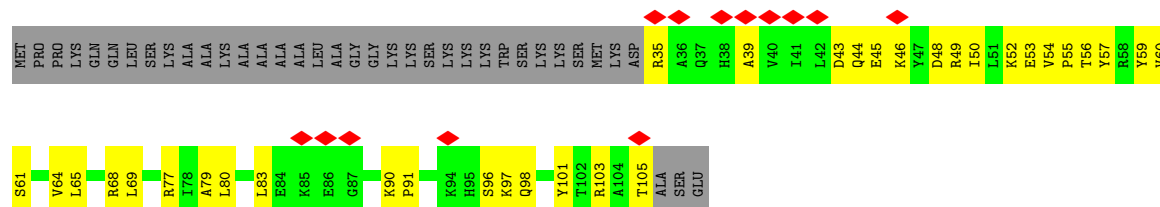
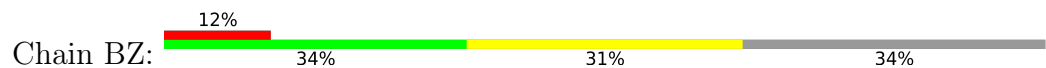
- Molecule 26: 40S ribosomal protein S19-A



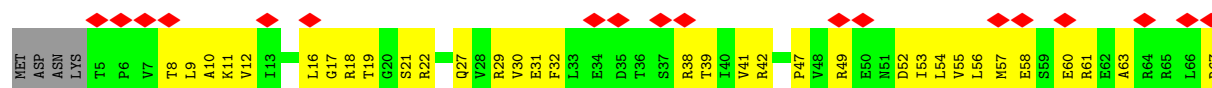
- Molecule 27: RPS20 isoform 1



- Molecule 28: RPS25A isoform 1



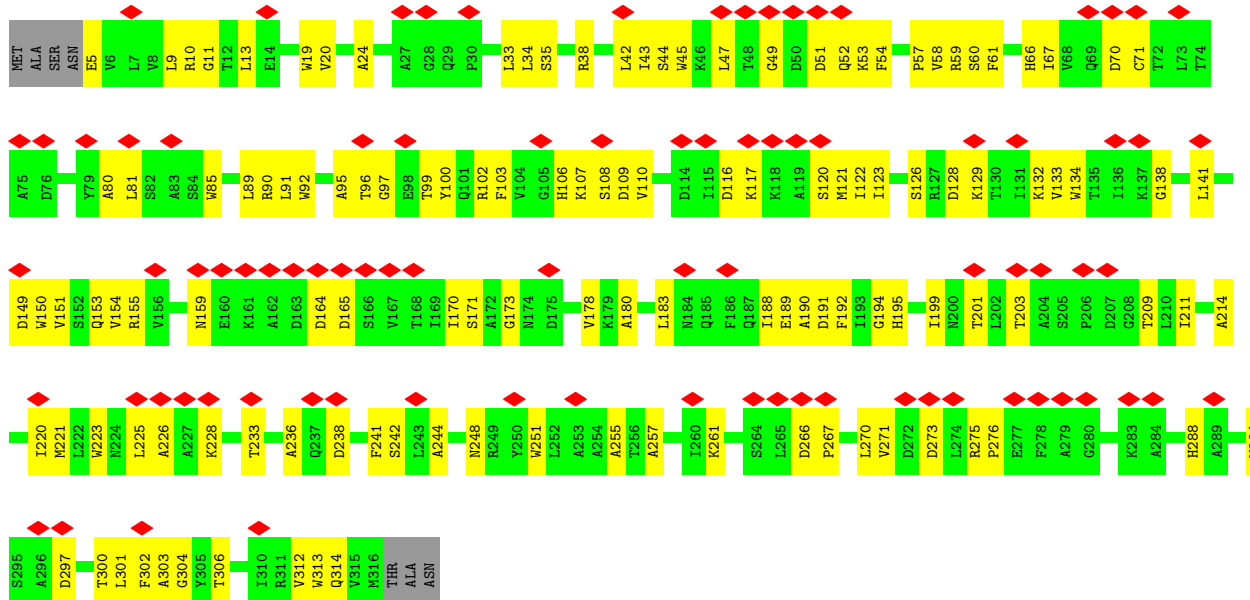
- Molecule 29: RPS28A isoform 1



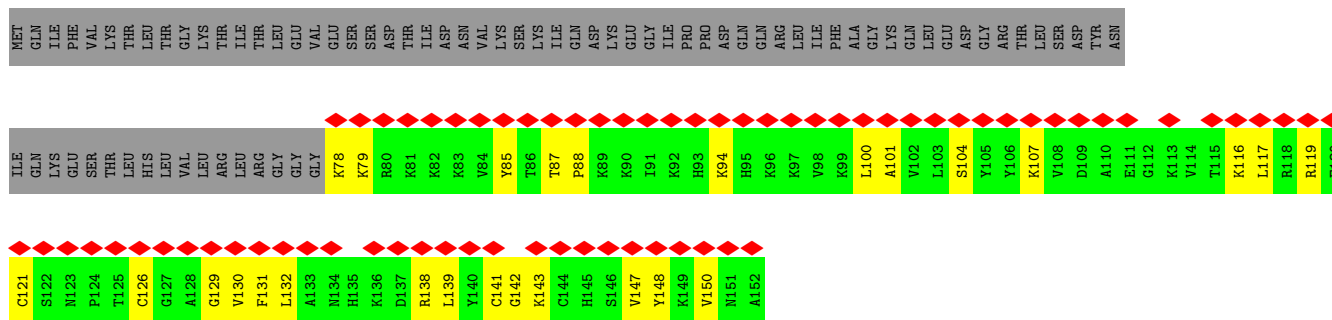
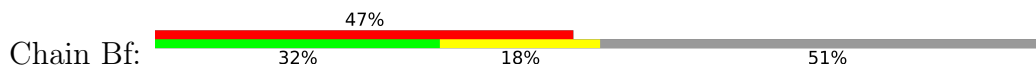
- Molecule 30: RPS29A isoform 1



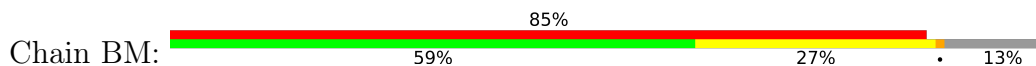
• Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein

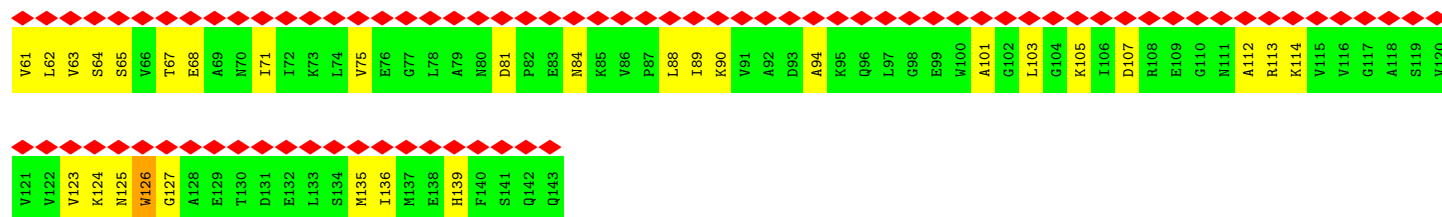


• Molecule 32: Ubiquitin-40S ribosomal protein S31

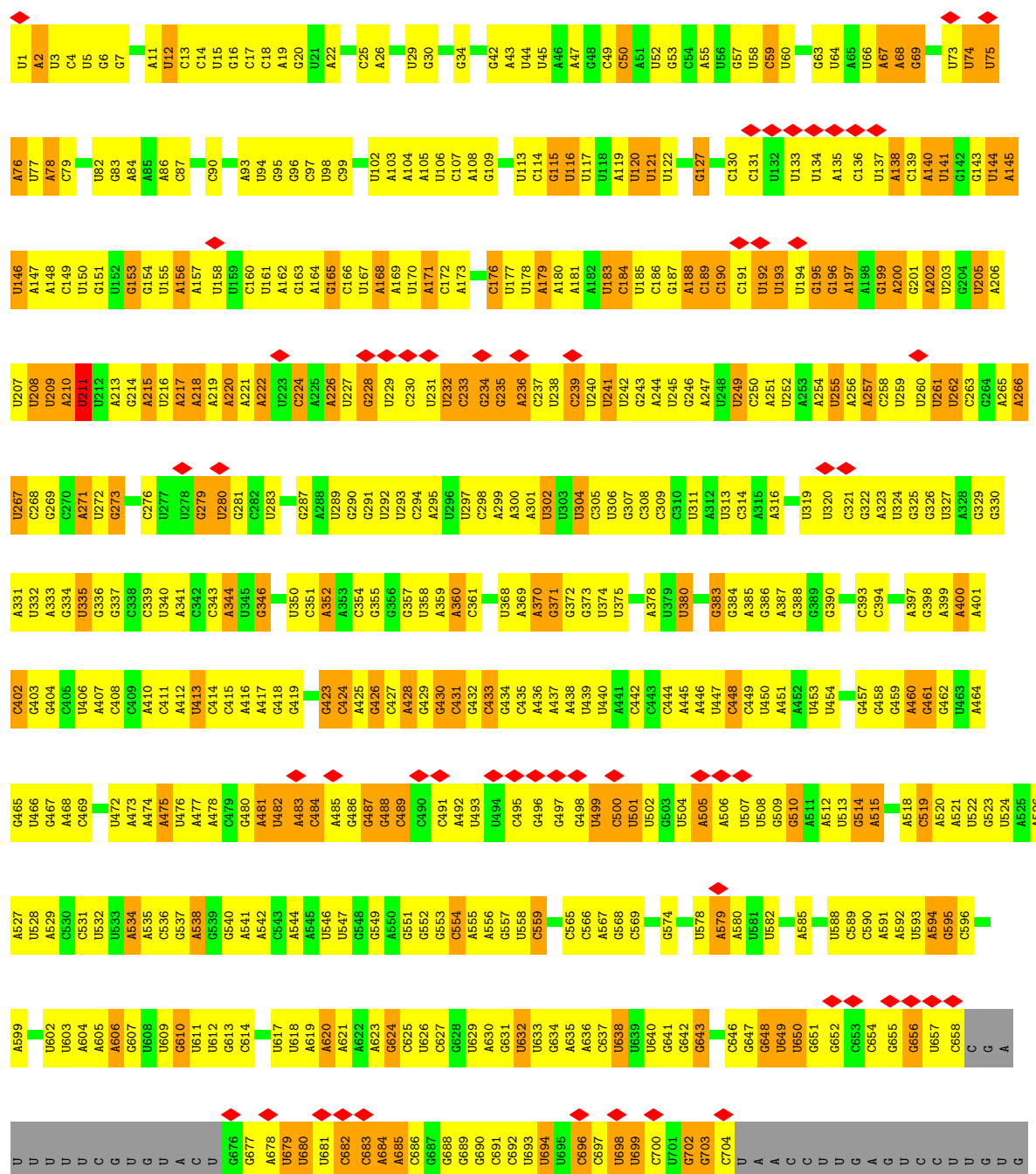


• Molecule 33: 40S ribosomal protein S12

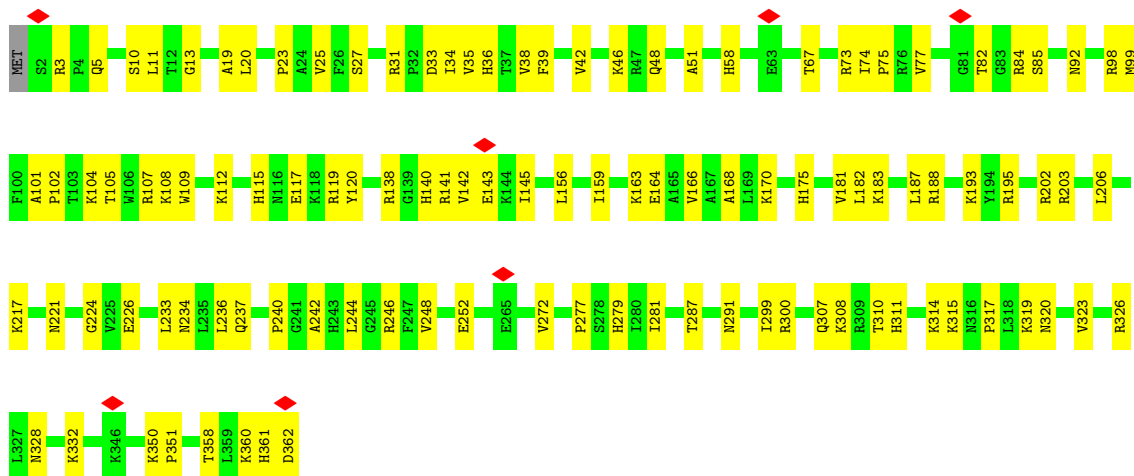




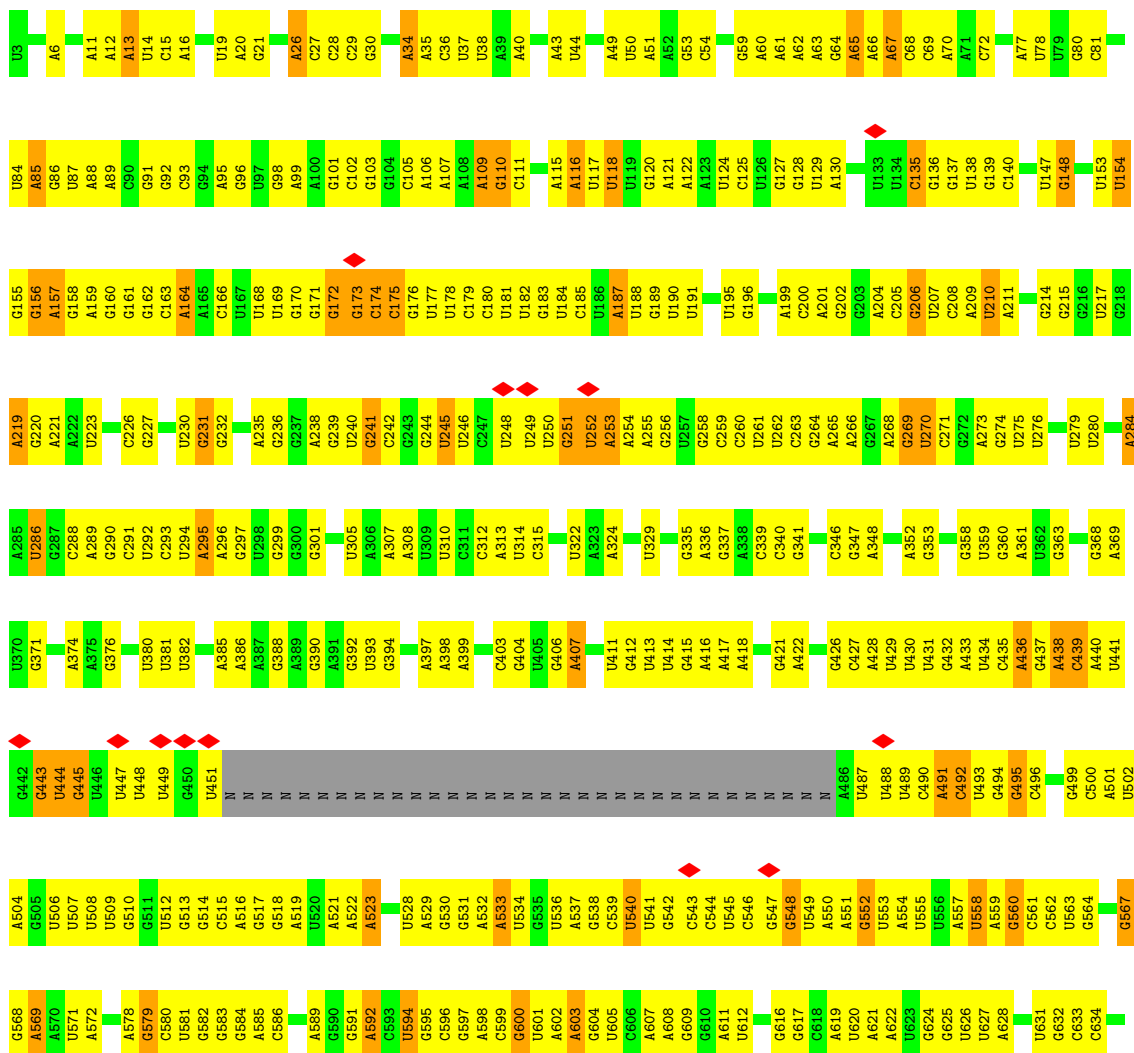
• Molecule 34: 18S rRNA

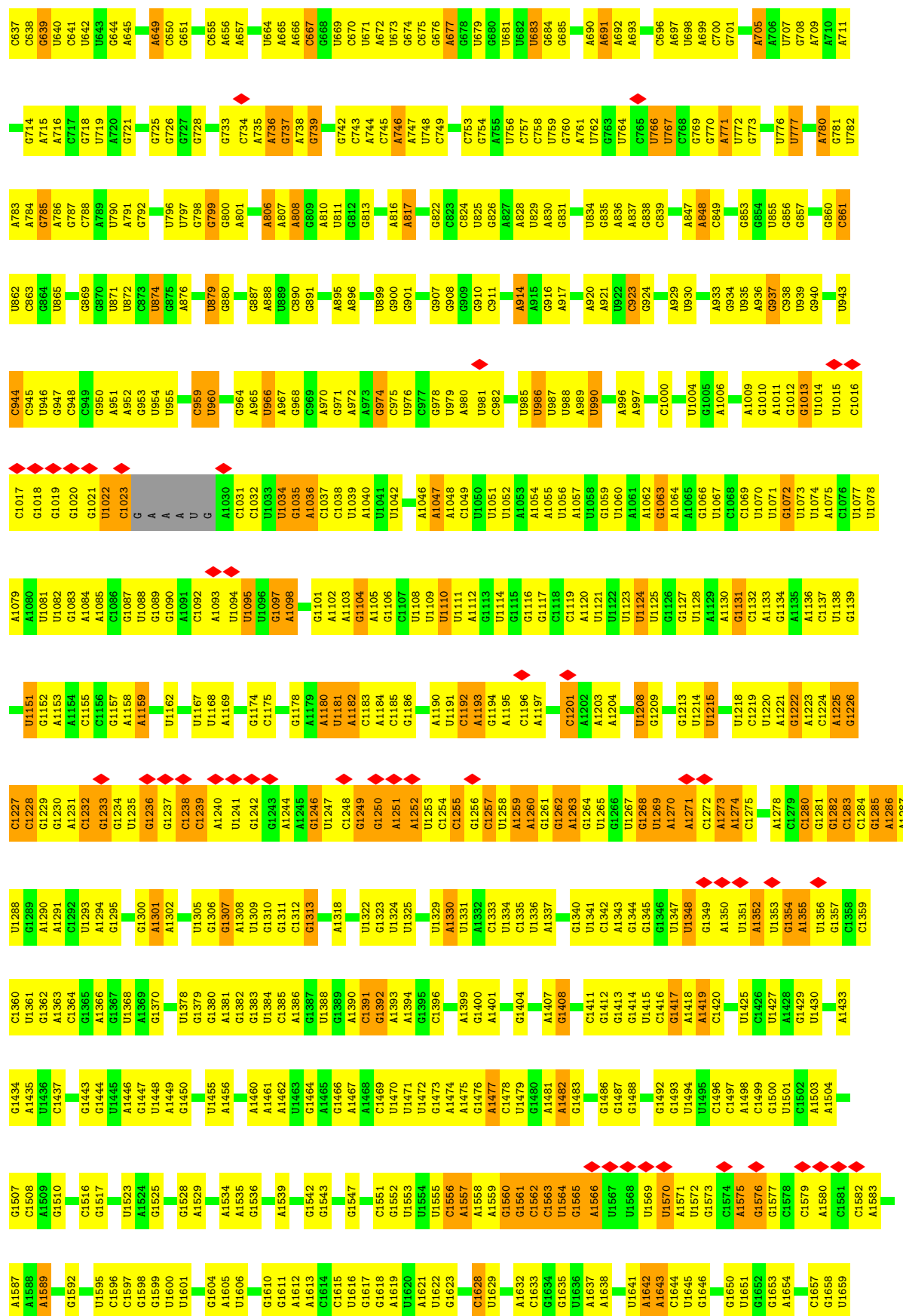


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C1537	G1411	U1262	A1202	U1135	G1064	G993	G925	A857	A789	U
G1540	U1412	G1267	A1203	U1136	C1067	G994	A926	G958	U790	C
G1541	U1413	G1270	A1204	A1137	C1068	U995	C927	A859	A791	U
G1542	U1414	G1270	U1205	A1138	C1069	U996	U928	U860	U792	U
A1543	U1415	G1270	U1206	U1144	A1068	G997	A829	U861	A793	G
U1544	G1416	C1274	A1207	U1145	C1070	U998	A930	A862	U794	
A1545	A1417	U1275	A1208	G1146	U1071	U999	C931	A863	G730	
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C1549	U1424	U1280	A1211	C1148	C1075	G1002	C934	G867	A733	
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U1560	G1433	G1294	A1220	A1160	G1085	C1021	U946	A811	U742	
U1561	U1434	G1295	A1221	C1161	A1086	C1022	U947	A812	U743	
G1562	G1435	A1296	C1222	U1162	A1087	A1023	C948	U813	U744	
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C1568	U1372	U1372	A1228	G1170	A1093	U1029	A955	G823	A753	
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U1579	U1448	G1316	G1233	G1176	U1103	C1035	G895	U829	G763	
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A1600	A1401	U1334	U1249	A1193	A1125	U1058	U918	C848	U781	
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	A1406	C1337	C1252	C1197	A1131	U1061	G987	U851	C784	
	U1407	C1338	U1253	G1198	A1132			G952	U785	
	G1408	U1340	U1254	G1199				G953	U786	
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			U1257							
			U1258							
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• Molecule 38: 25S rRNA

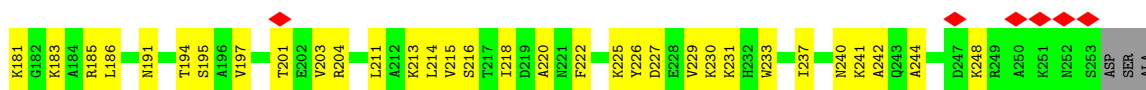
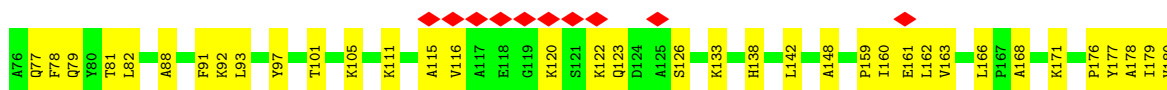




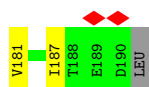
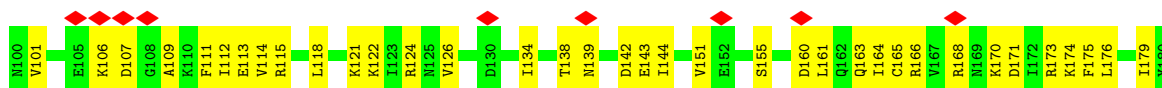
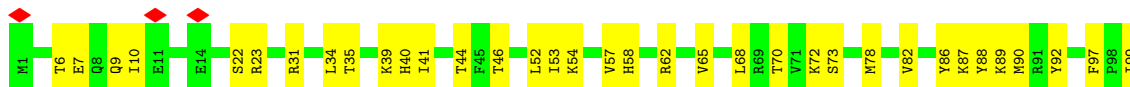
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G2584	A2514	U2453	C2389	U2313	A2243	C2163	C2094	G1882	G1728	G1662
G2585	A2515	U2454	A2390	U2314	A2244	A	C2095	A1883	G1729	C1663
G2586	A2520	U2455	G2391	G2315	C2245	A2167	U2096	U1885	G1664	G1665
G2587	U2521	G2456	G2392	G2316	C2246	A2168	U2097	A1886	A1806	A1806
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G2590	G2524	A2459	G2395	U2324	G2249	U2175	C2099	A1809	U1739	G1668
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G2594	G2528	A2463	A2399	C2329	U2253	G2179	C2098	G1813	G1743	G1675
G2595	G2529	G2464	A2402	C2330	U2254	G2180	U2099	A1814	G1744	G1676
G2596	G2530	U2465	G2403	C2331	A2255	C2181	A2100	U1815	C1745	G1677
G2597	G2531	G2466	A2404	U2334	U2256	A2182	C2101	A1816	G1747	G1678
G2598	G2533	G2467	G2405	G2335	U2258	A2183	U2102	G1817	G1748	A1679
G2599	A2536	A2468	G2406	G2336	A2259	U2184	G	U1818	A1749	G1680
G2600	U2537	G2469	G2407	U2337	U2260	G2185	A2106	U1819	A1750	U1681
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G2602	C2539	G2471	G2409	U2340	A2262	G2187	C2108	U1821	A1752	U1684
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G2604	U2541	C2473	G2412	G2342	U2264	G2189	G	A1823	C1757	U1686
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G2607	G2544	C2476	G2415	A2345	U2267	U2193	A2113	C1827	A1760	U1689
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G2609	G2546	U2478	U2417	A2347	U2269	C2195	U2114	G1829	C1762	U1694
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G2612	G2549	U2481	C2420	G2350	G2272	C2202	U2116	A1922	G1766	A1697
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G2642	C2578	G2511	A2450	G2382	G2312	G2237	C	G1806	G1730	G1729
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G2645	G2581	A2514	U2453	U2385	G2315	G2240	C	G1809	G1733	G1732
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G2667	G2605	C2539	G2475	U2407	U2262	G2262	C	U1831	G1755	U1684
G2668	U2606	A2540	G2476	U2408	U2263	G2263	C	A1832	G1756	C1685
G2669	G2607	U2541	U2477	U2409	U2264	G2264	C	U1833	C1757	U1686
G2670	G2608	G2542	G2478	U2410	U2265	G2265	C	G1834	U1758	U1687
G2671	U2609	U2543	U2479	U2411	U2266	G2266	C	U1835	G1759	U1688
G2672	C2610	G2544	U2480	U2412	U2267	U2267	C	G1836	A1760	U1689
G2673	U2611	U2545	A2481	U2413	U2268	U2268	C	U1837	G1761	C1690
G2674	G2612	C2546	G2482	U2414	U2269	U2269	C	G1838	C1762	U1694
G2675	U2613	G2547	U2483	U2415	U2270	U2270	C	U1839	U1764	A1695
G2676	G2614	U2548	G2484	U2416	U2271	U2271	C	A1840	G1765	A1696
G2677	U2615	G2549	A2485	U2417	U2272	U2272	C	U1841	U1766	A1697
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G2679	U2617	U2550	U2487	U2419	U2274	U2274	C	U1843	U1768	C1701
G2680	G2618	G2551	G2488	U2420	U2275	U2275	C	G1844	G1769	U1702
G2681	U2619	U2552	A2489	U2421	U2276	U2276	C	U1845	G1770	U1703
G2682	C2610	A2553	U2490	U2422	U2277	U2277	C	G1846	C1771	A1704
G2683	G2611	G2554	G2491	U2423	U2278	U2278	C	A1847	U1772	U1705
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G2685	C2612	C2556	U2493	U2425	U2280	U2280	C	C1849	G1774	C1707
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G2689	U2636	G2560	U2497	U2429	U2284	U2284	C	G1853	G1783	G1711
G2690	G2637	A2637	U2498	U2430	U2285	U2285	C	C1854	U1784	G1712
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G2692	G2639	G2639	U2500	U2432	U2287	U2287	C	U1856	G1786	A1715
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G2695	G2642	U2642	U2503	U2435	U2290	U2290	C	A1859	U1718	U1718
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G2697	C2644	U2644	U2505	U2437	U2292	U2292	C	G1861	U1720	U1720
G2698	A2645	G2645	U2506	U2438	U2293	U2293	C	U1862	U1721	U1721
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G2										



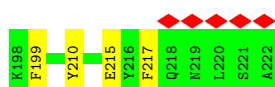
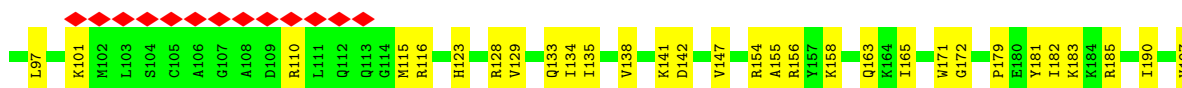
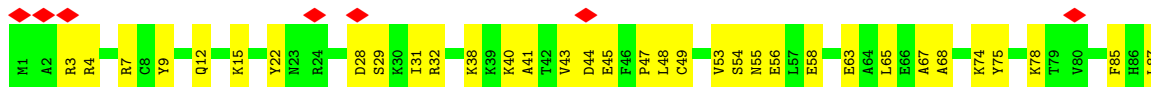
- Molecule 44: 60S ribosomal protein L8-A



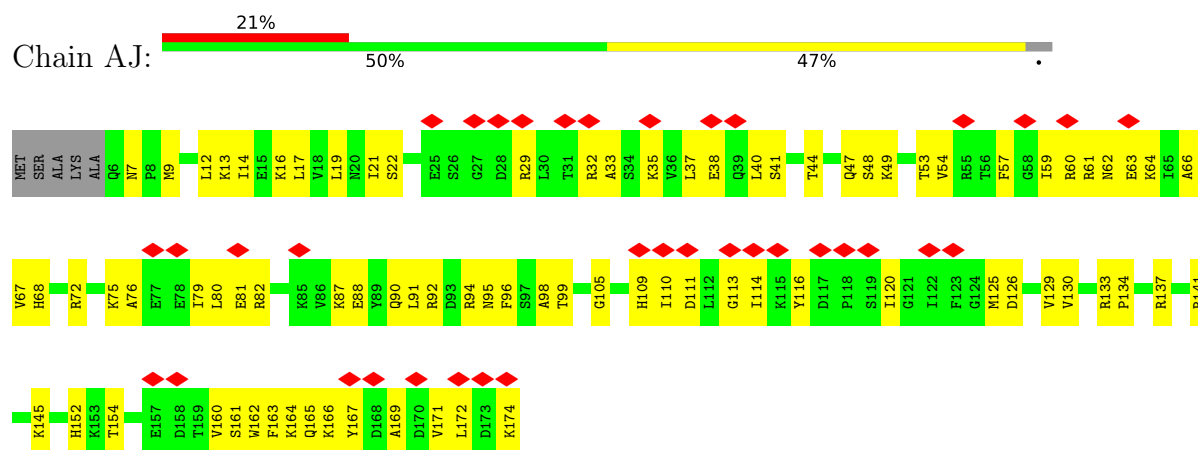
- Molecule 45: 60S ribosomal protein L9-A



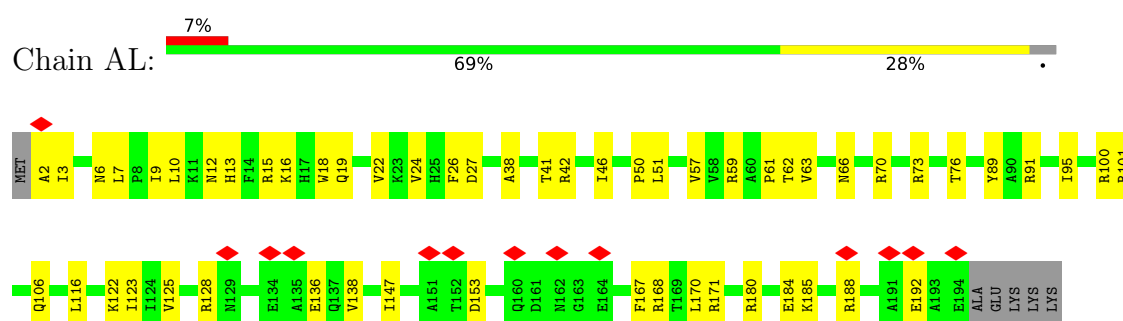
- Molecule 46: 60S ribosomal protein L10



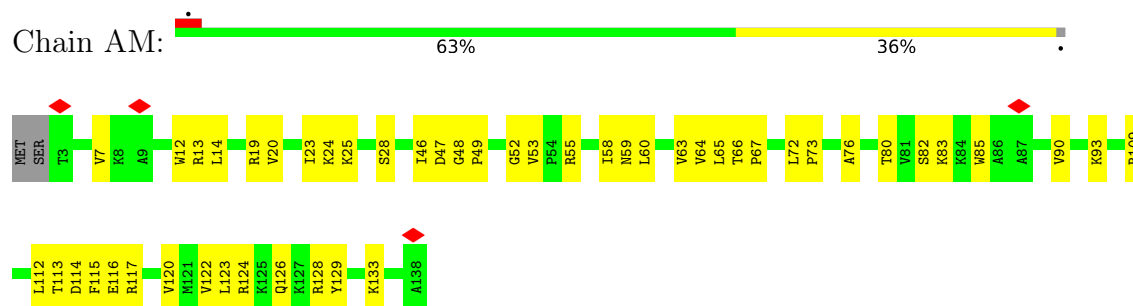
- Molecule 47: RPL11A isoform 1



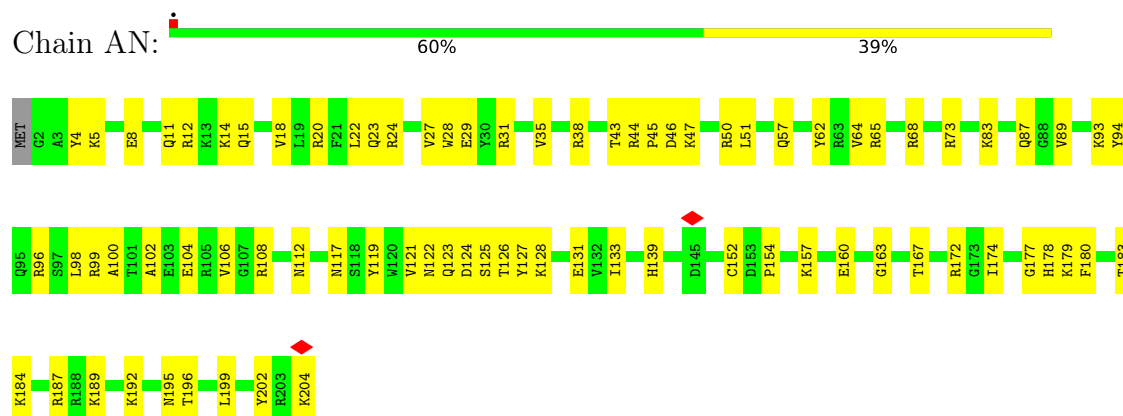
- Molecule 48: 60S ribosomal protein L13-A



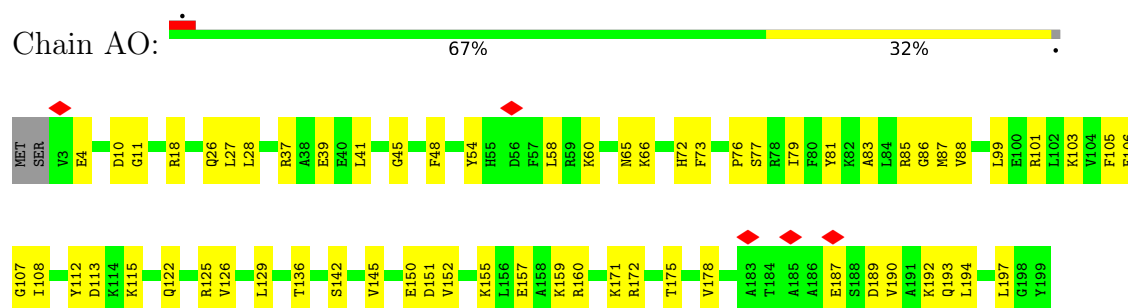
- Molecule 49: 60S ribosomal protein L14-A



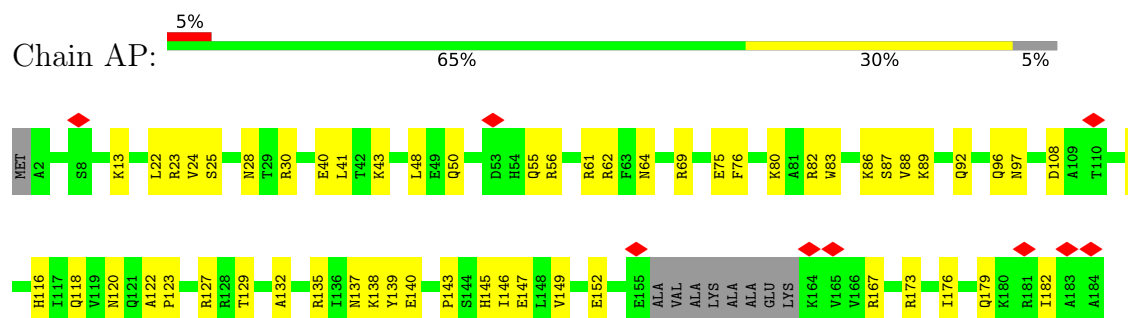
- Molecule 50: 60S ribosomal protein L15-A



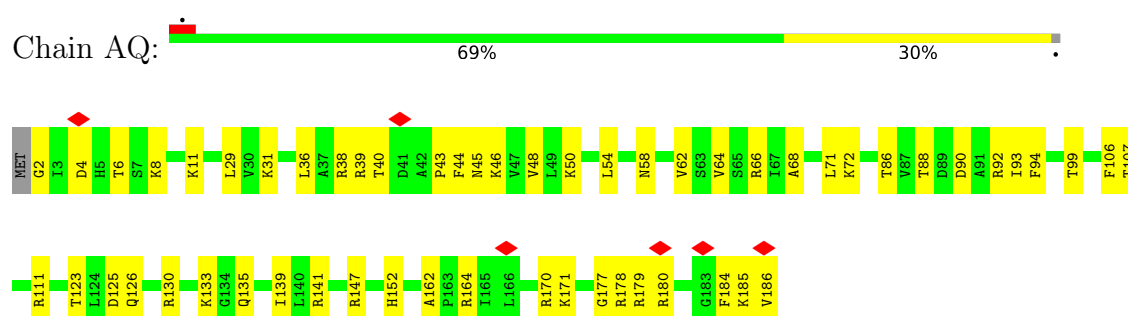
- Molecule 51: 60S ribosomal protein L16-A



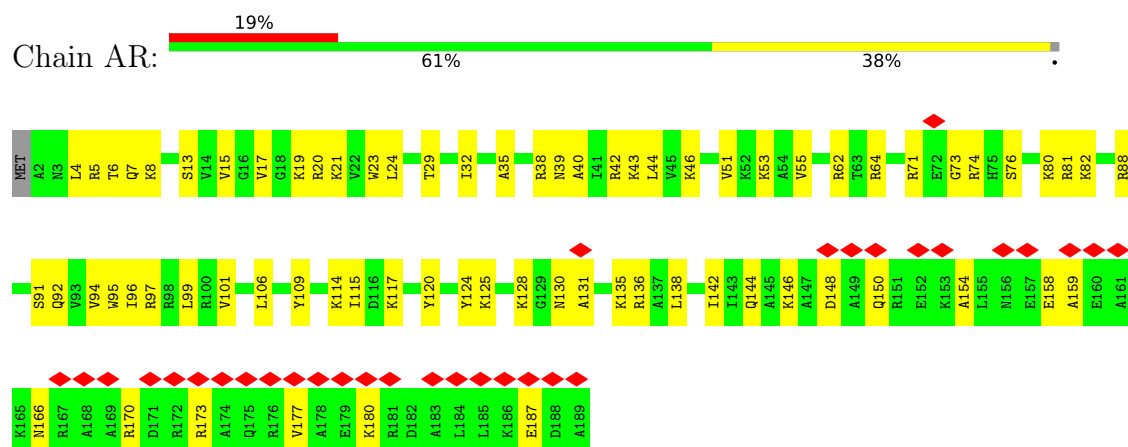
- Molecule 52: 60S ribosomal protein L17-A



- Molecule 53: 60S ribosomal protein L18-A

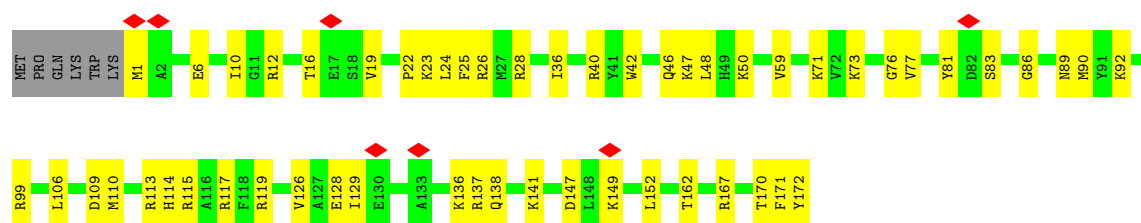


- Molecule 54: 60S ribosomal protein L19-A



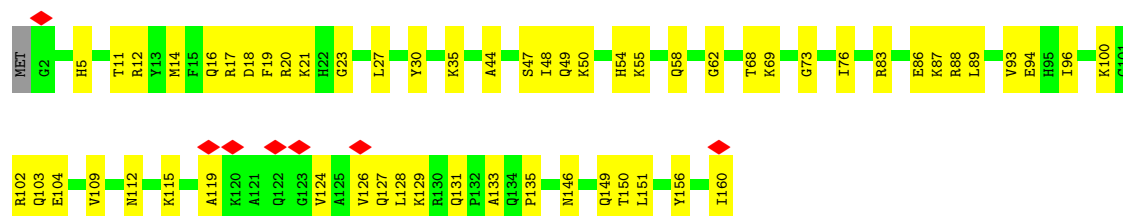
- Molecule 55: 60S ribosomal protein L20

Chain AS:  66% 30%



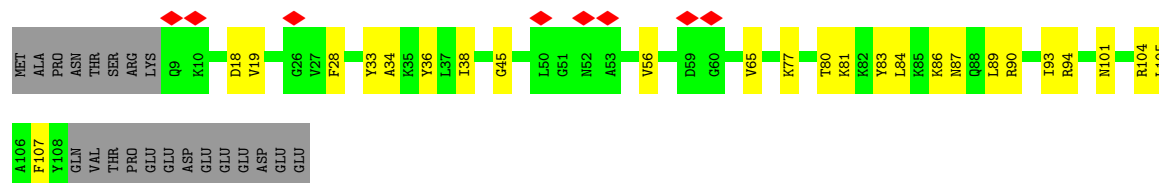
- Molecule 56: 60S ribosomal protein L21-A

Chain AT:  64% 36%



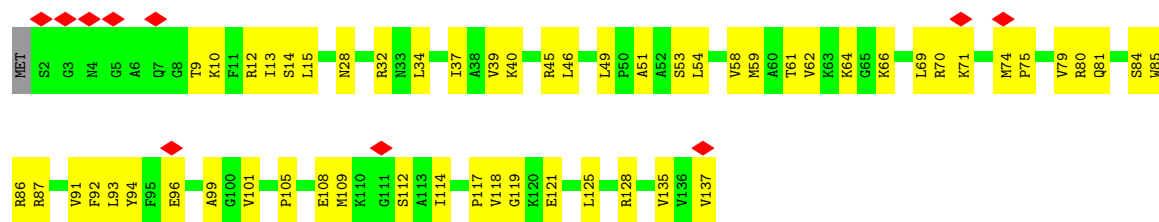
- Molecule 57: 60S ribosomal protein L22-A

Chain AU:  7% 62% 21% 17%



- Molecule 58: 60S ribosomal protein L23-A

Chain AV:  7% 58% 41%

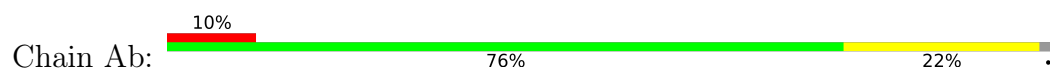


- Molecule 59: RPL24A isoform 1

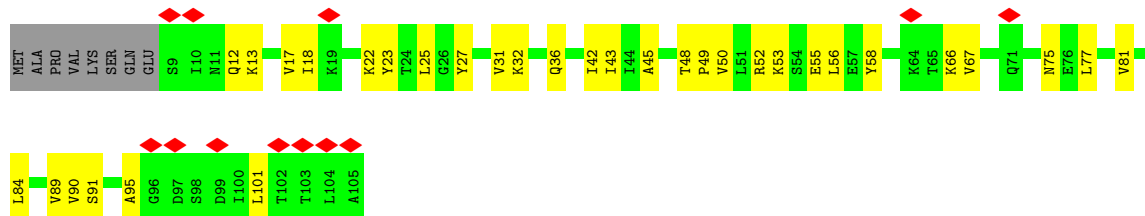
Chain AW:  28% 12% 59%



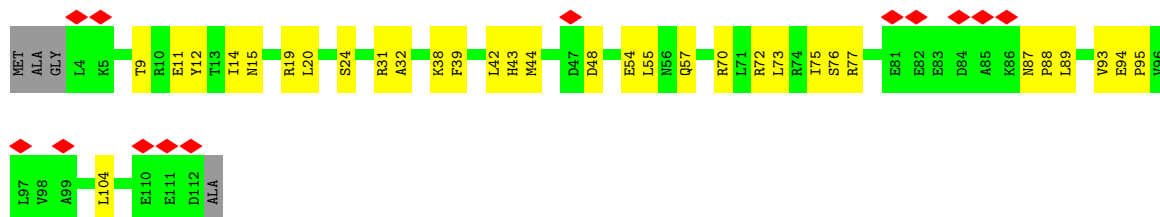
- Molecule 64: RPL29 isoform 1



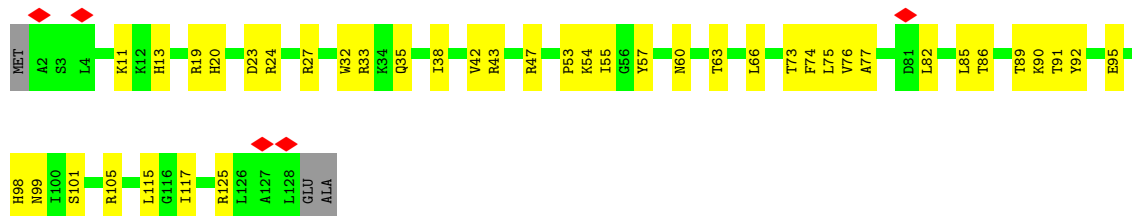
- Molecule 65: 60S ribosomal protein L30



- Molecule 66: 60S ribosomal protein L31-A

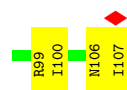


- Molecule 67: RPL32 isoform 1

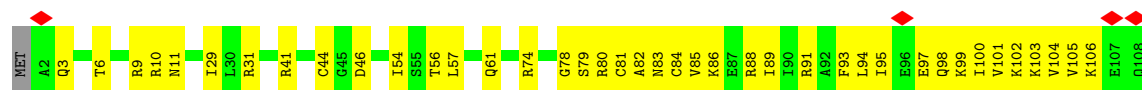


- Molecule 68: 60S ribosomal protein L33-A





- Molecule 69: 60S ribosomal protein L34-A



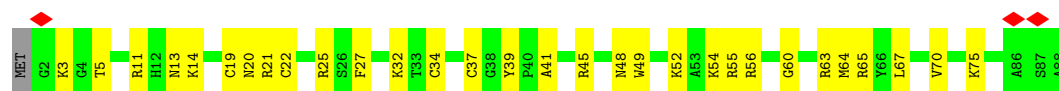
- Molecule 70: 60S ribosomal protein L35-A



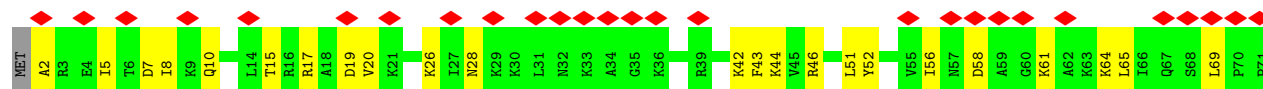
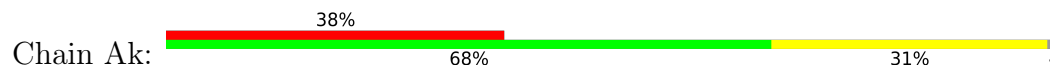
- Molecule 71: 60S ribosomal protein L36-A

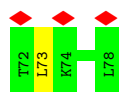


- Molecule 72: 60S ribosomal protein L37-A



- Molecule 73: RPL38 isoform 1

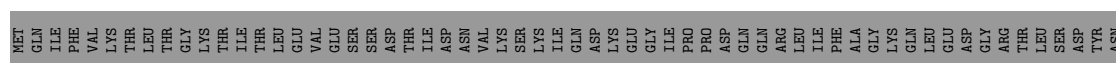
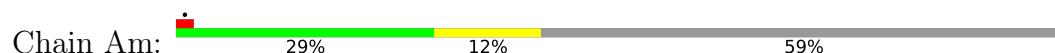




- Molecule 74: 60S ribosomal protein L39



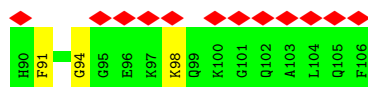
- Molecule 75: Ubiquitin-60S ribosomal protein L40



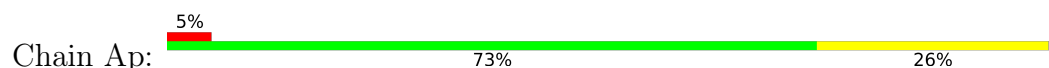
- Molecule 76: 60S ribosomal protein L41-A



- Molecule 77: 60S ribosomal protein L42-A



- Molecule 78: 60S ribosomal protein L43-A

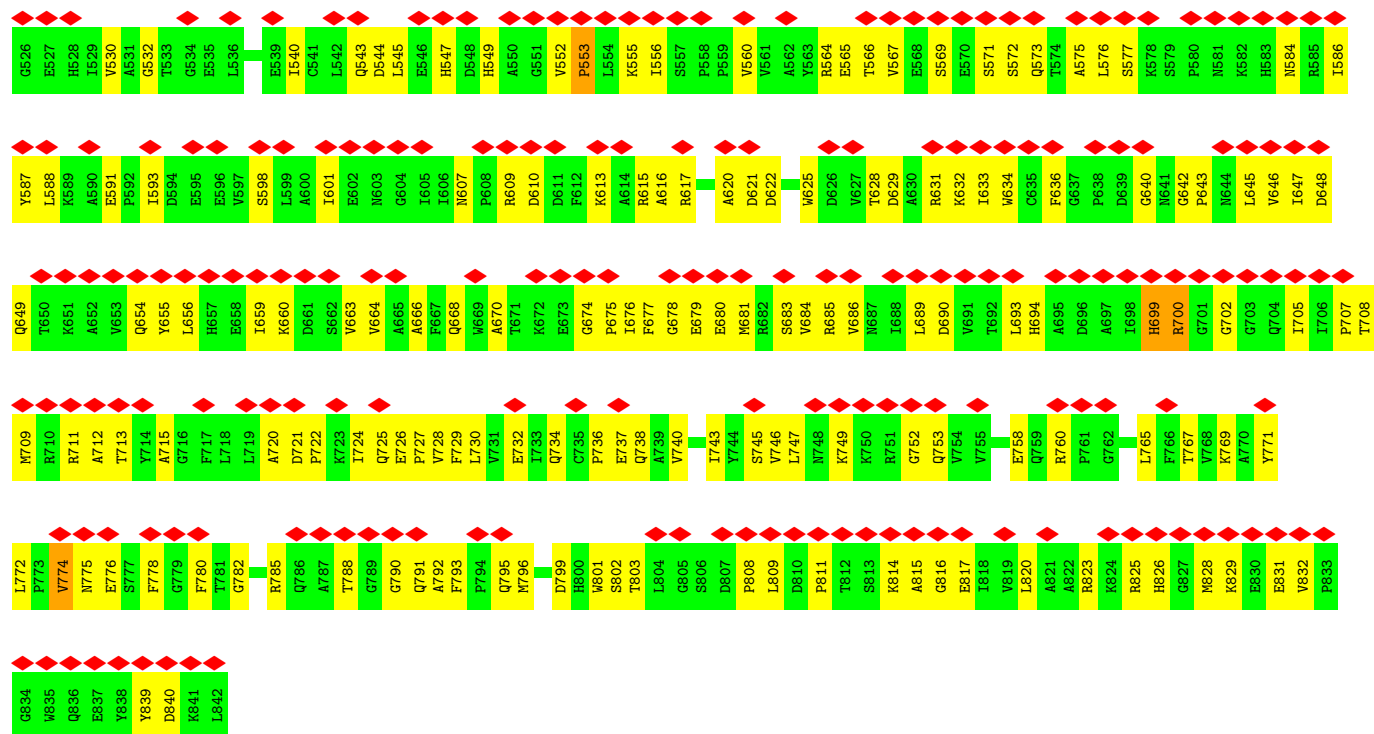


- Molecule 79: RPL1A isoform 1

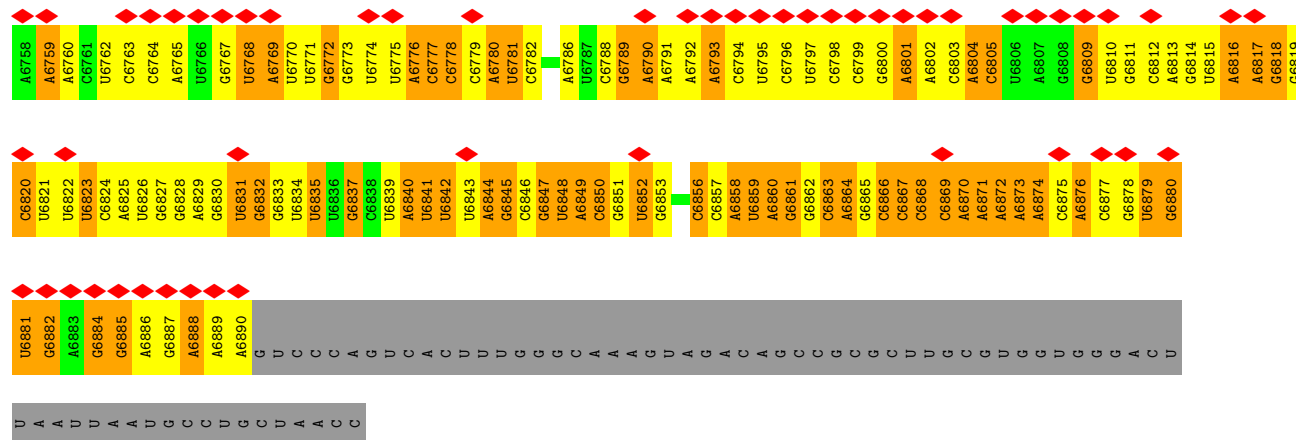


• Molecule 80: Elongation factor 2





● Molecule 81: TSV IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	49671	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	2.003	Depositor
Minimum map value	-0.878	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.101	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: B8N, UR3, DDE, OMG, 5MC, PSU, ZN, HIC, G7M, GDP, OMU, MA6, SO1, MG, 4AC, 1MA

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	1.98	13/1653 (0.8%)	0.47	1/2261 (0.0%)
2	BB	0.20	0/1735	0.43	0/2335
3	BC	0.20	0/1665	0.36	0/2263
4	BE	0.18	0/2109	0.37	0/2839
5	BG	0.14	0/1844	0.31	0/2464
6	BH	0.40	2/1506 (0.1%)	0.79	6/2028 (0.3%)
7	BI	0.18	0/1514	0.41	0/2021
8	BJ	0.18	0/1519	0.37	0/2035
9	BL	0.21	0/1272	0.36	0/1712
10	BN	0.18	0/1215	0.39	0/1638
11	BO	0.22	0/952	0.44	0/1279
12	BV	0.19	0/693	0.36	0/935
13	BW	0.24	0/1038	0.44	0/1395
14	BX	0.21	0/1139	0.39	0/1518
15	BY	0.16	0/1087	0.36	0/1449
16	Ba	0.21	0/782	0.42	0/1047
17	Bb	0.15	0/620	0.38	0/838
18	Be	0.15	0/483	0.48	1/643 (0.2%)
19	BD	0.14	0/1759	0.36	0/2368
20	BF	0.17	0/1629	0.34	0/2202
21	BK	0.15	0/837	0.42	0/1131
22	BP	0.14	0/1012	0.43	0/1356
23	BQ	0.63	2/1125 (0.2%)	1.06	5/1510 (0.3%)
24	BR	1.79	1/957 (0.1%)	0.49	2/1283 (0.2%)
25	BS	0.15	0/1211	0.38	0/1628
26	BT	0.14	0/1113	0.32	0/1494
27	BU	0.14	0/865	0.34	0/1169
28	BZ	0.21	0/582	0.50	0/782
29	Bc	0.17	0/499	0.40	0/670
30	Bd	0.16	0/452	0.29	0/600
31	Bg	0.12	0/2454	0.32	0/3340
32	Bf	0.11	0/616	0.35	0/817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.12	0/943	0.41	2/1274 (0.2%)
34	B5	0.19	0/41450	0.29	1/64582 (0.0%)
35	AA	0.24	0/1912	0.32	0/2569
36	AB	0.24	0/3139	0.37	0/4219
37	AC	0.22	0/2800	0.33	0/3790
38	A1	0.24	0/76161	0.29	0/118749
39	A3	0.20	0/2861	0.26	0/4457
40	A4	0.24	0/3724	0.28	0/5798
41	AD	0.16	0/2390	0.31	0/3225
42	AE	0.18	0/1324	0.35	0/1782
43	AF	0.23	0/1821	0.33	0/2451
44	AG	0.18	0/1830	0.34	0/2469
45	AH	0.21	0/1531	0.34	0/2062
46	AI	0.25	0/1843	0.43	0/2471
47	AJ	0.18	0/1374	0.41	0/1842
48	AL	0.19	0/1568	0.31	0/2106
49	AM	0.20	0/1068	0.35	0/1438
50	AN	0.25	0/1757	0.34	0/2354
51	AO	0.22	0/1585	0.35	0/2128
52	AP	0.21	0/1410	0.32	0/1893
53	AQ	0.21	0/1465	0.32	0/1965
54	AR	0.18	0/1538	0.31	0/2050
55	AS	0.23	0/1481	0.39	0/1990
56	AT	0.20	0/1300	0.33	0/1743
57	AU	0.21	0/812	0.39	0/1099
58	AV	0.22	0/1018	0.37	0/1369
59	AW	0.22	0/533	0.32	0/707
60	AX	0.21	0/983	0.32	0/1325
61	AY	0.19	0/1004	0.30	0/1341
62	AZ	0.21	0/1118	0.35	0/1497
63	Aa	0.22	0/1204	0.36	0/1612
64	Ab	0.19	0/473	0.41	0/629
65	Ac	0.21	0/751	0.35	0/1008
66	Ad	0.20	0/904	0.31	0/1213
67	Ae	0.21	0/1041	0.31	0/1394
68	Af	0.28	0/868	0.38	0/1168
69	Ag	0.23	0/890	0.33	0/1189
70	Ah	0.17	0/978	0.30	0/1301
71	Ai	0.16	0/778	0.35	0/1034
72	Aj	0.25	0/696	0.36	0/923
73	Ak	0.15	0/618	0.34	0/826
74	Al	0.27	0/443	0.54	0/588
75	Am	0.23	0/423	0.47	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.41	0/234	1.16	3/300 (1.0%)
77	Ao	0.17	0/860	0.30	0/1136
78	Ap	0.22	0/701	0.37	0/934
79	E	0.12	0/1745	0.33	0/2342
80	DC	0.39	4/6521 (0.1%)	0.53	6/8830 (0.1%)
81	EC	0.13	0/3138	0.33	0/4883
All	All	0.30	22/224946 (0.0%)	0.34	27/329667 (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
36	AB	0	1
64	Ab	0	1
All	All	0	3

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BA	197	ILE	CG1-CD1	62.96	3.97	1.51
24	BR	105	GLN	CB-CG	54.89	3.17	1.52
1	BA	38	PHE	CE1-CZ	21.53	2.03	1.38
1	BA	38	PHE	CD1-CE1	20.82	2.01	1.38
80	DC	553	PRO	CG-CD	-20.41	0.81	1.50

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	BQ	5	PRO	CB-CG-CD	-24.74	26.95	106.10
80	DC	553	PRO	CB-CG-CD	-24.73	26.96	106.10
23	BQ	5	PRO	CA-N-CD	-22.99	79.81	112.00
6	BH	32	PRO	N-CD-CG	-18.12	76.02	103.20
6	BH	32	PRO	CA-CB-CG	-15.56	74.93	104.50

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	AB	348	ARG	Peptide
64	Ab	41	ARG	Peptide
6	BH	64	VAL	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	137	0
2	BB	1709	0	1784	99	0
3	BC	1635	0	1723	86	0
4	BE	2068	0	2154	107	0
5	BG	1820	0	1918	80	0
6	BH	1481	0	1572	78	0
7	BI	1489	0	1525	98	0
8	BJ	1494	0	1573	109	0
9	BL	1244	0	1314	62	0
10	BN	1192	0	1255	46	0
11	BO	941	0	979	61	0
12	BV	684	0	672	40	0
13	BW	1021	0	1060	68	0
14	BX	1121	0	1196	60	0
15	BY	1073	0	1132	60	0
16	Ba	769	0	818	40	0
17	Bb	610	0	633	31	0
18	Be	475	0	525	23	0
19	BD	1734	0	1817	87	0
20	BF	1609	0	1675	88	0
21	BK	817	0	804	46	0
22	BP	991	0	1035	44	0
23	BQ	1105	0	1166	73	0
24	BR	948	0	990	74	0
25	BS	1192	0	1222	53	0
26	BT	1095	0	1114	48	0
27	BU	855	0	917	45	0
28	BZ	574	0	616	37	0
29	Bc	497	0	535	42	0
30	Bd	442	0	432	34	0
31	Bg	2401	0	2356	104	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	Bf	605	0	654	26	0
33	BM	935	0	975	30	0
34	B5	37463	0	18841	1210	0
35	AA	1878	0	1946	83	0
36	AB	3081	0	3162	133	0
37	AC	2748	0	2859	104	0
38	A1	68786	0	34576	1837	0
39	A3	2579	0	1304	73	0
40	A4	3353	0	1695	93	0
41	AD	2341	0	2290	84	0
42	AE	1303	0	1376	47	0
43	AF	1784	0	1862	63	0
44	AG	1798	0	1894	73	0
45	AH	1510	0	1576	65	0
46	AI	1804	0	1856	66	0
47	AJ	1353	0	1383	66	0
48	AL	1543	0	1608	57	0
49	AM	1053	0	1149	42	0
50	AN	1720	0	1779	69	0
51	AO	1555	0	1659	50	0
52	AP	1388	0	1423	48	0
53	AQ	1441	0	1543	51	0
54	AR	1521	0	1617	58	0
55	AS	1445	0	1487	49	0
56	AT	1276	0	1323	55	0
57	AU	796	0	812	25	0
58	AV	1003	0	1047	45	0
59	AW	521	0	551	16	0
60	AX	968	0	1036	34	0
61	AY	993	0	1081	28	0
62	AZ	1092	0	1155	65	0
63	Aa	1173	0	1215	62	0
64	Ab	462	0	490	11	0
65	Ac	743	0	797	26	0
66	Ad	890	0	938	26	0
67	Ae	1020	0	1090	32	0
68	Af	850	0	880	35	0
69	Ag	880	0	945	39	0
70	Ah	969	0	1078	46	0
71	Ai	771	0	849	27	0
72	Aj	681	0	687	31	0
73	Ak	612	0	682	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
74	Al	436	0	475	30	0
75	Am	417	0	459	13	0
76	An	233	0	284	17	0
77	Ao	847	0	914	37	0
78	Ap	694	0	738	26	0
79	E	1718	0	1811	70	0
80	DC	6419	0	6491	361	0
81	EC	2808	0	1416	103	0
82	Ao	1	0	0	0	0
83	DC	28	0	12	3	0
84	DC	1	0	0	0	0
85	DC	35	0	40	1	0
All	All	211022	0	157945	6499	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 18.

The worst 5 of 6499 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:38:PHE:CD2	1:BA:38:PHE:CE2	1.94	1.52
1:BA:38:PHE:CE2	1:BA:38:PHE:CZ	1.98	1.52
80:DC:553:PRO:CG	80:DC:553:PRO:N	1.69	1.51
1:BA:38:PHE:CD1	1:BA:38:PHE:CE1	2.01	1.47
1:BA:38:PHE:CZ	1:BA:38:PHE:CE1	2.03	1.46

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	191 (94%)	13 (6%)	0	100	100
2	BB	212/255 (83%)	189 (89%)	23 (11%)	0	100	100
3	BC	215/254 (85%)	206 (96%)	9 (4%)	0	100	100
4	BE	258/261 (99%)	233 (90%)	25 (10%)	0	100	100
5	BG	224/236 (95%)	211 (94%)	13 (6%)	0	100	100
6	BH	182/190 (96%)	166 (91%)	16 (9%)	0	100	100
7	BI	184/200 (92%)	167 (91%)	17 (9%)	0	100	100
8	BJ	183/197 (93%)	165 (90%)	18 (10%)	0	100	100
9	BL	153/156 (98%)	140 (92%)	13 (8%)	0	100	100
10	BN	148/151 (98%)	136 (92%)	12 (8%)	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%)	116 (91%)	11 (9%)	0	100	100
14	BX	142/145 (98%)	132 (93%)	10 (7%)	0	100	100
15	BY	132/135 (98%)	123 (93%)	9 (7%)	0	100	100
16	Ba	95/119 (80%)	87 (92%)	8 (8%)	0	100	100
17	Bb	79/82 (96%)	74 (94%)	5 (6%)	0	100	100
18	Be	58/63 (92%)	51 (88%)	7 (12%)	0	100	100
19	BD	221/240 (92%)	210 (95%)	11 (5%)	0	100	100
20	BF	204/225 (91%)	187 (92%)	17 (8%)	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%)	133 (96%)	6 (4%)	0	100	100
24	BR	117/136 (86%)	112 (96%)	5 (4%)	0	100	100
25	BS	143/146 (98%)	129 (90%)	14 (10%)	0	100	100
26	BT	139/144 (96%)	126 (91%)	13 (9%)	0	100	100
27	BU	105/121 (87%)	97 (92%)	8 (8%)	0	100	100
28	BZ	69/108 (64%)	61 (88%)	8 (12%)	0	100	100
29	Bc	61/67 (91%)	56 (92%)	5 (8%)	0	100	100
30	Bd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
31	Bg	310/319 (97%)	288 (93%)	22 (7%)	0	100	100
32	Bf	73/152 (48%)	69 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	BM	122/143 (85%)	113 (93%)	9 (7%)	0	100	100
35	AA	245/254 (96%)	226 (92%)	19 (8%)	0	100	100
36	AB	383/387 (99%)	360 (94%)	23 (6%)	0	100	100
37	AC	359/362 (99%)	328 (91%)	31 (9%)	0	100	100
41	AD	290/297 (98%)	268 (92%)	22 (8%)	0	100	100
42	AE	163/176 (93%)	145 (89%)	18 (11%)	0	100	100
43	AF	220/244 (90%)	209 (95%)	11 (5%)	0	100	100
44	AG	228/256 (89%)	213 (93%)	15 (7%)	0	100	100
45	AH	188/191 (98%)	173 (92%)	15 (8%)	0	100	100
46	AI	220/222 (99%)	207 (94%)	13 (6%)	0	100	100
47	AJ	167/174 (96%)	155 (93%)	12 (7%)	0	100	100
48	AL	191/199 (96%)	179 (94%)	12 (6%)	0	100	100
49	AM	134/138 (97%)	126 (94%)	8 (6%)	0	100	100
50	AN	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
51	AO	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
52	AP	171/184 (93%)	164 (96%)	7 (4%)	0	100	100
53	AQ	183/186 (98%)	176 (96%)	7 (4%)	0	100	100
54	AR	186/189 (98%)	178 (96%)	8 (4%)	0	100	100
55	AS	170/178 (96%)	160 (94%)	10 (6%)	0	100	100
56	AT	157/160 (98%)	145 (92%)	12 (8%)	0	100	100
57	AU	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
58	AV	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
59	AW	61/155 (39%)	59 (97%)	2 (3%)	0	100	100
60	AX	119/142 (84%)	111 (93%)	8 (7%)	0	100	100
61	AY	124/127 (98%)	120 (97%)	4 (3%)	0	100	100
62	AZ	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
63	Aa	146/149 (98%)	135 (92%)	11 (8%)	0	100	100
64	Ab	56/59 (95%)	47 (84%)	9 (16%)	0	100	100
65	Ac	95/105 (90%)	92 (97%)	3 (3%)	0	100	100
66	Ad	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
67	Ae	125/130 (96%)	123 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	Af	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
69	Ag	110/121 (91%)	102 (93%)	8 (7%)	0	100	100
70	Ah	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
71	Ai	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
72	Aj	85/88 (97%)	81 (95%)	4 (5%)	0	100	100
73	Ak	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
74	Al	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
75	Am	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	103/106 (97%)	95 (92%)	8 (8%)	0	100	100
78	Ap	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
79	E	215/217 (99%)	203 (94%)	12 (6%)	0	100	100
80	DC	819/842 (97%)	741 (90%)	76 (9%)	2 (0%)	43	73
All	All	11960/12946 (92%)	11119 (93%)	839 (7%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
80	DC	700	ARG
80	DC	774	VAL

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	101/124 (82%)	101 (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	62/89 (70%)	62 (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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	AD	241/245 (98%)	241 (100%)	0	100	100
42	AE	137/153 (90%)	137 (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	190/190 (100%)	190 (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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
All	All	10195/10903 (94%)	10195 (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 183 such sidechains are listed below:

Mol	Chain	Res	Type
51	AO	72[A]	HIS
62	AZ	78	ASN
52	AP	64	ASN
56	AT	26	HIS
64	Ab	17	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1754/1798 (97%)	502 (28%)	6 (0%)
38	A1	3212/3393 (94%)	708 (22%)	21 (0%)
39	A3	120/121 (99%)	17 (14%)	1 (0%)
40	A4	157/158 (99%)	30 (19%)	1 (0%)
81	EC	129/202 (63%)	82 (63%)	7 (5%)
All	All	5372/5672 (94%)	1339 (24%)	36 (0%)

5 of 1339 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	2	A
34	B5	4	C

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Mol	Chain	Res	Type
34	B5	11	A
34	B5	12	U
34	B5	25	C

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
40	A4	88	A
81	EC	6889	A
81	EC	6771	U
81	EC	6804	A
38	A1	1287	A

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

60 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	OMG	A1	2922	38	23,26,27	1.20	3 (13%)	32,38,41	1.96	6 (18%)
34	PSU	B5	1181	34	18,21,22	1.36	2 (11%)	21,30,33	2.05	4 (19%)
38	1MA	A1	645	38	21,25,26	1.36	4 (19%)	30,37,40	1.76	6 (20%)
34	PSU	B5	211	34	18,21,22	1.42	3 (16%)	21,30,33	2.04	3 (14%)
38	PSU	A1	986	38	18,21,22	1.39	4 (22%)	21,30,33	2.01	3 (14%)
38	PSU	A1	2735	38	18,21,22	1.41	3 (16%)	21,30,33	2.16	4 (19%)
38	PSU	A1	2314	38	18,21,22	1.39	3 (16%)	21,30,33	2.05	5 (23%)
34	PSU	B5	1415	34	18,21,22	1.41	3 (16%)	21,30,33	2.05	4 (19%)
38	PSU	A1	2865	38	18,21,22	1.48	4 (22%)	21,30,33	2.14	4 (19%)
38	PSU	A1	1004	38	18,21,22	1.36	2 (11%)	21,30,33	2.03	3 (14%)
38	PSU	A1	960	38	18,21,22	1.40	3 (16%)	21,30,33	2.11	4 (19%)
38	PSU	A1	2944	38	18,21,22	1.42	3 (16%)	21,30,33	2.07	4 (19%)
34	PSU	B5	1290	34	18,21,22	1.36	3 (16%)	21,30,33	2.10	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	MA6	B5	1782	34	23,26,27	1.71	3 (13%)	33,38,41	2.24	11 (33%)
34	4AC	B5	1280	34	21,24,25	1.09	1 (4%)	28,34,37	1.08	2 (7%)
38	PSU	A1	2923	38	18,21,22	1.39	2 (11%)	21,30,33	2.14	4 (19%)
38	PSU	A1	2880	38	18,21,22	1.38	3 (16%)	21,30,33	2.11	4 (19%)
38	5MC	A1	2278	38	19,22,23	1.49	3 (15%)	26,32,35	1.15	3 (11%)
34	PSU	B5	999	34	18,21,22	1.40	3 (16%)	21,30,33	2.13	4 (19%)
38	UR3	A1	2634	38	19,22,23	0.92	1 (5%)	26,32,35	1.75	4 (15%)
38	PSU	A1	2133	38	18,21,22	1.46	3 (16%)	21,30,33	2.18	5 (23%)
34	PSU	B5	120	34	18,21,22	1.37	2 (11%)	21,30,33	2.02	3 (14%)
80	DDE	DC	699	-	18,20,21	1.04	1 (5%)	17,28,30	0.83	0
39	PSU	A3	50	39	18,21,22	1.36	2 (11%)	21,30,33	2.12	4 (19%)
34	MA6	B5	1781	34	23,26,27	1.53	5 (21%)	33,38,41	2.03	10 (30%)
38	PSU	A1	1042	38	18,21,22	1.39	3 (16%)	21,30,33	2.02	3 (14%)
38	PSU	A1	2258	38	18,21,22	1.38	2 (11%)	21,30,33	2.07	3 (14%)
38	PSU	A1	2416	38	18,21,22	1.41	4 (22%)	21,30,33	2.11	3 (14%)
34	PSU	B5	302	34	18,21,22	1.40	3 (16%)	21,30,33	2.10	4 (19%)
38	PSU	A1	2129	38	18,21,22	1.40	3 (16%)	21,30,33	2.12	4 (19%)
40	PSU	A4	73	40	18,21,22	1.39	2 (11%)	21,30,33	2.07	3 (14%)
38	PSU	A1	2260	38	18,21,22	1.41	3 (16%)	21,30,33	2.02	4 (19%)
38	PSU	A1	966	38	18,21,22	1.38	4 (22%)	21,30,33	2.05	3 (14%)
38	PSU	A1	2826	38	18,21,22	1.41	4 (22%)	21,30,33	2.12	5 (23%)
38	PSU	A1	2340	38	18,21,22	1.44	4 (22%)	21,30,33	2.03	3 (14%)
38	PSU	A1	776	38	18,21,22	1.42	4 (22%)	21,30,33	1.87	5 (23%)
38	PSU	A1	1110	38	18,21,22	1.41	3 (16%)	21,30,33	2.06	3 (14%)
38	5MC	A1	2870	38	19,22,23	1.37	3 (15%)	26,32,35	1.14	3 (11%)
38	PSU	A1	2349	38	18,21,22	1.38	4 (22%)	21,30,33	1.96	4 (19%)
38	PSU	A1	2351	38	18,21,22	1.42	4 (22%)	21,30,33	2.14	4 (19%)
38	PSU	A1	2266	38	18,21,22	1.45	4 (22%)	21,30,33	2.10	5 (23%)
34	G7M	B5	1575	34	23,26,27	2.54	7 (30%)	34,39,42	1.70	7 (20%)
38	PSU	A1	2975	38	18,21,22	1.40	4 (22%)	21,30,33	2.11	4 (19%)
34	PSU	B5	766	34	18,21,22	1.39	2 (11%)	21,30,33	2.09	4 (19%)
38	PSU	A1	2264	38	18,21,22	1.39	2 (11%)	21,30,33	2.04	3 (14%)
34	PSU	B5	759	34	18,21,22	1.36	2 (11%)	21,30,33	2.07	4 (19%)
38	PSU	A1	1056	38	18,21,22	1.37	3 (16%)	21,30,33	2.05	4 (19%)
34	PSU	B5	106	34	18,21,22	1.38	3 (16%)	21,30,33	2.00	3 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	PSU	B5	632	34	18,21,22	1.38	3 (16%)	21,30,33	2.09	3 (14%)
38	PSU	A1	990	38	18,21,22	1.42	3 (16%)	21,30,33	2.10	4 (19%)
36	HIC	AB	243	36	10,11,12	1.43	1 (10%)	9,14,16	1.25	1 (11%)
38	PSU	A1	1124	38	18,21,22	1.35	3 (16%)	21,30,33	2.07	4 (19%)
38	PSU	A1	1052	38	18,21,22	1.40	3 (16%)	21,30,33	2.10	4 (19%)
34	PSU	B5	466	34	18,21,22	1.35	3 (16%)	21,30,33	2.06	4 (19%)
38	1MA	A1	2142	38	21,25,26	1.33	4 (19%)	30,37,40	1.70	5 (16%)
38	OMU	A1	2921	38	19,22,23	1.26	3 (15%)	25,31,34	1.84	5 (20%)
38	PSU	A1	2191	38	18,21,22	1.39	5 (27%)	21,30,33	2.08	4 (19%)
34	PSU	B5	1187	34	18,21,22	1.35	2 (11%)	21,30,33	2.02	4 (19%)
34	4AC	B5	1773	34	21,24,25	1.03	2 (9%)	28,34,37	1.71	4 (14%)
34	B8N	B5	1191	34	25,29,30	1.37	3 (12%)	28,42,45	1.86	5 (17%)

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	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
34	PSU	B5	1181	34	-	0/7/25/26	0/2/2/2
38	1MA	A1	645	38	-	0/7/25/26	0/3/3/3
34	PSU	B5	211	34	-	3/7/25/26	0/2/2/2
38	PSU	A1	986	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2735	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2314	38	-	2/7/25/26	0/2/2/2
34	PSU	B5	1415	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2865	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1004	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	960	38	-	4/7/25/26	0/2/2/2
38	PSU	A1	2944	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	1290	34	-	0/7/25/26	0/2/2/2
34	MA6	B5	1782	34	-	1/11/29/30	0/3/3/3
34	4AC	B5	1280	34	-	2/11/29/30	0/2/2/2
38	PSU	A1	2923	38	-	3/7/25/26	0/2/2/2
38	PSU	A1	2880	38	-	0/7/25/26	0/2/2/2
38	5MC	A1	2278	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	999	34	-	0/7/25/26	0/2/2/2
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	PSU	A1	2133	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	120	34	-	0/7/25/26	0/2/2/2
80	DDE	DC	699	-	-	1/20/21/23	0/1/1/1
39	PSU	A3	50	39	-	3/7/25/26	0/2/2/2
34	MA6	B5	1781	34	-	0/11/29/30	0/3/3/3
38	PSU	A1	1042	38	-	2/7/25/26	0/2/2/2
38	PSU	A1	2258	38	-	2/7/25/26	0/2/2/2
38	PSU	A1	2416	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	302	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2129	38	-	0/7/25/26	0/2/2/2
40	PSU	A4	73	40	-	0/7/25/26	0/2/2/2
38	PSU	A1	2260	38	-	3/7/25/26	0/2/2/2
38	PSU	A1	966	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2826	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2340	38	-	3/7/25/26	0/2/2/2
38	PSU	A1	776	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1110	38	-	2/7/25/26	0/2/2/2
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
38	PSU	A1	2349	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2351	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2266	38	-	3/7/25/26	0/2/2/2
34	G7M	B5	1575	34	-	0/7/25/26	0/3/3/3
38	PSU	A1	2975	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	766	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2264	38	-	3/7/25/26	0/2/2/2
34	PSU	B5	759	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	1056	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	106	34	-	0/7/25/26	0/2/2/2
34	PSU	B5	632	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	990	38	-	0/7/25/26	0/2/2/2
36	HIC	AB	243	36	-	0/5/6/8	0/1/1/1
38	PSU	A1	1124	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1052	38	-	1/7/25/26	0/2/2/2
34	PSU	B5	466	34	-	0/7/25/26	0/2/2/2
38	1MA	A1	2142	38	-	0/7/25/26	0/3/3/3
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
38	PSU	A1	2191	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	1187	34	-	1/7/25/26	0/2/2/2
34	4AC	B5	1773	34	-	4/11/29/30	0/2/2/2
34	B8N	B5	1191	34	-	2/16/34/35	0/2/2/2

The worst 5 of 181 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	O6-C6	7.58	1.37	1.23
34	B5	1782	MA6	C5-C4	5.70	1.49	1.39
34	B5	1575	G7M	C2-N2	5.60	1.47	1.34
38	A1	2278	5MC	C5-C4	5.18	1.48	1.44
34	B5	1575	G7M	C5-N7	-5.07	1.33	1.39

The worst 5 of 243 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2133	PSU	N1-C2-N3	6.98	122.53	115.17
38	A1	2634	UR3	C4-N3-C2	-6.91	119.02	124.58
38	A1	2735	PSU	N1-C2-N3	6.75	122.29	115.17
38	A1	2923	PSU	N1-C2-N3	6.73	122.27	115.17
38	A1	2351	PSU	N1-C2-N3	6.69	122.22	115.17

There are no chirality outliers.

5 of 49 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B5	211	PSU	C2'-C1'-C5-C4
34	B5	211	PSU	C2'-C1'-C5-C6
34	B5	1280	4AC	N3-C4-N4-C7
34	B5	1280	4AC	C5-C4-N4-C7
34	B5	1773	4AC	N3-C4-N4-C7

There are no ring outliers.

28 monomers are involved in 59 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	B5	211	PSU	2	0
38	A1	986	PSU	2	0
38	A1	2314	PSU	1	0
38	A1	2865	PSU	1	0
34	B5	1290	PSU	1	0
34	B5	1782	MA6	12	0
34	B5	1280	4AC	4	0
38	A1	2880	PSU	1	0
38	A1	2634	UR3	1	0
38	A1	2133	PSU	1	0
34	B5	120	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
80	DC	699	DDE	2	0
34	B5	1781	MA6	5	0
38	A1	2258	PSU	2	0
34	B5	302	PSU	1	0
38	A1	2129	PSU	2	0
38	A1	966	PSU	2	0
38	A1	1110	PSU	1	0
38	A1	2870	5MC	1	0
38	A1	2349	PSU	1	0
38	A1	2351	PSU	1	0
38	A1	2266	PSU	7	0
38	A1	2975	PSU	1	0
34	B5	632	PSU	2	0
38	A1	990	PSU	1	0
38	A1	1124	PSU	1	0
38	A1	2191	PSU	1	0
34	B5	1773	4AC	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
83	GDP	DC	901	84	29,30,30	1.19	3 (10%)	45,47,47	1.75	6 (13%)
85	SO1	DC	903	-	34,39,39	0.67	1 (2%)	38,64,64	1.08	3 (7%)

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
83	GDP	DC	901	84	-	5/16/32/32	0/3/3/3
85	SO1	DC	903	-	1/1/15/16	3/21/104/104	0/7/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	DC	901	GDP	C5-C4	3.11	1.47	1.38
85	DC	903	SO1	O14-C5	-2.95	1.19	1.30
83	DC	901	GDP	C6-N1	-2.54	1.34	1.38
83	DC	901	GDP	C5-N7	-2.26	1.34	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	DC	901	GDP	C5-C4-N3	-6.27	118.40	128.39
83	DC	901	GDP	N9-C4-N3	4.89	135.72	125.95
83	DC	901	GDP	C2-N3-C4	4.71	120.41	112.30
85	DC	903	SO1	C12-C6-C2	-3.96	98.96	105.09
85	DC	903	SO1	C21-C13-C4	2.67	119.53	112.41

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
85	DC	903	SO1	C4

5 of 8 torsion outliers are listed below:

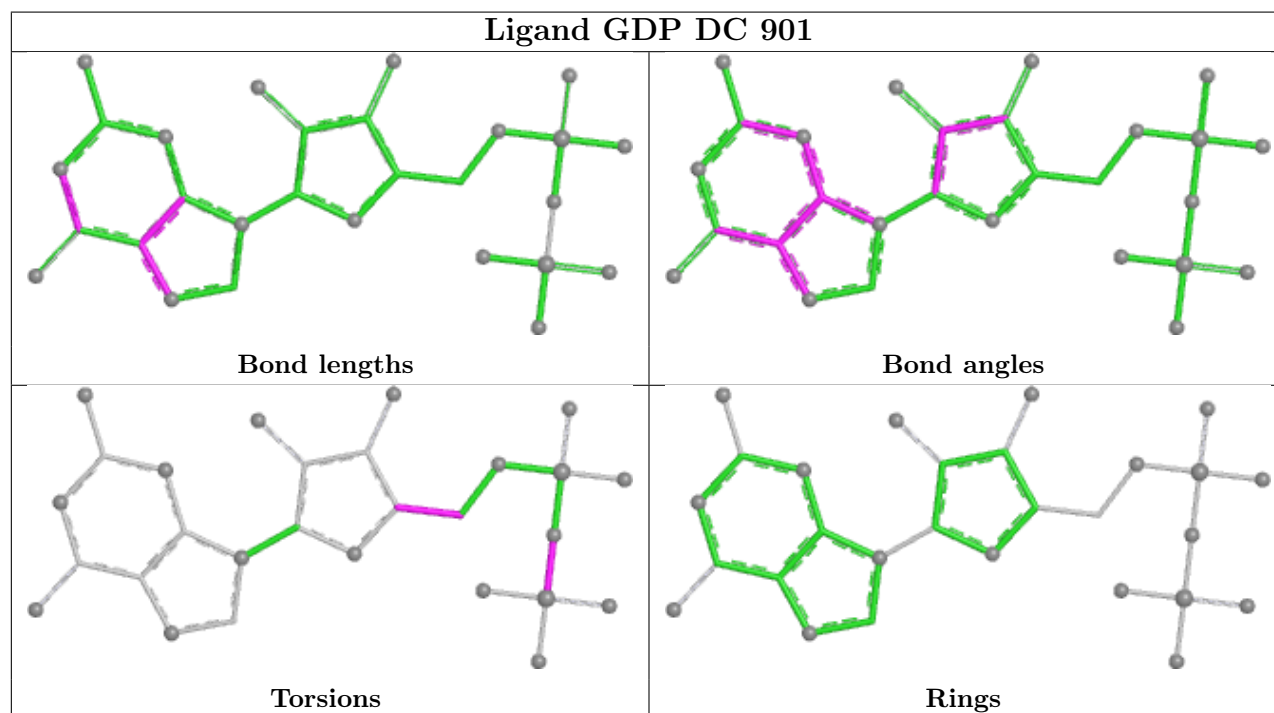
Mol	Chain	Res	Type	Atoms
83	DC	901	GDP	O4'-C4'-C5'-O5'
85	DC	903	SO1	C2-C1-C5-O14
85	DC	903	SO1	C2-C1-C5-O15
83	DC	901	GDP	C3'-C4'-C5'-O5'
85	DC	903	SO1	C54-C55-O64-C65

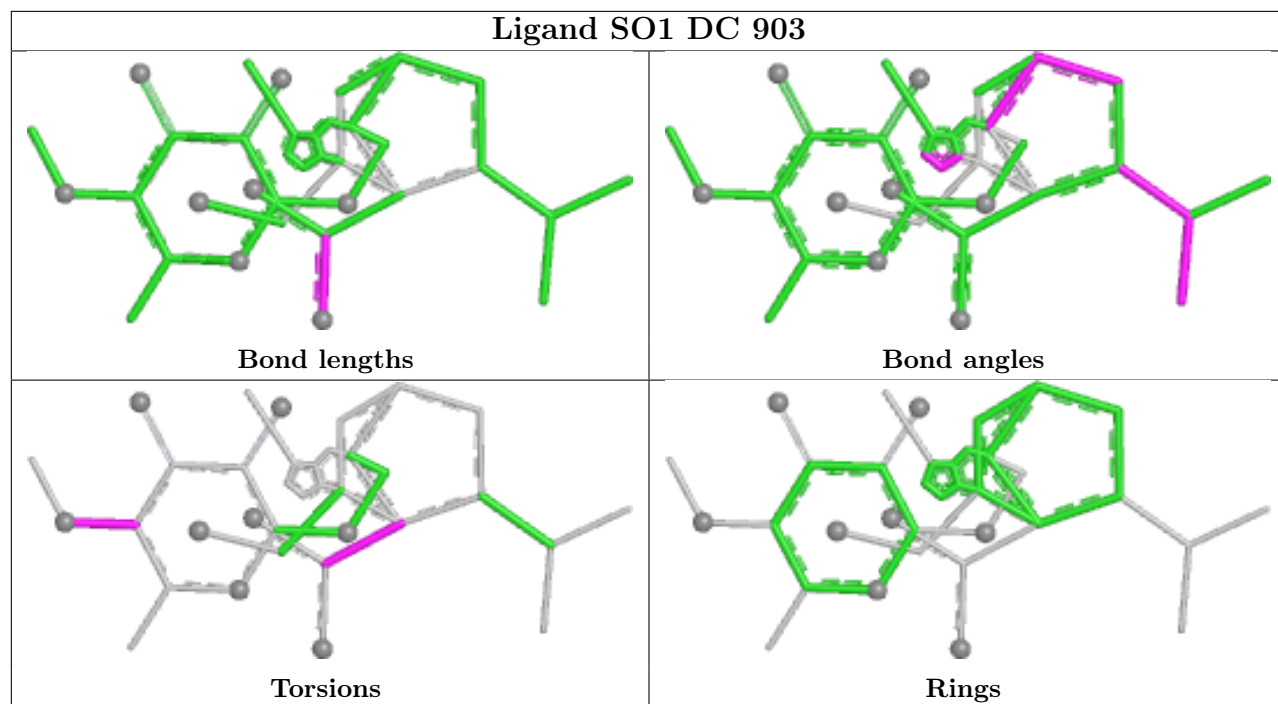
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
83	DC	901	GDP	3	0
85	DC	903	SO1	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.

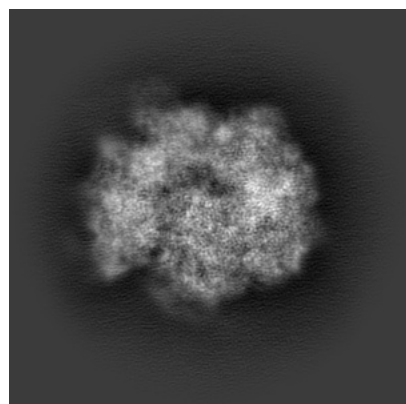
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41002. These allow visual inspection of the internal detail of the map and identification of artifacts.

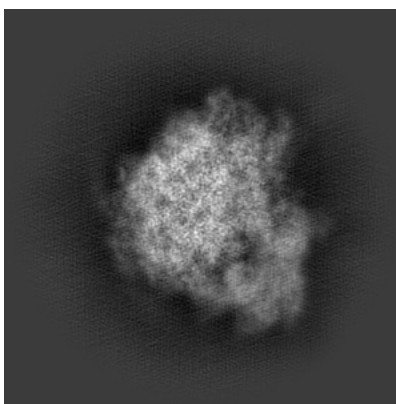
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

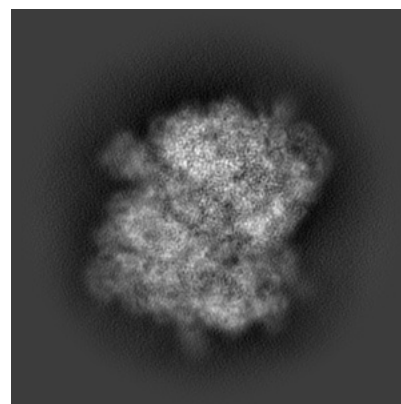
6.1.1 Primary map



X

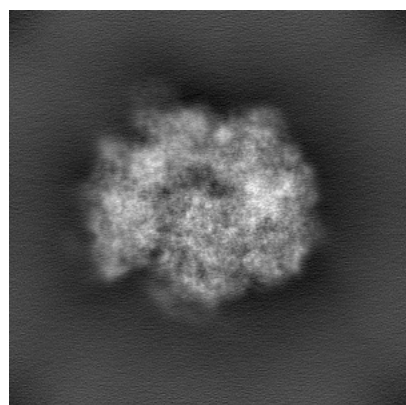


Y

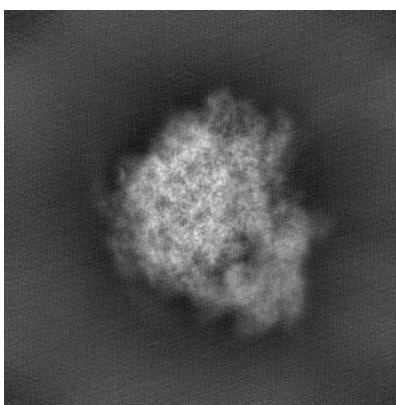


Z

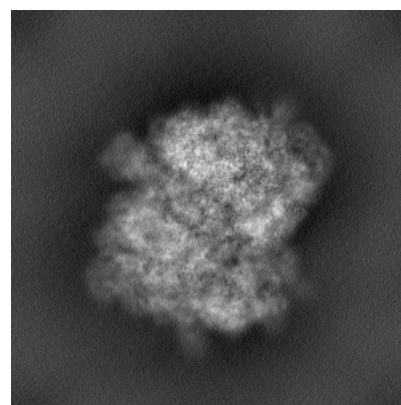
6.1.2 Raw map



X



Y

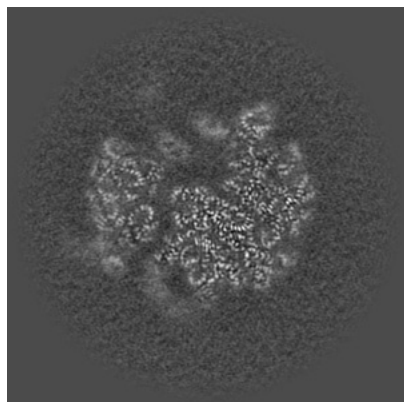


Z

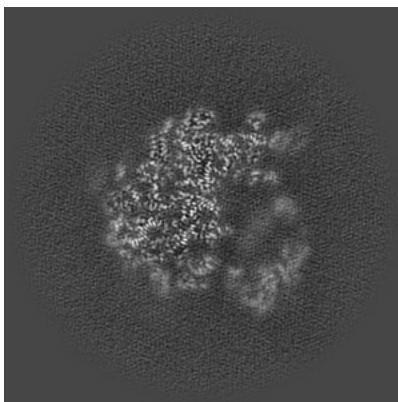
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

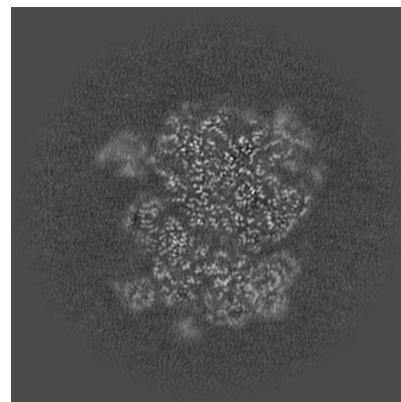
6.2.1 Primary map



X Index: 200

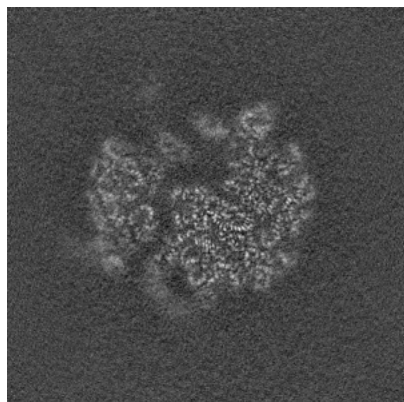


Y Index: 200

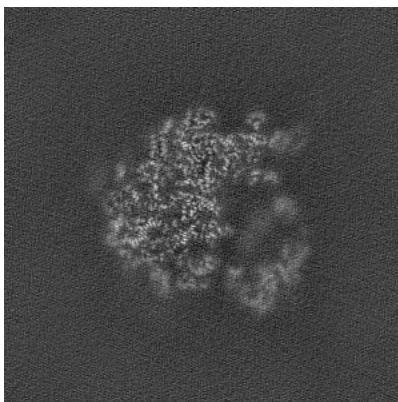


Z Index: 200

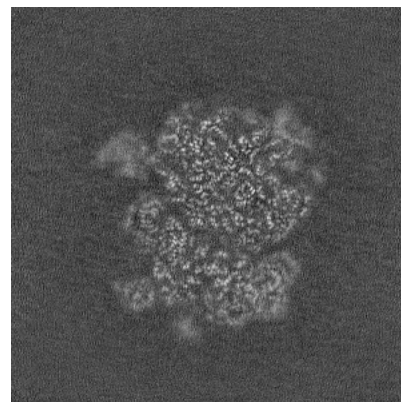
6.2.2 Raw map



X Index: 200



Y Index: 200

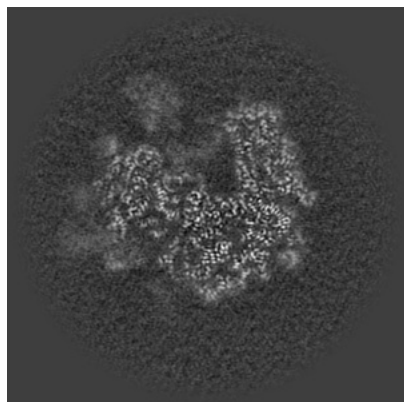


Z Index: 200

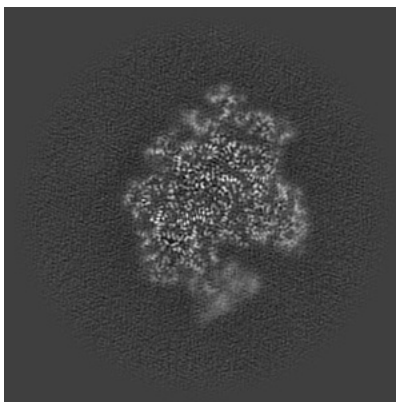
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

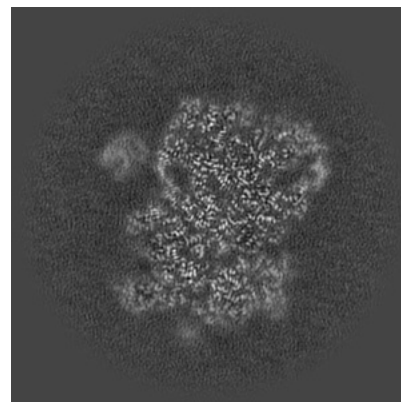
6.3.1 Primary map



X Index: 185

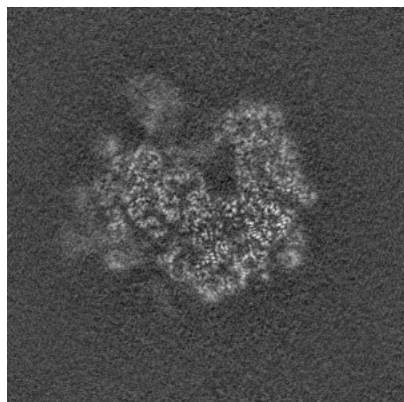


Y Index: 244

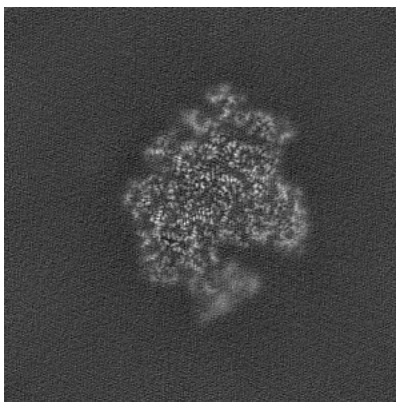


Z Index: 207

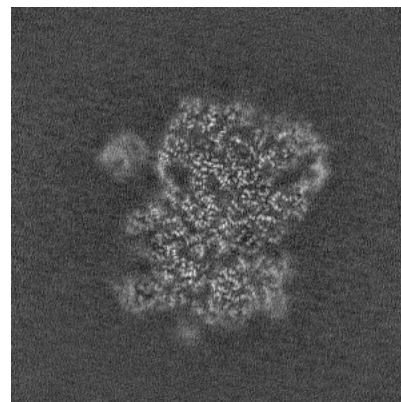
6.3.2 Raw map



X Index: 184



Y Index: 244

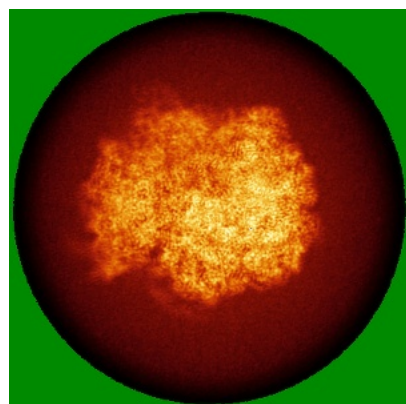


Z Index: 207

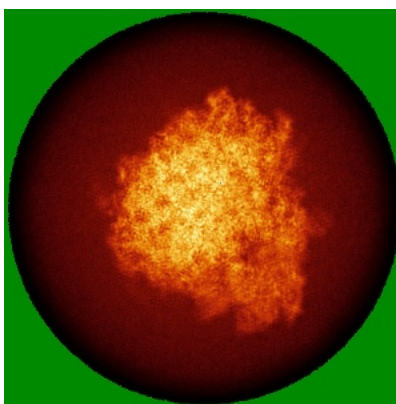
The images above show the largest variance slices of the map in three orthogonal directions.

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

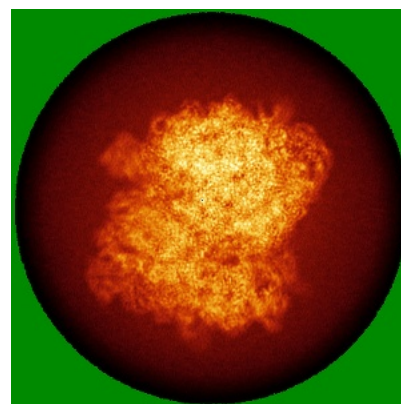
6.4.1 Primary map



X

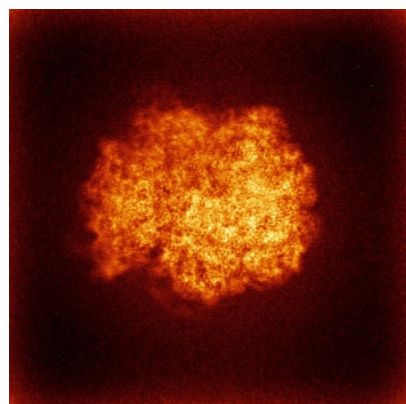


Y

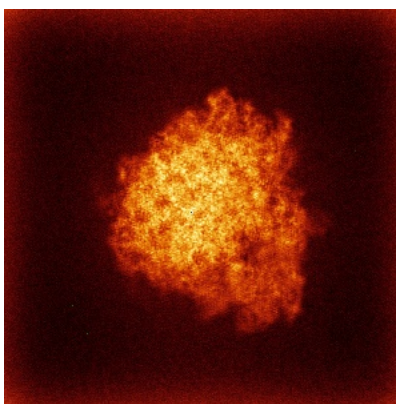


Z

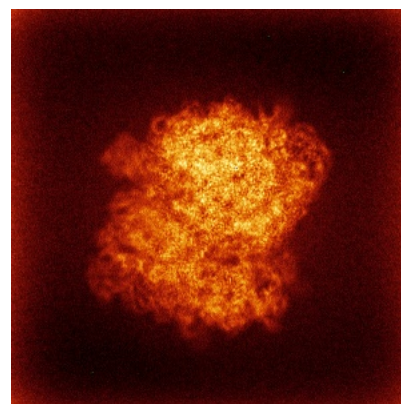
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

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

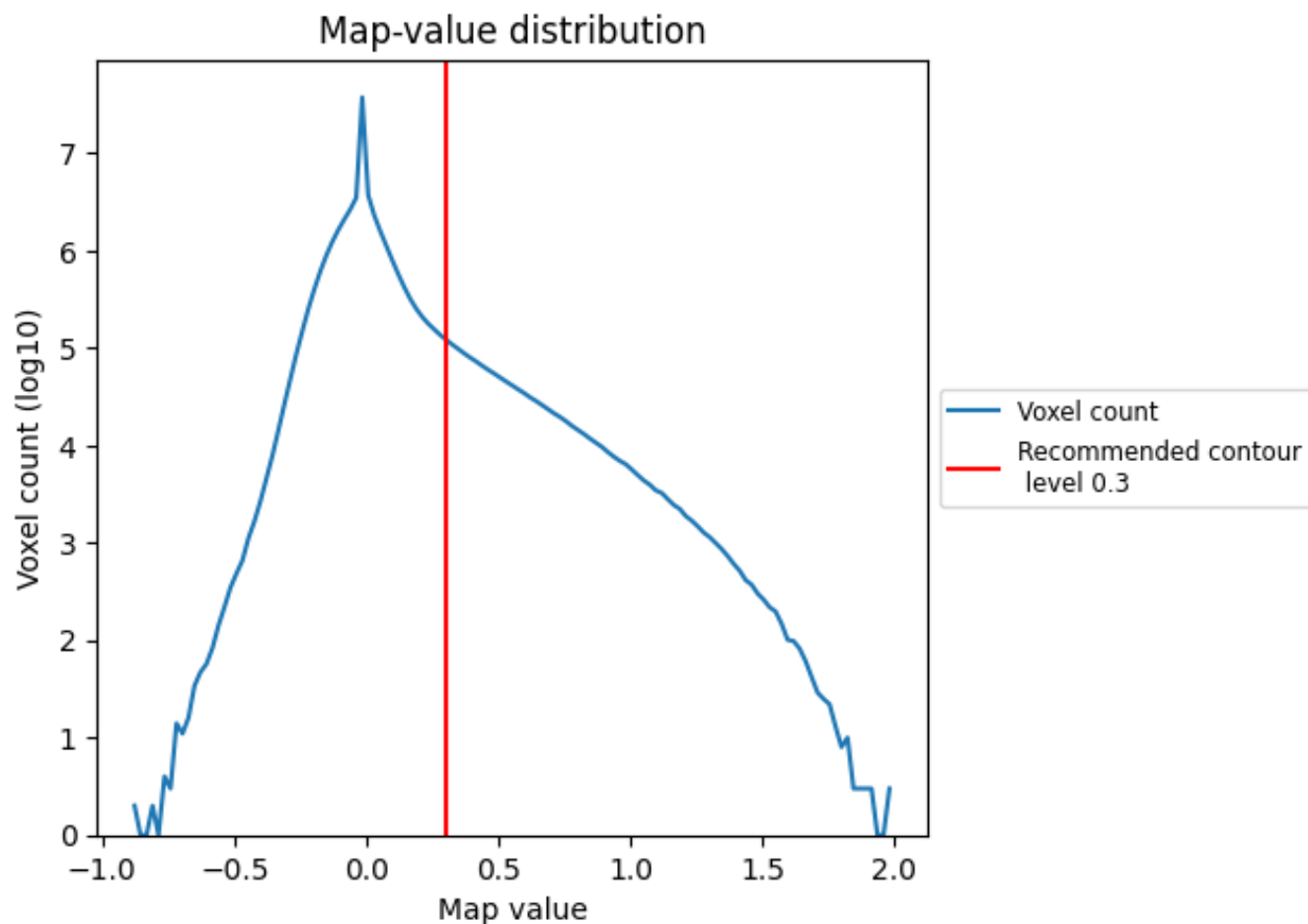
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

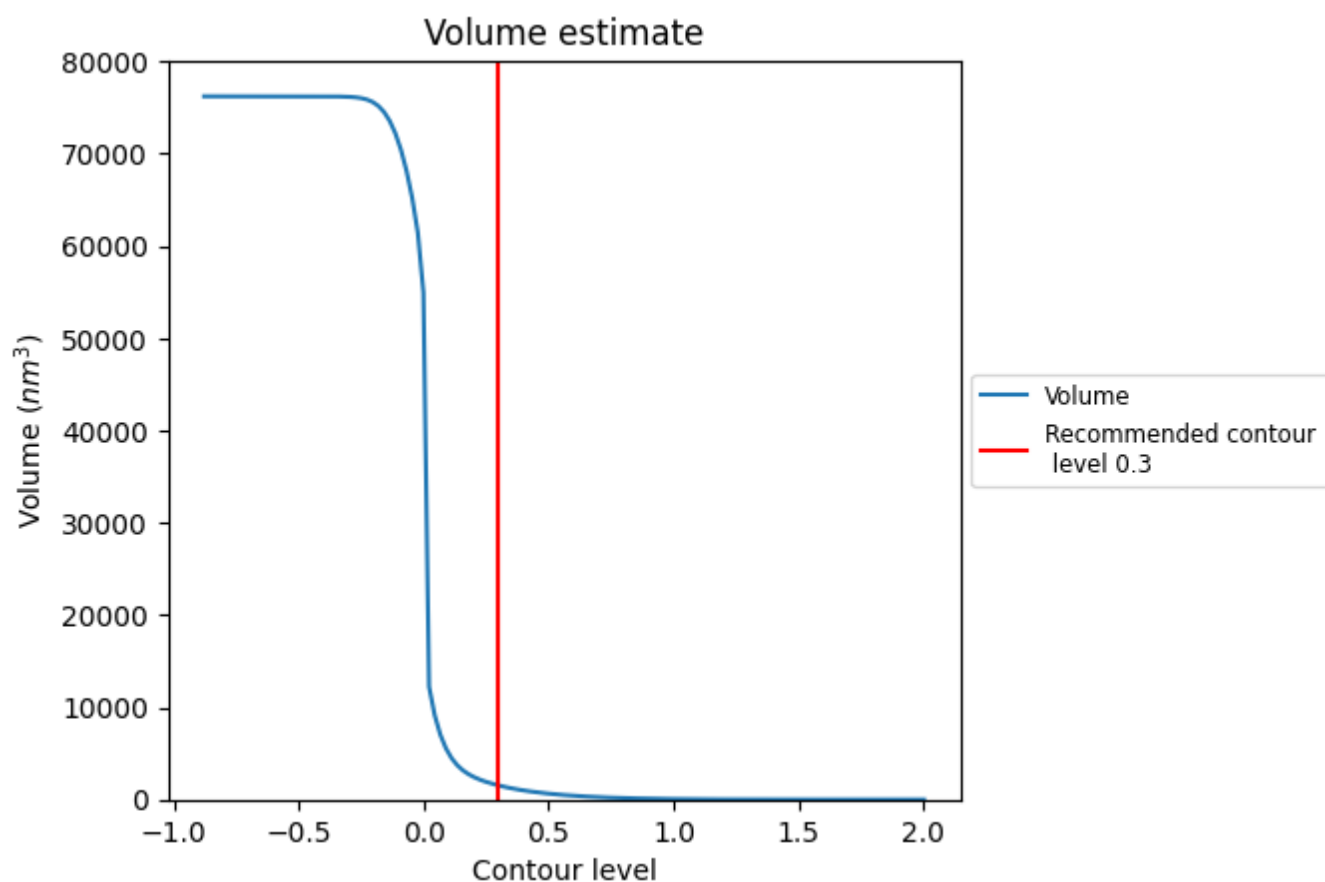
This section contains the results of statistical analysis of the map.

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.

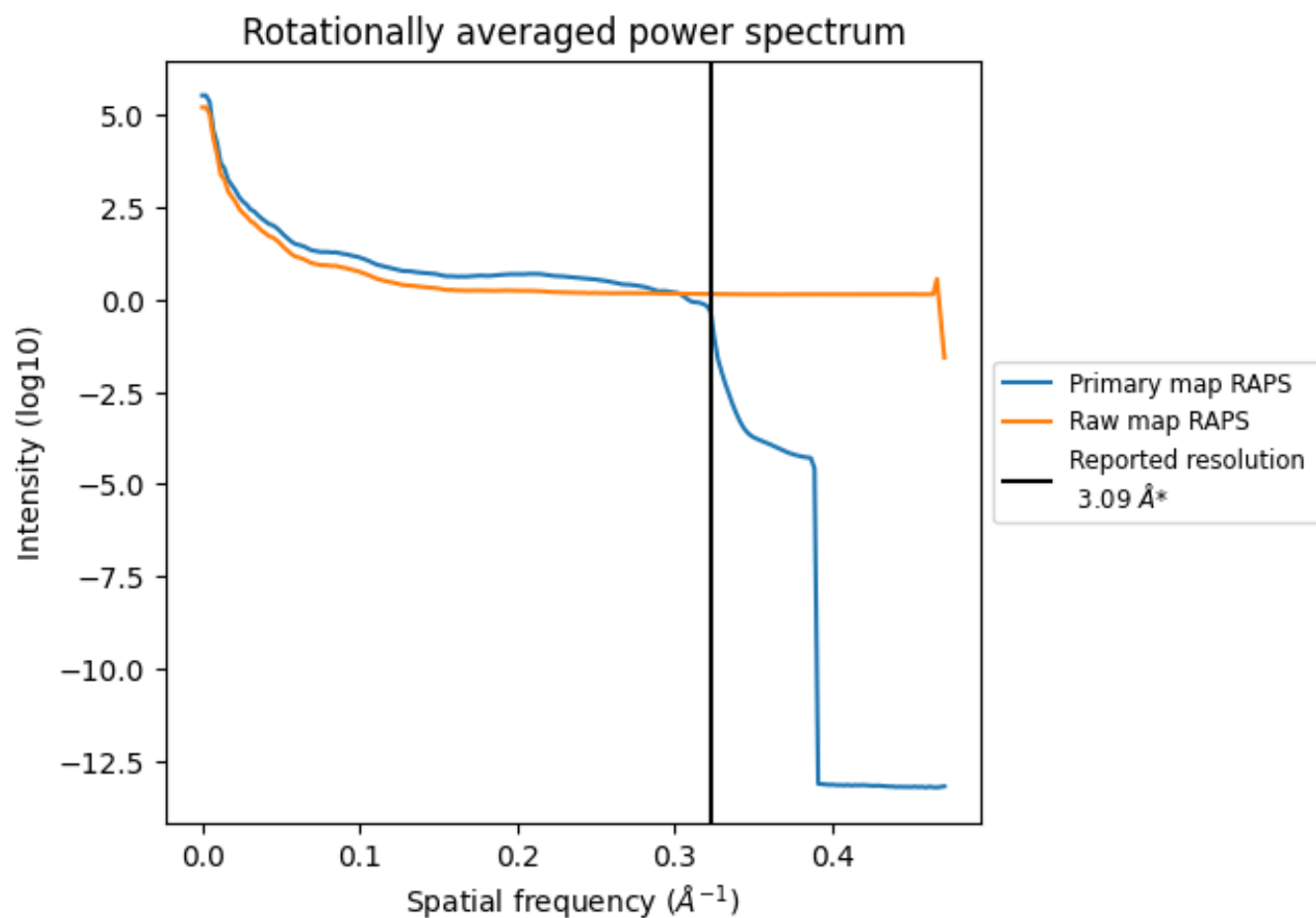
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1532 nm³; this corresponds to an approximate mass of 1384 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 ⓘ

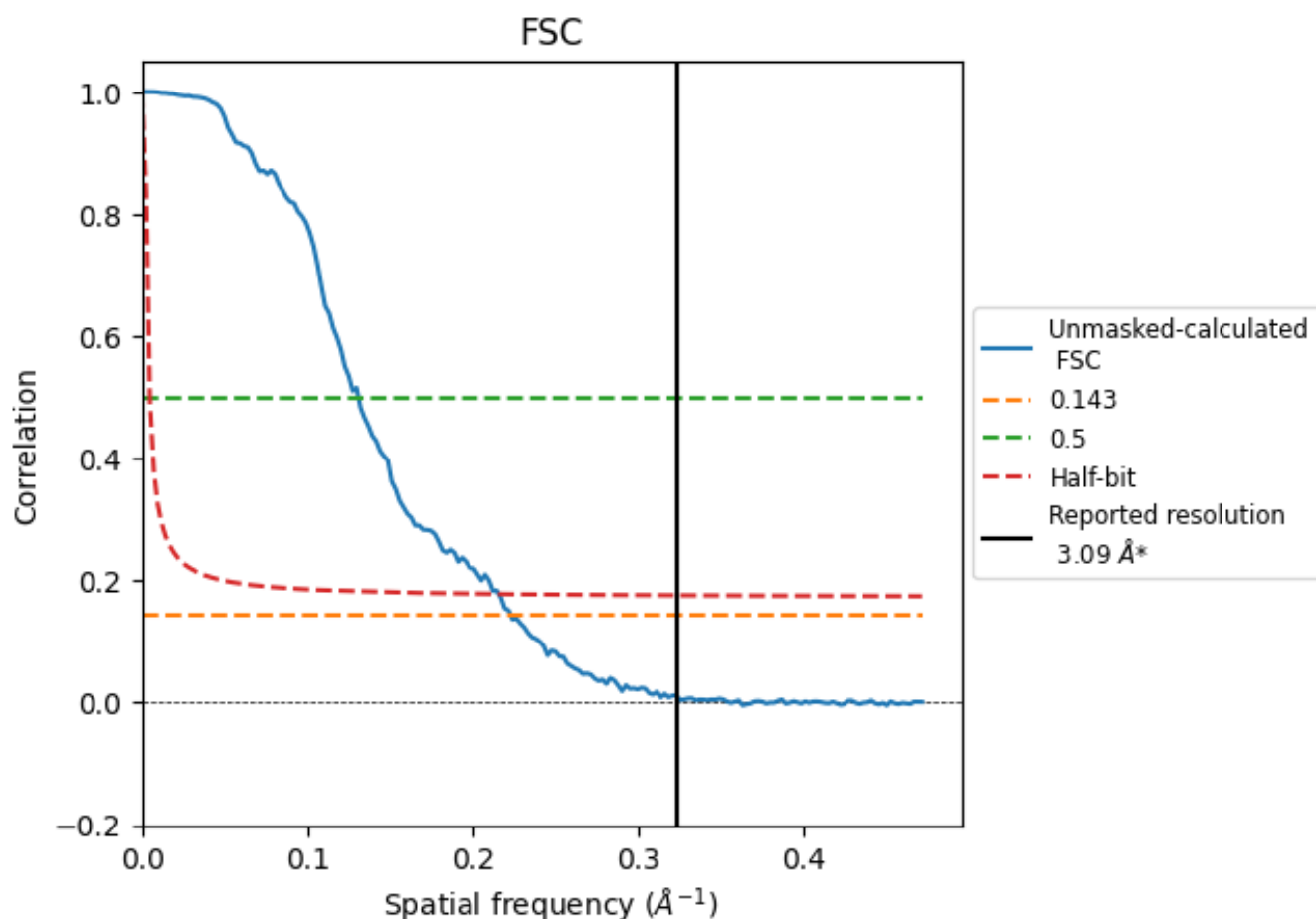


*Reported resolution corresponds to spatial frequency of 0.324 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.324 Å⁻¹

8.2 Resolution estimates [i](#)

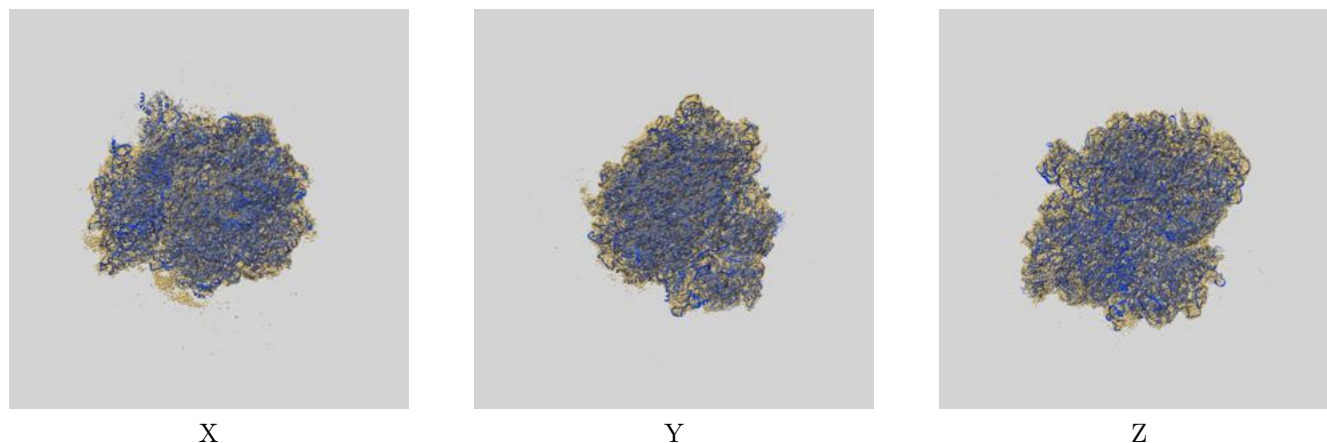
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.09	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.48	7.65	4.63

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.48 differs from the reported value 3.09 by more than 10 %

9 Map-model fit [i](#)

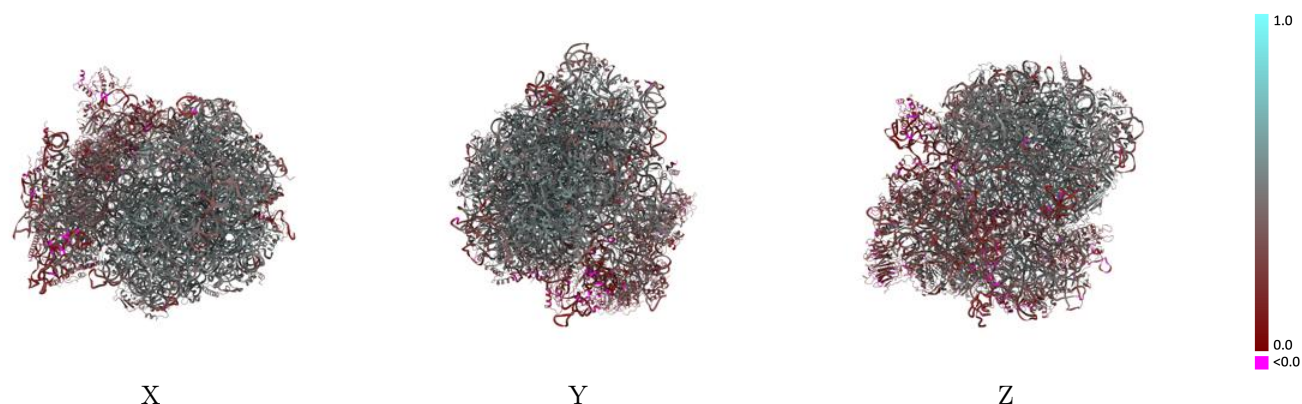
This section contains information regarding the fit between EMDB map EMD-41002 and PDB model 8T3F. Per-residue inclusion information can be found in section [3](#) on page [21](#).

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](#)

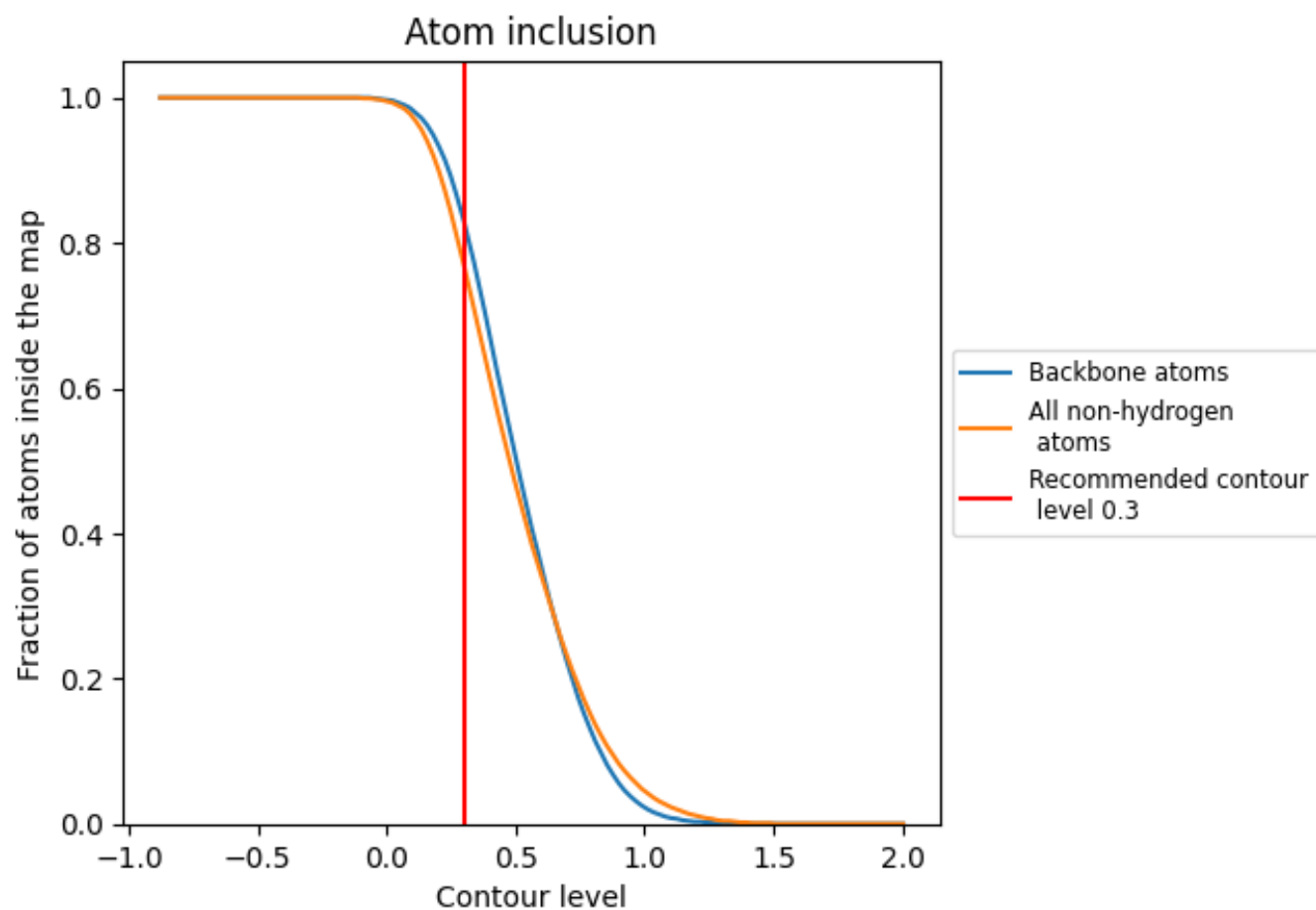


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7680	 0.4230
A1	 0.8870	 0.4700
A3	 0.9500	 0.4680
A4	 0.9280	 0.4940
AA	 0.7220	 0.5200
AB	 0.8030	 0.4980
AC	 0.8030	 0.4910
AD	 0.7870	 0.4190
AE	 0.7720	 0.4410
AF	 0.8350	 0.4970
AG	 0.7350	 0.4490
AH	 0.7290	 0.4740
AI	 0.6750	 0.4290
AJ	 0.6330	 0.3700
AL	 0.7980	 0.4950
AM	 0.8070	 0.4660
AN	 0.8090	 0.5280
AO	 0.7780	 0.4950
AP	 0.7700	 0.4960
AQ	 0.7930	 0.5060
AR	 0.6420	 0.4290
AS	 0.7910	 0.4920
AT	 0.7850	 0.4800
AU	 0.7740	 0.4140
AV	 0.6580	 0.4880
AW	 0.7720	 0.4980
AX	 0.7240	 0.4720
AY	 0.8000	 0.4860
AZ	 0.7770	 0.4580
Aa	 0.7970	 0.5050
Ab	 0.7210	 0.4690
Ac	 0.6880	 0.4570
Ad	 0.7730	 0.4790
Ae	 0.7760	 0.5120
Af	 0.8280	 0.5160



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Chain	Atom inclusion	Q-score
Ag	 0.7340	 0.4860
Ah	 0.8030	 0.4630
Ai	 0.7570	 0.4540
Aj	 0.8350	 0.5260
Ak	 0.4910	 0.3980
Al	 0.7730	 0.5150
Am	 0.7250	 0.4820
An	 0.6600	 0.4580
Ao	 0.6320	 0.4820
Ap	 0.7030	 0.5000
B5	 0.8180	 0.3860
BA	 0.6440	 0.3770
BB	 0.6110	 0.3750
BC	 0.7030	 0.4380
BD	 0.5360	 0.3220
BE	 0.7070	 0.4030
BF	 0.5680	 0.3480
BG	 0.6420	 0.3380
BH	 0.5540	 0.3370
BI	 0.6870	 0.3930
BJ	 0.6320	 0.2680
BK	 0.4960	 0.2650
BL	 0.6580	 0.4360
BM	 0.0650	 0.1910
BN	 0.6860	 0.4430
BO	 0.6550	 0.4250
BP	 0.3340	 0.2700
BQ	 0.6190	 0.3410
BR	 0.5010	 0.3020
BS	 0.5070	 0.2820
BT	 0.6670	 0.3070
BU	 0.5490	 0.3090
BV	 0.7000	 0.4070
BW	 0.7370	 0.4740
BX	 0.6840	 0.4680
BY	 0.6490	 0.3190
BZ	 0.6290	 0.2910
Ba	 0.7000	 0.4760
Bb	 0.6010	 0.3770
Bc	 0.5090	 0.3270
Bd	 0.6760	 0.3660
Be	 0.5580	 0.3660

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Chain	Atom inclusion	Q-score
Bf	 0.1030	 0.2130
Bg	 0.5570	 0.2540
DC	 0.3890	 0.2750
E	 0.3320	 0.1870
EC	 0.4670	 0.1530