



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:02 AM UTC

PDB ID : 8T3E / pdb_00008t3e
EMDB ID : EMD-41001
Title : Hypomethylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), eEF2, GDP, and sordarin, Structure IV
Authors : Zhao, Y.; Li, H.
Deposited on : 2023-06-07
Resolution : 3.04 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

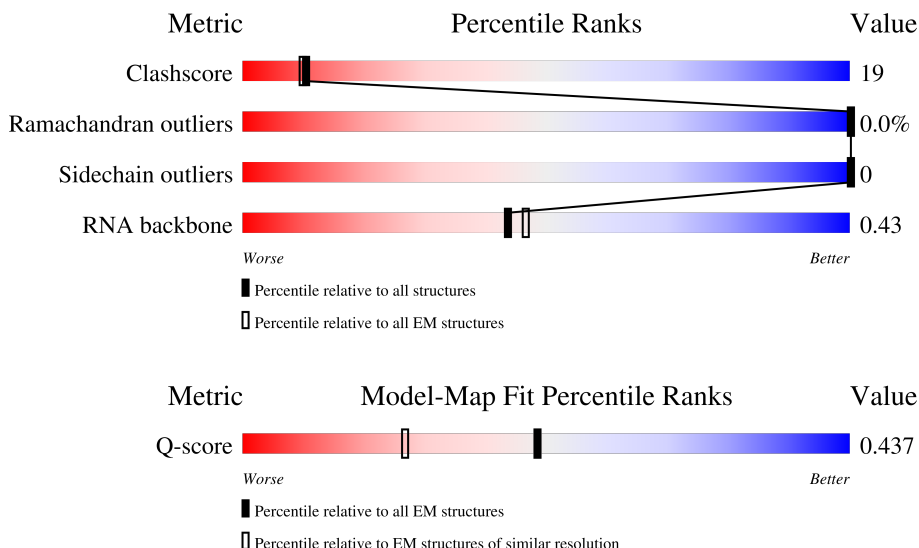
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.04 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	13952 (2.54 - 3.54)

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	3394	
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
85	SO1	DC	903	X	-	-	-

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 210978 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		

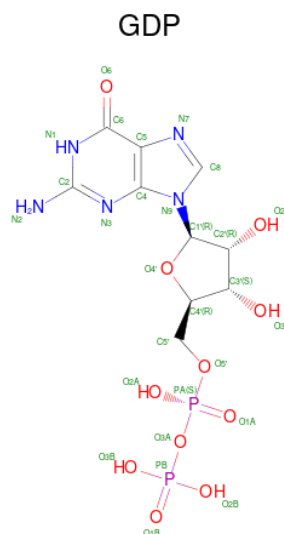
- Molecule 81 is a RNA chain called TSV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	EC	131	Total	C	N	O	P	0	0
			2764	1234	489	910	131		

- 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).

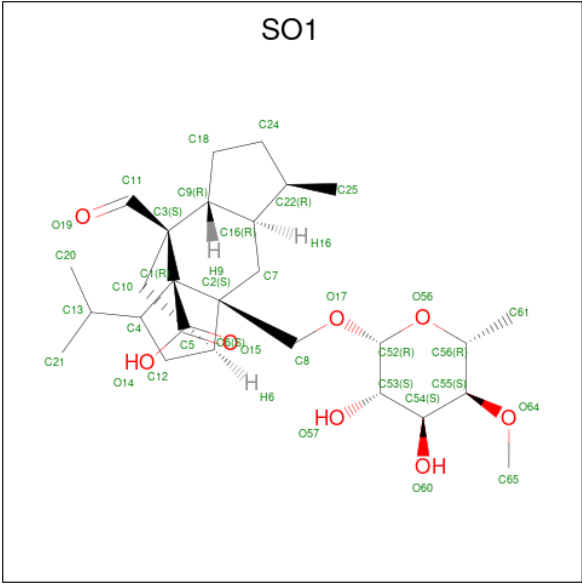


Mol	Chain	Residues	Atoms					AltConf
83	DC	1	Total 28	C 10	N 5	O 11	P 2	0

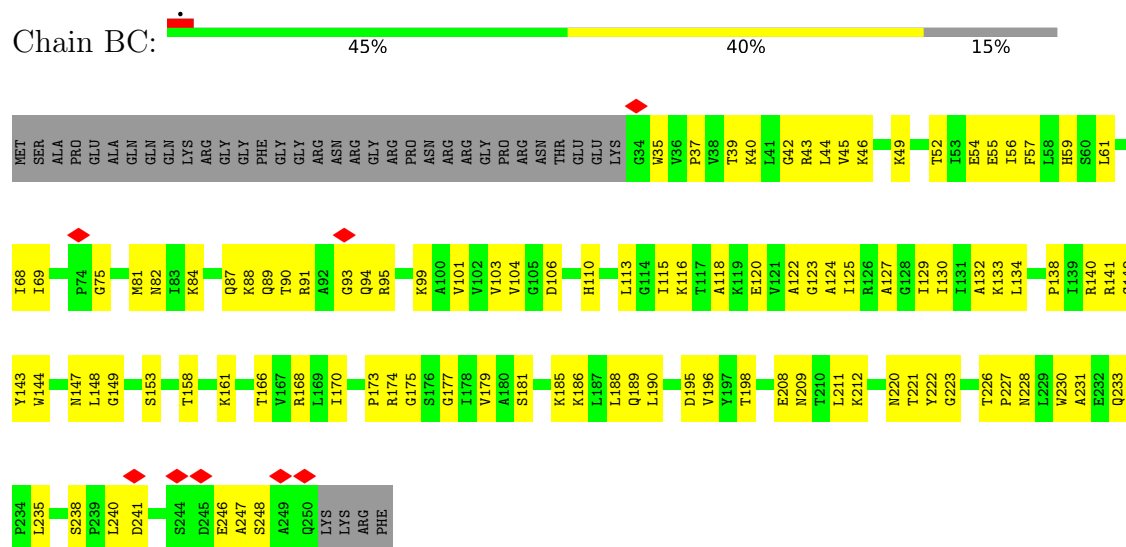
- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

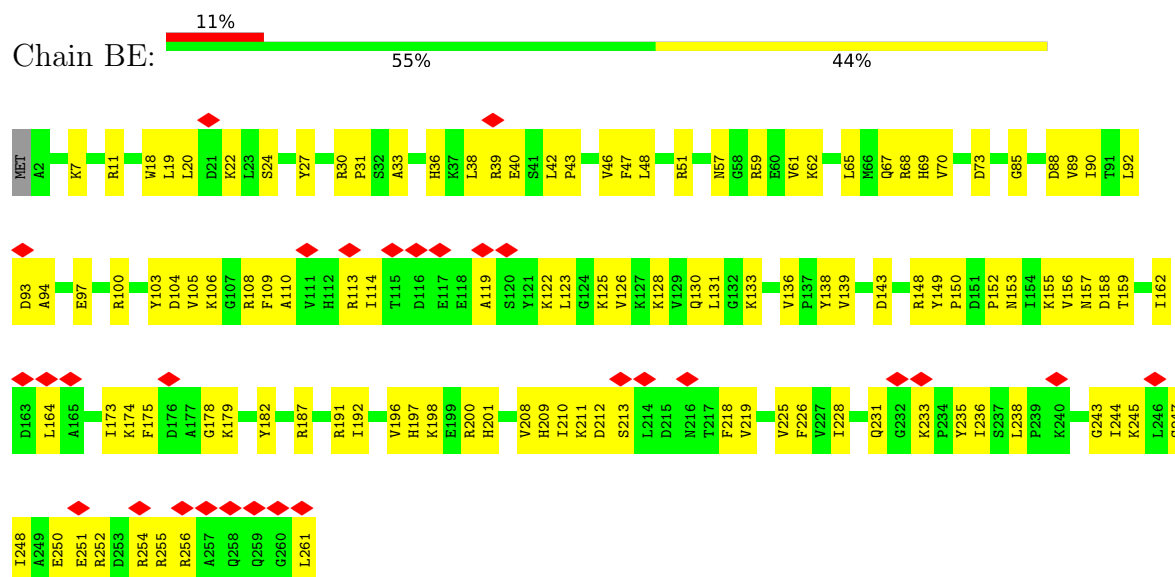
- Molecule 85 is [1R-(1.ALPHA.,3A.BETA.,4.BETA.,4A.BETA.,7.BETA.,7A.ALPHA.,8A.BETA.)]8A-[(6-DEOXY-4-O-METHYL-BETA-D-ALTROPYRANOSYLOXY)METHYL]-4-FORMYL-4,4A,5,6,7,7A,8,8A-OCTAHYDRO-7-METHYL-3-(1-METHYLETHYL)-1,4-METHANO-S-INDACENE-3A(1H)-CARBOXYLIC ACID (CCD ID: SO1) (formula: $C_{27}H_{42}O_8$).



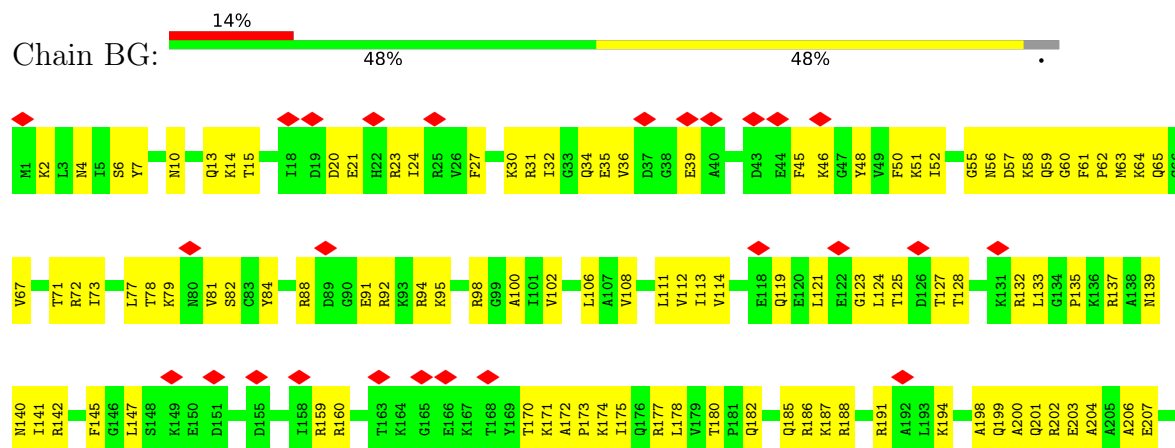
Mol	Chain	Residues	Atoms			AltConf
85	DC	1	Total	C	O	0
			35	27	8	



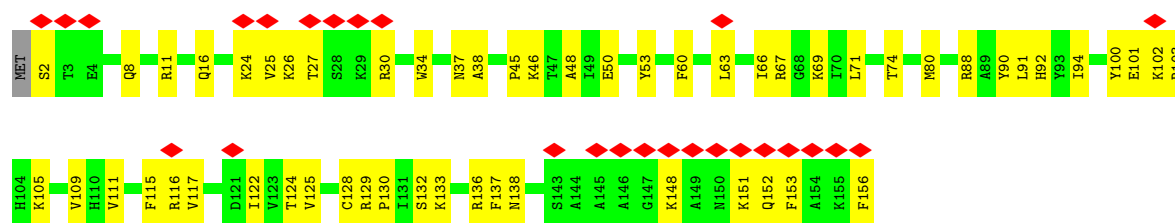
• Molecule 4: 40S ribosomal protein S4-A



• Molecule 5: 40S ribosomal protein S6-A

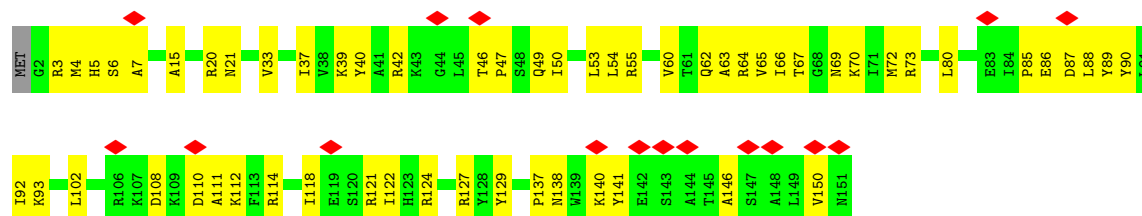


Chain BL: 17% 63% 36% .



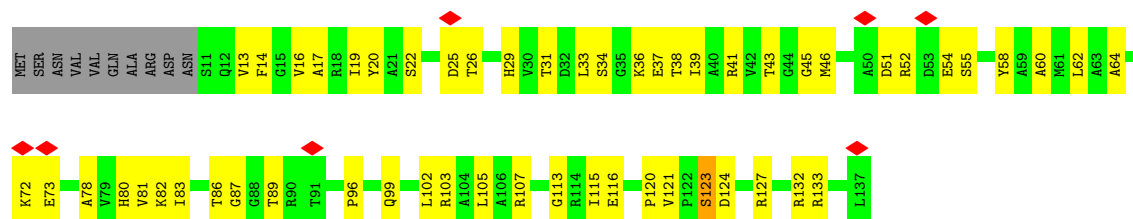
- Molecule 10: 40S ribosomal protein S13

Chain BN: 11% 61% 38% .



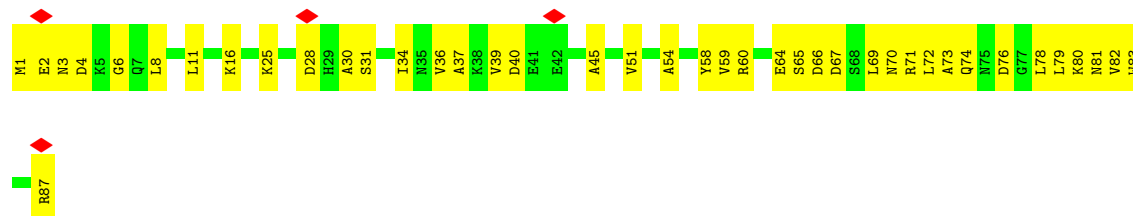
- Molecule 11: 40S ribosomal protein S14-A

Chain BO: 5% 53% 39% 7% .



- Molecule 12: 40S ribosomal protein S21-A

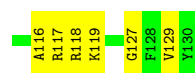
Chain BV: 5% 53% 47% .



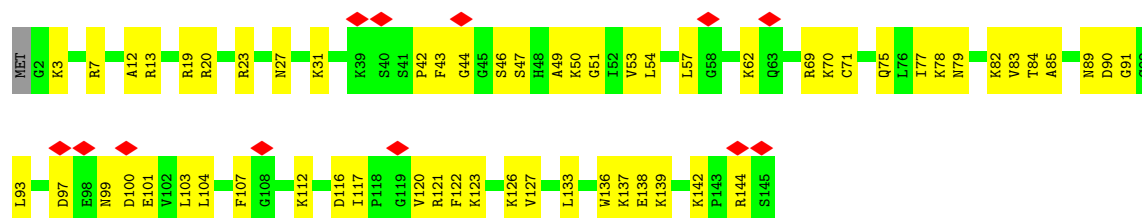
- Molecule 13: RPS22A isoform 1

Chain BW: 68% 32% .

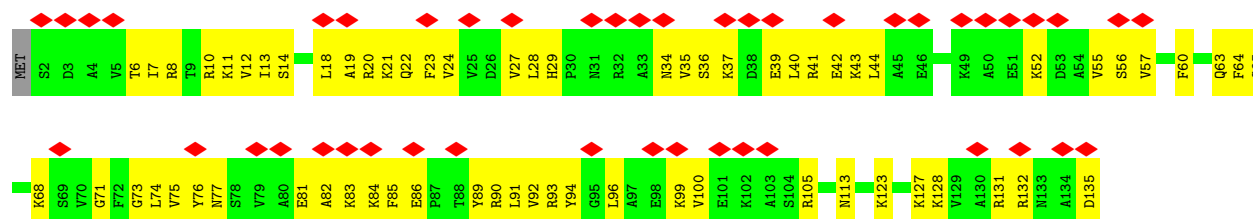




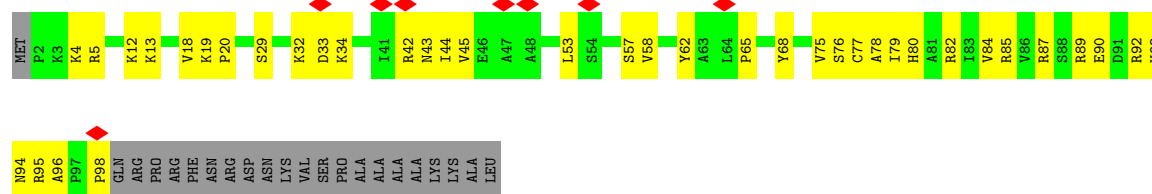
- Molecule 14: 40S ribosomal protein S23-A



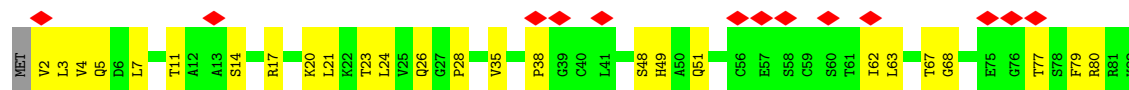
- Molecule 15: 40S ribosomal protein S24-A



- Molecule 16: RPS26B isoform 1

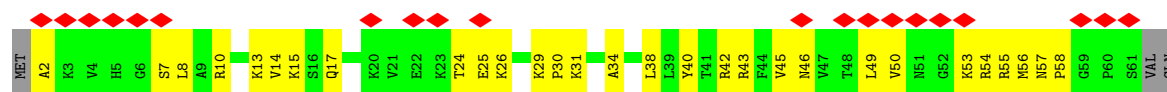


- Molecule 17: 40S ribosomal protein S27-A

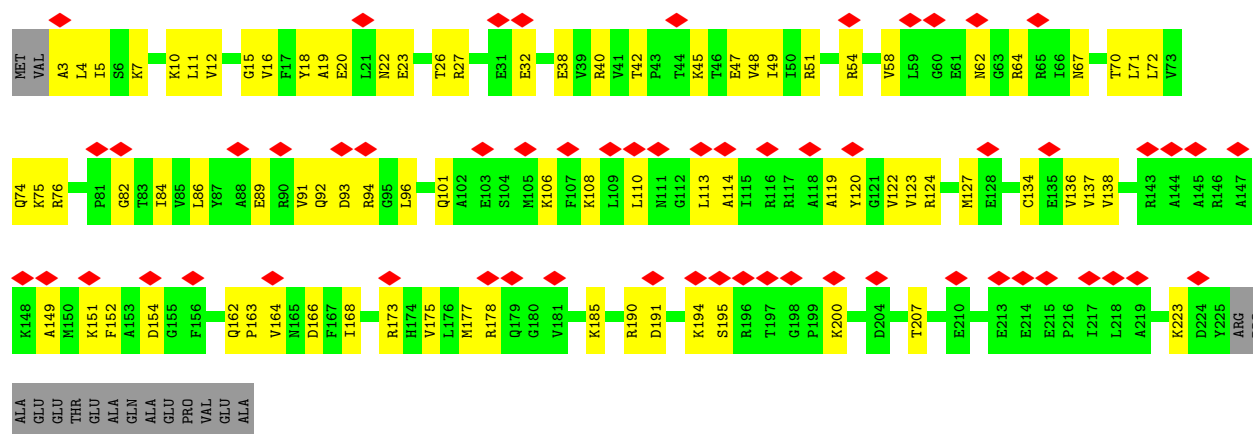


- Molecule 18: 40S ribosomal protein S30-A

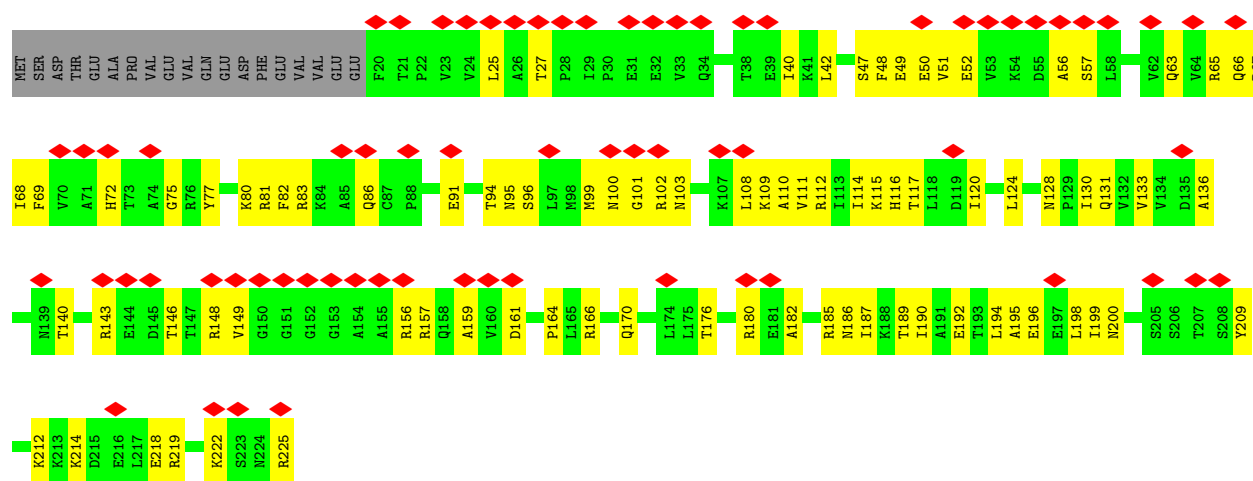




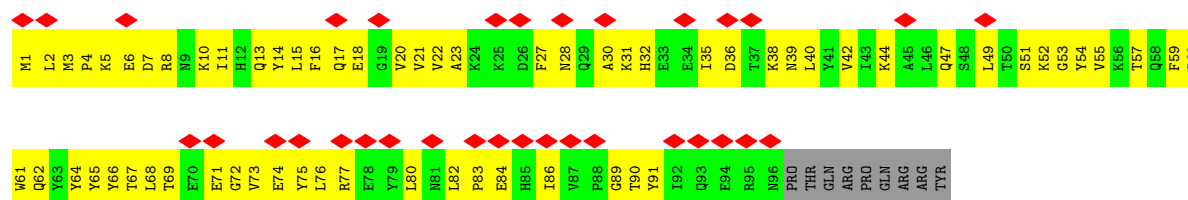
• Molecule 19: RPS3 isoform 1



• Molecule 20: Rps5p

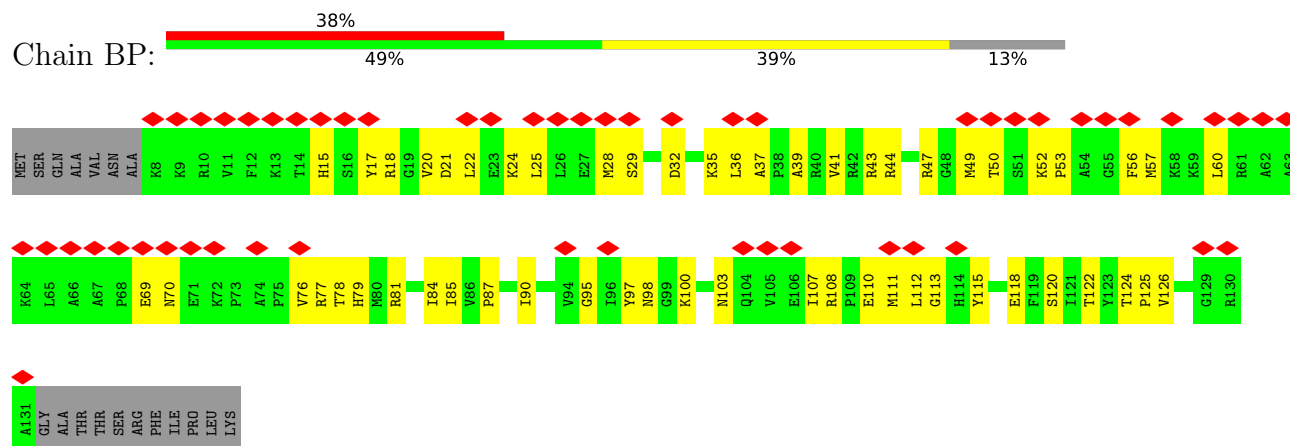


• Molecule 21: 40S ribosomal protein S10-A



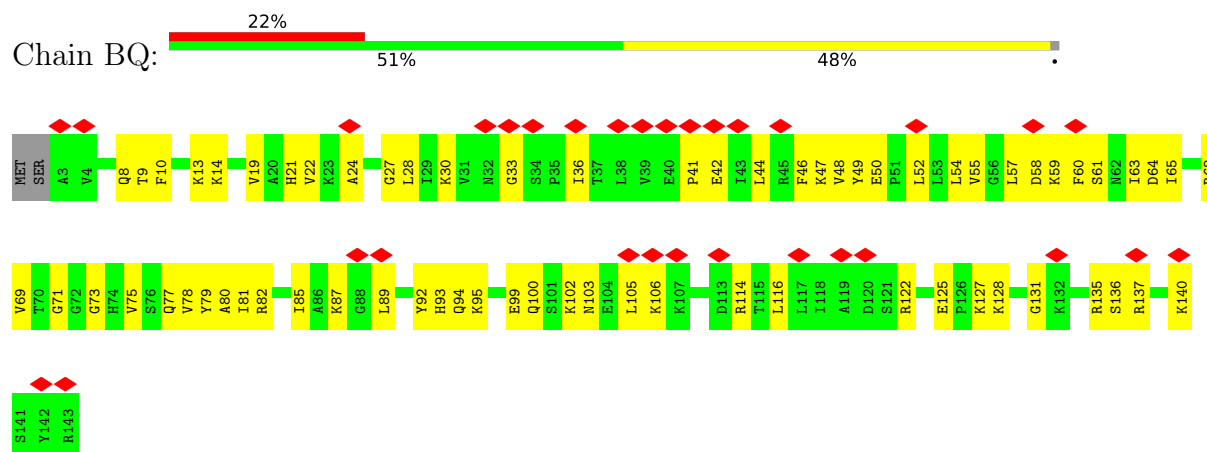
- Molecule 22: RPS15 isoform 1

Chain BP:



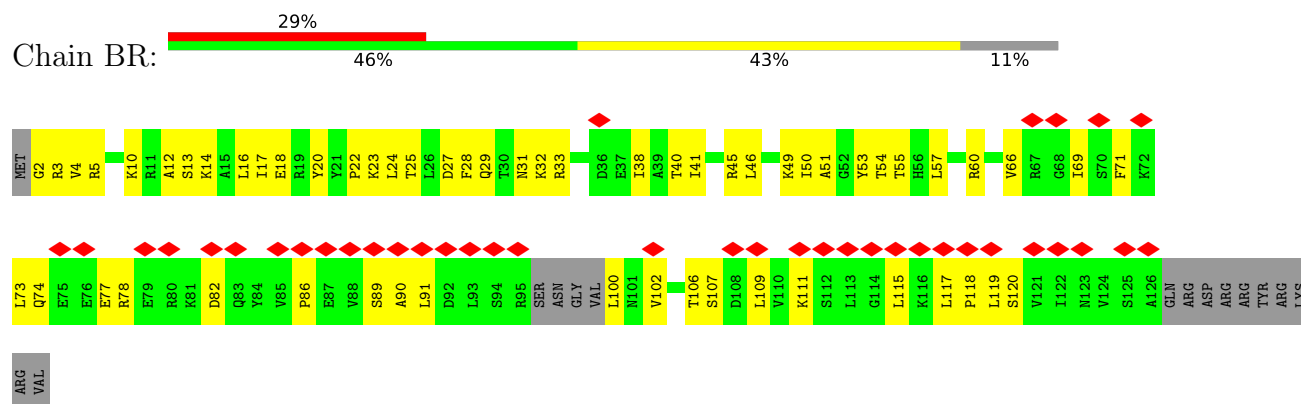
- Molecule 23: 40S ribosomal protein S16-A

Chain BQ:



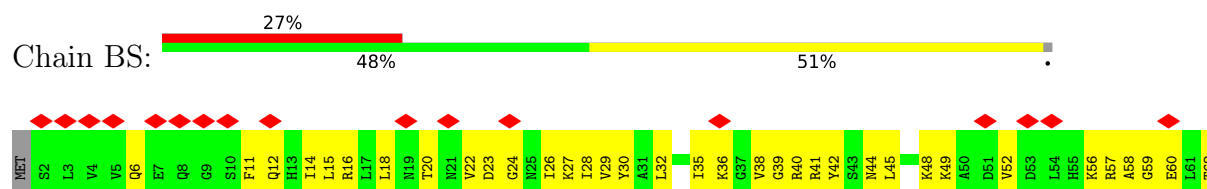
- Molecule 24: 40S ribosomal protein S17-A

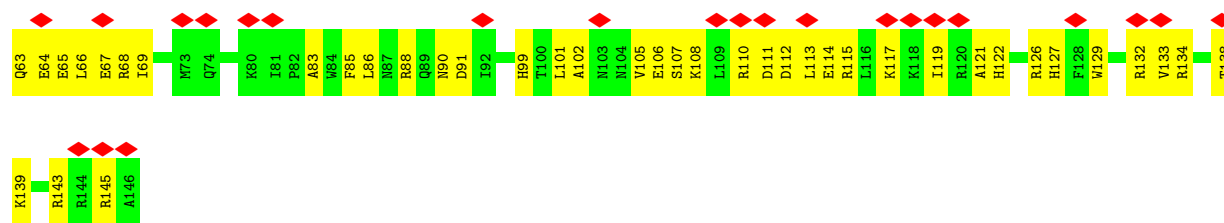
Chain BR:



- Molecule 25: 40S ribosomal protein S18-A

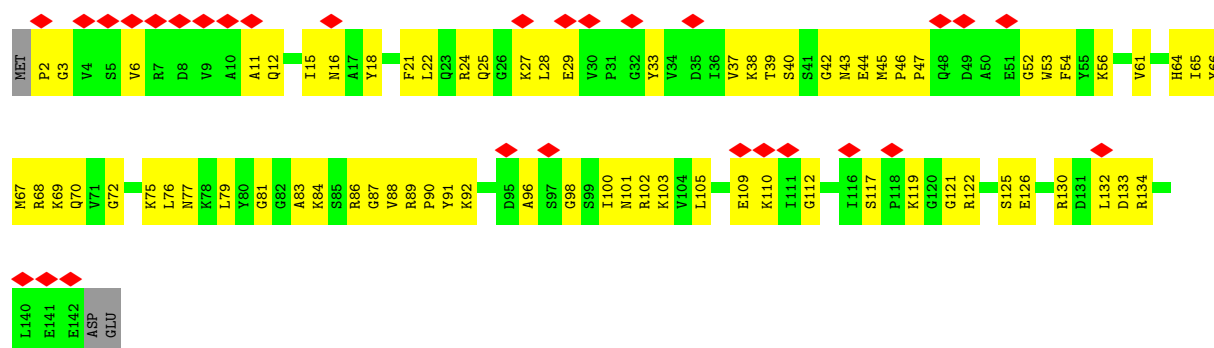
Chain BS:





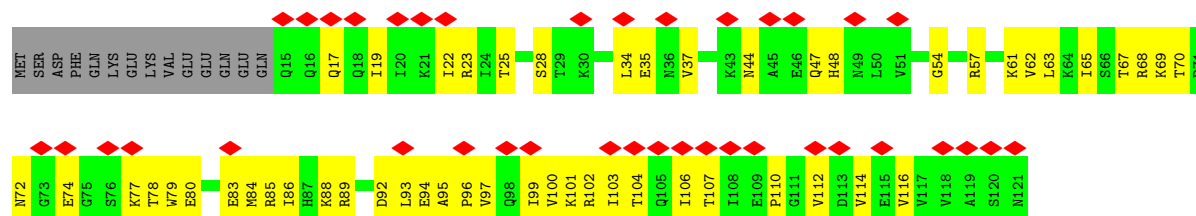
• Molecule 26: 40S ribosomal protein S19-A

Chain BT:



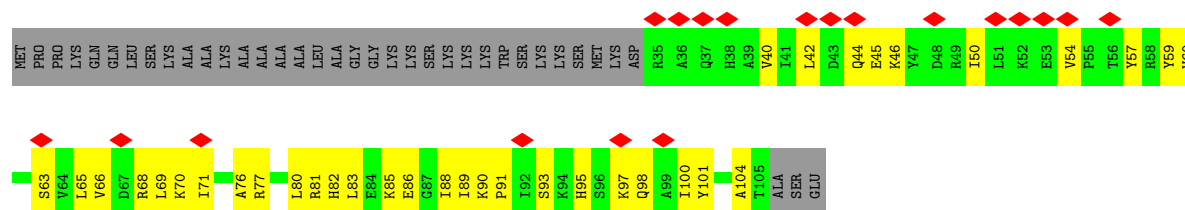
• Molecule 27: RPS20 isoform 1

Chain BU:



• Molecule 28: RPS25A isoform 1

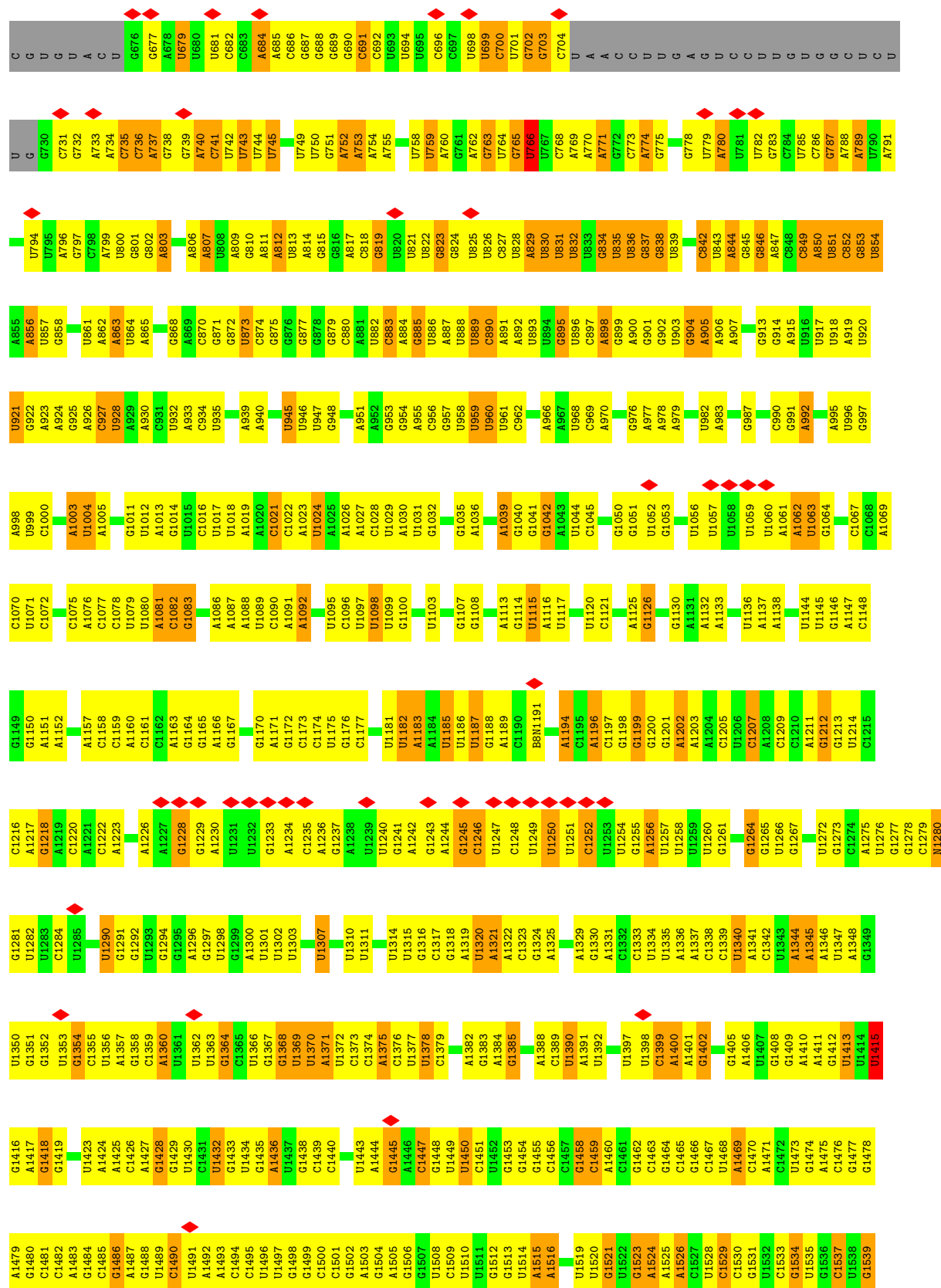
Chain BZ:

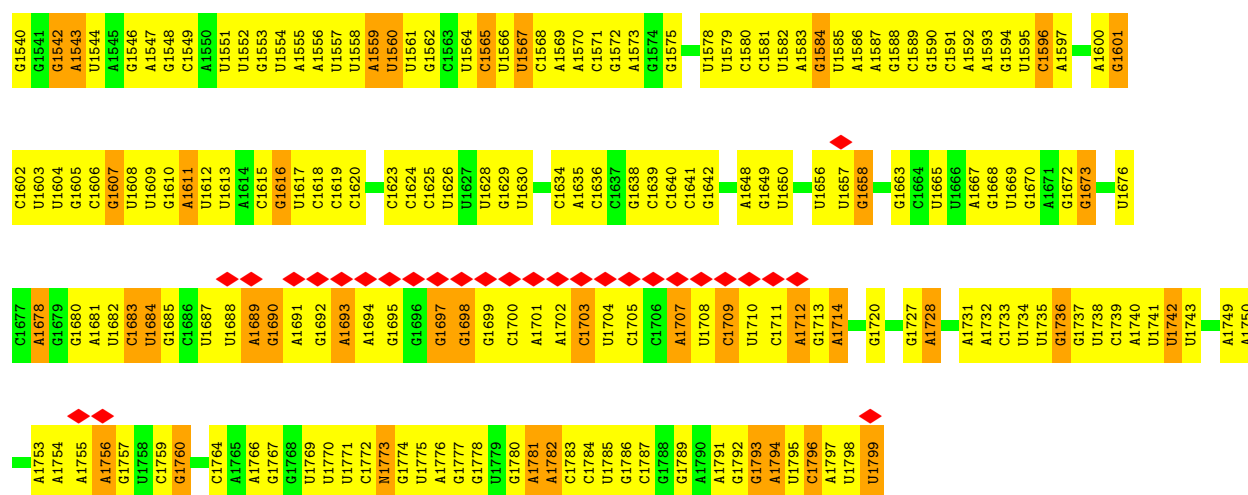


• Molecule 29: RPS28A isoform 1

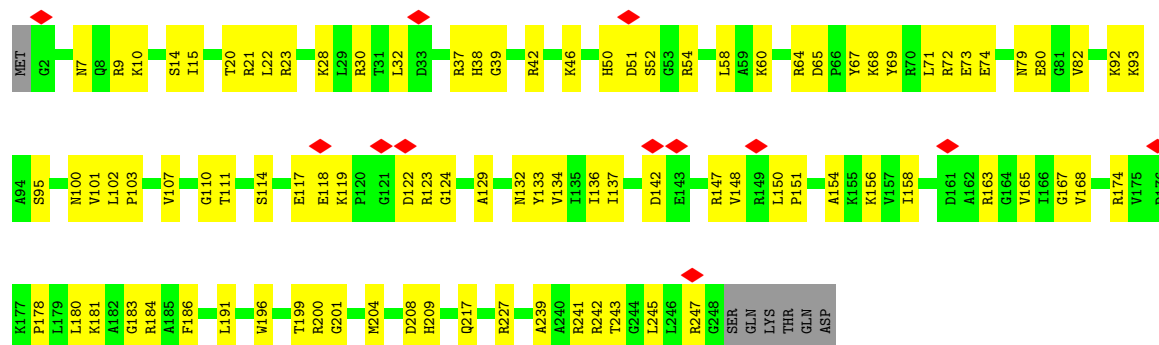
Chain Bc:



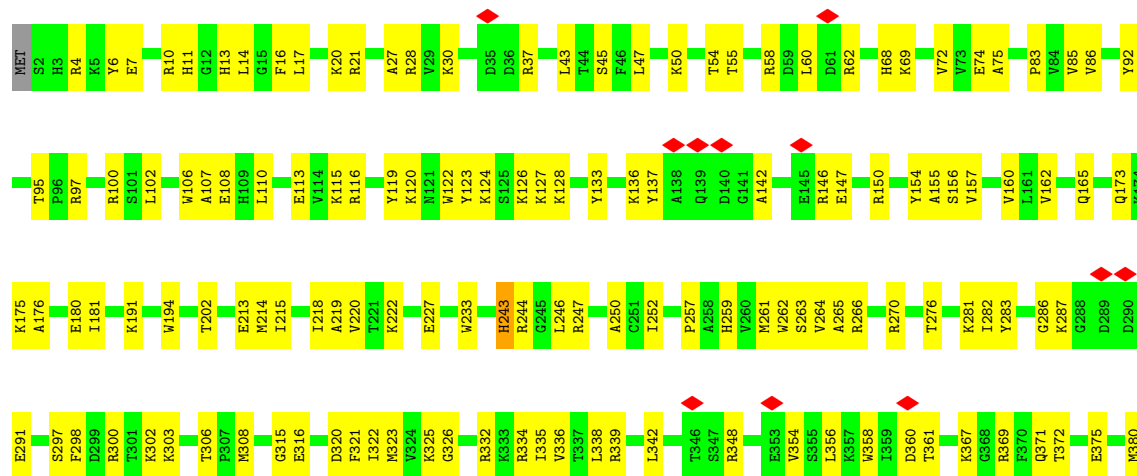




• Molecule 35: 60S ribosomal protein L2-A



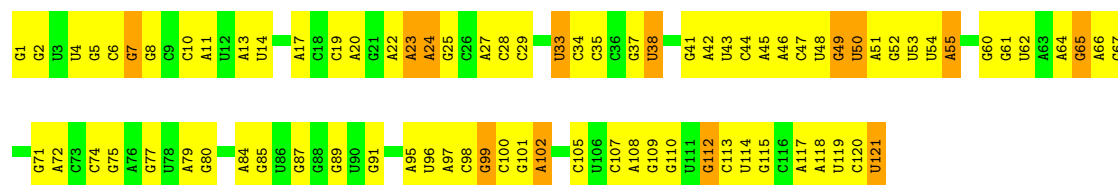
• Molecule 36: 60S ribosomal protein L3



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G1437	G1357	G1289	C1227	A1153	A1084	G1018	U946	C851	U766	U766	U766	U623	C562	C499
U1438	C1358	A1290	G1228	A1154	A1085	G1019	G947	G853	U852	U852	U852	G624	U563	C500
U1439	C1359	A1291	G1229	A1155	C1086	G1020	C948	U854	C768	C768	C768	G625	U564	A501
G1440	C1360	U1292	G1230	C1156	U1087	G1021	C949	G860	C769	C769	C769	U626	U565	U502
G1441	U1293	U1293	A1231	C1157	U1088	U1022	C950	C861	C770	C770	C770	U627	U566	C503
G1442	C1364	G1295	G1232	G1157	G1089	U1023	A951	U871	C771	C771	C771	A628	U567	A504
G1443	G1365	G1296	G1233	A1158	C1092	C1023	A952	U872	C772	C772	C772	U631	U568	G505
G1444	C1366	U1297	G1235	U1167	A1093	G	C959	C873	C773	C773	C773	G632	U569	U506
U1445	G1367	U1298	G1236	U1168	U1094	A	U960	U874	C774	C774	C774	G633	U570	U507
U1446	C1368	C1298	G1237	U1169	U1095	A	U961	U875	C775	C775	C775	C634	U571	U508
G1447	A1369	G1300	U1238	A1170	U1096	U	G964	A876	U776	U776	U776	U637	U572	U512
U1448	G1370	A1301	C1239	G1171	G1097	G	A965	U877	U777	U777	U777	C637	C573	U574
A1449	G1374	A1304	A1240	G1172	A1098	A1030	A966	U879	A780	A780	A780	C638	C575	C515
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A1456	U1376	G1306	G1242	G1177	A1103	C1032	A968	G881	U782	U782	U782	U640	C577	G517
U1457	G1379	G1307	G1243	G1178	G1104	U1033	C969	A882	A783	A783	A783	U643	A578	G518
G1458	G1382	A1308	A1244	A1180	A1105	U1034	A970	G887	A785	A785	A785	U644	A579	A519
C1459	G1383	U1309	A1245	U1181	G1106	U1035	G971	A888	A786	A786	A786	A645	C580	U520
A1460	U1384	G1310	G1246	A1182	C1107	A1036	A972	U889	A787	A787	A787	A649	A521	A521
A1461	C1385	C1312	U1247	C1183	U1108	A1037	A973	C890	C788	C788	C788	C650	A522	A522
U1462	A1386	U1315	C1248	A1184	U1109	C1038	G974	G891	A789	A789	A789	C651	U524	U524
U1463	G1387	G1249	G1250	C1185	U1110	C1039	A980	G894	U790	U790	U790	C655	C525	C525
G1464	U1388	A1251	A1251	C1186	U1111	A1040	U981	G895	A791	A791	A791	C657	C526	C526
A1467	G1389	G1321	A1252	C1187	U1112	U1041	C982	A895	C792	C792	C792	A657	U527	A527
U1471	C1390	U1322	G1253	U1188	G1115	C1042	A983	A896	C793	C793	C793	U662	U528	U528
U1472	G1392	G1323	U1254	C1189	G1116	C1043	G984	U899	U796	U796	U796	C663	A529	A529
G1473	A1393	U1324	C1255	U1191	G1117	U1044	U985	G901	U797	U797	U797	C664	G530	G530
A1474	C1394	U1325	G1256	C1192	C1118	A1045	U986	A904	A806	A806	A806	A665	A532	A532
A1475	G1395	C1257	C1257	A1193	U1119	A1046	U987	G907	A807	A807	A807	A666	A533	A533
G1476	C1396	U1329	U1258	A1194	U1120	U1047	U988	G908	A808	A808	A808	C667	U534	U534
C1397	U1330	U1331	U1259	A1195	U1121	C1049	A989	U909	C732	C732	C732	U668	G535	G535
U1398	A1332	U1332	A1260	C1196	U1122	U1050	U990	G910	C733	C733	C733	U669	U536	U536
G1400	C1333	G1261	G1261	A1200	U1123	U1051	G991	C907	C734	C734	C734	U671	A537	A537
G1404	U1334	G1262	G1262	C1201	U1124	U1052	G992	G908	A735	A735	A735	U672	G538	G538
U1407	U1335	A1263	A1263	C1202	G1125	A1055	G993	G909	U741	U741	U741	A673	C539	C539
U1408	G1336	G1264	G1264	A1203	G1126	U1056	U994	C911	U742	U742	U742	U674	U540	U540
U1409	U1337	U1265	U1265	A1204	U1127	U1056	U995	C912	C743	C743	C743	G675	G542	G542
U1410	C1338	G1266	G1266	U1208	U1128	U1060	A996	A913	A744	A744	A744	G676	C543	C543
C1411	G1339	U1267	U1267	G1209	A1129	A1061	A997	A914	C745	C745	C745	A677	U544	U544
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G1417	G1345	C1272	C1272	G1213	A1136	A1065	U1001	A921	U750	U750	U750	U682	G548	G548
U1418	U1346	C1273	C1273	U1214	G1137	U1066	U1002	U922	A751	A751	A751	U683	U549	U549
A1419	U1347	A1274	A1274	U1218	U1138	C1069	A1003	C923	G754	G754	G754	U684	A550	A550
U1423	U1348	G1275	G1275	U1219	U1139	U1070	U1004	G924	A755	A755	A755	G685	G552	G552
C1424	G1349	C1279	C1279	U1220	U1140	U1071	U1007	A929	C758	C758	C758	U687	U553	U553
U1425	U1350	G1280	G1280	U1221	G1141	U1072	U1008	A937	U759	U759	U759	G688	A554	A554
U1426	U1351	U1281	U1281	G1222	G1142	U1073	A1009	G837	G617	G617	G617	U689	U555	U555
U1427	A1352	G1282	G1282	G1223	A1143	U1074	G1010	C938	C618	C618	C618	A691	U556	U556
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U1436	U1355	A1285	A1285	U1287	U1080	U1081	U1015	U1016	C949	C949	C949	C694	A559	A559
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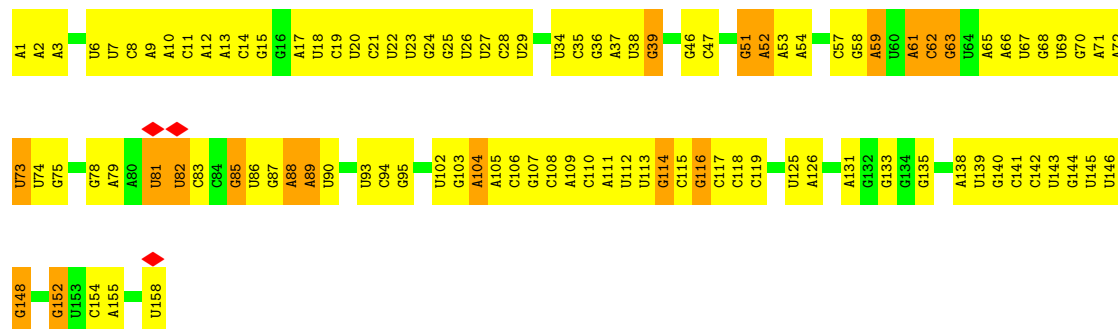
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A2456		G2305	A2228	A2158	A	A		A1748	C1865	G1591	U1518
G2457	A2386	C2306	A2229	U2159	A	A	A1813	G1749	G1666	G1592	G1519
A2458		G2307		G2160	U	U	A1814	A1890	A1667	A1593	G1520
A2459	C2389	C2308	A2232	G2161	U	U	U1815	A1891	A1668	A1594	G1521
U2460	A2390	A2309	A2233		A	U	A1816	A1752	U1595	U1595	U1522
A2461	G2311	U2310		A2168	G	G	G1817	G1753	A1676	C1596	G1523
A2462	G2312	G2169	G2239	C2169	C	A	U1818	C1754	G1677	G1597	U1524
G2463	A2313	G2096	A2243	G2170	G	C	U1819	C1755	G1680	G1598	
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G2465	G2315	U2097		U2172	C	C	U1821	G1757	U1682	U1601	
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G2467	A2321	A2099	G2250	U2174	C	C	C1822	C1759	U1684	U1533	U1534
A2468	C2322	A2100		U2175	C	C	U1823		U1685	A1535	
G2469	G2323	U2101	G2251	G2176	U	U	U1824	A1760	U1686	U1606	G1536
A2470	A2324	U2102	A2252	A2177	U	U	G1825	C1761	U1687	U1607	
U2471	G2325	U2103	C2179	C2178	U	C	C1826	C1762	U1688	C1608	A1539
U2472	A2326	U2104	G2180	C2179	U	C	U1827	U1763	U1689		
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G2474	C2329	A2107	A2182	A2183	U	U	U1829	U1765	U1691	G1612	G1543
G2475	C2330	G2111	G2185	U2184	A	G	G1830	U1766	U1692	A1613	G1544
A2476	C2331	U2112	U2186	G2186	G	C	C1831	C1767	U1693	C1614	
G2477	A2332	A2113	G2187	U2187	C	U	U1832	U1768	U1694	C1615	
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G2481	U2340	U2266	C2192	U2192	U	A	U1836	C1772	U1703	U1553	
U2482	A2341	C2267	U2193	U2193	U	C	A1839	C1773	U1554	U1555	
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A2491	G2434	A2131	A2131	G1947	C	C	G1861	U1782	U1567	U1567	
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A2494	A2438	U2137	U2137	U1950	U	U	A1864	G1789	U1570	C1639	
C2495	U2439	U2140	U2140	C1951	A	A	G1865	U1790	A1571	G1640	
G2496	G2440	U2141	U2141	G1952	G	G	C1866	C1791	U1572	U1641	
U2497	A2441	A2142	A2142	U1953	A	C	A1867	C1792	G1573	A1642	
U2498	G2442	A2143	A2143	G1954	C	C	G1868	G1793	C1574	A1643	
U2499	A2443	A2144	A2144	U	C	U	U1868	U1794	A1575	U1644	
A2500	C2444	G2216	G2216	A	G	U	U1873	U1795	G1576	U1645	
U2501	A2445	U2217	U2217	G	U	C	A1874	U1796	G1577	G1646	
U2502	U2446	G2218	G2218	U	C	C	U1875	A1797	C1578	C1578	
G2503	A2447	A2146	A2146	C	C	U	A1876	U1798	A1580	A1580	
U2504	G2371	U2219	U2219	C	A	A	G1878	A1799	G1658	U1659	
U2505	A2372	A2220	A2220	U	C	C	U1879	A1800	U1740	C1581	
U2506	A2373	G2221	G2221	G	G	G	A1880	U1799	U1742	G1582	
C2507	C2374	A2222	A2222	U	C	C	U1881	U1800	G1743	A1583	
U2508	G2375	A2223	A2223	C	C	C	A1884	C1803	G1744	G1661	
U2509		A2224	A2224	C	C	C	U1885	C1804	C1745	G1662	
U2510		U2225	U2225	U	G	G		C1805		G1586	
A2511					U	U		A1806		A1587	
C2512					G	G				A1588	
U2513											





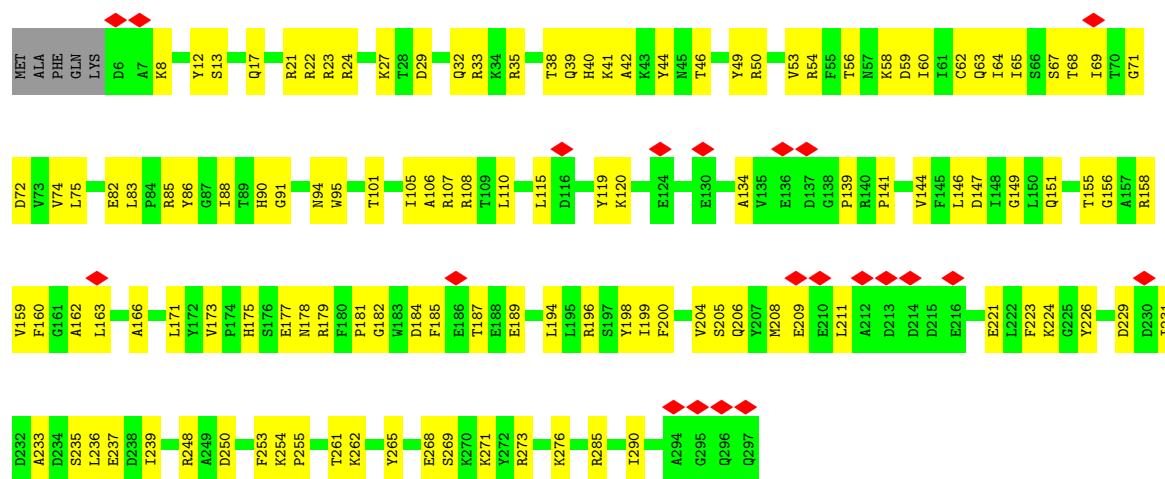
• Molecule 40: 5.8 S rRNA

Chain A4: 32% 56% 11%



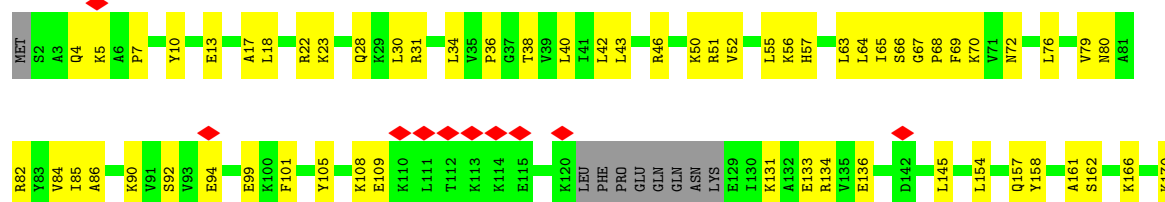
• Molecule 41: RPL5 isoform 1

Chain AD: 7% 57% 41%



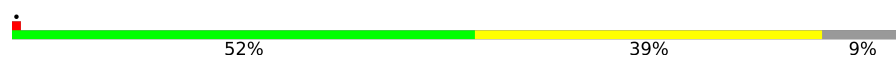
• Molecule 42: 60S ribosomal protein L6-A

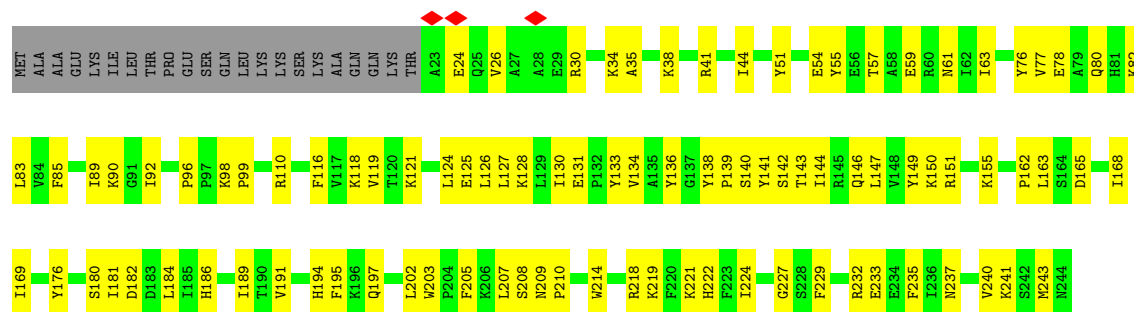
Chain AE: 6% 58% 37% 5%



P171
H172
M173
L174
K176
E176

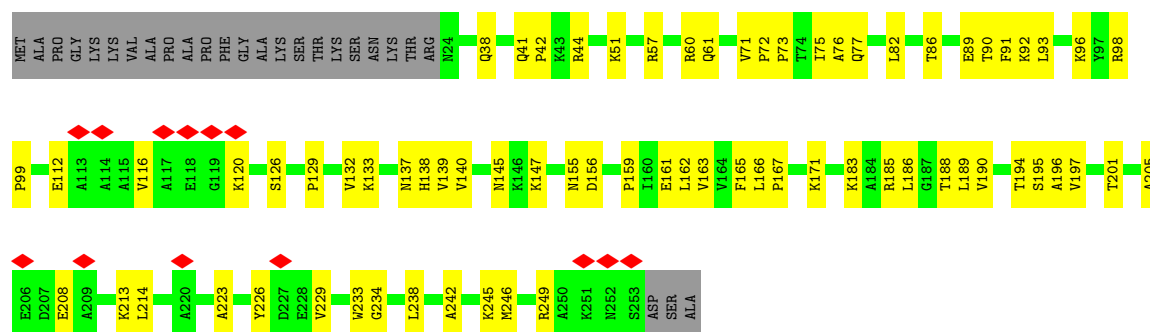
• Molecule 43: 60S ribosomal protein L7-A

Chain AF:  52% 39% 9%



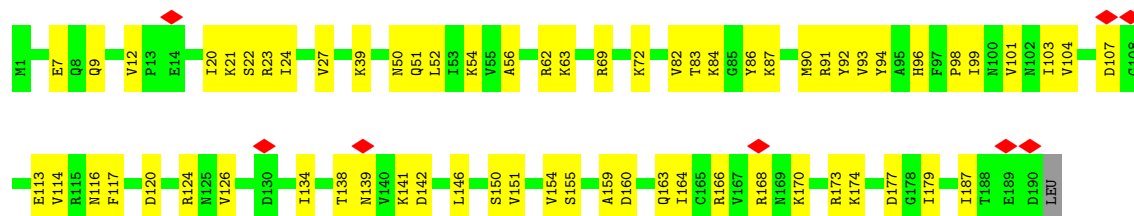
• Molecule 44: 60S ribosomal protein L8-A

Chain AG:  5% 62% 28% 10%



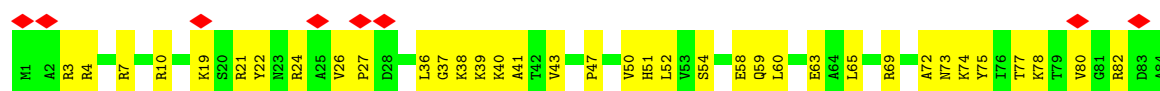
• Molecule 45: 60S ribosomal protein L9-A

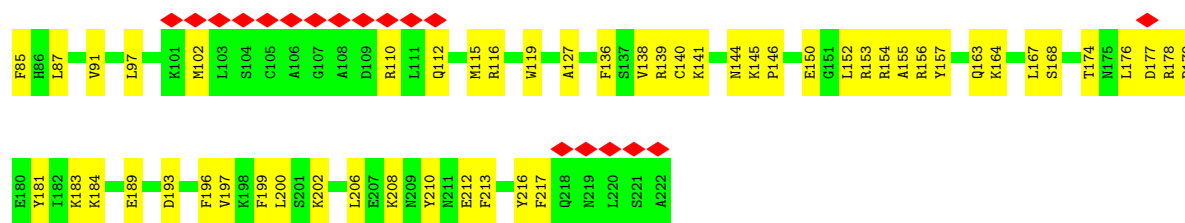
Chain AH:  65% 34%



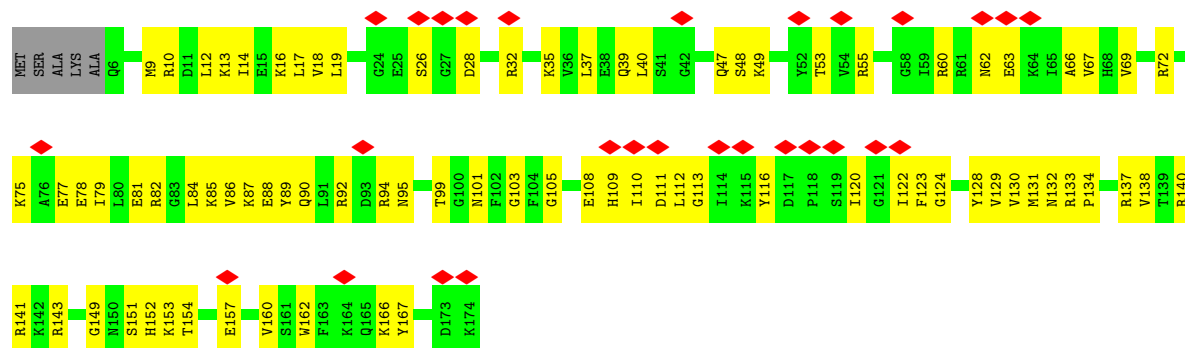
• Molecule 46: 60S ribosomal protein L10

Chain AI:  12% 60% 40%

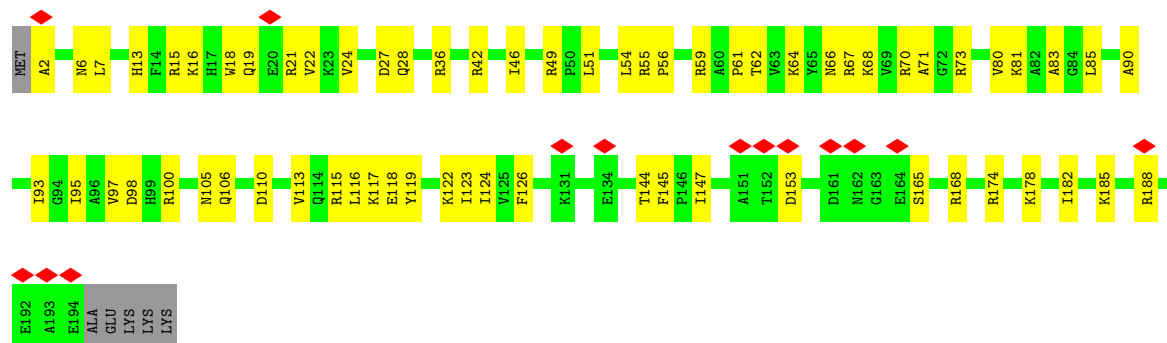




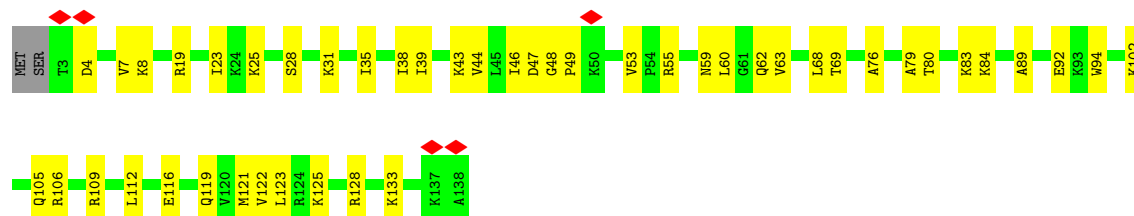
• Molecule 47: RPL11A isoform 1



• Molecule 48: 60S ribosomal protein L13-A



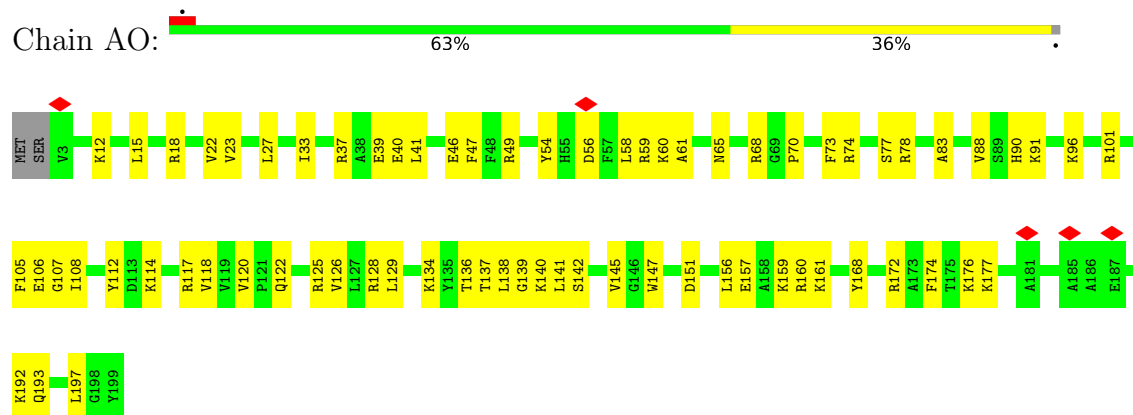
• Molecule 49: 60S ribosomal protein L14-A



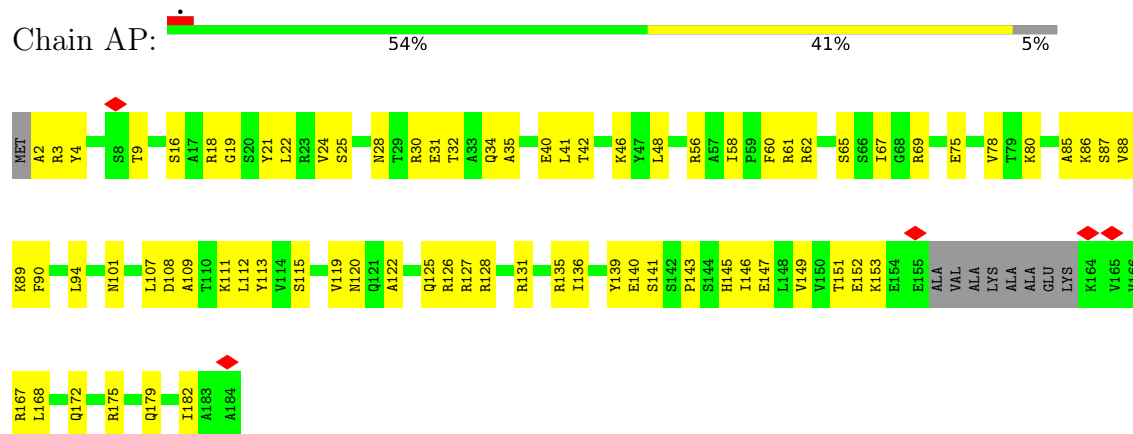
• Molecule 50: 60S ribosomal protein L15-A



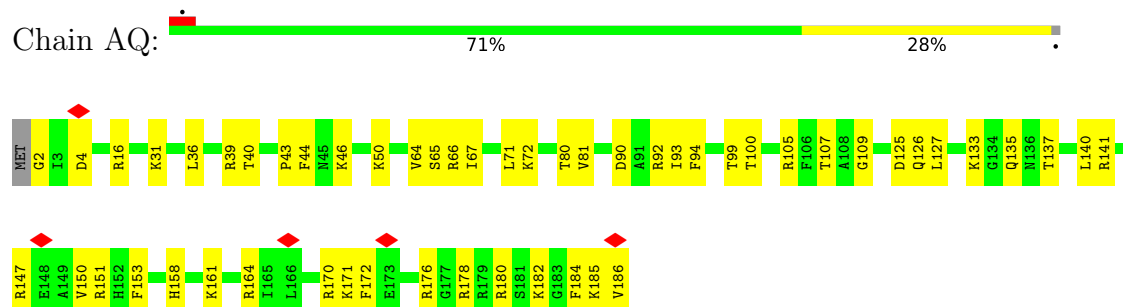
• Molecule 51: 60S ribosomal protein L16-A



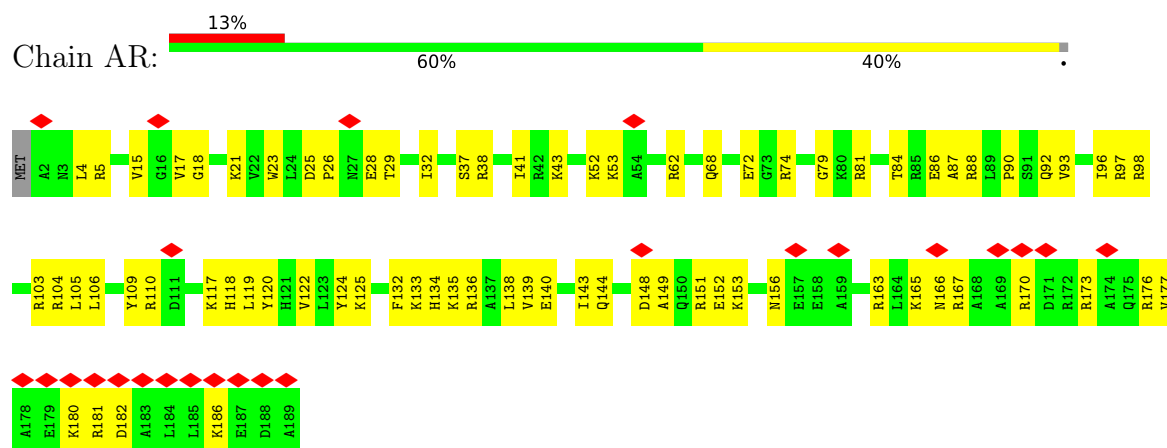
• Molecule 52: 60S ribosomal protein L17-A



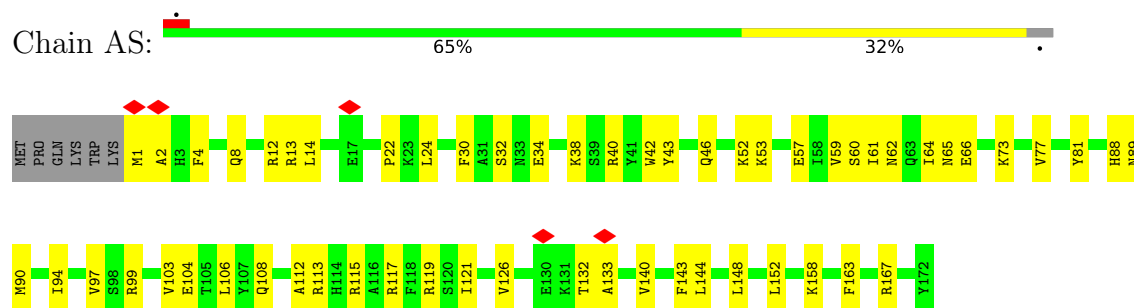
• Molecule 53: 60S ribosomal protein L18-A



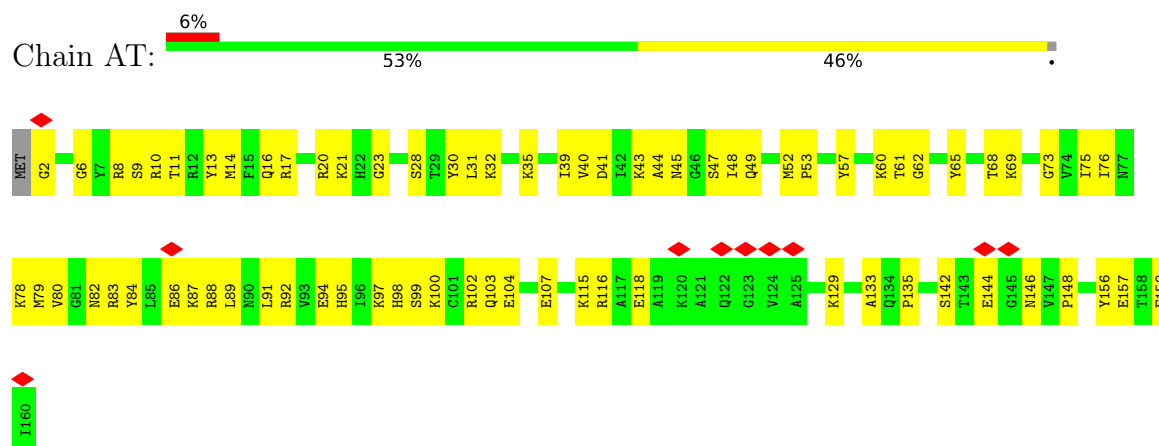
- Molecule 54: 60S ribosomal protein L19-A



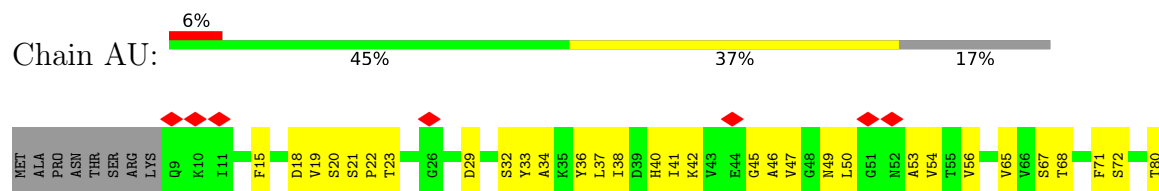
- Molecule 55: 60S ribosomal protein L20



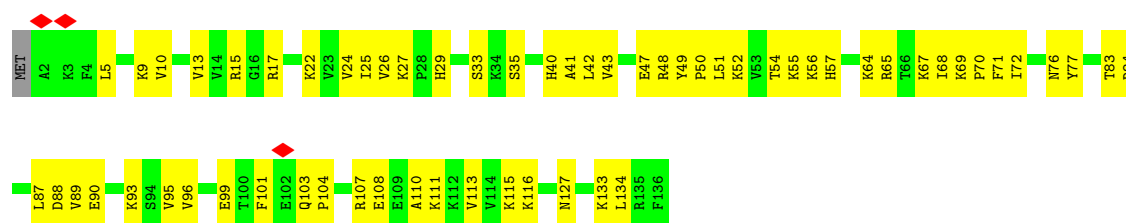
- Molecule 56: 60S ribosomal protein L21-A



- Molecule 57: 60S ribosomal protein L22-A

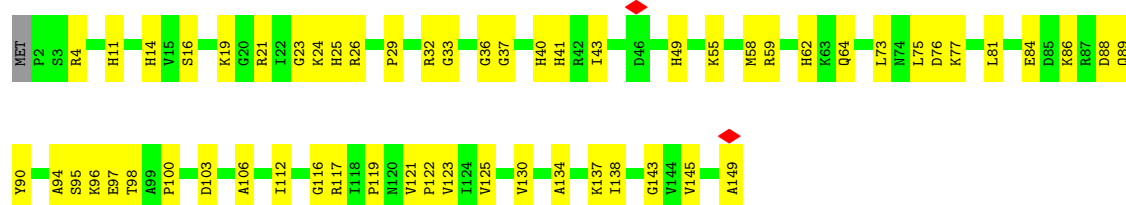


Chain AZ: 



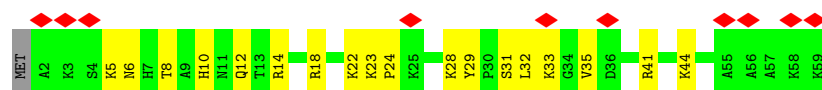
- Molecule 63: 60S ribosomal protein L28

Chain Aa: 



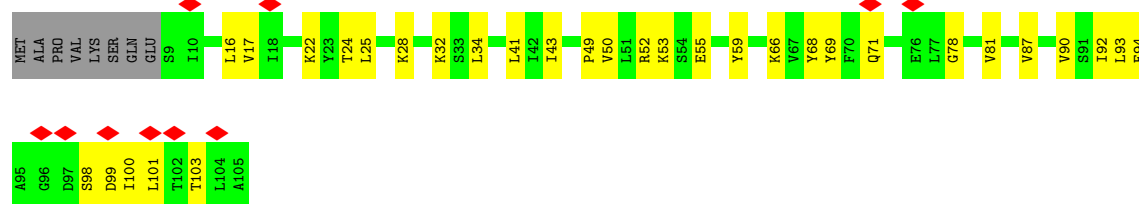
- Molecule 64: RPL29 isoform 1

Chain Ab: 



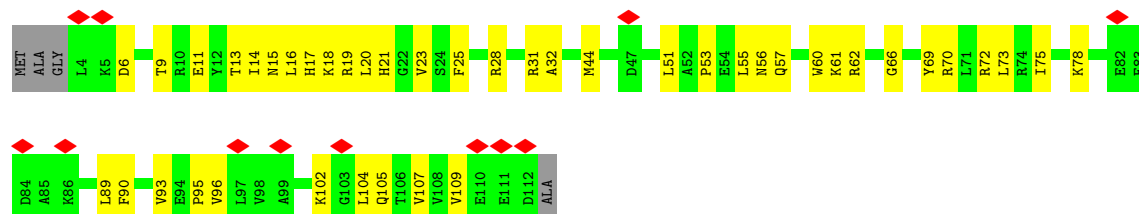
- Molecule 65: 60S ribosomal protein L30

Chain Ac: 

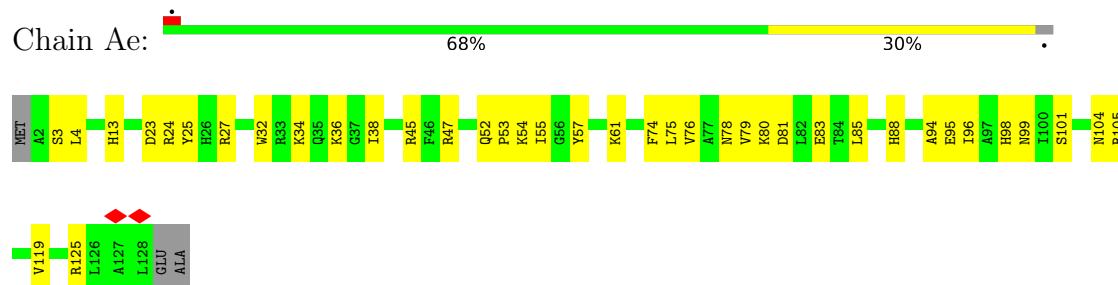


- Molecule 66: 60S ribosomal protein L31-A

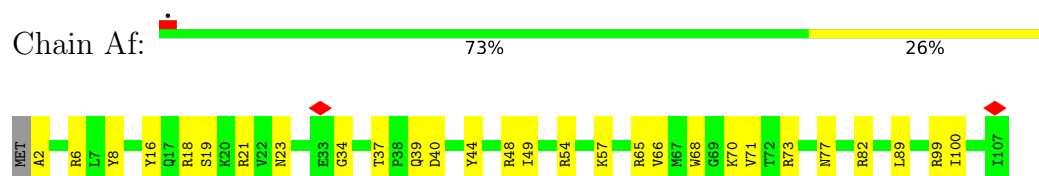
Chain Ad: 



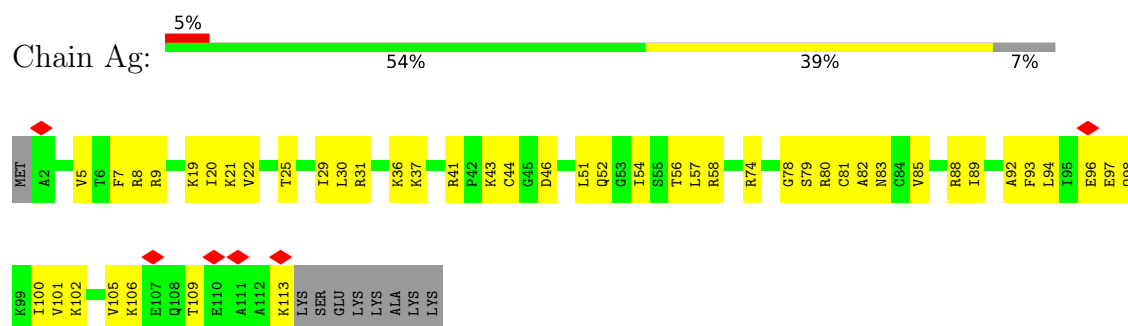
- Molecule 67: RPL32 isoform 1



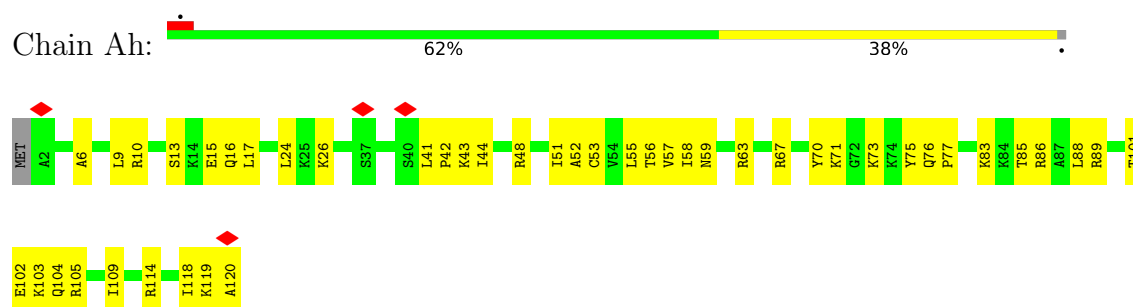
- Molecule 68: 60S ribosomal protein L33-A



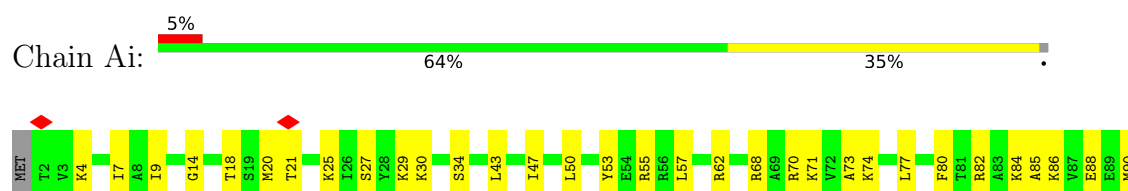
- Molecule 69: 60S ribosomal protein L34-A



- Molecule 70: 60S ribosomal protein L35-A

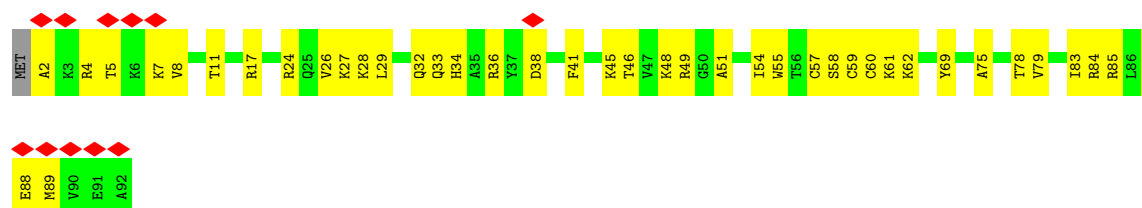


- Molecule 71: 60S ribosomal protein L36-A

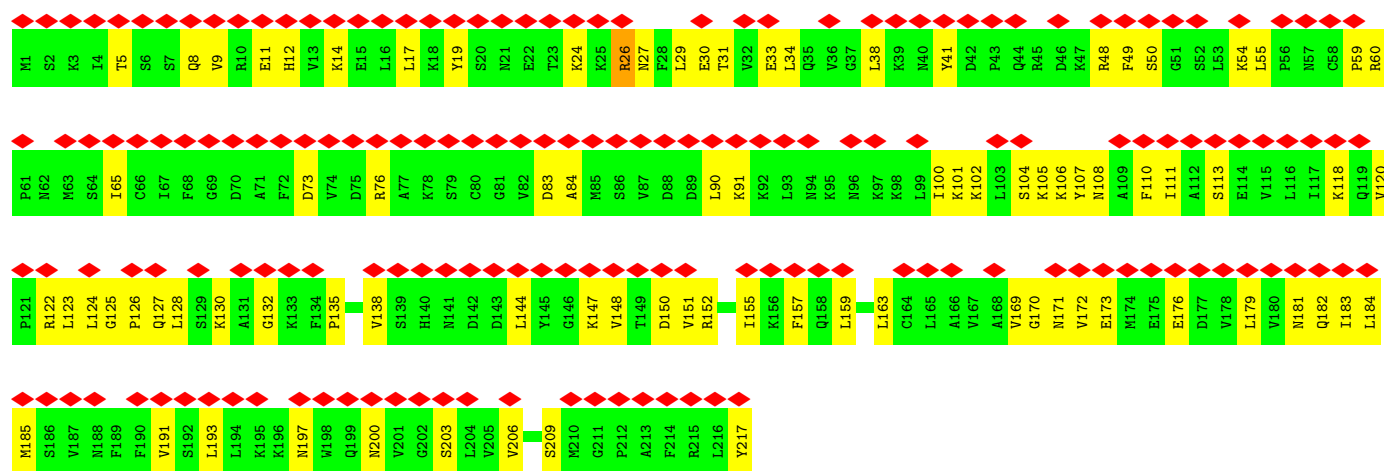




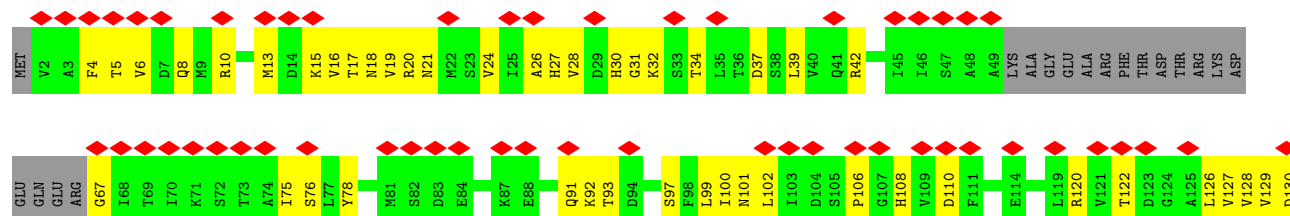
Chain Ap: 12% 54% 45%

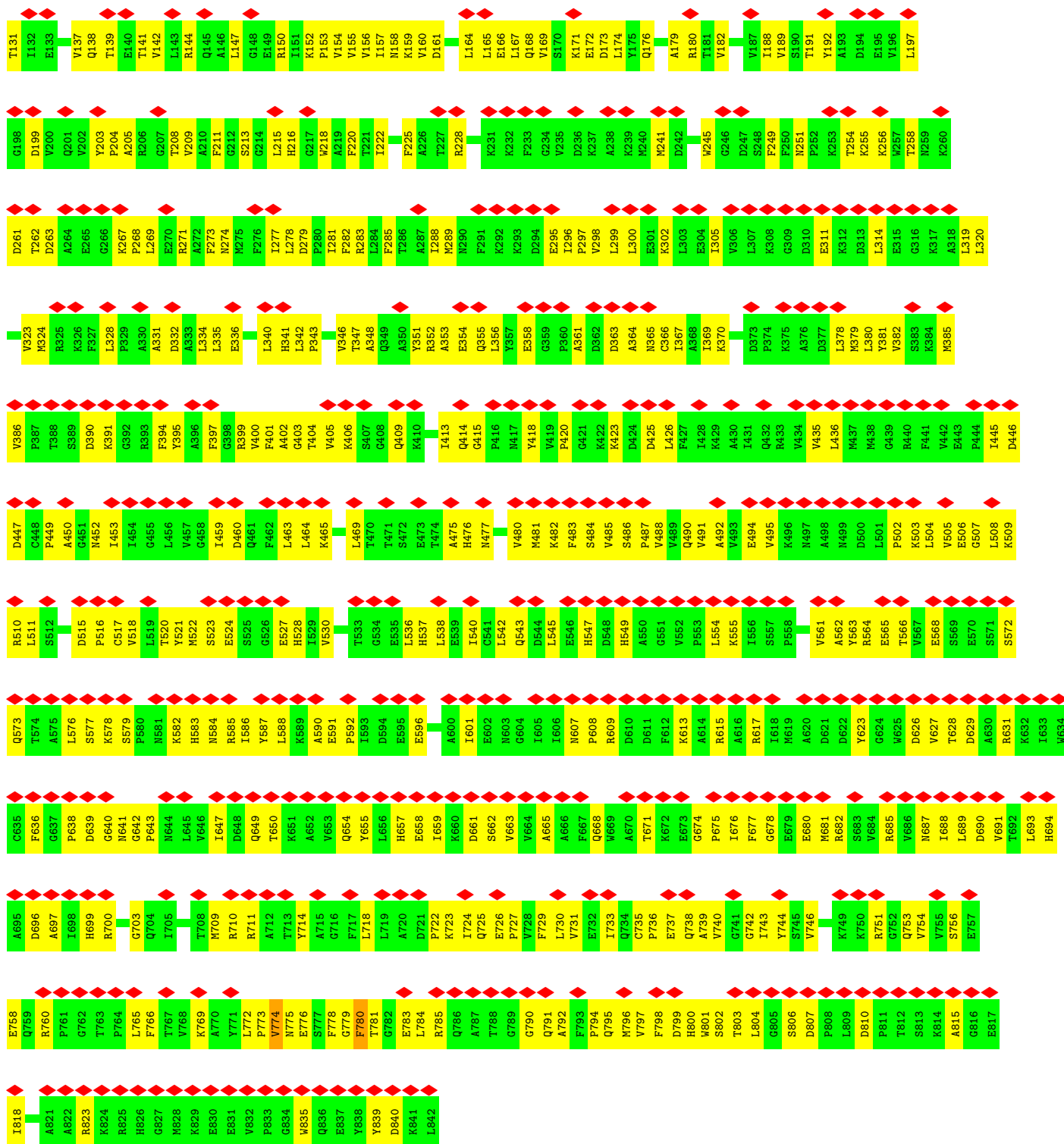


Chain E: 79% 60% 39%



Chain DC: 55% 49% 48%





A	G6878	G6818
C	U6879	G6819
U	G6880	G6820
U	U6881	U6821
A	U6882	U6822
A	G6883	G6823
U	A6884	A6825
U	G6885	U6826
U	A6886	G6827
U	G6887	G6828
U	A6888	A6829
A		G6830
G	A	U6831
G	A	G6832
C	G	G6833
U	U	U6834
U	C	U6835
A	C	U6836
C	C	U6837
C	G	C6838
C	U	U6839
C	C	A6840
A	C	U6841
A	U	U6842
A	U	U6843
G	U	U6844
G	G	G6845
C	G	C6846
C	C	G6847
A	A	U6848
A	A	A6849
A	G	C6850
A	U	G6851
U	U	U6852
G	A	G6853
A	C	U6854
C	C	A6855
A	G	C6856
C	C	G6857
G	G	A6858
G	C	U6859
C	G	A6860
C	C	G6861
U	U	G6862
U	U	C6863
C	G	A6864
C	G	G6865
G	U	C6866
U	G	C6867
G	G	C6868
U	U	C6869
G	G	A6870
G	G	A6871
G	G	A6872
G		A6873
		A6874
		C6875
		A6876
		C6877

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75068	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	2.167	Depositor
Minimum map value	-1.037	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.104	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: UR3, SO1, OMU, OMG, GDP, PSU, HIC, G7M, ZN, MG, MA6, 4AC, B8N, 1MA, DDE, 5MC

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	0.27	0/1653	0.53	0/2261
2	BB	0.27	0/1735	0.49	0/2335
3	BC	0.27	0/1665	0.41	0/2263
4	BE	0.25	0/2109	0.47	0/2839
5	BG	0.22	0/1844	0.43	0/2464
6	BH	0.23	0/1506	0.50	2/2028 (0.1%)
7	BI	0.27	0/1514	0.49	0/2021
8	BJ	0.26	0/1519	0.53	1/2035 (0.0%)
9	BL	0.26	0/1272	0.41	0/1712
10	BN	0.29	0/1215	0.48	0/1638
11	BO	0.31	0/952	0.59	2/1279 (0.2%)
12	BV	0.23	0/693	0.41	0/935
13	BW	0.32	0/1038	0.48	0/1395
14	BX	0.28	0/1139	0.44	0/1518
15	BY	0.21	0/1087	0.44	0/1449
16	Ba	0.34	0/782	0.69	3/1047 (0.3%)
17	Bb	0.24	0/620	0.45	0/838
18	Be	0.18	0/483	0.42	0/643
19	BD	0.21	0/1759	0.44	0/2368
20	BF	0.21	0/1629	0.44	0/2202
21	BK	0.22	0/837	0.59	0/1131
22	BP	0.18	0/1012	0.40	0/1356
23	BQ	0.20	0/1125	0.42	0/1510
24	BR	0.22	0/957	0.45	0/1283
25	BS	0.22	0/1211	0.48	0/1628
26	BT	0.19	0/1113	0.43	0/1494
27	BU	0.24	0/865	0.46	0/1169
28	BZ	0.21	0/582	0.41	0/782
29	Bc	0.21	0/499	0.47	0/670
30	Bd	0.21	0/452	0.40	0/600
31	Bg	0.18	0/2454	0.43	0/3340
32	Bf	0.11	0/616	0.29	0/817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
33	BM	0.14	0/943	0.43	2/1274 (0.2%)
34	B5	0.26	0/41450	0.31	0/64582
35	AA	0.35	0/1912	0.45	0/2569
36	AB	0.32	0/3139	0.43	0/4219
37	AC	0.30	0/2800	0.40	0/3790
38	A1	0.33	0/76160	0.32	0/118745
39	A3	0.26	0/2861	0.30	0/4457
40	A4	0.33	0/3724	0.32	0/5798
41	AD	0.22	0/2390	0.37	0/3225
42	AE	0.26	0/1324	0.39	0/1782
43	AF	0.35	0/1821	0.47	0/2451
44	AG	0.27	0/1830	0.45	0/2469
45	AH	0.27	0/1531	0.46	0/2062
46	AI	0.24	0/1843	0.40	0/2471
47	AJ	0.22	0/1374	0.47	0/1842
48	AL	0.29	0/1568	0.39	0/2106
49	AM	0.28	0/1068	0.43	0/1438
50	AN	0.35	0/1757	0.45	0/2354
51	AO	0.33	0/1585	0.44	0/2128
52	AP	0.33	0/1410	0.44	0/1893
53	AQ	0.29	0/1465	0.39	0/1965
54	AR	0.31	0/1538	0.47	0/2050
55	AS	0.34	0/1481	0.48	0/1990
56	AT	0.28	0/1300	0.45	0/1743
57	AU	0.26	0/812	0.47	0/1099
58	AV	0.33	0/1018	0.50	0/1369
59	AW	0.31	0/533	0.50	0/707
60	AX	0.29	0/983	0.43	0/1325
61	AY	0.27	0/1004	0.42	0/1341
62	AZ	0.29	0/1118	0.45	0/1497
63	Aa	0.31	0/1204	0.40	0/1612
64	Ab	0.34	0/473	0.57	0/629
65	Ac	0.27	0/751	0.39	0/1008
66	Ad	0.29	0/904	0.41	0/1213
67	Ae	0.30	0/1041	0.37	0/1394
68	Af	0.34	0/868	0.40	0/1168
69	Ag	0.33	0/890	0.40	0/1189
70	Ah	0.26	0/978	0.43	0/1301
71	Ai	0.26	0/778	0.48	0/1034
72	Aj	0.34	0/696	0.41	0/923
73	Ak	0.27	0/618	0.52	0/826
74	Al	0.35	0/443	0.52	0/588
75	Am	0.26	0/423	0.45	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.38	0/234	0.61	0/300
77	Ao	0.23	0/859	0.42	0/1133
78	Ap	0.31	0/701	0.47	0/934
79	E	0.17	0/1745	0.43	0/2342
80	DC	0.18	0/6521	0.41	1/8830 (0.0%)
81	EC	0.16	0/3088	0.37	0/4805
All	All	0.29	0/224894	0.38	11/329582 (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
43	AF	0	1
64	Ab	0	1
79	E	0	1
All	All	0	4

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Ba	20	PRO	N-CD-CG	-10.63	87.26	103.20
16	Ba	20	PRO	CA-N-CD	-7.99	100.81	112.00
16	Ba	20	PRO	CA-CB-CG	-7.65	89.97	104.50
8	BJ	80	LEU	CA-CB-CG	6.19	137.98	116.30
11	BO	123	SER	CA-C-N	6.14	133.28	121.54

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
43	AF	232	ARG	Peptide
64	Ab	41	ARG	Sidechain
6	BH	64	VAL	Peptide
79	E	26	ARG	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	91	0
2	BB	1709	0	1784	106	0
3	BC	1635	0	1723	91	0
4	BE	2068	0	2154	103	0
5	BG	1820	0	1918	111	0
6	BH	1481	0	1572	82	0
7	BI	1489	0	1525	106	0
8	BJ	1494	0	1573	121	0
9	BL	1244	0	1312	46	0
10	BN	1192	0	1255	49	0
11	BO	941	0	979	61	0
12	BV	684	0	672	46	0
13	BW	1021	0	1060	47	0
14	BX	1121	0	1196	53	0
15	BY	1073	0	1132	85	0
16	Ba	769	0	818	38	0
17	Bb	610	0	633	27	0
18	Be	475	0	525	35	0
19	BD	1734	0	1817	71	0
20	BF	1609	0	1675	97	0
21	BK	817	0	804	61	0
22	BP	991	0	1035	55	0
23	BQ	1105	0	1166	75	0
24	BR	948	0	990	62	0
25	BS	1192	0	1222	78	0
26	BT	1095	0	1114	69	0
27	BU	855	0	917	57	0
28	BZ	574	0	616	41	0
29	Bc	497	0	535	31	0
30	Bd	442	0	432	27	0
31	Bg	2401	0	2356	148	0
32	Bf	605	0	654	32	0
33	BM	935	0	975	38	0
34	B5	37463	0	18842	1276	0
35	AA	1878	0	1946	89	0
36	AB	3081	0	3162	119	0
37	AC	2748	0	2859	114	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	A1	68786	0	34576	1749	0
39	A3	2579	0	1304	91	0
40	A4	3353	0	1695	101	0
41	AD	2341	0	2290	108	0
42	AE	1303	0	1376	59	0
43	AF	1784	0	1862	77	0
44	AG	1798	0	1894	65	0
45	AH	1510	0	1576	55	0
46	AI	1804	0	1856	74	0
47	AJ	1353	0	1383	70	0
48	AL	1543	0	1608	66	0
49	AM	1053	0	1149	39	0
50	AN	1720	0	1779	67	0
51	AO	1555	0	1659	61	0
52	AP	1388	0	1423	68	0
53	AQ	1441	0	1543	48	0
54	AR	1521	0	1617	76	0
55	AS	1445	0	1487	61	0
56	AT	1276	0	1323	79	0
57	AU	796	0	812	33	0
58	AV	1003	0	1046	56	0
59	AW	521	0	551	23	0
60	AX	968	0	1036	32	0
61	AY	993	0	1081	47	0
62	AZ	1092	0	1155	52	0
63	Aa	1173	0	1215	49	0
64	Ab	462	0	490	21	0
65	Ac	743	0	797	27	0
66	Ad	890	0	938	38	0
67	Ae	1020	0	1090	37	0
68	Af	850	0	880	32	0
69	Ag	880	0	945	41	0
70	Ah	969	0	1078	41	0
71	Ai	771	0	849	30	0
72	Aj	681	0	687	24	0
73	Ak	612	0	682	40	0
74	Al	436	0	475	31	0
75	Am	417	0	459	24	0
76	An	233	0	283	23	0
77	Ao	847	0	913	45	0
78	Ap	694	0	738	34	0
79	E	1718	0	1811	86	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	DC	6419	0	6492	363	0
81	EC	2764	0	1394	105	0
82	AO	1	0	0	0	0
83	DC	28	0	12	4	0
84	DC	1	0	0	0	0
85	DC	35	0	40	8	0
All	All	210978	0	157920	6840	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 19.

The worst 5 of 6840 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)
79:E:126:PRO:O	79:E:130:LYS:HB2	1.31	1.26
34:B5:976:G:H1	34:B5:1023:A:HO2'	1.06	1.03
34:B5:649:U:H3	34:B5:684:A:N6	1.55	1.03
34:B5:1335:U:H3	34:B5:1416:G:H1	1.05	0.98
5:BG:56:ASN:HD21	34:B5:153:G:H21	1.09	0.97

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%)	185 (91%)	19 (9%)	0	100	100
2	BB	212/255 (83%)	185 (87%)	27 (13%)	0	100	100
3	BC	215/254 (85%)	208 (97%)	7 (3%)	0	100	100
4	BE	258/261 (99%)	235 (91%)	23 (9%)	0	100	100
5	BG	224/236 (95%)	209 (93%)	15 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	BH	182/190 (96%)	168 (92%)	14 (8%)	0	100	100
7	BI	184/200 (92%)	162 (88%)	22 (12%)	0	100	100
8	BJ	183/197 (93%)	164 (90%)	19 (10%)	0	100	100
9	BL	153/156 (98%)	138 (90%)	15 (10%)	0	100	100
10	BN	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
11	BO	125/137 (91%)	111 (89%)	14 (11%)	0	100	100
12	BV	85/87 (98%)	76 (89%)	9 (11%)	0	100	100
13	BW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
14	BX	142/145 (98%)	127 (89%)	15 (11%)	0	100	100
15	BY	132/135 (98%)	125 (95%)	7 (5%)	0	100	100
16	Ba	95/119 (80%)	82 (86%)	13 (14%)	0	100	100
17	Bb	79/82 (96%)	74 (94%)	5 (6%)	0	100	100
18	Be	58/63 (92%)	49 (84%)	9 (16%)	0	100	100
19	BD	221/240 (92%)	209 (95%)	12 (5%)	0	100	100
20	BF	204/225 (91%)	189 (93%)	15 (7%)	0	100	100
21	BK	94/105 (90%)	80 (85%)	14 (15%)	0	100	100
22	BP	122/142 (86%)	114 (93%)	8 (7%)	0	100	100
23	BQ	139/143 (97%)	131 (94%)	8 (6%)	0	100	100
24	BR	117/136 (86%)	109 (93%)	8 (7%)	0	100	100
25	BS	143/146 (98%)	129 (90%)	14 (10%)	0	100	100
26	BT	139/144 (96%)	125 (90%)	14 (10%)	0	100	100
27	BU	105/121 (87%)	99 (94%)	6 (6%)	0	100	100
28	BZ	69/108 (64%)	64 (93%)	5 (7%)	0	100	100
29	Bc	61/67 (91%)	58 (95%)	3 (5%)	0	100	100
30	Bd	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
31	Bg	310/319 (97%)	276 (89%)	34 (11%)	0	100	100
32	Bf	73/152 (48%)	65 (89%)	8 (11%)	0	100	100
33	BM	122/143 (85%)	114 (93%)	8 (7%)	0	100	100
35	AA	245/254 (96%)	231 (94%)	14 (6%)	0	100	100
36	AB	383/387 (99%)	355 (93%)	28 (7%)	0	100	100
37	AC	359/362 (99%)	332 (92%)	27 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	AD	290/297 (98%)	271 (93%)	19 (7%)	0	100	100
42	AE	163/176 (93%)	146 (90%)	17 (10%)	0	100	100
43	AF	220/244 (90%)	208 (94%)	12 (6%)	0	100	100
44	AG	228/256 (89%)	213 (93%)	15 (7%)	0	100	100
45	AH	188/191 (98%)	175 (93%)	13 (7%)	0	100	100
46	AI	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
47	AJ	167/174 (96%)	154 (92%)	13 (8%)	0	100	100
48	AL	191/199 (96%)	178 (93%)	13 (7%)	0	100	100
49	AM	134/138 (97%)	128 (96%)	6 (4%)	0	100	100
50	AN	201/204 (98%)	186 (92%)	15 (8%)	0	100	100
51	AO	195/199 (98%)	188 (96%)	7 (4%)	0	100	100
52	AP	171/184 (93%)	165 (96%)	6 (4%)	0	100	100
53	AQ	183/186 (98%)	174 (95%)	9 (5%)	0	100	100
54	AR	186/189 (98%)	172 (92%)	14 (8%)	0	100	100
55	AS	170/178 (96%)	155 (91%)	15 (9%)	0	100	100
56	AT	157/160 (98%)	141 (90%)	16 (10%)	0	100	100
57	AU	98/121 (81%)	92 (94%)	6 (6%)	0	100	100
58	AV	134/137 (98%)	127 (95%)	7 (5%)	0	100	100
59	AW	61/155 (39%)	58 (95%)	3 (5%)	0	100	100
60	AX	119/142 (84%)	113 (95%)	6 (5%)	0	100	100
61	AY	124/127 (98%)	116 (94%)	8 (6%)	0	100	100
62	AZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
63	Aa	146/149 (98%)	134 (92%)	12 (8%)	0	100	100
64	Ab	56/59 (95%)	49 (88%)	7 (12%)	0	100	100
65	Ac	95/105 (90%)	92 (97%)	3 (3%)	0	100	100
66	Ad	107/113 (95%)	97 (91%)	10 (9%)	0	100	100
67	Ae	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
68	Af	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
69	Ag	110/121 (91%)	107 (97%)	3 (3%)	0	100	100
70	Ah	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
71	Ai	97/100 (97%)	89 (92%)	8 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	Aj	85/88 (97%)	80 (94%)	5 (6%)	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%)	48 (96%)	2 (4%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	102/106 (96%)	95 (93%)	7 (7%)	0	100	100
78	Ap	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
79	E	215/217 (99%)	190 (88%)	25 (12%)	0	100	100
80	DC	819/842 (97%)	744 (91%)	73 (9%)	2 (0%)	43	73
All	All	11959/12946 (92%)	11051 (92%)	906 (8%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
80	DC	171	LYS
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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 190 such sidechains are listed below:

Mol	Chain	Res	Type
46	AI	162	GLN
59	AW	59	HIS
48	AL	99	HIS
54	AR	130	ASN
63	Aa	67	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1754/1798 (97%)	482 (27%)	11 (0%)
38	A1	3211/3394 (94%)	698 (21%)	22 (0%)
39	A3	120/121 (99%)	17 (14%)	1 (0%)
40	A4	157/158 (99%)	29 (18%)	1 (0%)
81	EC	127/202 (62%)	88 (69%)	7 (5%)
All	All	5369/5673 (94%)	1314 (24%)	42 (0%)

5 of 1314 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	2	A
34	B5	4	C
34	B5	25	C
34	B5	34	G
34	B5	42	G

5 of 42 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A1	2772	C
81	EC	6789	G
38	A1	3022	G
38	A1	3169	U
81	EC	6818	G

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	PSU	A1	776	38	18,21,22	1.29	3 (16%)	21,30,33	2.19	6 (28%)
38	PSU	A1	2735	38	18,21,22	1.40	4 (22%)	21,30,33	2.11	4 (19%)
38	PSU	A1	960	38	18,21,22	1.45	3 (16%)	21,30,33	2.07	4 (19%)
38	PSU	A1	2340	38	18,21,22	1.47	4 (22%)	21,30,33	2.04	3 (14%)
80	DDE	DC	699	-	18,20,21	1.02	1 (5%)	17,28,30	0.79	1 (5%)
38	PSU	A1	2975	38	18,21,22	1.46	4 (22%)	21,30,33	2.20	4 (19%)
34	MA6	B5	1781	34	23,26,27	1.49	6 (26%)	33,38,41	2.01	11 (33%)
34	PSU	B5	211	34	18,21,22	1.41	3 (16%)	21,30,33	2.01	3 (14%)
34	PSU	B5	1290	34	18,21,22	1.39	3 (16%)	21,30,33	2.15	4 (19%)
38	PSU	A1	2349	38	18,21,22	1.39	4 (22%)	21,30,33	2.07	3 (14%)
38	PSU	A1	1042	38	18,21,22	1.36	3 (16%)	21,30,33	1.96	3 (14%)
34	PSU	B5	106	34	18,21,22	1.41	3 (16%)	21,30,33	2.01	3 (14%)
34	PSU	B5	1181	34	18,21,22	1.39	2 (11%)	21,30,33	2.15	4 (19%)
34	MA6	B5	1782	34	23,26,27	1.47	5 (21%)	33,38,41	2.14	10 (30%)
38	PSU	A1	2133	38	18,21,22	1.55	4 (22%)	21,30,33	2.26	5 (23%)
34	PSU	B5	766	34	18,21,22	1.41	4 (22%)	21,30,33	2.22	5 (23%)
38	PSU	A1	1004	38	18,21,22	1.43	4 (22%)	21,30,33	2.09	3 (14%)
38	1MA	A1	2142	38	21,25,26	1.33	3 (14%)	30,37,40	1.72	5 (16%)
38	PSU	A1	2191	38	18,21,22	1.43	4 (22%)	21,30,33	2.15	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	4AC	B5	1773	34	21,24,25	1.11	2 (9%)	28,34,37	2.10	5 (17%)
38	PSU	A1	2264	38	18,21,22	1.42	3 (16%)	21,30,33	2.08	3 (14%)
38	OMU	A1	2921	38	19,22,23	1.26	4 (21%)	25,31,34	1.89	6 (24%)
34	PSU	B5	466	34	18,21,22	1.39	3 (16%)	21,30,33	2.07	4 (19%)
38	PSU	A1	2266	38	18,21,22	1.46	5 (27%)	21,30,33	2.02	3 (14%)
38	OMG	A1	2922	38	23,26,27	1.19	4 (17%)	32,38,41	1.98	6 (18%)
38	5MC	A1	2870	38	19,22,23	1.30	3 (15%)	26,32,35	1.12	2 (7%)
38	PSU	A1	2880	38	18,21,22	1.45	4 (22%)	21,30,33	2.19	4 (19%)
34	PSU	B5	120	34	18,21,22	1.36	3 (16%)	21,30,33	2.03	4 (19%)
34	B8N	B5	1191	34	25,29,30	1.38	3 (12%)	28,42,45	7.25	5 (17%)
38	PSU	A1	1124	38	18,21,22	1.40	4 (22%)	21,30,33	2.09	4 (19%)
38	PSU	A1	966	38	18,21,22	1.41	4 (22%)	21,30,33	2.10	4 (19%)
38	PSU	A1	990	38	18,21,22	1.39	3 (16%)	21,30,33	2.07	4 (19%)
34	PSU	B5	999	34	18,21,22	1.43	4 (22%)	21,30,33	2.17	4 (19%)
38	1MA	A1	645	38	21,25,26	1.33	4 (19%)	30,37,40	1.75	6 (20%)
39	PSU	A3	50	39	18,21,22	1.39	2 (11%)	21,30,33	2.06	3 (14%)
34	PSU	B5	759	34	18,21,22	1.40	3 (16%)	21,30,33	2.12	4 (19%)
36	HIC	AB	243	36	10,11,12	1.43	1 (10%)	9,14,16	1.22	1 (11%)
38	PSU	A1	2416	38	18,21,22	1.52	5 (27%)	21,30,33	2.13	4 (19%)
38	PSU	A1	2923	38	18,21,22	1.35	2 (11%)	21,30,33	2.10	3 (14%)
38	PSU	A1	2351	38	18,21,22	1.44	4 (22%)	21,30,33	2.10	4 (19%)
38	PSU	A1	2865	38	18,21,22	1.48	4 (22%)	21,30,33	2.15	4 (19%)
38	PSU	A1	1056	38	18,21,22	1.43	4 (22%)	21,30,33	2.19	4 (19%)
34	G7M	B5	1575	34	23,26,27	2.48	6 (26%)	34,39,42	1.82	7 (20%)
38	PSU	A1	2314	38	18,21,22	1.37	3 (16%)	21,30,33	2.04	4 (19%)
40	PSU	A4	73	40	18,21,22	1.36	3 (16%)	21,30,33	1.99	4 (19%)
38	PSU	A1	2944	38	18,21,22	1.44	5 (27%)	21,30,33	2.23	5 (23%)
38	PSU	A1	986	38	18,21,22	1.46	5 (27%)	21,30,33	2.18	5 (23%)
38	UR3	A1	2634	38	19,22,23	0.93	0	26,32,35	1.76	3 (11%)
38	PSU	A1	1110	38	18,21,22	1.43	4 (22%)	21,30,33	2.14	3 (14%)
38	PSU	A1	1052	38	18,21,22	1.38	4 (22%)	21,30,33	2.10	4 (19%)
38	5MC	A1	2278	38	19,22,23	1.37	3 (15%)	26,32,35	1.13	3 (11%)
34	PSU	B5	1415	34	18,21,22	1.35	3 (16%)	21,30,33	2.07	4 (19%)
34	PSU	B5	302	34	18,21,22	1.44	4 (22%)	21,30,33	2.16	4 (19%)
34	PSU	B5	1187	34	18,21,22	1.38	3 (16%)	21,30,33	2.05	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	1.47	4 (22%)	21,30,33	2.16	4 (19%)
34	4AC	B5	1280	34	21,24,25	1.11	1 (4%)	28,34,37	0.98	1 (3%)
38	PSU	A1	2258	38	18,21,22	1.37	3 (16%)	21,30,33	2.16	4 (19%)
38	PSU	A1	2826	38	18,21,22	1.42	5 (27%)	21,30,33	2.12	5 (23%)
38	PSU	A1	2260	38	18,21,22	1.38	2 (11%)	21,30,33	2.14	5 (23%)
38	PSU	A1	2129	38	18,21,22	1.47	4 (22%)	21,30,33	2.18	4 (19%)

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	PSU	A1	776	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	960	38	-	1/7/25/26	0/2/2/2
38	PSU	A1	2340	38	-	2/7/25/26	0/2/2/2
80	DDE	DC	699	-	-	12/20/21/23	0/1/1/1
38	PSU	A1	2975	38	-	0/7/25/26	0/2/2/2
34	MA6	B5	1781	34	-	3/11/29/30	0/3/3/3
34	PSU	B5	211	34	-	2/7/25/26	0/2/2/2
34	PSU	B5	1290	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2349	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1042	38	-	2/7/25/26	0/2/2/2
34	PSU	B5	106	34	-	0/7/25/26	0/2/2/2
34	PSU	B5	1181	34	-	1/7/25/26	0/2/2/2
34	MA6	B5	1782	34	-	5/11/29/30	0/3/3/3
38	PSU	A1	2133	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	766	34	-	2/7/25/26	0/2/2/2
38	PSU	A1	1004	38	-	0/7/25/26	0/2/2/2
38	1MA	A1	2142	38	-	0/7/25/26	0/3/3/3
38	PSU	A1	2191	38	-	0/7/25/26	0/2/2/2
34	4AC	B5	1773	34	-	3/11/29/30	0/2/2/2
38	PSU	A1	2264	38	-	1/7/25/26	0/2/2/2
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
34	PSU	B5	466	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2266	38	-	3/7/25/26	0/2/2/2
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	PSU	A1	2880	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	120	34	-	0/7/25/26	0/2/2/2
34	B8N	B5	1191	34	-	1/16/34/35	0/2/2/2
38	PSU	A1	1124	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	966	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	990	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	999	34	-	0/7/25/26	0/2/2/2
38	1MA	A1	645	38	-	2/7/25/26	0/3/3/3
39	PSU	A3	50	39	-	0/7/25/26	0/2/2/2
34	PSU	B5	759	34	-	0/7/25/26	0/2/2/2
36	HIC	AB	243	36	-	2/5/6/8	0/1/1/1
38	PSU	A1	2416	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2923	38	-	3/7/25/26	0/2/2/2
38	PSU	A1	2351	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2865	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1056	38	-	0/7/25/26	0/2/2/2
34	G7M	B5	1575	34	-	2/7/25/26	0/3/3/3
38	PSU	A1	2314	38	-	1/7/25/26	0/2/2/2
40	PSU	A4	73	40	-	0/7/25/26	0/2/2/2
38	PSU	A1	2944	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	986	38	-	0/7/25/26	0/2/2/2
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1110	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1052	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	1415	34	-	1/7/25/26	0/2/2/2
34	PSU	B5	302	34	-	0/7/25/26	0/2/2/2
34	PSU	B5	1187	34	-	2/7/25/26	0/2/2/2
34	PSU	B5	632	34	-	0/7/25/26	0/2/2/2
34	4AC	B5	1280	34	-	2/11/29/30	0/2/2/2
38	PSU	A1	2258	38	-	2/7/25/26	0/2/2/2
38	PSU	A1	2826	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2260	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2129	38	-	0/7/25/26	0/2/2/2

The worst 5 of 207 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	O6-C6	7.11	1.37	1.23
34	B5	1575	G7M	C2-N2	5.74	1.47	1.34
34	B5	1575	G7M	C5-N7	-4.66	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1781	MA6	C5-C4	4.46	1.47	1.39
38	A1	2278	5MC	C5-C4	4.42	1.47	1.44

The worst 5 of 248 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1191	B8N	C32-C31-N3	37.44	177.60	112.16
34	B5	1773	4AC	N4-C4-N3	7.81	126.55	113.87
38	A1	2133	PSU	N1-C2-N3	7.25	122.82	115.17
38	A1	2634	UR3	C4-N3-C2	-7.13	118.84	124.58
34	B5	766	PSU	N1-C2-N3	7.00	122.55	115.17

There are no chirality outliers.

5 of 59 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
80	DC	699	DDE	O-C-CA-CB
80	DC	699	DDE	N-CA-CB-CG
80	DC	699	DDE	C-CA-CB-CG
80	DC	699	DDE	CBI-CBW-NCB-CAB
80	DC	699	DDE	CAT-CAU-CBW-NCB

There are no ring outliers.

35 monomers are involved in 53 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	776	PSU	1	0
38	A1	2735	PSU	1	0
38	A1	2975	PSU	1	0
34	B5	1781	MA6	2	0
34	B5	1290	PSU	1	0
38	A1	2349	PSU	1	0
38	A1	2133	PSU	2	0
34	B5	766	PSU	1	0
34	B5	1773	4AC	3	0
38	A1	2266	PSU	2	0
38	A1	2870	5MC	1	0
38	A1	2880	PSU	1	0
34	B5	120	PSU	1	0
38	A1	1124	PSU	1	0
38	A1	966	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	990	PSU	1	0
39	A3	50	PSU	1	0
34	B5	759	PSU	1	0
36	AB	243	HIC	2	0
38	A1	2416	PSU	1	0
38	A1	2351	PSU	1	0
38	A1	2865	PSU	2	0
38	A1	2314	PSU	1	0
40	A4	73	PSU	1	0
38	A1	2944	PSU	1	0
38	A1	986	PSU	3	0
38	A1	1110	PSU	3	0
38	A1	2278	5MC	3	0
34	B5	1415	PSU	1	0
34	B5	302	PSU	1	0
34	B5	1187	PSU	1	0
34	B5	632	PSU	1	0
34	B5	1280	4AC	4	0
38	A1	2258	PSU	2	0
38	A1	2129	PSU	2	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	$\# Z > 2$
85	SO1	DC	903	-	34,39,39	0.68	1 (2%)	38,64,64	1.23	5 (13%)
83	GDP	DC	901	84	29,30,30	1.16	3 (10%)	45,47,47	1.79	7 (15%)

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	SO1	DC	903	-	1/1/15/16	4/21/104/104	0/7/5/5
83	GDP	DC	901	84	-	3/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	DC	901	GDP	C5-C4	3.17	1.47	1.38
85	DC	903	SO1	O14-C5	-2.95	1.19	1.30
83	DC	901	GDP	C5-N7	-2.31	1.34	1.39
83	DC	901	GDP	C6-N1	-2.28	1.34	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	DC	901	GDP	C5-C4-N3	-6.41	118.19	128.39
83	DC	901	GDP	C2-N3-C4	4.97	120.85	112.30
83	DC	901	GDP	N9-C4-N3	4.92	135.79	125.95
85	DC	903	SO1	C12-C6-C2	-4.51	98.10	105.09
83	DC	901	GDP	C6-C5-N7	2.66	135.13	130.29

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
85	DC	903	SO1	C4

5 of 7 torsion outliers are listed below:

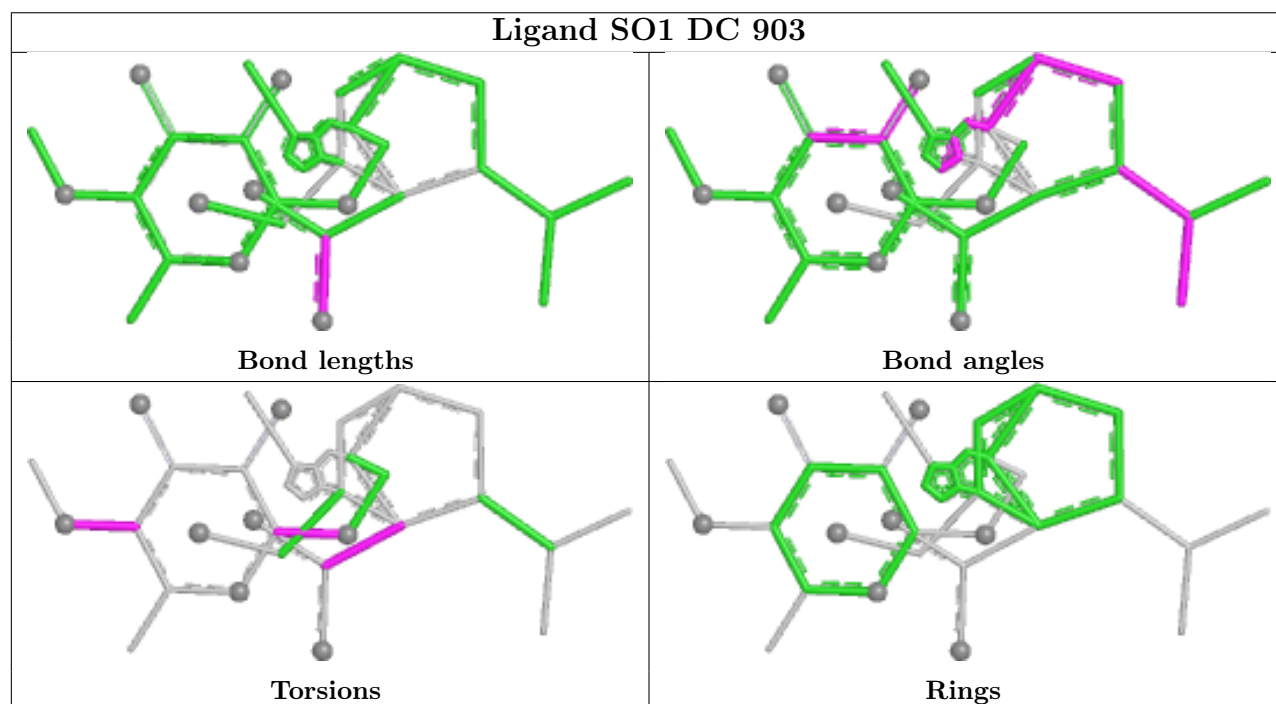
Mol	Chain	Res	Type	Atoms
85	DC	903	SO1	C2-C1-C5-O14
85	DC	903	SO1	C2-C1-C5-O15
85	DC	903	SO1	O56-C52-O17-C8
85	DC	903	SO1	C54-C55-O64-C65
83	DC	901	GDP	PA-O3A-PB-O2B

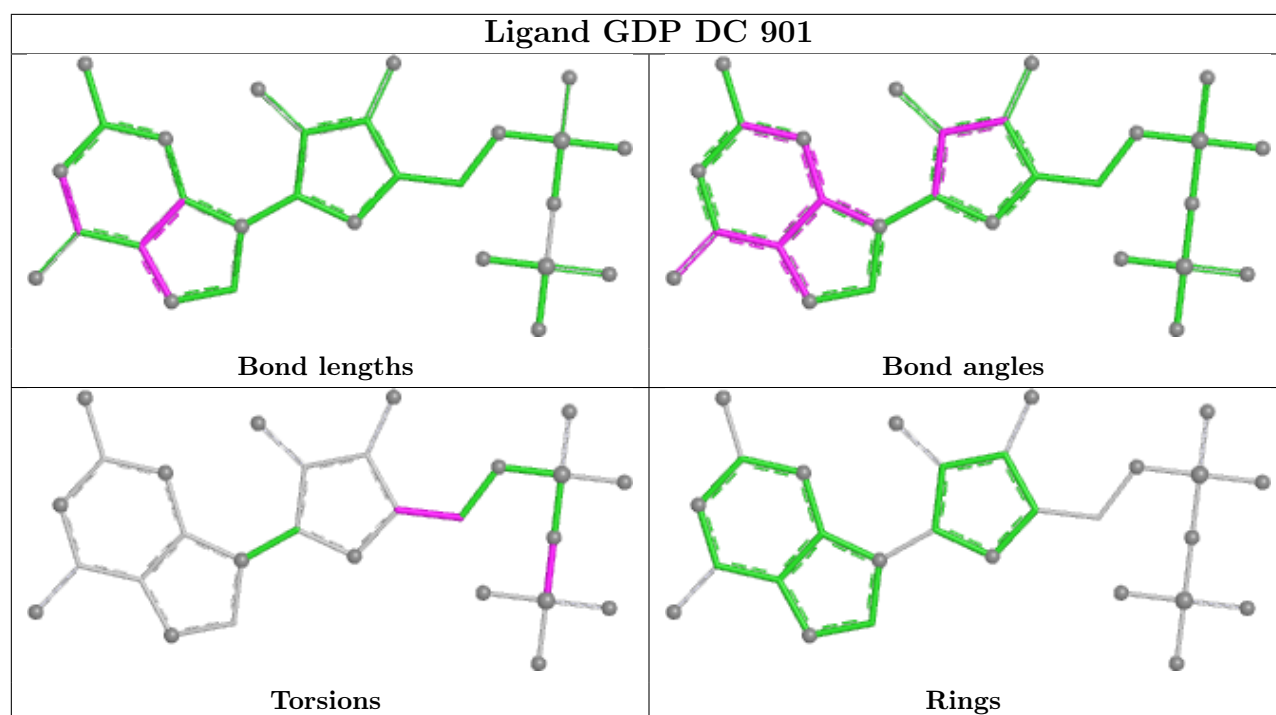
There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	DC	903	SO1	8	0
83	DC	901	GDP	4	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
38	A1	1
77	Ao	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	1282:G	O3'	1283:C	P	4.95
1	Ao	105:GLN	C	106:PHE	N	3.24

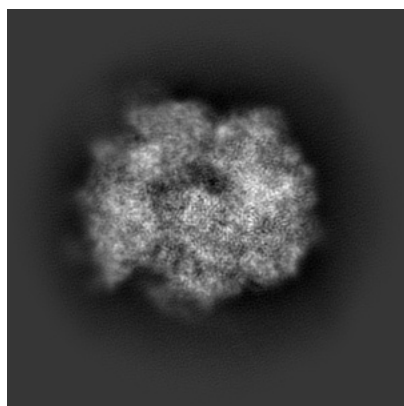
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41001. These allow visual inspection of the internal detail of the map and identification of artifacts.

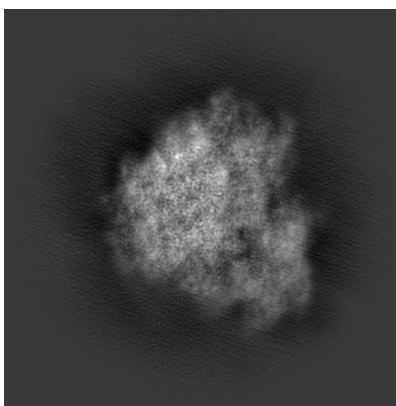
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

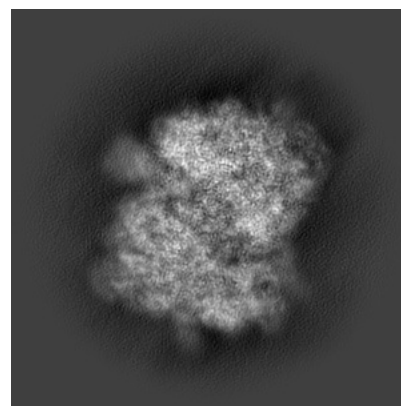
6.1.1 Primary map



X

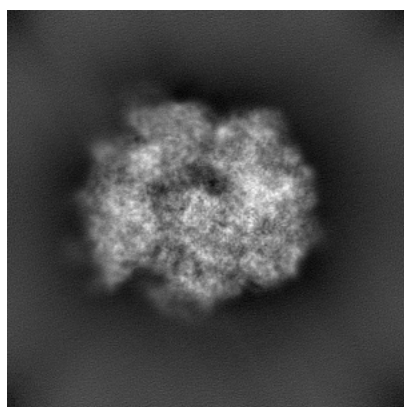


Y

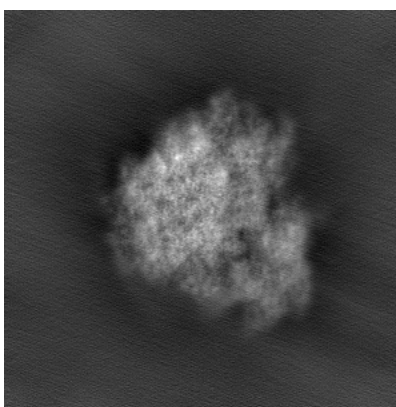


Z

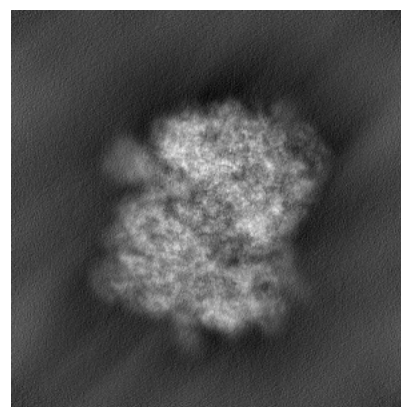
6.1.2 Raw map



X



Y

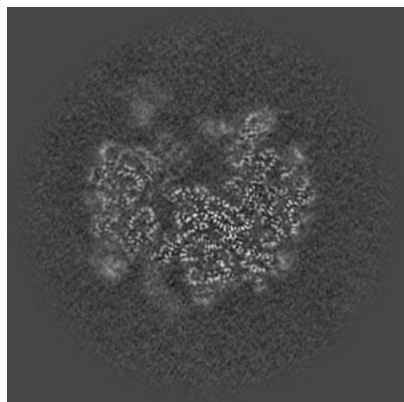


Z

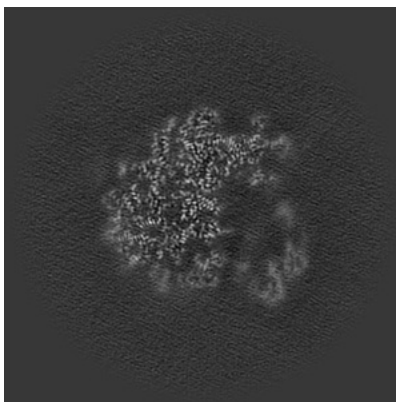
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

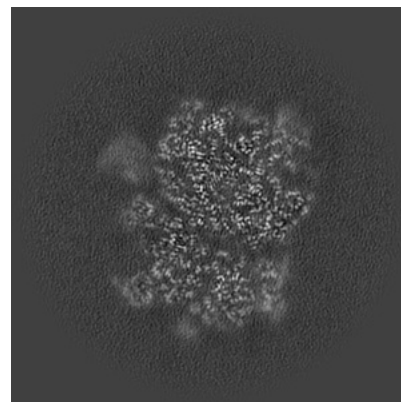
6.2.1 Primary map



X Index: 200

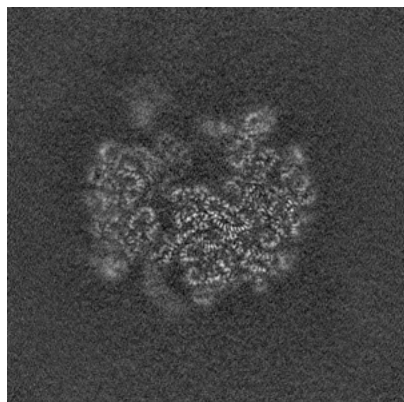


Y Index: 200

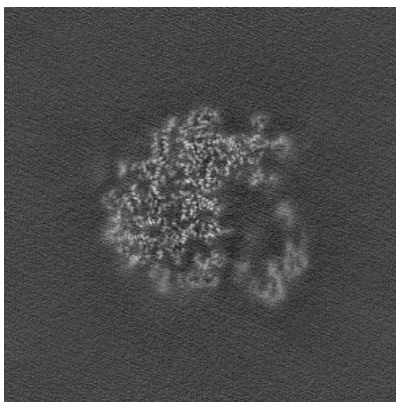


Z Index: 200

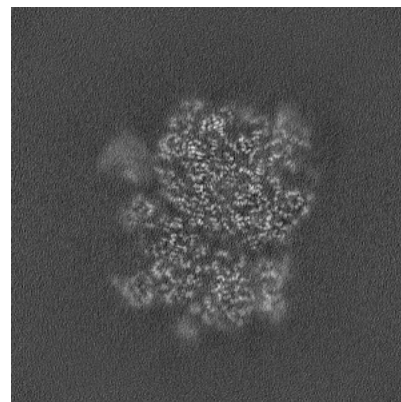
6.2.2 Raw map



X Index: 200



Y Index: 200

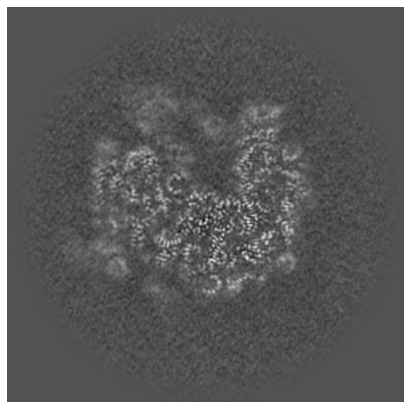


Z Index: 200

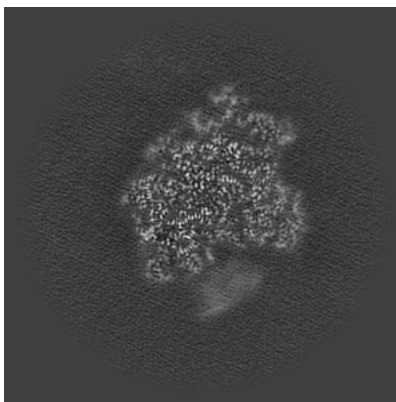
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

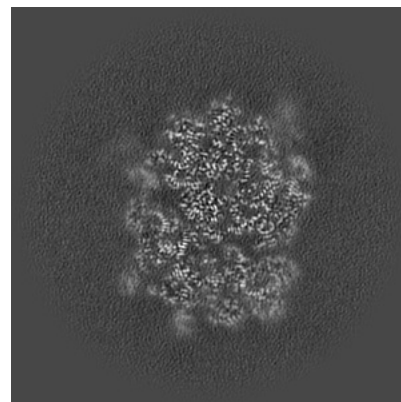
6.3.1 Primary map



X Index: 192

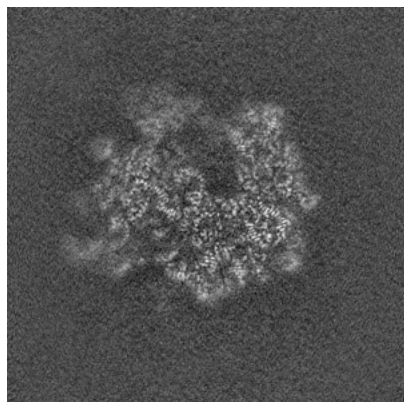


Y Index: 245

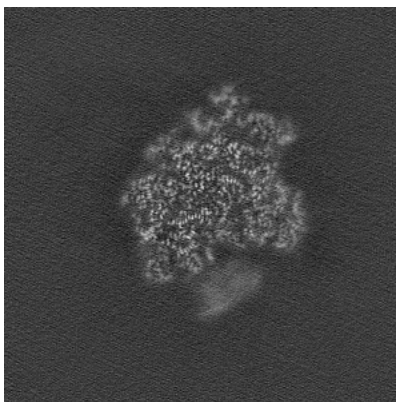


Z Index: 190

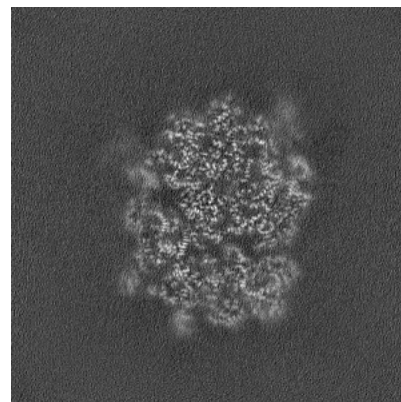
6.3.2 Raw map



X Index: 185



Y Index: 245

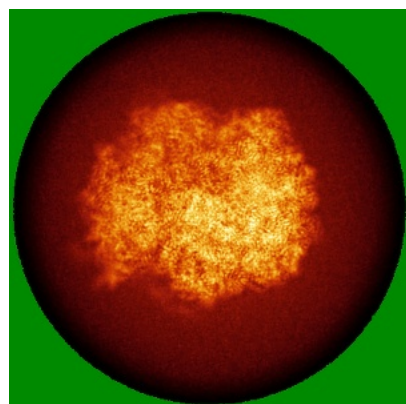


Z Index: 190

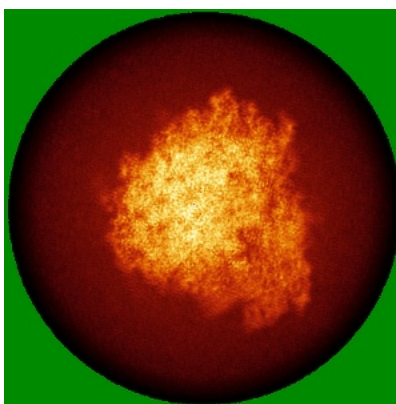
The images above show the largest variance slices of the map in three orthogonal directions.

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

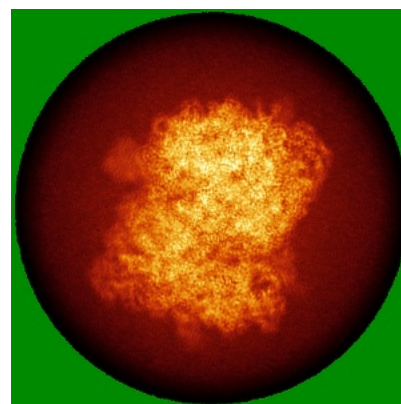
6.4.1 Primary map



X

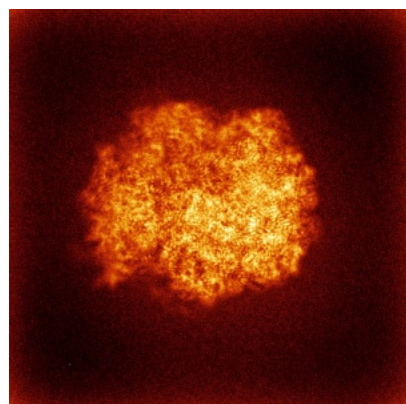


Y

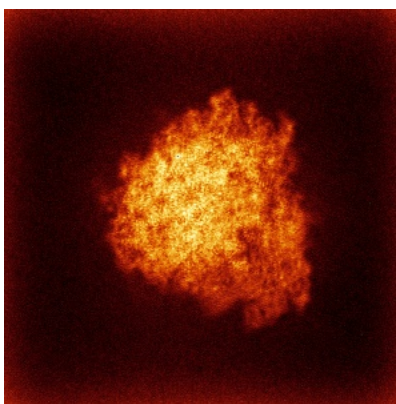


Z

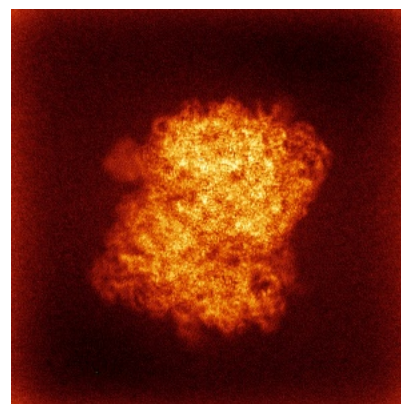
6.4.2 Raw map



X



Y

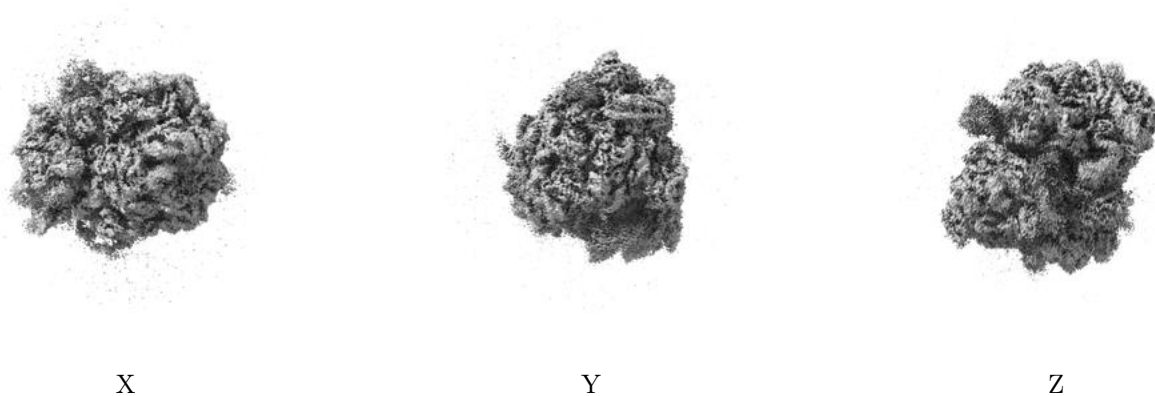


Z

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

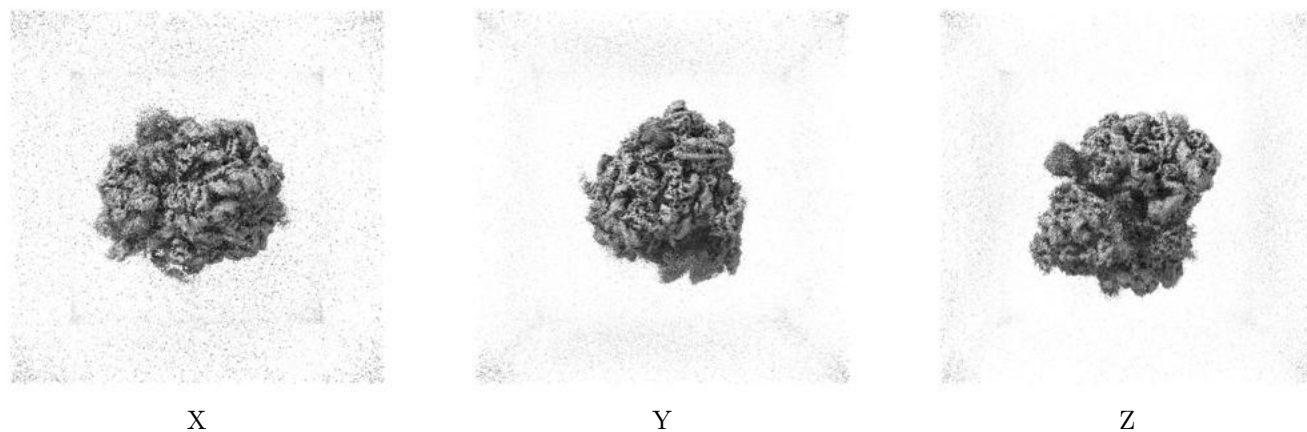
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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

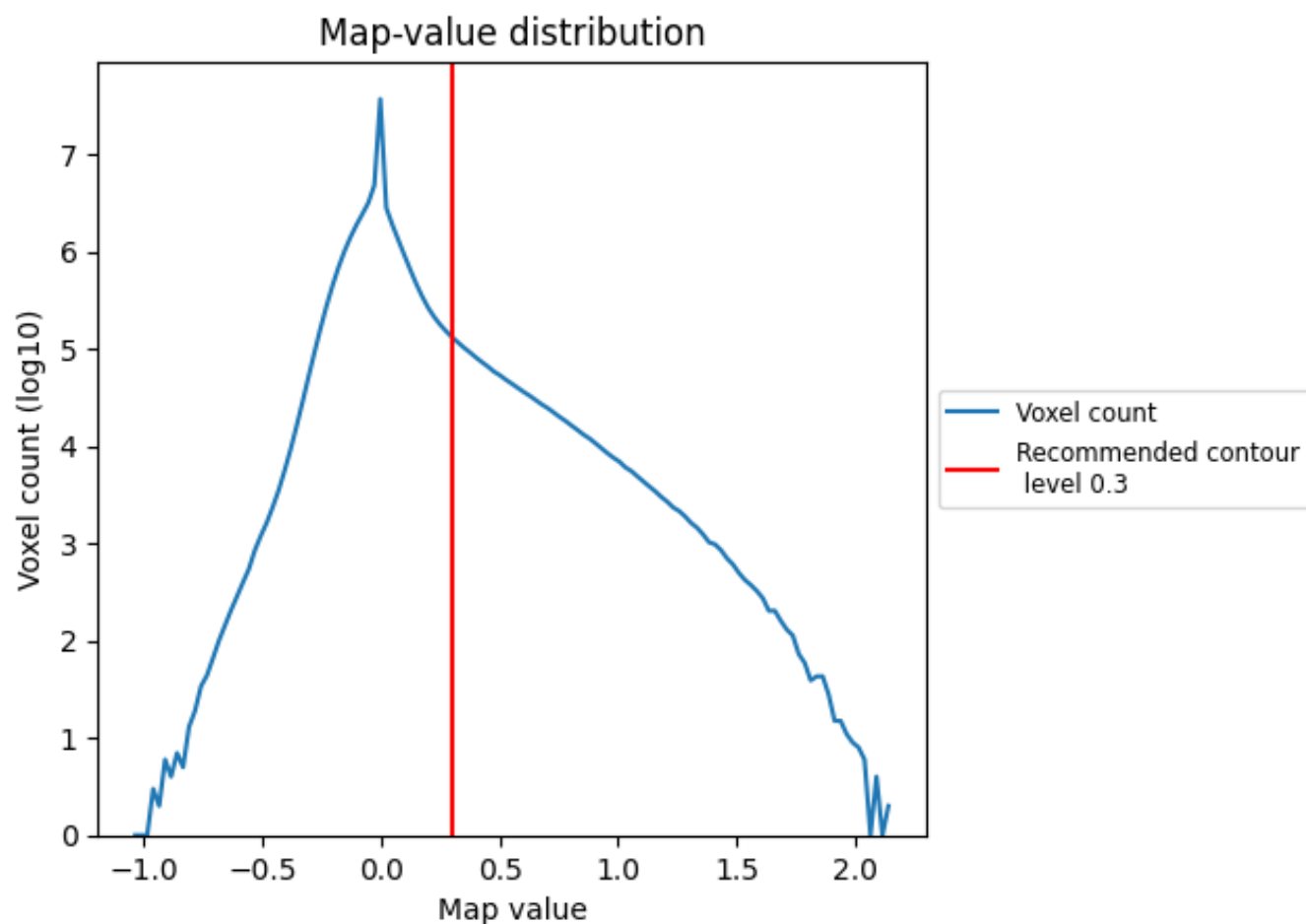
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

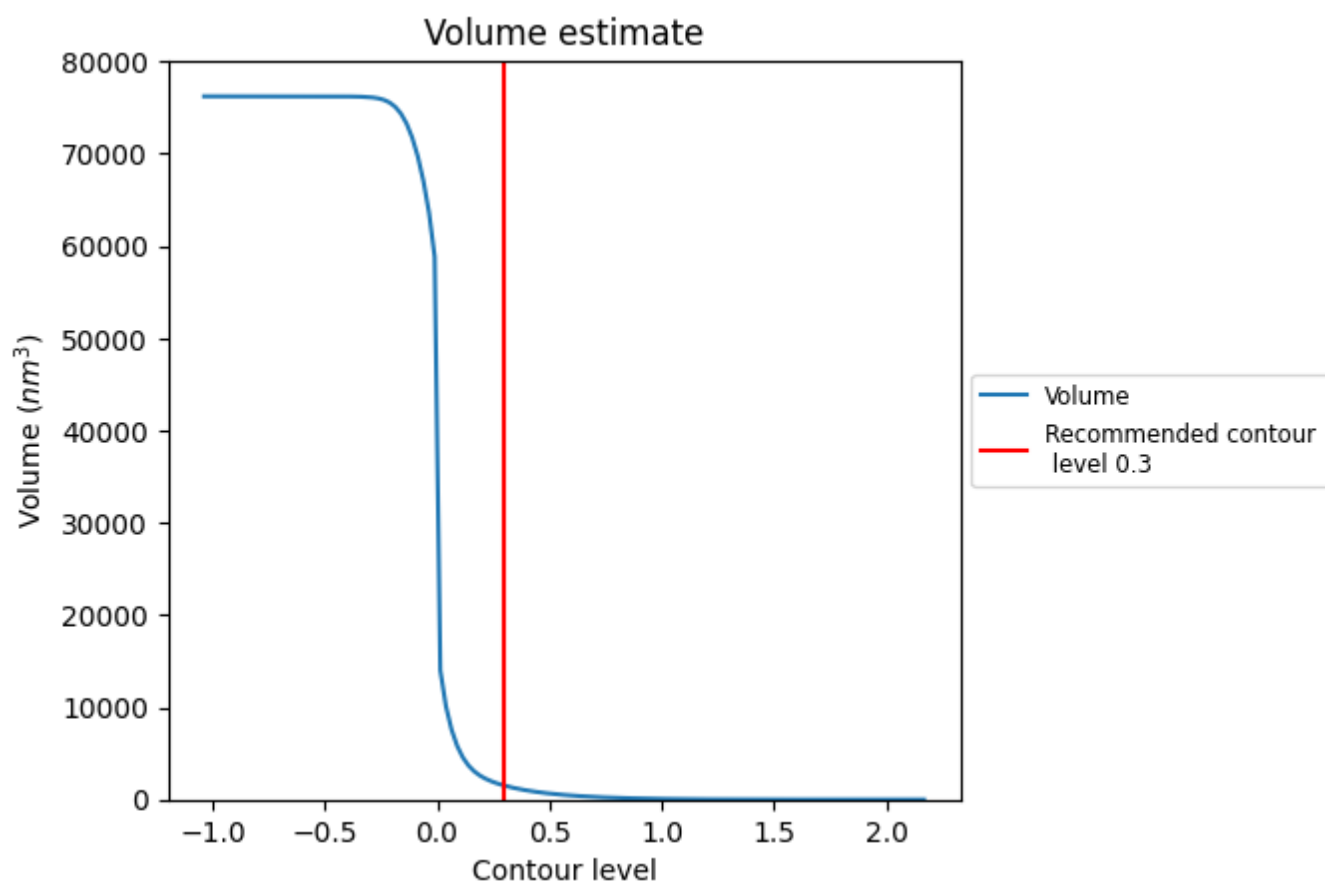
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

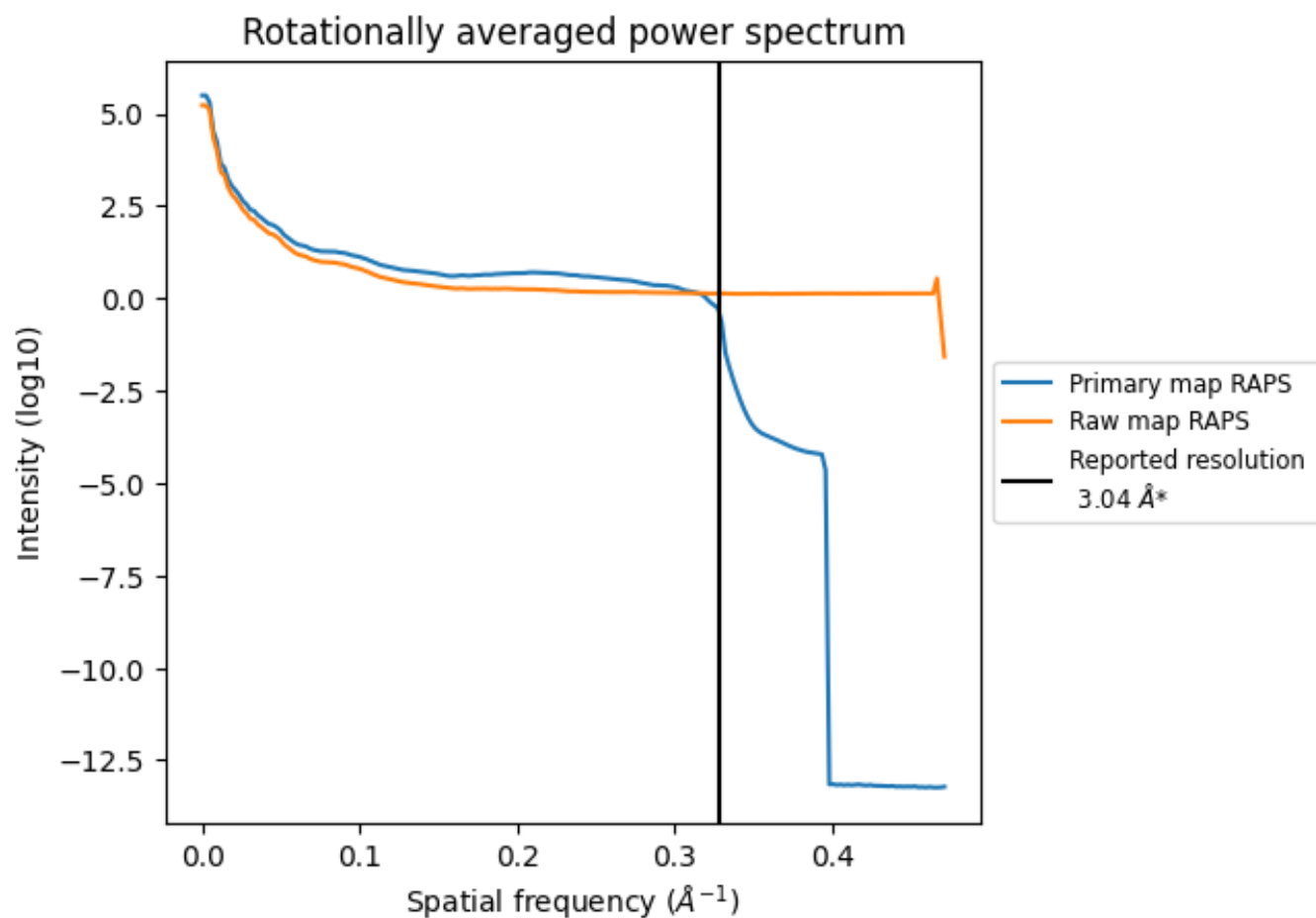
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1514 nm³; this corresponds to an approximate mass of 1367 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 ⓘ

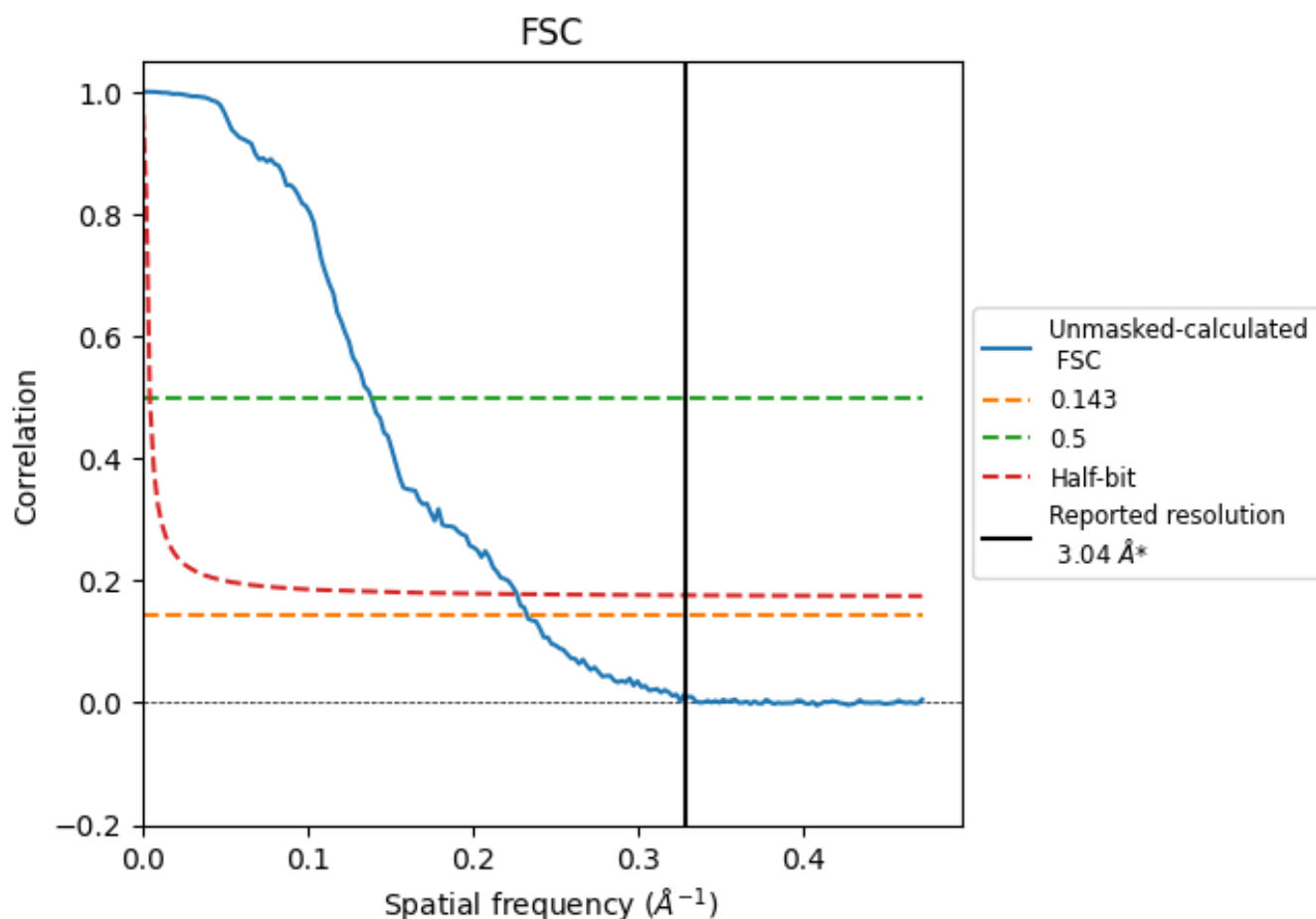


*Reported resolution corresponds to spatial frequency of 0.329 Å⁻¹

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 0.329 Å⁻¹

8.2 Resolution estimates [i](#)

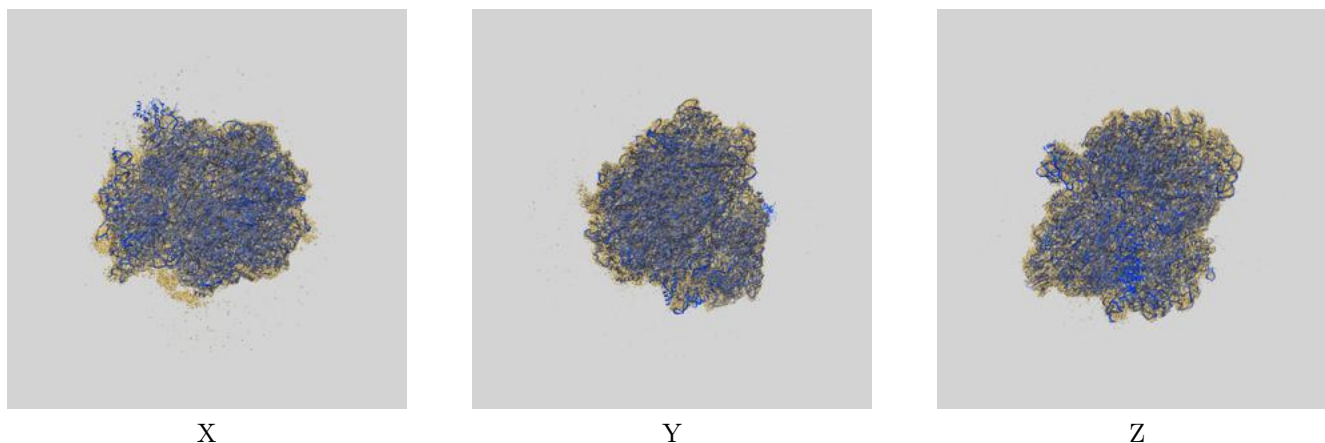
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.04	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.30	7.23	4.41

*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 4.30 differs from the reported value 3.04 by more than 10 %

9 Map-model fit [i](#)

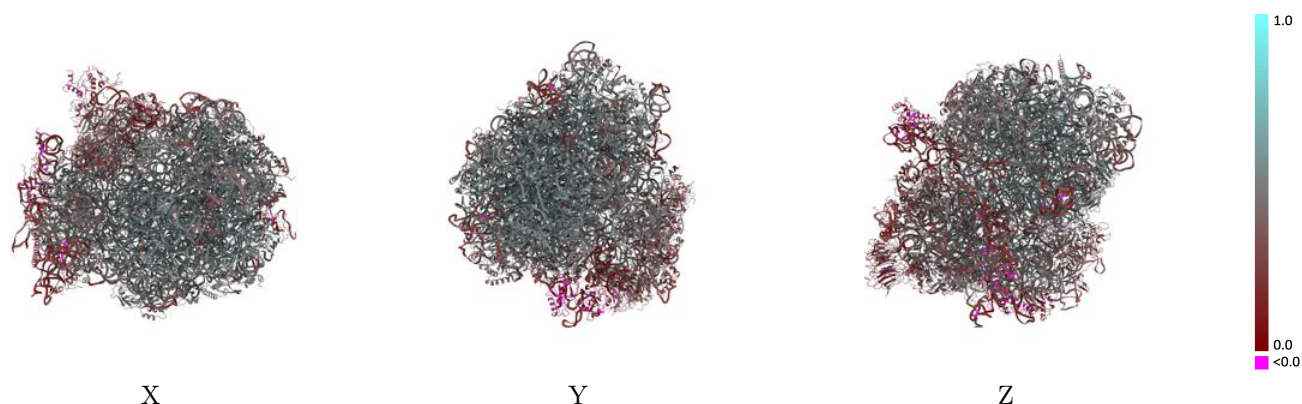
This section contains information regarding the fit between EMDB map EMD-41001 and PDB model 8T3E. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



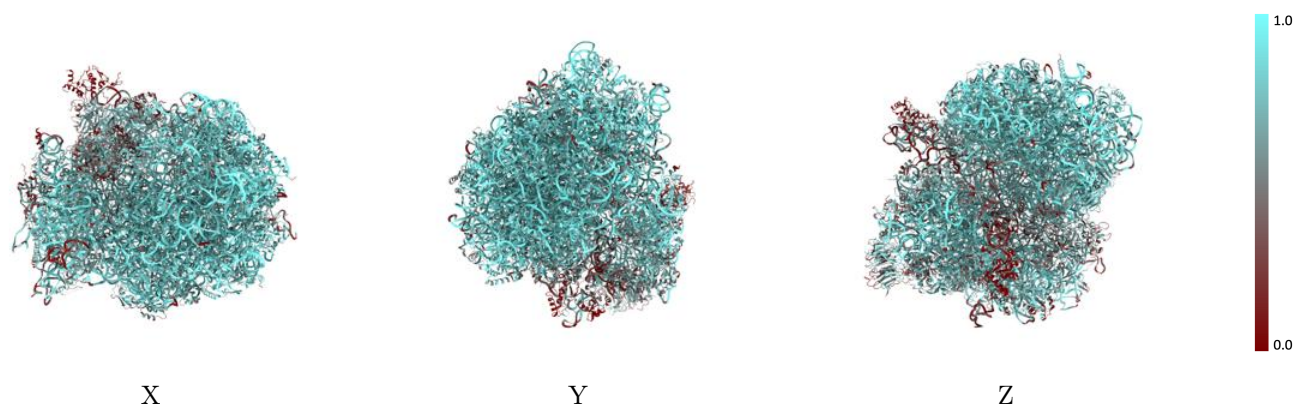
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



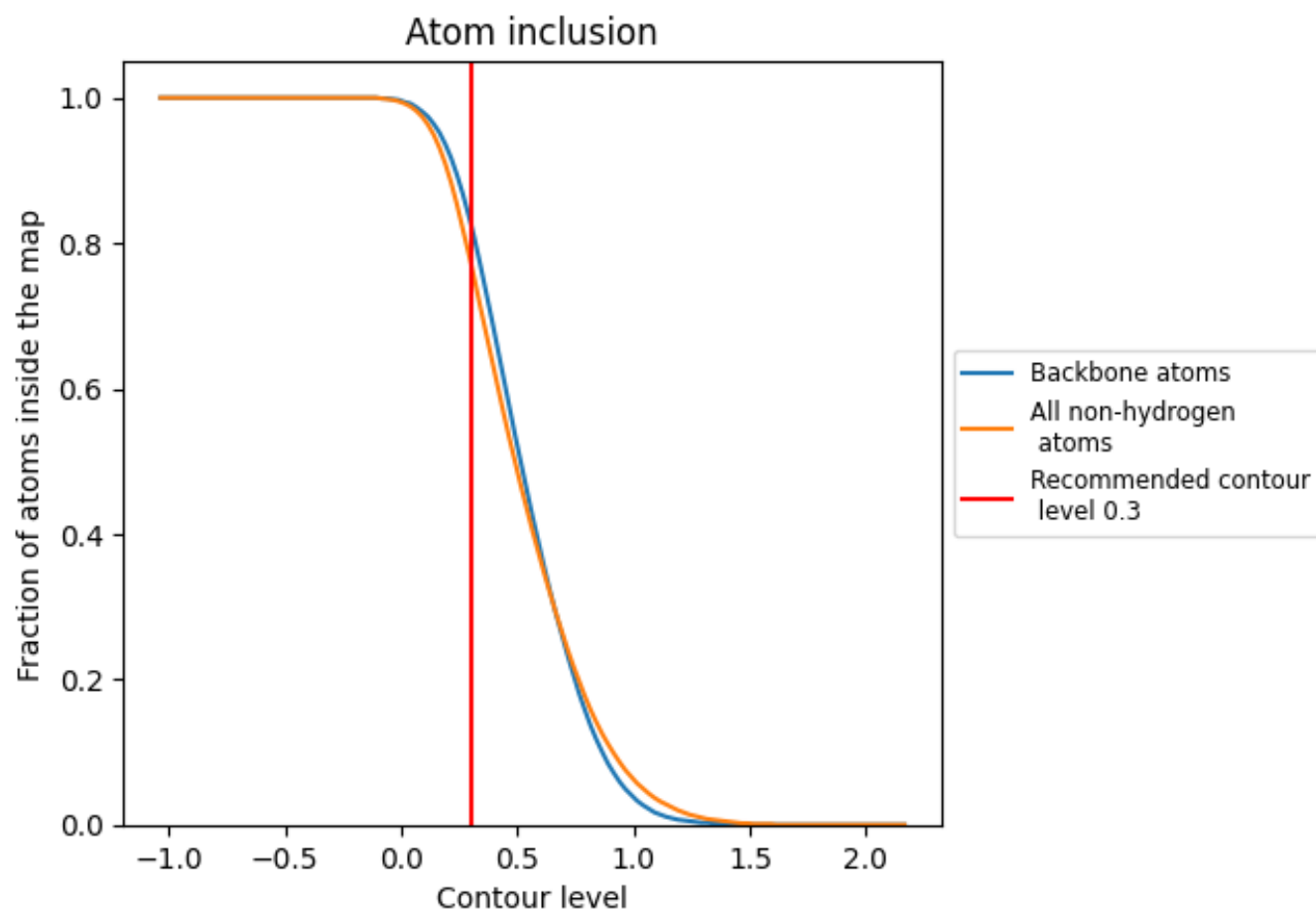
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 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	 0.7720	 0.4370
A1	 0.8870	 0.4840
A3	 0.9390	 0.4710
A4	 0.9290	 0.5070
AA	 0.7400	 0.5350
AB	 0.8200	 0.5040
AC	 0.8130	 0.5060
AD	 0.7520	 0.4110
AE	 0.8030	 0.4450
AF	 0.8400	 0.5040
AG	 0.7820	 0.4580
AH	 0.7600	 0.4780
AI	 0.7100	 0.4540
AJ	 0.6210	 0.3900
AL	 0.8200	 0.4960
AM	 0.7890	 0.4660
AN	 0.8170	 0.5300
AO	 0.7960	 0.4990
AP	 0.8200	 0.5080
AQ	 0.7840	 0.5120
AR	 0.6920	 0.4560
AS	 0.8240	 0.4970
AT	 0.7640	 0.4940
AU	 0.7350	 0.4280
AV	 0.7140	 0.4980
AW	 0.8080	 0.4940
AX	 0.7470	 0.4860
AY	 0.8180	 0.4920
AZ	 0.8260	 0.4790
Aa	 0.8350	 0.5110
Ab	 0.6440	 0.4660
Ac	 0.6840	 0.4830
Ad	 0.7750	 0.4700
Ae	 0.8060	 0.5190
Af	 0.8660	 0.5360



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Chain	Atom inclusion	Q-score
Ag	 0.7560	 0.5020
Ah	 0.7980	 0.4800
Ai	 0.7600	 0.4590
Aj	 0.8630	 0.5480
Ak	 0.5930	 0.4110
Al	 0.7900	 0.5240
Am	 0.7490	 0.5000
An	 0.7080	 0.5070
Ao	 0.6250	 0.4820
Ap	 0.6790	 0.4890
B5	 0.8200	 0.4070
BA	 0.6870	 0.4000
BB	 0.6770	 0.4040
BC	 0.7450	 0.4620
BD	 0.5620	 0.3630
BE	 0.6930	 0.4060
BF	 0.5080	 0.3340
BG	 0.6830	 0.3420
BH	 0.6710	 0.3880
BI	 0.7230	 0.4390
BJ	 0.5830	 0.2440
BK	 0.5220	 0.2880
BL	 0.6860	 0.4610
BM	 0.0210	 0.1830
BN	 0.7090	 0.4750
BO	 0.7140	 0.4630
BP	 0.4510	 0.2980
BQ	 0.5850	 0.3350
BR	 0.5480	 0.3170
BS	 0.5690	 0.3310
BT	 0.6330	 0.3160
BU	 0.5120	 0.3430
BV	 0.7400	 0.4430
BW	 0.8030	 0.5010
BX	 0.6710	 0.4880
BY	 0.5470	 0.2320
BZ	 0.5580	 0.2970
Ba	 0.7280	 0.4830
Bb	 0.6960	 0.4340
Bc	 0.4650	 0.3270
Bd	 0.7590	 0.4110
Be	 0.5250	 0.3320

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Chain	Atom inclusion	Q-score
Bf	 0.0350	 0.1960
Bg	 0.5830	 0.2470
DC	 0.3660	 0.3210
E	 0.2200	 0.1130
EC	 0.3200	 0.2000