



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 06:15 PM UTC

PDB ID : 6GQV / pdb_00006gqv
EMDB ID : EMD-0049
Title : Cryo-EM reconstruction of yeast 80S ribosome in complex with mRNA, tRNA and eEF2 (GMPPCP)
Authors : Pellegrino, S.; Yusupov, M.; Yusupova, G.; Hashem, Y.
Deposited on : 2018-06-08
Resolution : 4.00 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:

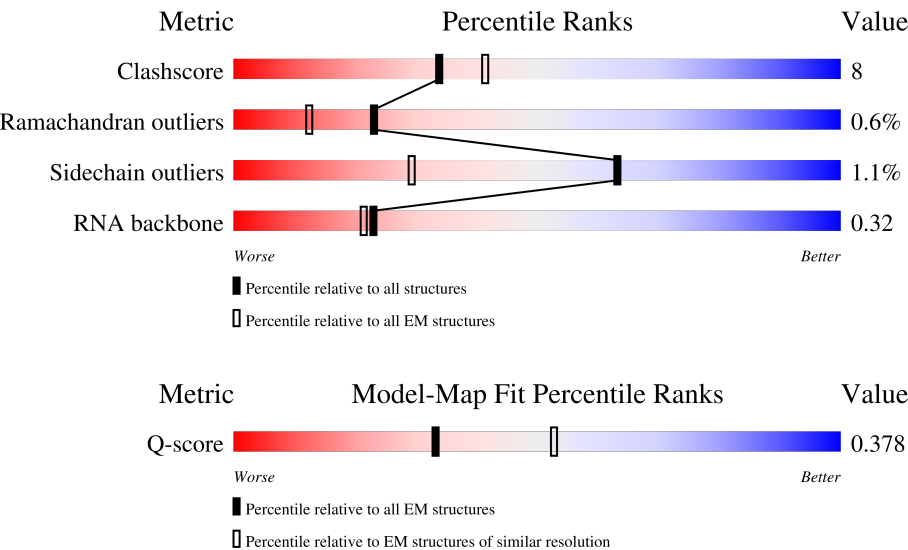
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 4.00 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	7587 (3.50 - 4.50)

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	1	3396	46% 40% 9% 5%
2	3	121	52% 37% 11%
3	4	158	49% 41% 10%

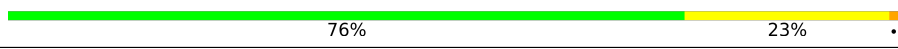
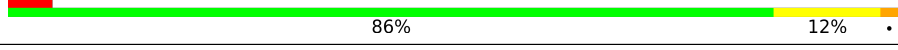
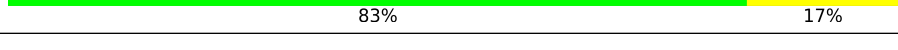
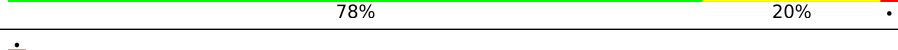
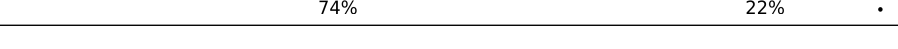
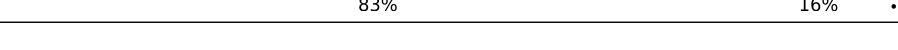
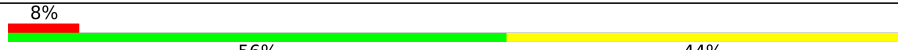
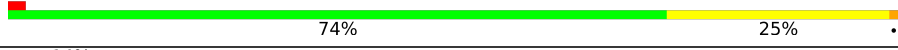
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Mol	Chain	Length	Quality of chain
4	P0	189	
5	P2	94	
6	A	252	
7	B	386	
8	C	361	
9	D	296	
10	E	175	
11	F	222	
12	G	233	
13	H	191	
14	I	220	
15	J	169	
16	L	193	
17	M	136	
18	N	203	
19	O	197	
20	P	183	
21	Q	185	
22	R	188	
23	S	172	
24	T	159	
25	U	100	
26	V	136	
27	W	62	
28	X	121	

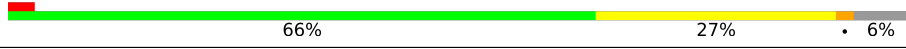
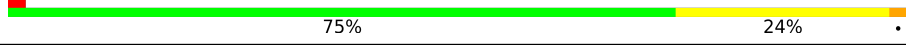
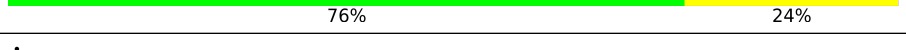
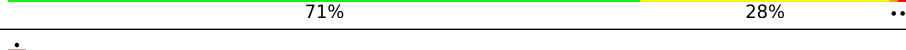
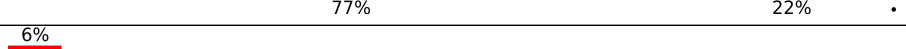
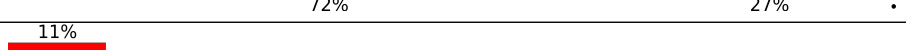
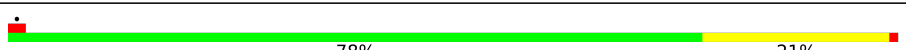
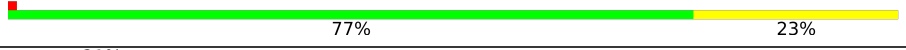
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Mol	Chain	Length	Quality of chain
29	Y	126	
30	Z	135	
31	a	148	
32	b	58	
33	c	97	
34	d	109	
35	e	127	
36	f	106	
37	g	112	
38	h	119	
39	i	99	
40	j	87	
41	k	77	
42	l	50	
43	m	52	
44	n	25	
45	o	105	
46	p	91	
47	2	1797	
48	q	206	
49	r	214	
50	s	217	
51	t	223	
52	u	260	
53	v	206	

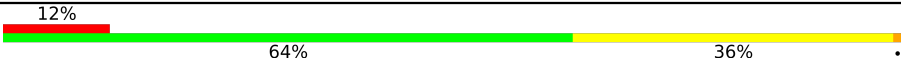
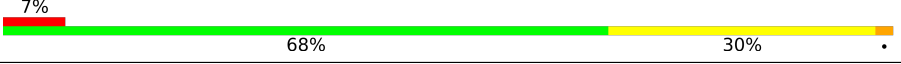
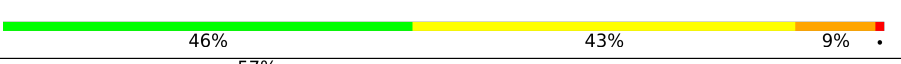
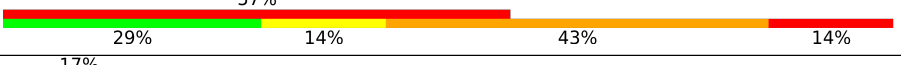
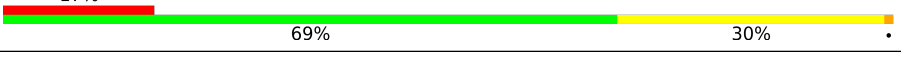
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Mol	Chain	Length	Quality of chain
54	w	223	
55	x	184	
56	y	199	
57	z	185	
58	AA	105	
59	AB	153	
60	AC	124	
61	AD	150	
62	AE	127	
63	AF	124	
64	AG	141	
65	AH	125	
66	AI	145	
67	AJ	143	
68	AK	107	
69	AL	87	
70	AM	129	
71	AN	144	
72	AO	134	
73	AP	70	
74	AQ	97	
75	AR	81	
76	AS	63	
77	AT	53	
78	AU	60	

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Mol	Chain	Length	Quality of chain
79	AV	318	
80	AW	37	
81	AX	837	
82	AY	76	
83	AZ	7	
84	BA	204	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 212058 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3223	Total	C	N	O	P	0	0
			68931	30790	12416	22502	3223		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P0	189	Total	C	N	O	S	0	0
			1473	942	257	270	4		

- Molecule 5 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P2	94	Total	C	N	O	S	0	0
			723	448	138	135	2		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 7 is a protein called 60S ribosomal protein L3.

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

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L5.

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

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 14 is a protein called 60S ribosomal protein L10.

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

- Molecule 15 is a protein called 60S ribosomal protein L11-B.

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

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	183	Total	C	N	O	S	0	0
			1420	882	281	257			

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	136	Total	C	N	O	S	0	0
			997	625	186	179	7		

- Molecule 27 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	62	Total	C	N	O	S	0	0
			513	330	101	81	1		

- Molecule 28 is a protein called 60S ribosomal protein L25.

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

- Molecule 29 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 31 is a protein called 60S ribosomal protein L28.

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

- Molecule 32 is a protein called 60S ribosomal protein L29.

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

- Molecule 33 is a protein called 60S ribosomal protein L30.

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

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 35 is a protein called 60S ribosomal protein L32.

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

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 41 is a protein called 60S ribosomal protein L38.

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

- Molecule 42 is a protein called 60S ribosomal protein L39.

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

- Molecule 43 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 44 is a protein called 60S ribosomal protein L41-B.

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

- Molecule 45 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	1776	Total	C	N	O	P	0	0
			37845	16918	6702	12449	1776		

- Molecule 48 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 49 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 50 is a protein called 40S ribosomal protein S2.

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

- Molecule 51 is a protein called 40S ribosomal protein S3.

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

- Molecule 52 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 53 is a protein called 40S ribosomal protein S5.

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

- Molecule 54 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	223	Total	C	N	O	S	0	0
			1790	1123	346	318	3		

- Molecule 55 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	x	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 56 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 57 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 58 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 59 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AB	153	Total	C	N	O	S	0	0
			1220	780	231	206	3		

- Molecule 60 is a protein called 40S ribosomal protein S12.

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

- Molecule 61 is a protein called 40S ribosomal protein S13.

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

- Molecule 62 is a protein called 40S ribosomal protein S14-B.

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

- Molecule 63 is a protein called 40S ribosomal protein S15.

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

- Molecule 64 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AG	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 65 is a protein called 40S ribosomal protein S17-B.

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

- Molecule 66 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 67 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 68 is a protein called 40S ribosomal protein S20.

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

- Molecule 69 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 70 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 71 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 72 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 73 is a protein called 40S ribosomal protein S25-A.

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

- Molecule 74 is a protein called 40S ribosomal protein S26-B.

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

- Molecule 75 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 76 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 77 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 78 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	AV	318	Total	C	N	O	S	0	0
			2437	1541	418	470	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
80	AW	37	Total	C	N	O	S	0	0
			287	177	57	49	4		

- Molecule 81 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AX	837	Total	C	N	O	S	0	0
			6523	4143	1120	1231	29		

- Molecule 82 is a RNA chain called Transfer RNA - Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	AY	76	Total	C	N	O	P	0	0
			1626	725	293	532	76		

- Molecule 83 is a RNA chain called Messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	AZ	7	Total	C	N	O	P	0	0
			144	65	21	51	7		

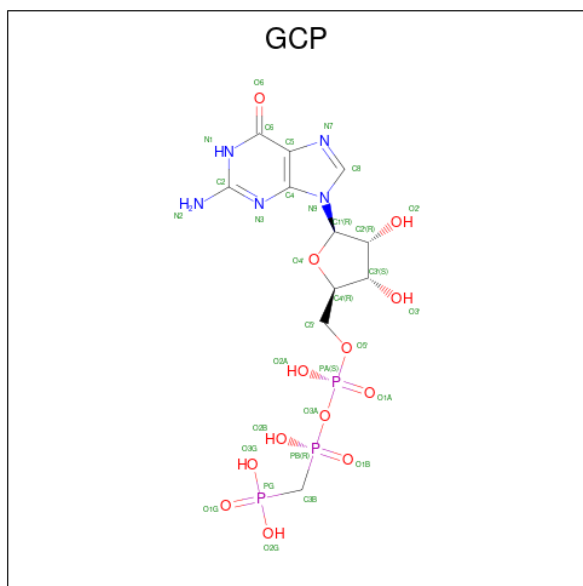
- Molecule 84 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	BA	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	j	1	Total	Zn	0
			1	1	
85	m	1	Total	Zn	0
			1	1	
85	o	1	Total	Zn	0
			1	1	
85	p	1	Total	Zn	0
			1	1	
85	AQ	1	Total	Zn	0
			1	1	
85	AR	1	Total	Zn	0
			1	1	
85	AT	1	Total	Zn	0
			1	1	
85	AW	1	Total	Zn	0
			1	1	

- Molecule 86 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

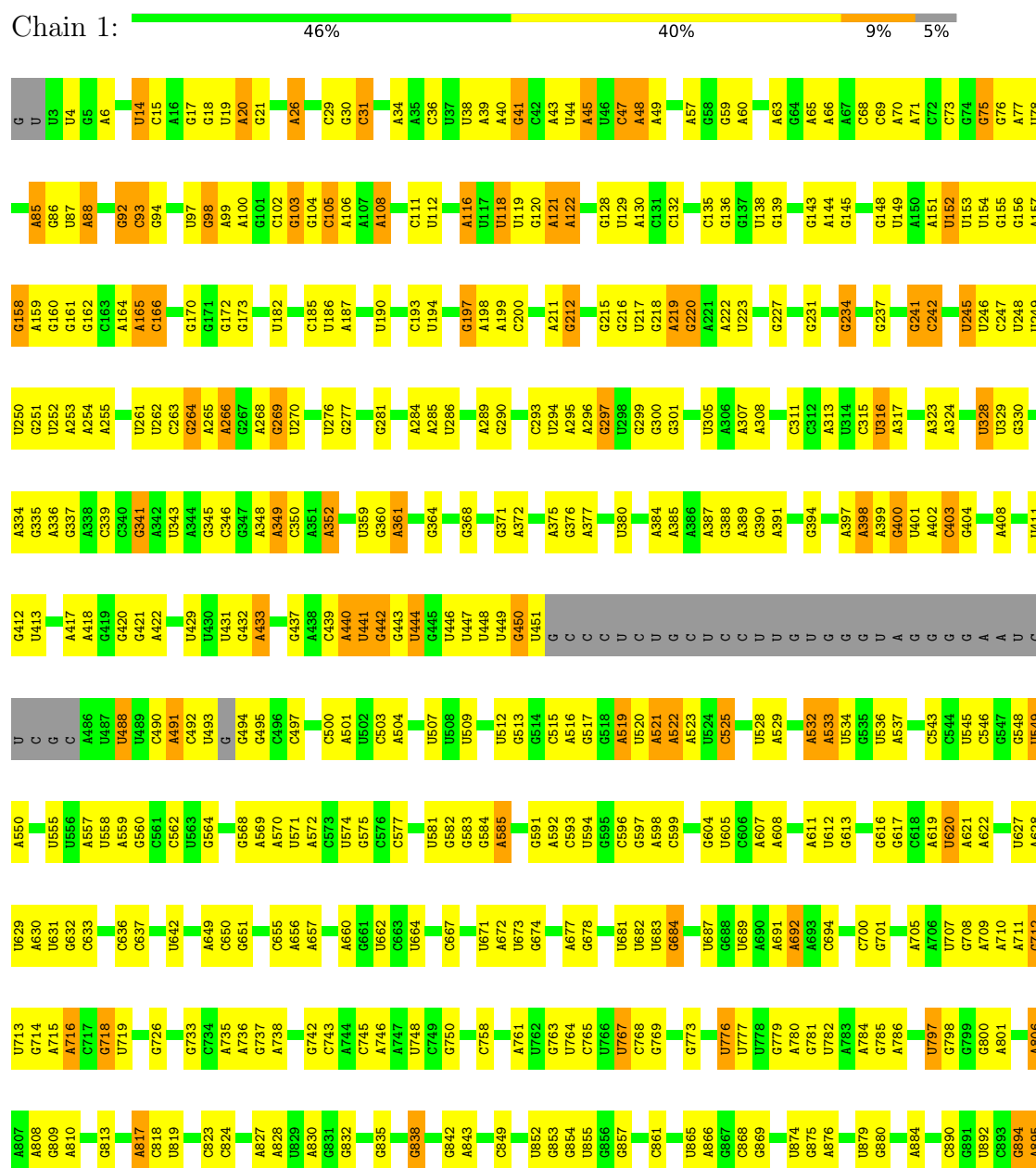


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
86	AX	1	32	11	5	13	3	0

3 Residue-property plots

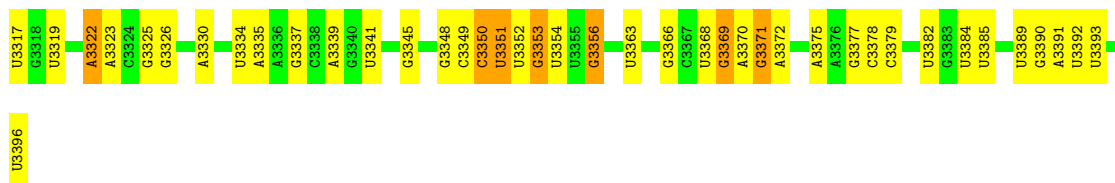
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 25S ribosomal RNA



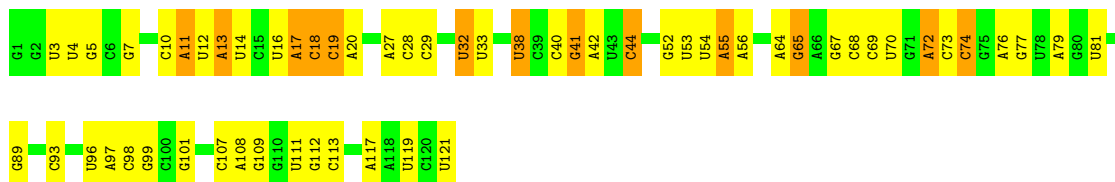
C	A1850	U1765	G1678	C1596	A1524	C1420	U1341	G1264	A1200	A1120	U1051	U981	A896
U	G1851	G1766	G1680	C1597	G1525	U1425	C1342	U1267	C1201	G1126	U1054	C982	U899
G	U1855	C1767	A1683	A1603	U1530	G1429	G1344	G1268	A1203	U1128	A1054	A983	G900
G	A1858	G1770	U1691	G1604	U1533	G1431	U1347	A1271	G1206	A1130	U1056	U985	U903
G	A1859	U1772	U1692	U1606	U1536	G1434	U1348	C1272	G1209	G1131	G1059	A889	A904
G	G1860	C1773	C1693	U1607	A1537	C1437	G1349	U1275	U1210	A1136	U1060	G991	G907
G	G1861	G1774	A1696	A1613	U1538	C1437	U1351	C1276	U1211	C1137	A1061	A992	G908
C	G1862	G1775	U1702	U1616	A1539	G1441	U1352	C1277	A1212	A1142	A1062	G993	G909
C	G1863	U1776	G1703	U1617	A1542	U1442	U1353	C1278	G1213	G1142	G1063	G994	G910
U	A1864	U1777	U1703	G1617	G1543	U1446	G1354	C1279	U1214	A1143	A1064	U995	C911
G	G1865	G1778	U1706	G1617	A1546	U1447	U1355	C1280	U1215	A1144	A1065	A996	
C	C1866	C1779	C1706	U1620	G1543	A1446	A1355	G1281	C1216	U1147	G1066	G999	A914
C	A1867	G1780	C1709	A1621	A1546	G1447	G1357	U1282	A1217	U1147	U1067	A915	A915
C	G1868	U1783	C1709	G1622	A1546	G1447	U1357	C1283	U1218	G1147	C1068	G916	A917
C	C1869	U1784	C1709	G1623	A1546	G1447	U1357	C1284	U1219	G1148	G1001	A1002	
C	U1877	G1788	C1710	U1626	C1551	G1450	C1360	G1285	U1220	G1149	U1071	U922	U922
C	G1878	U1789	C1711	U1626	G1552	G1451	U1361	U1286	A1221	A1150	G1072	G923	G923
U	A1879	C1793	G1712	U1629	U1553	A1452	U1362	A1287	G1222	U1151	U1073	G924	G924
A	U1880	G1794	G1713	U1630	U1554	A1452	A1363	U1287	A1223	G1152	A1079	U1007	U1007
G	A1881	U1795	A1714	U1631	U1555	U1455	C1364	A1291	G1224	A1153	A1080	U1008	U1008
G	G1882	U1796	U1715	C1631	C1556	A1456	G1365	C1292	A1225	A1154	U1081	A1009	C928
G	U1885	G1797	U1716	A1632	A1557	A1456	A1366	G1292	G1226	G1155	U1082	G1010	A929
G	A1886	A1797	U1717	C1633	A1558	A1460	G1367	G1295	C1227	G1156	U1083	A1011	
C	G1888	A1798	G1718	A1633	A1559	A1460	U1368	U1301	C1228	G1157	G1083	G1012	U932
C	G1892	A1799	U1722	A1638	G1560	G1466	A1369	A1302	G1229	A1158	A1084	G1013	A933
C	U1893	A1800	A1723	C1639	G1561	G1466	G1370	A1303	G1230	A1159	A1085	U1014	
C	A1894	U1724	U1724	U1641	C1563	U1470	G1374	A1304	A1231	U1167	C1086	U1015	A936
A	U1895	C1803	U1728	A1642	U1564	U1471	G1375	U1305	G1232	U1168	G1087	C1016	G937
C	A1896	A1804	A1729	A1643	G1565	A1475	A1381	G1306	G1233	A1169	U1088	C1017	C938
U	G1897	G1807	G1730	U1644	U1567	G1476	G1382	G1307	U1235	G1170	G1089	G1019	G941
G	G1898	A1813	A1731	C1645	U1567	A1477	U1383	U1308	G1236	G1171	A1091	U942	U942
C	A1900	U1814	U1736	G1646	U1568	A1477	A1386	U1309	G1237	U1173	C1092	G1021	U943
C	G1905	U1815	G1736	A1647	U1569	A1482	U1387	G1310	G1238	G1174	U1094	G1022	C944
C	C1907	A1816	U1737	U1648	U1570	U1482	G1388	G1311	A1240	G1177	U1095	G1023	G950
C	A1908	G1817	U1737	U1650	A1571	U1484	G1389	G1312	U1241	G1178	A1096	G1024	A951
C	U1909	U1820	C1738	G1654	U1572	G1485	A1390	C1313	A1244	A1179	G1097	A1025	A952
C	A1910	U1821	U1740	A1654	G1573	G1485	C1391	U1314	A1245	A1180	A1098	A1026	G953
C	A1911	U1821	U1740	G1655	U1574	G1488	G1392	C1315	G1246	U1181	U1099	A1027	
G	U1912	U1824	G1748	C1657	G1575	A1489	A1393	A1316	U1247	A1182	G1101	U1028	C959
U	A1913	G1825	A1749	C1660	C1576	A1490	A1394	A1317	G1248	C1183	U1100	G1029	U960
U	G1914	U1750	G1751	G1661	A1580	A1490	U1398	A1318	G1249	A1184	A1102	C1031	A962
C	A1915	A1752	G1752	G1662	C1581	A1497	A1399	C1320	A1252	G1185	A1103	U1033	G963
A	U1916	G1753	G1753	C1663	A1582	A1498	G1400	G1321	A1253	G1186	A1104	C1032	G964
C	C1917	G1754	G1754	G1664	U1583	A1502	U1405	U1325	C1254	A1190	G1106	U1034	
C	U1920	U1837	C1755	C1665	U1584	C1502	A1406	A1326	U1255	U1191	U1111	G1035	C969
C	A1921	G1838	C1756	G1666	A1587	G1507	U1406	U1331	C1256	C1192	A1112	A1036	A970
C	U1922	A1839	A1757	G1667	A1588	C1508	C1411	U1332	G1257	A1193	G1113	C1037	G971
G	C1923	U1840	U1757	G1668	A1589	C1508	U1415	U1336	U1258	G1194	U1114	U1039	
C	U1924	A1841	G1758	C1670	G1590	U1511	U1416	A1337	A1259	A1195	G1115	U1041	G974
C	C1926	C1842	C1759	C1671	G1591	U1512	C1417	A1338	A1260	C1196	G1116	U1042	C977
U		A1846	A1760	G1674	G1592	U1512	G1417	C1339	G1261	A1197	G1117	U1043	G978
U	G1929	A1847	C1761	G1677	A1593	U1523	A1418	C1340	G1262	C1198	U1118	U1044	U979
C	U1931		U1764	G1677			A1419		A1263	C1199		A1047	A980
G													





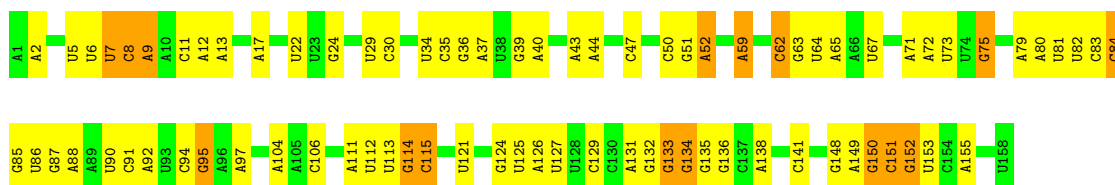
- Molecule 2: 5S ribosomal RNA

Chain 3: 52% 37% 11%



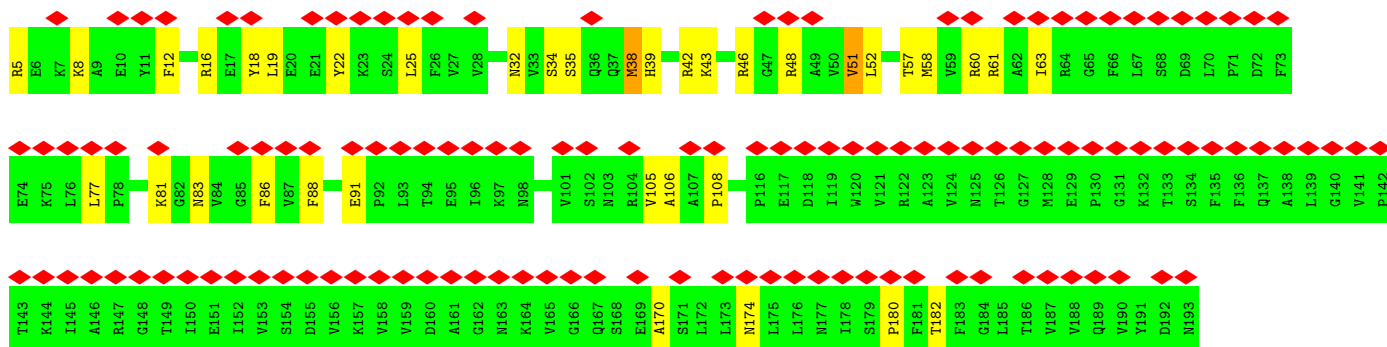
- Molecule 3: 5.8S ribosomal RNA

Chain 4: 49% 41% 10%



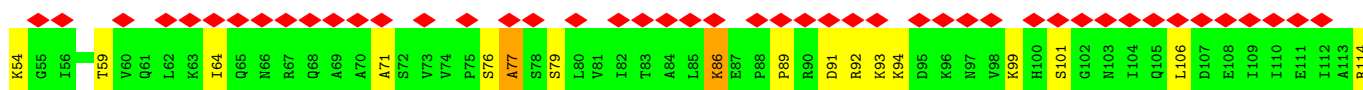
- Molecule 4: 60S acidic ribosomal protein P0

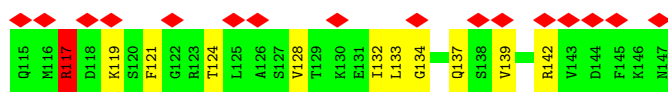
Chain P0: 67% 80% 19%



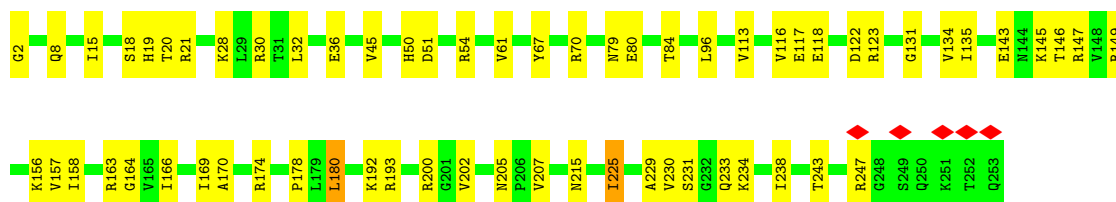
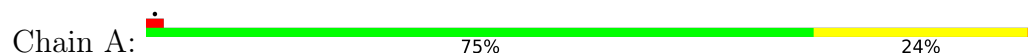
- Molecule 5: 60S ribosomal protein L12-A

Chain P2: 66% 70% 27%

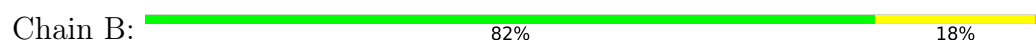




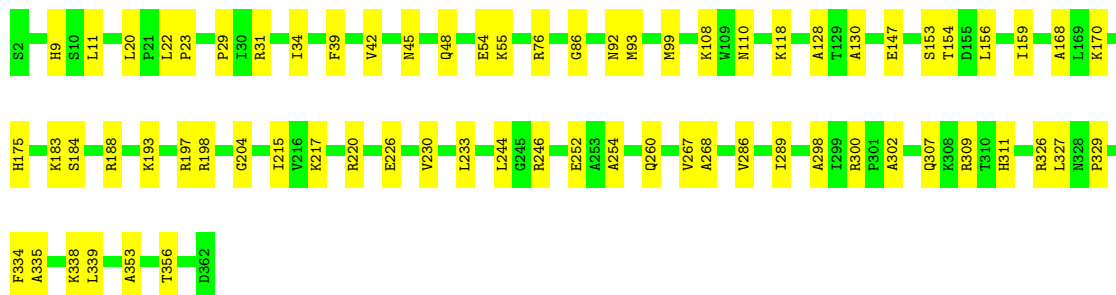
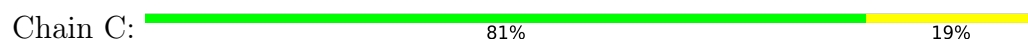
• Molecule 6: 60S ribosomal protein L2-A



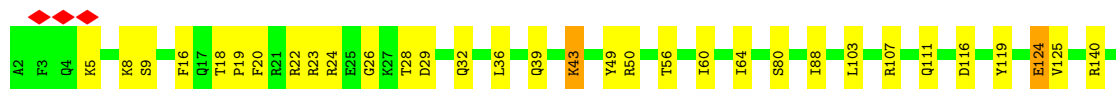
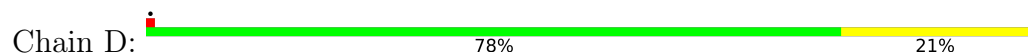
• Molecule 7: 60S ribosomal protein L3

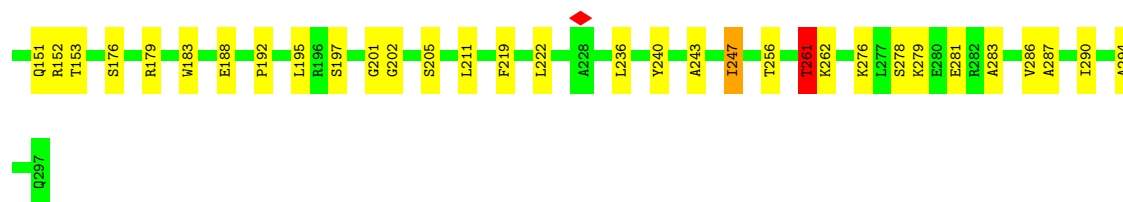


• Molecule 8: 60S ribosomal protein L4-A

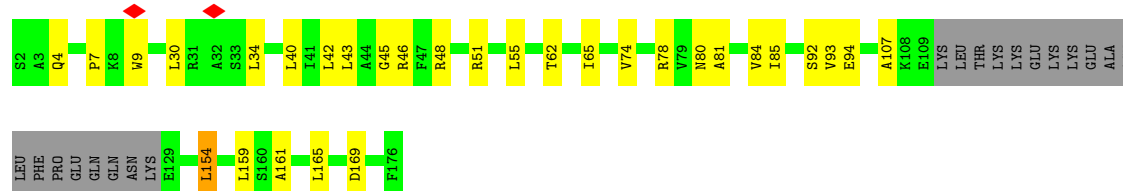


• Molecule 9: 60S ribosomal protein L5

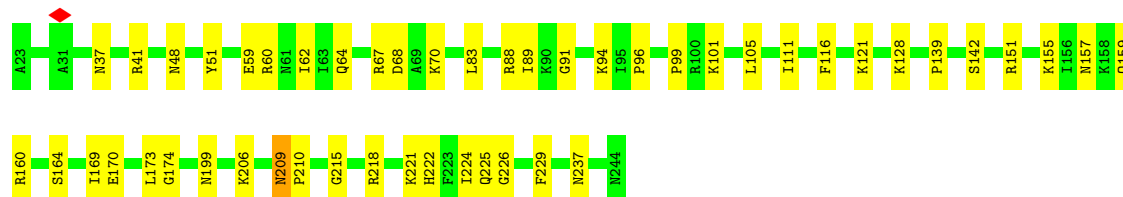
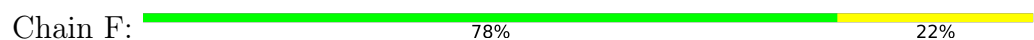




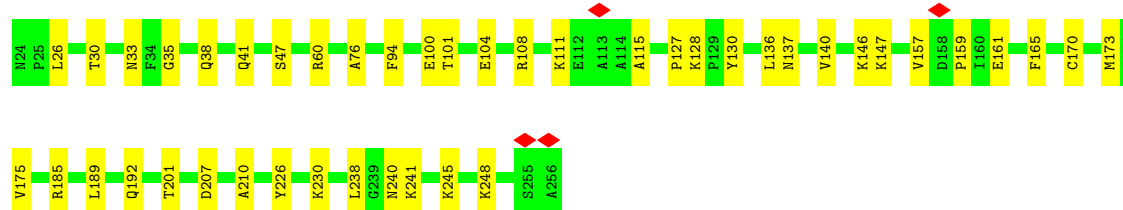
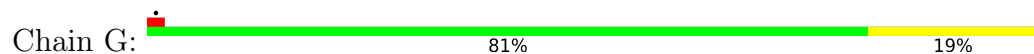
- Molecule 10: 60S ribosomal protein L6-A



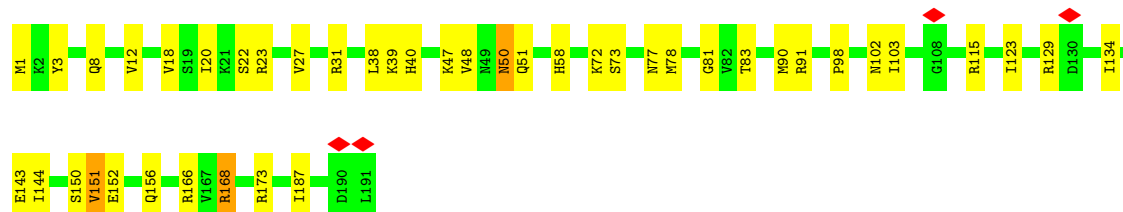
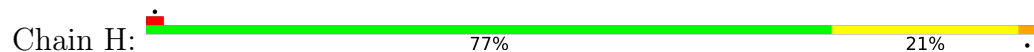
- Molecule 11: 60S ribosomal protein L7-A



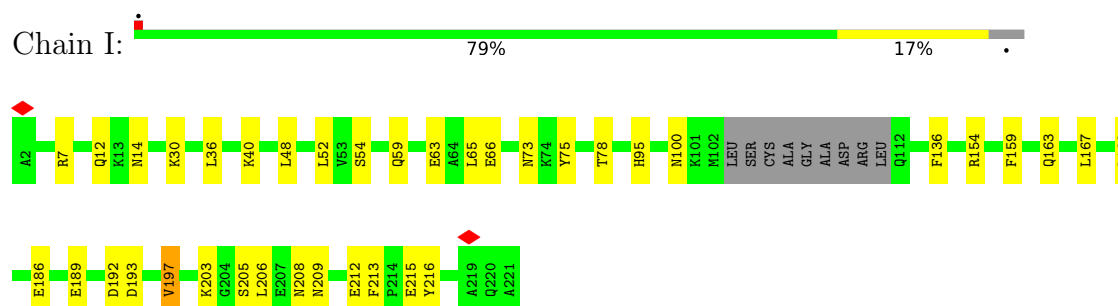
- Molecule 12: 60S ribosomal protein L8-A



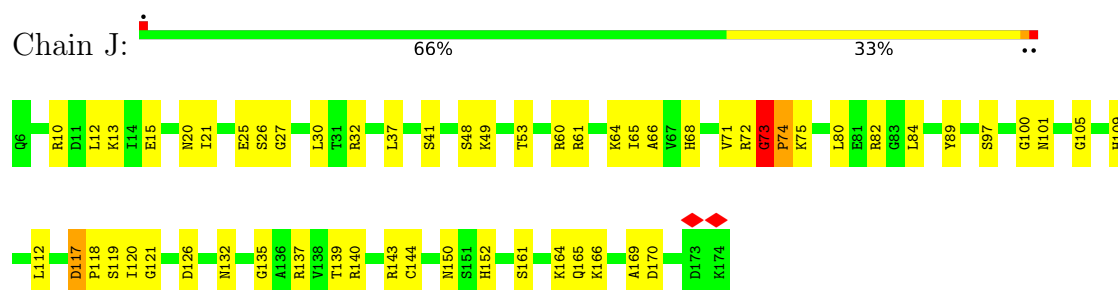
- Molecule 13: 60S ribosomal protein L9-A



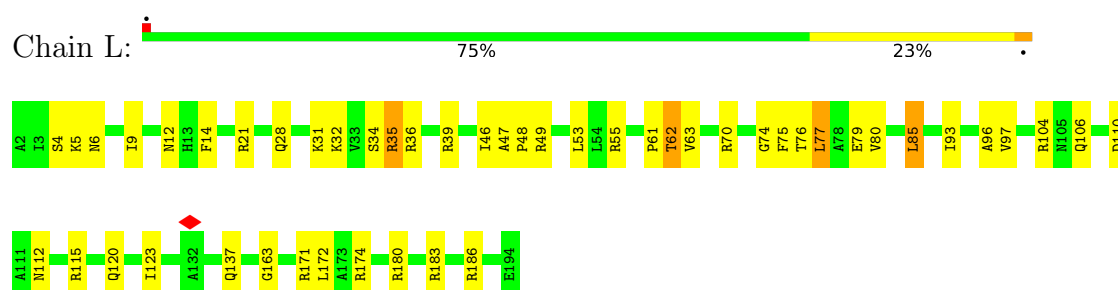
- Molecule 14: 60S ribosomal protein L10



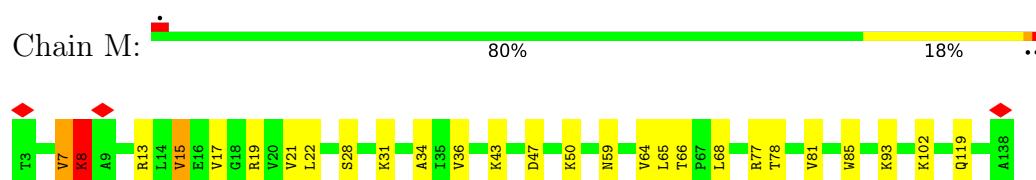
- Molecule 15: 60S ribosomal protein L11-B



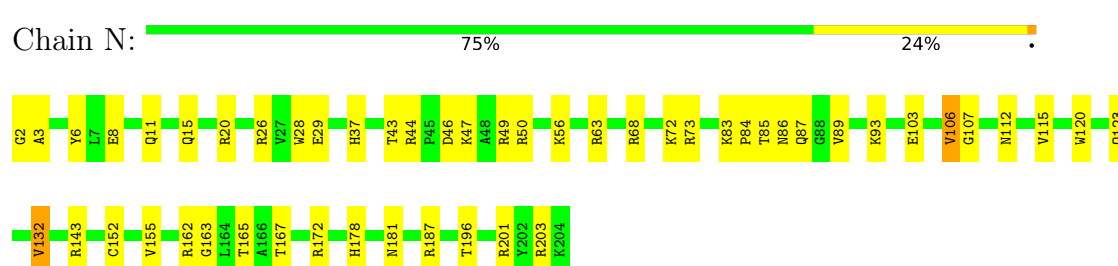
- Molecule 16: 60S ribosomal protein L13-A



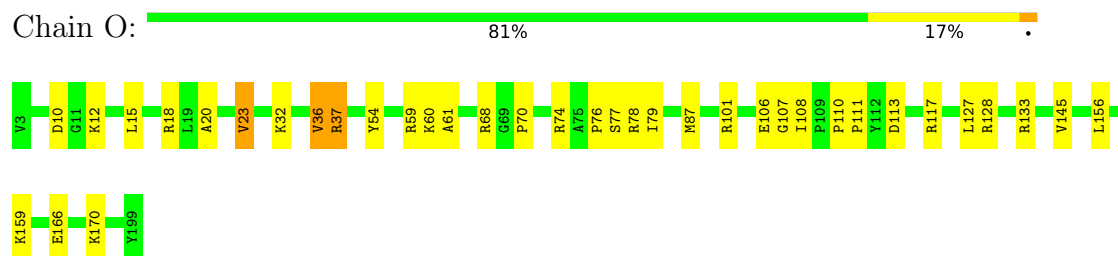
- Molecule 17: 60S ribosomal protein L14-A



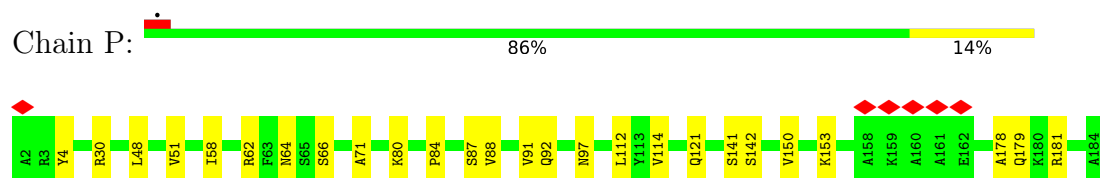
- Molecule 18: 60S ribosomal protein L15-A



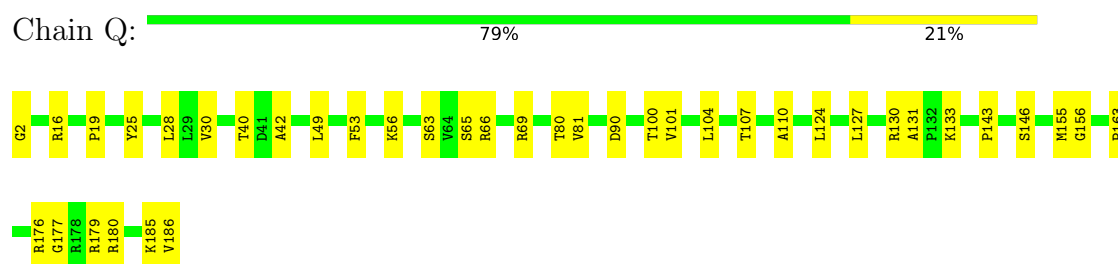
- Molecule 19: 60S ribosomal protein L16-A



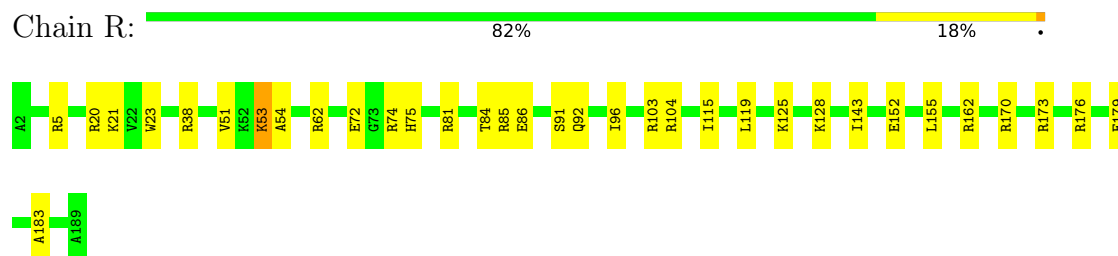
- Molecule 20: 60S ribosomal protein L17-A



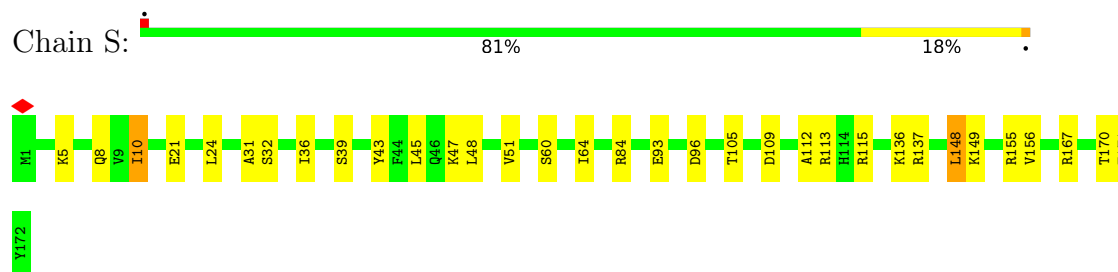
- Molecule 21: 60S ribosomal protein L18-A



- Molecule 22: 60S ribosomal protein L19-A



- Molecule 23: 60S ribosomal protein L20-A



- Molecule 24: 60S ribosomal protein L21-A

Chain T:  83% 17%



- Molecule 25: 60S ribosomal protein L22-A

Chain U:  88% 12%



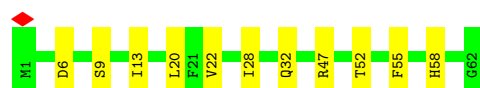
- Molecule 26: 60S ribosomal protein L23-A

Chain V:  81% 18%



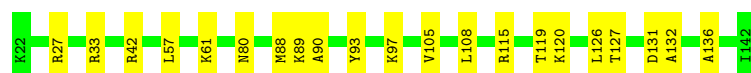
- Molecule 27: 60S ribosomal protein L24-A

Chain W:  82% 18%



- Molecule 28: 60S ribosomal protein L25

Chain X:  83% 17%



- Molecule 29: 60S ribosomal protein L26-A

Chain Y:  79% 21%

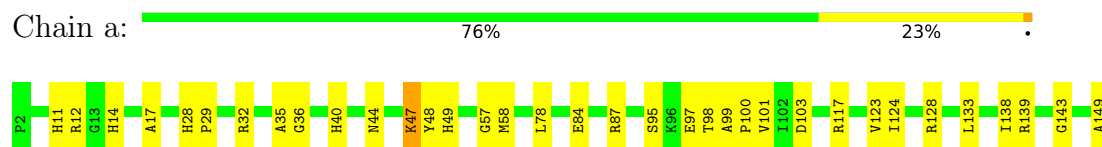


- Molecule 30: 60S ribosomal protein L27-A

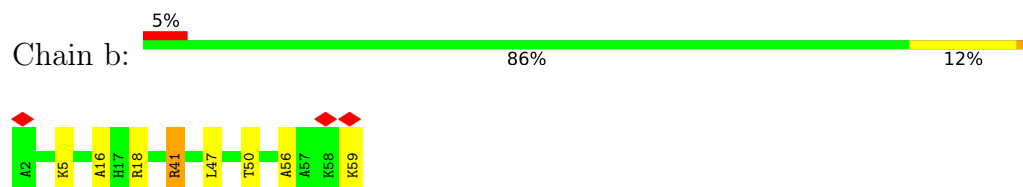
Chain Z:  76% 23%



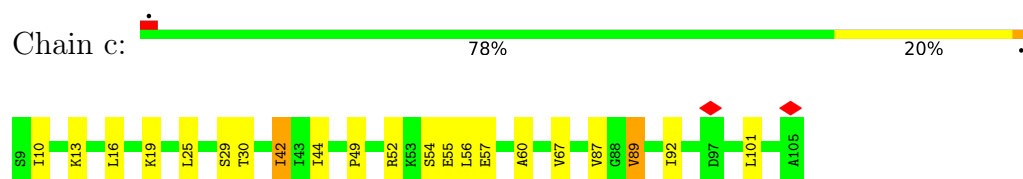
- Molecule 31: 60S ribosomal protein L28



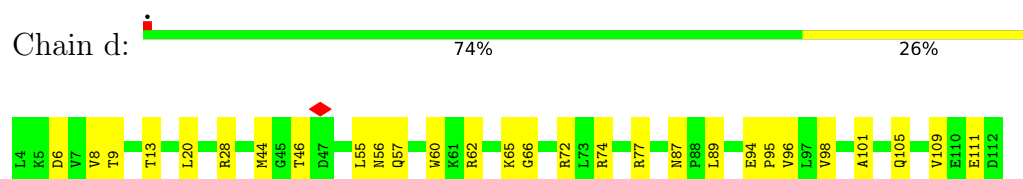
- Molecule 32: 60S ribosomal protein L29



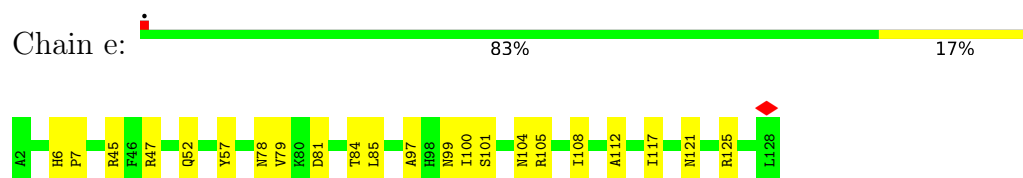
- Molecule 33: 60S ribosomal protein L30



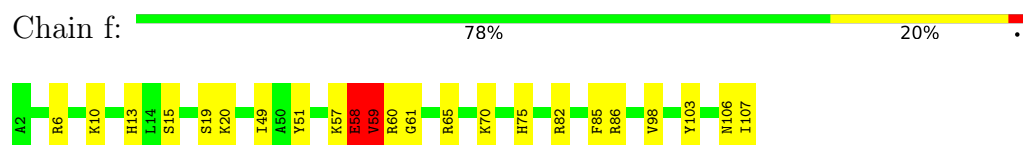
- Molecule 34: 60S ribosomal protein L31-A



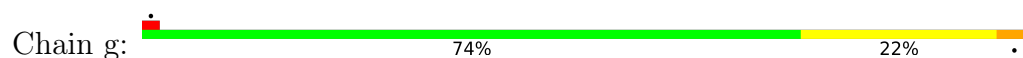
- Molecule 35: 60S ribosomal protein L32



- Molecule 36: 60S ribosomal protein L33-A

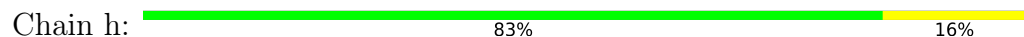


- Molecule 37: 60S ribosomal protein L34-A





- Molecule 38: 60S ribosomal protein L35-A



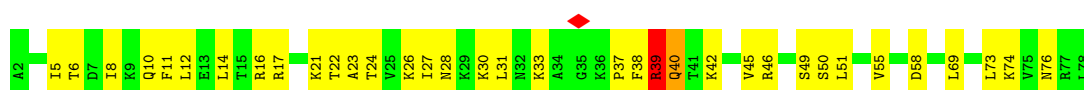
- Molecule 39: 60S ribosomal protein L36-A



- Molecule 40: 60S ribosomal protein L37-A



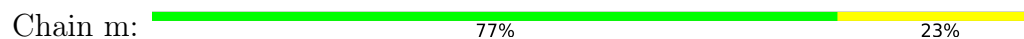
- Molecule 41: 60S ribosomal protein L38



- Molecule 42: 60S ribosomal protein L39

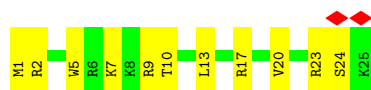


- Molecule 43: Ubiquitin-60S ribosomal protein L40

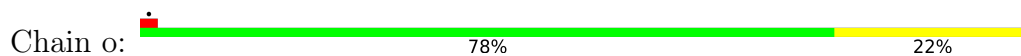


- Molecule 44: 60S ribosomal protein L41-B

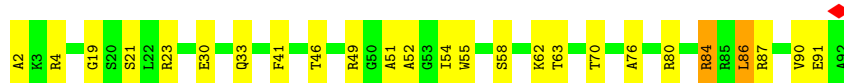




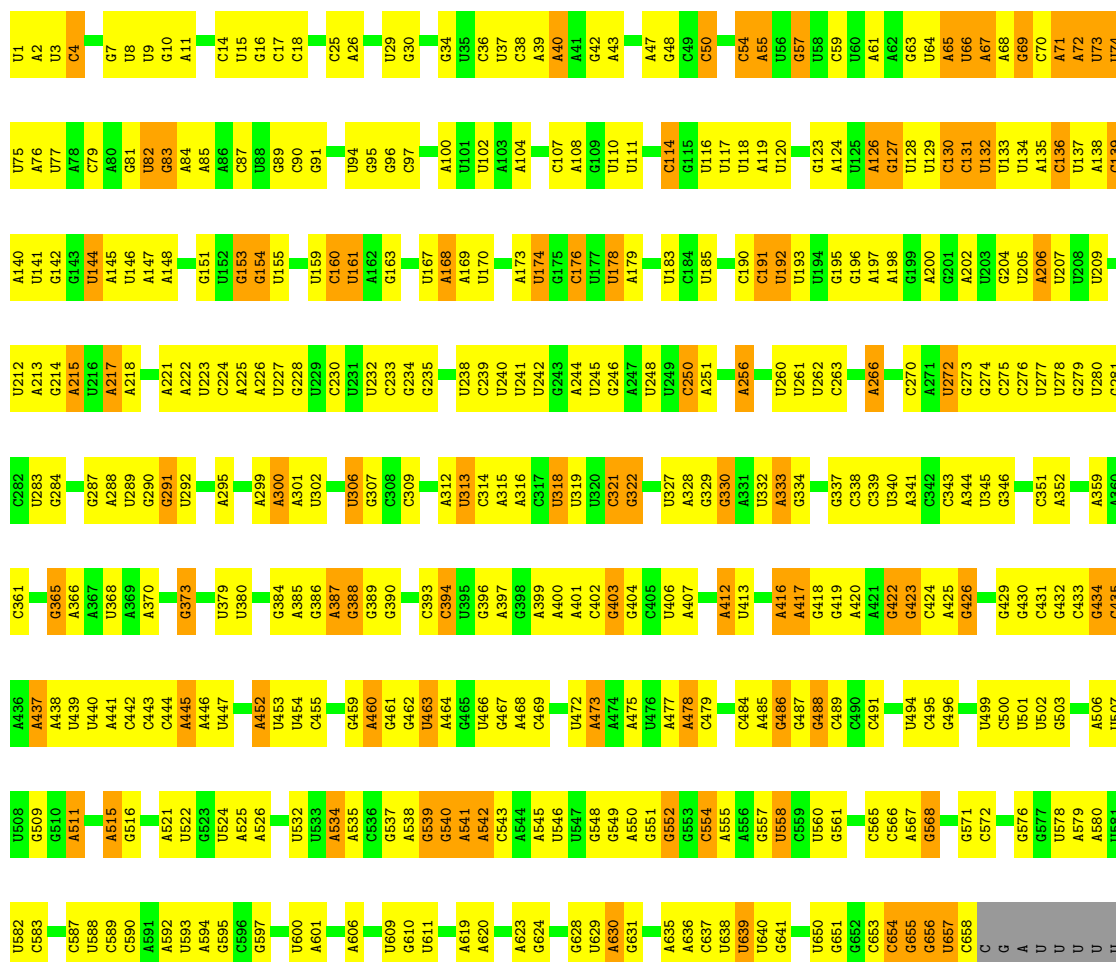
- Molecule 45: 60S ribosomal protein L42-A



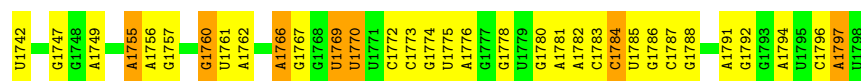
- Molecule 46: 60S ribosomal protein L43-A



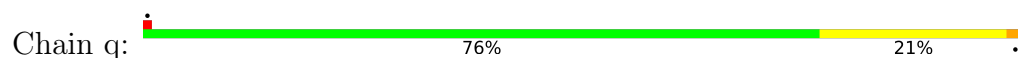
- Molecule 47: 18S ribosomal RNA



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A1671	G1594	G1455	A1329	U1254	C1192	A1124	A1030	G949	C853	A814	C735	G
G1672	U1595	C1456	C1332	G1255	A1193	A1125	A1031	C950	A854	G815	C736	U
G1673	C1596	C1457	C1333	U1256	A1194	A1125	G1032	A951	G855	G816	A737	G
G1674	A1597	G1458	U1334	U1257	C1195	A1125	A1033	A952	U886	A817	G738	U
U1675	U1598	C1459	U1335	U1258	A1196	A1132	A1036	G953	C818	C818	G739	A
U1676	G1599	A1460	U1336	U1259	C1199	A1133	A1039	G954	G819	G819	A740	C
C1677	U1528	C1398	A1337	U1260	G1199	C1134	A1039	G957	U820	U820	C741	U
A1678	U1529	C1399	A1337	G1261	G1200	C1135	G1040	C957	A821	U821	U742	G876
G1679	C1530	A1400	C1338	U1262	G1201	U1135	G1041	U958	G895	G895	U743	G877
G1680	G1531	A1401	C1339	G1263	A1202	U1136	G1042	U959	G896	G896	U744	A878
C1681	U1532	C1402	U1340	G1264	A1203	A1137	A1043	U960	U896	U896	U745	U879
G1682	C1533	G1403	A1341	G1265	A1204	A1138	U1044	U961	C827	U826	U749	U879
U1683	G1534	C1404	C1342	U1266	C1205	G1140	C1045	C962	U827	U827	U749	U881
G1684	U1535	G1405	U1343	G1267	U1206	G1046	G1046	A963	A899	A899	A752	C886
U1685	G1536	A1406	A1344	U1268	C1207	U964	G1047	U964	A900	A900	A753	G887
C1686	C1537	U1407	A1345	U1269	A1208	U965	U1052	A965	G901	U831	A757	G887
U1688	U1538	U1408	A1346	G1270	C1209	A1147	U1052	A966	G902	U832	A757	C892
U1689	G1539	G1409	U1347	G1271	G1210	C1148	G1053	A967	G903	U833	A760	U893
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C1699	U1554	A1487	A1357	U1285	C1220	C1158	U1070	G986	G913	U843	A766	C702
U1700	A1555	G1488	A1357	U1286	A1221	C1159	C1071	G987	G914	A844	A766	G703
A1701	U1556	U1489	A1360	U1287	G1222	A1160	U1071	G987	U915	G845	A766	C704
U1702	U1557	C1490	U1361	G1288	A1223	C1161	G1074	C990	U916	G846	A766	C705
C1703	U1558	U1491	U1362	U1289	G1224	C1162	U1075	G991	U917	G847	A766	C706
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A1707	U1560	G1493	G1364	U1291	A1226	G1164	G1083	A993	U919	C849	A766	C708
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C1709	G1562	U1495	U1366	U1293	G1228	A1166	A1081	A993	U921	U851	A766	C710
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G1711	U1564	U1497	G1368	U1298	A1230	U1168	G1083	G1002	G923	G853	A766	C712
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G1713	U1566	U1499	U1370	A1300	U1232	G1170	A1087	U1004	G925	A855	A766	C714
A1714	U1567	G1502	U1371	U1301	G1233	A1171	A1088	A1005	A926	A859	A766	C715
U1715	C1568	A1503	U1372	U1302	A1234	G1172	A1088	A1005	U927	U859	A766	C716
G1716	U1568	U1497	C1373	C1306	G1235	C1173	A1091	C1010	U928	U860	A766	C717
C1717	G1572	G1504	C1374	C1307	A1236	C1174	A1092	G1011	A929	U861	A766	C718
U1720	A1573	U1505	A1375	C1309	G1237	U1175	A1092	U1012	A930	A862	A766	C719
G1727	U1574	G1506	C1376	U1310	A1238	C1176	U1097	A1013	C931	A863	A766	C720
A1730	C1575	U1507	C1376	U1311	U1239	G1178	U1098	G1014	U932	U864	A766	C721
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A1732	A1577	C1509	C1377	U1313	G1241	C1180	G1100	C1016	C934	G866	A766	C723
G1733	U1582	U1510	C1379	A1314	A1242	U1181	G1108	A1020	U935	G867	A766	C724
U1734	U1583	G1512	U1380	U1315	G1243	U1182	G1109	C1021	G936	G868	A766	C725
G1735	G1584	U1513	A1382	G1316	A1244	A1183	G1109	C1022	G937	G871	A766	C726
U1736	U1585	U1514	G1383	G1316	G1245	A1184	G1110	A1023	U938	G872	A766	C727
C1737	A1586	A1515	G1385	U1320	C1246	U1185	A1113	U1024	A941	U873	A766	C728
U1738	U1587	U1448	G1386	A1329	U1249	U1186	A1113	U1025	A944	G877	A766	C729
G1739	G1588	U1449	G1387	A1321	U1250	G1187	A1116	A1026	U947	G877	A766	C730
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G1741	C1591	U1451	U1389	A1326	C1252	C1190	G1118	C1028	U947	G877	A766	C732
U1742	U1592	U1452	U1390	C1327	C1252	C1190	G1118	C1028	U947	G877	A766	C733
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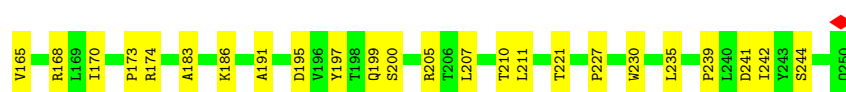
• Molecule 48: 40S ribosomal protein S0-A



• Molecule 49: 40S ribosomal protein S1-A



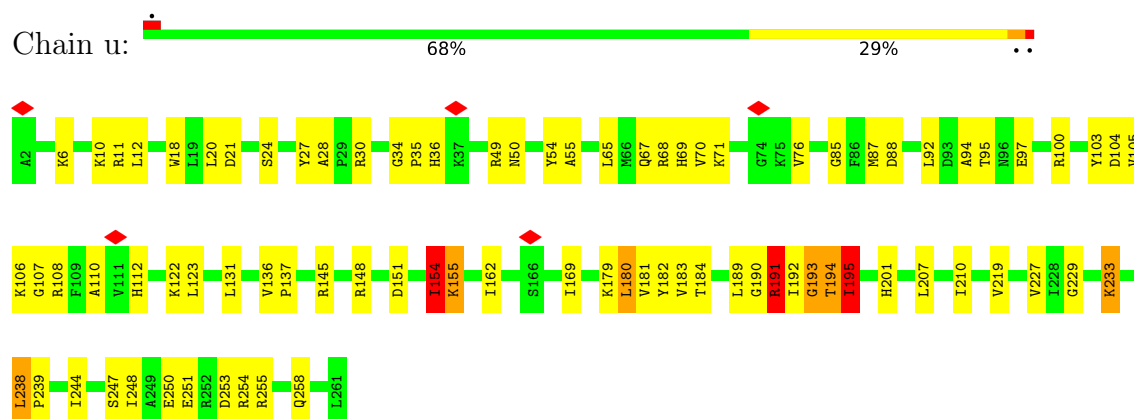
• Molecule 50: 40S ribosomal protein S2



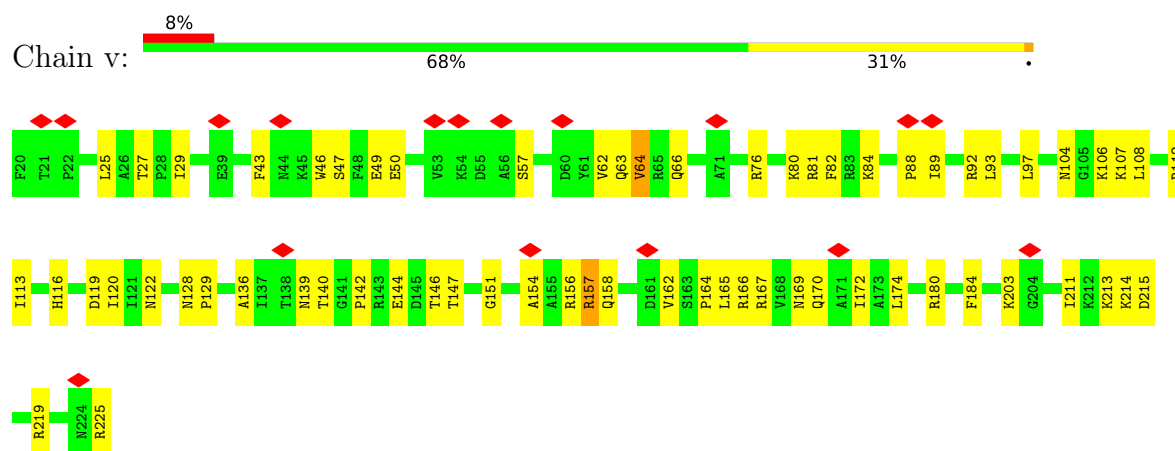
• Molecule 51: 40S ribosomal protein S3



- Molecule 52: 40S ribosomal protein S4-A



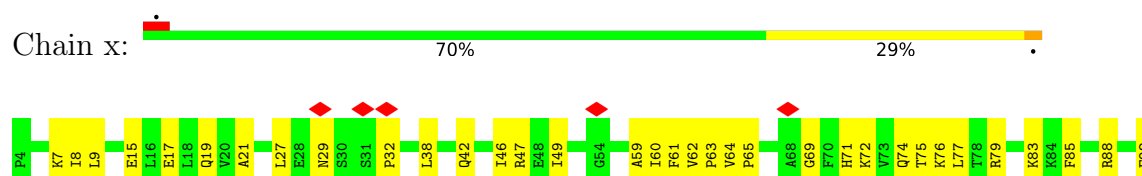
- Molecule 53: 40S ribosomal protein S5

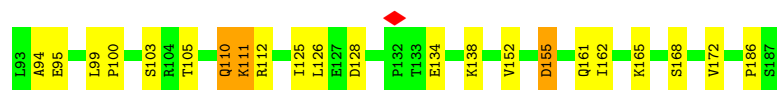


- Molecule 54: 40S ribosomal protein S6-A

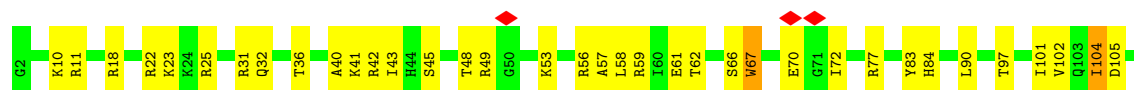


- Molecule 55: 40S ribosomal protein S7-A

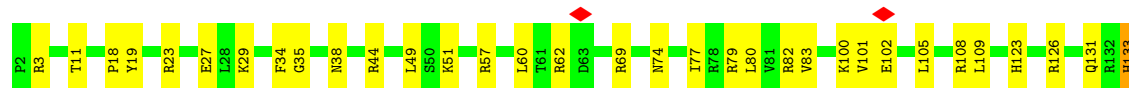
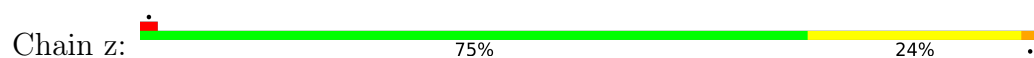




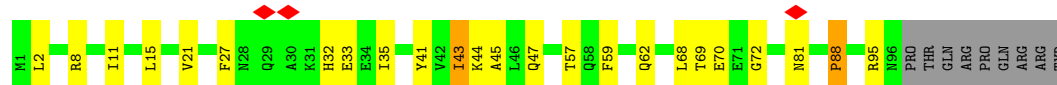
- Molecule 56: 40S ribosomal protein S8-A



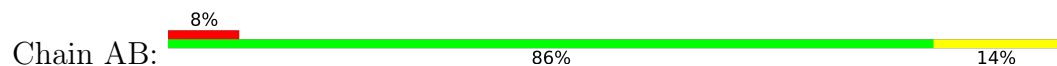
- Molecule 57: 40S ribosomal protein S9-A



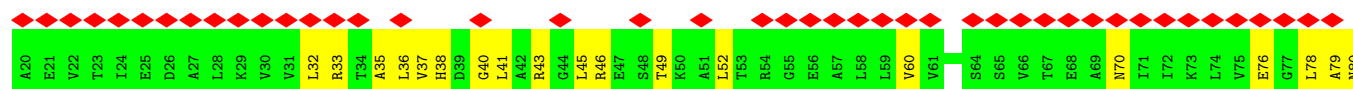
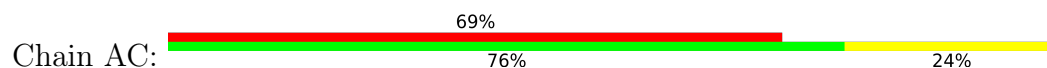
- Molecule 58: 40S ribosomal protein S10-A

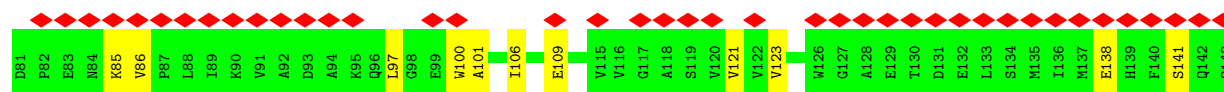


- Molecule 59: 40S ribosomal protein S11-A



- Molecule 60: 40S ribosomal protein S12

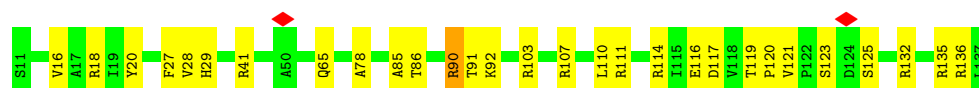
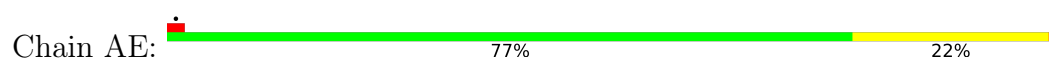




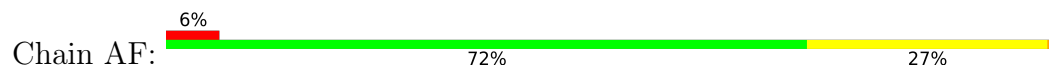
- Molecule 61: 40S ribosomal protein S13



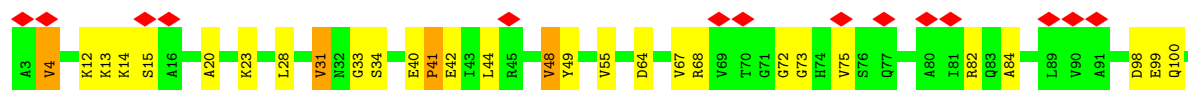
- Molecule 62: 40S ribosomal protein S14-B



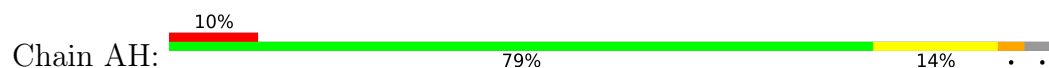
- Molecule 63: 40S ribosomal protein S15

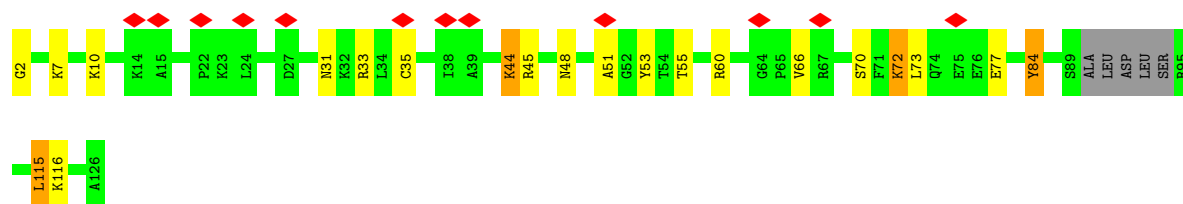


- Molecule 64: 40S ribosomal protein S16-A

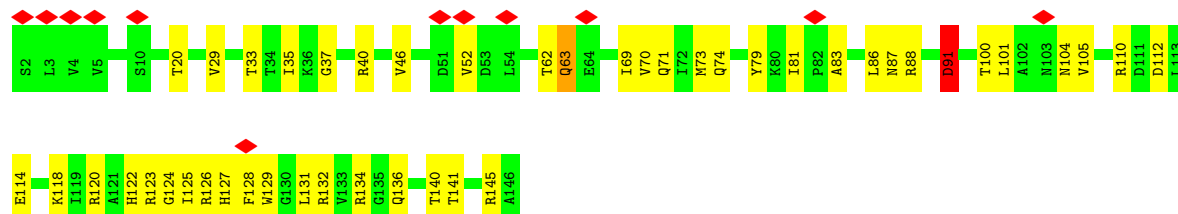


- Molecule 65: 40S ribosomal protein S17-B

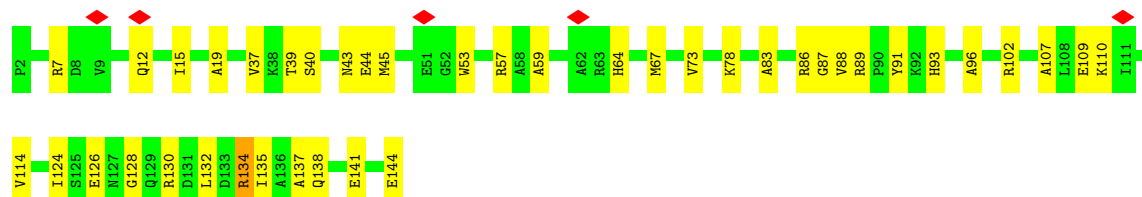




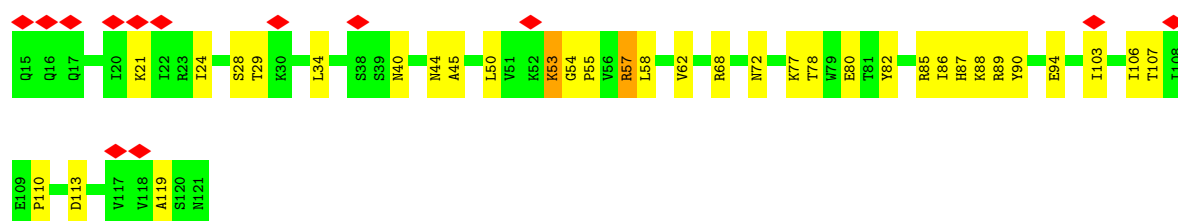
- Molecule 66: 40S ribosomal protein S18-A



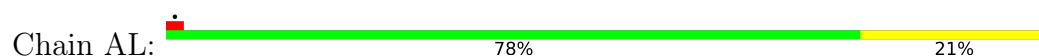
- Molecule 67: 40S ribosomal protein S19-A



- Molecule 68: 40S ribosomal protein S20



- Molecule 69: 40S ribosomal protein S21-A



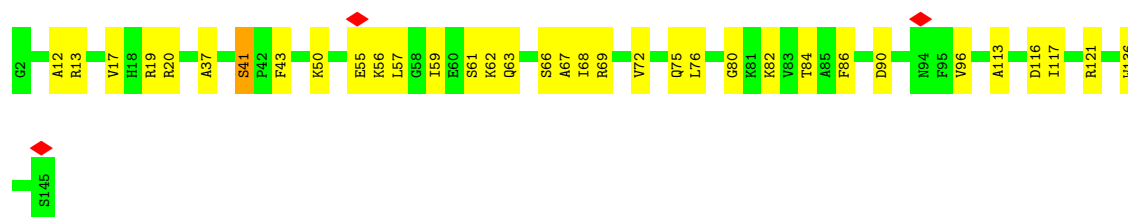
- Molecule 70: 40S ribosomal protein S22-A

Chain AM:  80% 20%



- Molecule 71: 40S ribosomal protein S23-A

Chain AN:  76% 23%



- Molecule 72: 40S ribosomal protein S24-A

Chain AO:  74% 26%



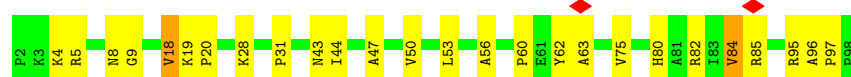
- Molecule 73: 40S ribosomal protein S25-A

Chain AP:  23% 63% 37%



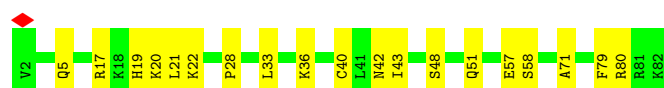
- Molecule 74: 40S ribosomal protein S26-B

Chain AQ:  73% 25%



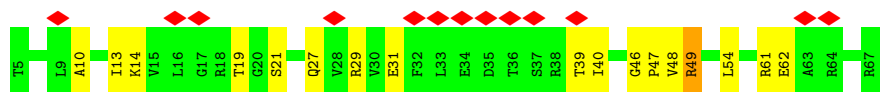
- Molecule 75: 40S ribosomal protein S27-A

Chain AR:  77% 23%

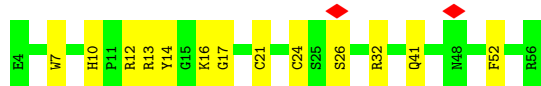
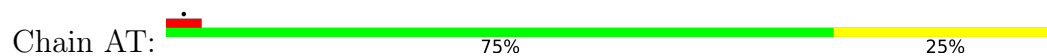


- Molecule 76: 40S ribosomal protein S28-A

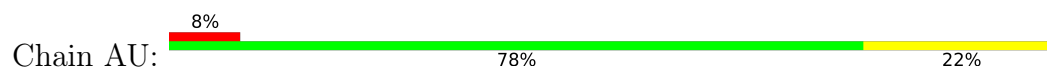
Chain AS:  21% 73% 25%



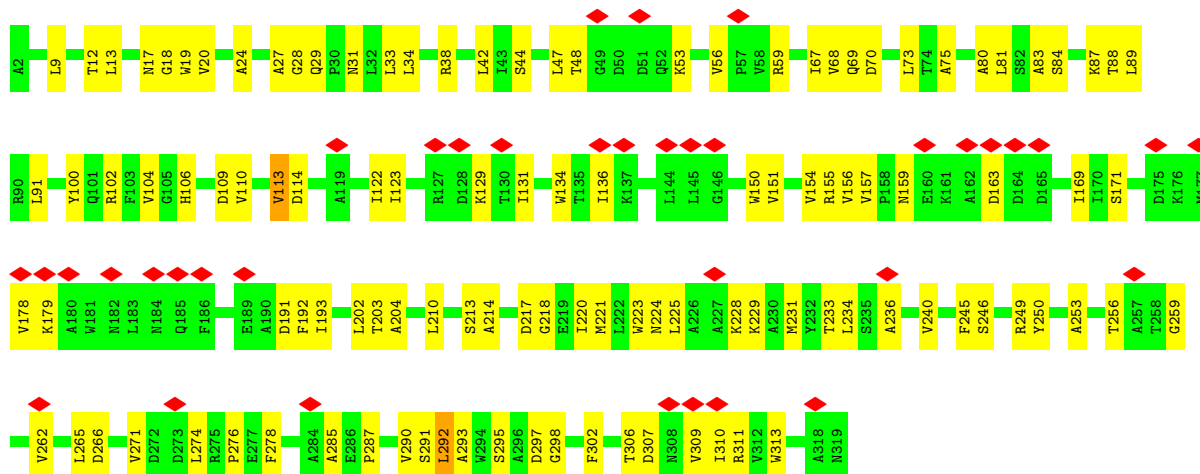
- Molecule 77: 40S ribosomal protein S29-A



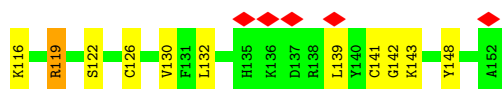
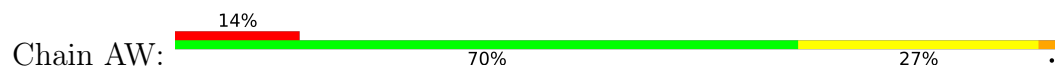
- Molecule 78: 40S ribosomal protein S30-A



- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein

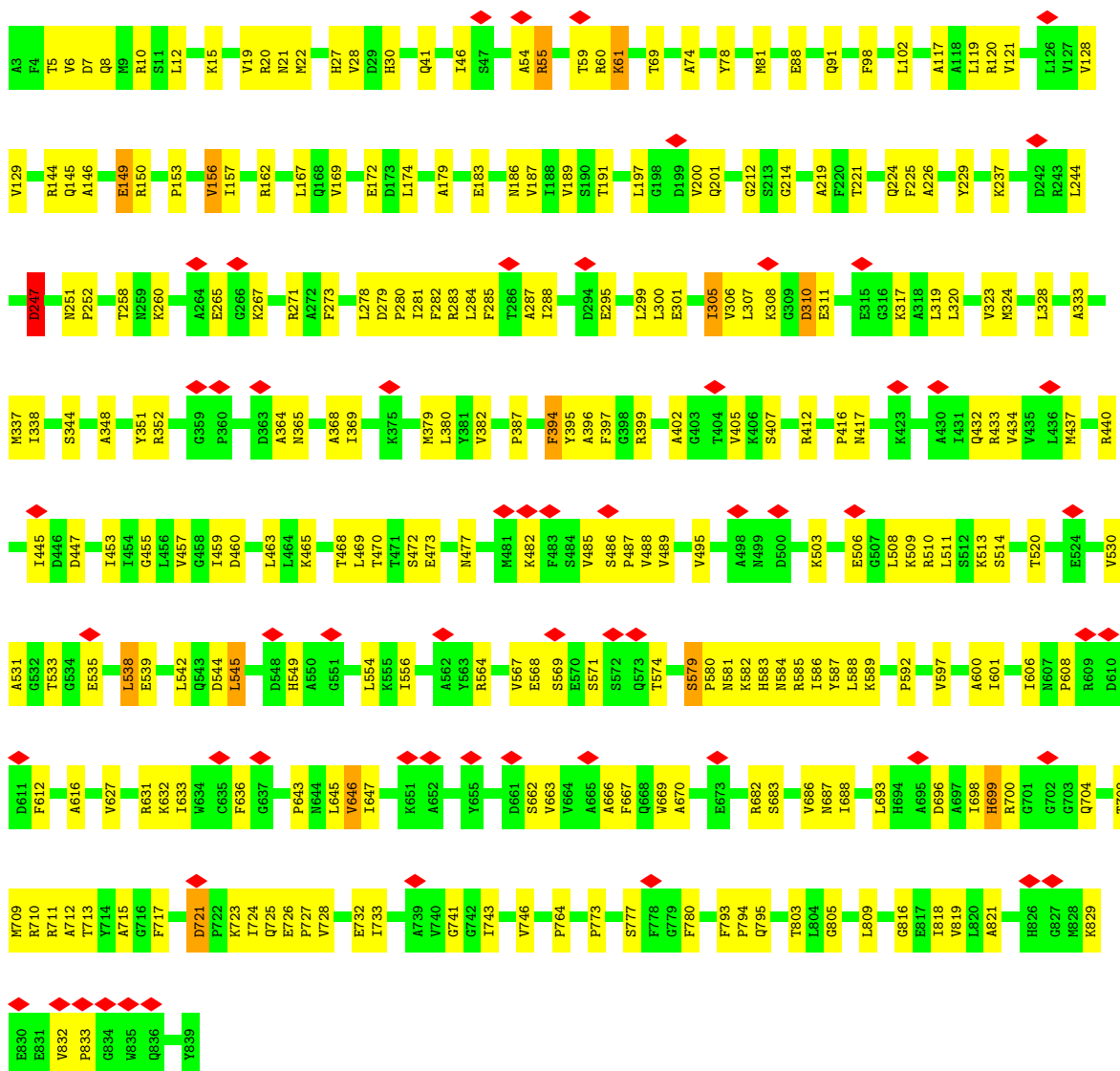


- Molecule 80: Ubiquitin-40S ribosomal protein S31



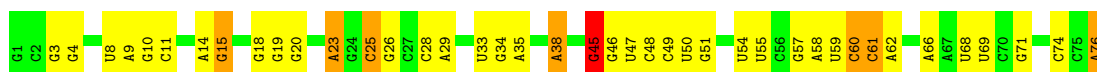
- Molecule 81: Elongation factor 2





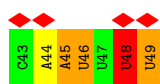
- Molecule 82: Transfer RNA - Phe

Chain AY: 46% 43% 9% .



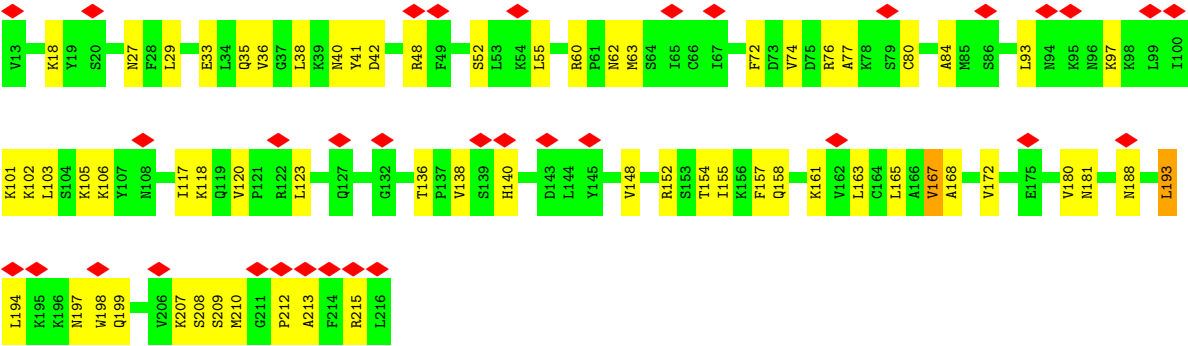
- Molecule 83: Messenger RNA

Chain AZ: 29% 14% 43% 14%



- Molecule 84: 60S ribosomal protein L1-A

Chain BA: 17% 69% 30% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	86500	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.306	Depositor
Minimum map value	-0.179	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.033	Depositor
Map size ($\text{\AA}$)	396.0, 396.0, 396.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: DDE, ZN, GCP

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	1	0.32	0/77157	0.49	2/120295 (0.0%)
2	3	0.29	0/2883	0.48	0/4491
3	4	0.33	0/3746	0.51	0/5832
4	P0	0.32	1/1498 (0.1%)	0.71	0/2025
5	P2	0.33	0/728	1.05	3/975 (0.3%)
6	A	0.39	0/1948	0.77	2/2617 (0.1%)
7	B	0.34	0/3146	0.71	2/4228 (0.0%)
8	C	0.34	0/2800	0.77	1/3790 (0.0%)
9	D	0.28	0/2425	0.71	4/3271 (0.1%)
10	E	0.28	0/1260	0.74	2/1694 (0.1%)
11	F	0.34	0/1821	0.76	0/2451
12	G	0.29	0/1836	0.71	0/2481
13	H	0.33	0/1539	0.79	3/2073 (0.1%)
14	I	0.31	0/1741	0.72	2/2335 (0.1%)
15	J	0.30	0/1374	0.90	2/1842 (0.1%)
16	L	0.33	0/1568	0.79	2/2106 (0.1%)
17	M	0.28	0/1068	0.69	1/1438 (0.1%)
18	N	0.37	0/1757	0.72	0/2354
19	O	0.35	0/1585	0.73	0/2128
20	P	0.31	0/1443	0.69	1/1944 (0.1%)
21	Q	0.33	0/1465	0.73	0/1965
22	R	0.29	0/1538	0.70	1/2050 (0.0%)
23	S	0.33	0/1481	0.71	0/1990
24	T	0.34	0/1300	0.70	2/1743 (0.1%)
25	U	0.27	0/812	0.68	0/1099
26	V	0.36	0/1012	0.76	0/1362
27	W	0.29	0/525	0.69	0/696
28	X	0.26	0/979	0.57	0/1321
29	Y	0.29	0/1004	0.66	0/1341
30	Z	0.34	0/1118	0.71	1/1497 (0.1%)
31	a	0.34	0/1204	0.78	3/1612 (0.2%)
32	b	0.31	0/473	0.67	0/629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.25	0/751	0.59	0/1008
34	d	0.35	0/897	0.70	0/1205
35	e	0.33	0/1041	0.71	0/1394
36	f	0.35	0/868	0.77	3/1168 (0.3%)
37	g	0.31	0/890	0.81	1/1189 (0.1%)
38	h	0.29	0/978	0.77	1/1301 (0.1%)
39	i	0.33	0/778	0.79	0/1034
40	j	0.34	0/696	0.83	0/923
41	k	0.32	0/618	0.86	2/826 (0.2%)
42	l	0.35	0/443	0.98	2/588 (0.3%)
43	m	0.30	0/423	0.69	0/562
44	n	0.31	0/234	0.80	0/300
45	o	0.33	0/860	0.83	2/1136 (0.2%)
46	p	0.39	0/701	0.76	0/934
47	2	0.28	0/42328	0.52	5/65955 (0.0%)
48	q	0.29	0/1617	0.77	3/2215 (0.1%)
49	r	0.31	0/1735	0.88	7/2335 (0.3%)
50	s	0.28	0/1665	0.71	2/2263 (0.1%)
51	t	0.26	0/1759	0.68	0/2368
52	u	0.29	0/2109	0.87	9/2839 (0.3%)
53	v	0.29	0/1629	0.83	4/2202 (0.2%)
54	w	0.33	0/1814	0.96	4/2425 (0.2%)
55	x	0.28	0/1506	0.82	0/2028
56	y	0.29	0/1514	0.81	4/2021 (0.2%)
57	z	0.29	0/1519	0.79	0/2035
58	AA	0.29	0/789	0.82	1/1067 (0.1%)
59	AB	0.31	0/1247	0.69	0/1681
60	AC	0.24	0/898	0.70	0/1220
61	AD	0.30	0/1215	0.85	2/1638 (0.1%)
62	AE	0.31	0/901	0.75	0/1217
63	AF	0.30	0/998	0.84	0/1341
64	AG	0.29	0/1125	0.80	5/1510 (0.3%)
65	AH	0.27	0/935	0.75	0/1254
66	AI	0.27	0/1211	0.72	0/1628
67	AJ	0.26	0/1130	0.69	0/1517
68	AK	0.30	0/865	0.92	2/1169 (0.2%)
69	AL	0.35	0/693	0.92	1/935 (0.1%)
70	AM	0.28	0/1038	0.65	0/1395
71	AN	0.33	0/1139	0.79	0/1518
72	AO	0.27	0/1087	0.65	0/1449
73	AP	0.33	0/571	0.84	0/768
74	AQ	0.33	0/782	0.93	2/1047 (0.2%)
75	AR	0.25	0/620	0.83	1/838 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AS	0.27	0/499	0.76	0/670
77	AT	0.28	0/452	0.75	0/600
78	AU	0.27	0/483	0.79	0/643
79	AV	0.25	0/2490	0.67	0/3389
80	AW	0.23	0/292	0.70	0/390
81	AX	0.32	0/6626	0.87	8/8970 (0.1%)
82	AY	0.25	0/1818	0.55	2/2831 (0.1%)
83	AZ	0.50	0/159	1.60	4/244 (1.6%)
84	BA	0.30	0/1634	0.83	1/2195 (0.0%)
All	All	0.31	1/227304 (0.0%)	0.63	112/333053 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	P0	0	2
5	P2	0	1
7	B	0	1
8	C	0	1
9	D	0	4
10	E	0	2
11	F	0	2
12	G	0	3
14	I	0	3
15	J	0	6
16	L	0	2
17	M	0	2
18	N	0	1
19	O	0	3
22	R	0	1
23	S	0	2
30	Z	0	1
31	a	0	2
32	b	0	1
34	d	0	1
36	f	0	2
37	g	0	4
38	h	0	2
39	i	0	3
40	j	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
41	k	0	2
45	o	0	2
46	p	0	1
48	q	0	2
49	r	0	3
50	s	0	1
51	t	0	4
52	u	0	7
53	v	0	4
54	w	0	6
55	x	0	3
56	y	0	1
57	z	0	3
58	AA	0	2
59	AB	0	1
61	AD	0	2
62	AE	0	3
63	AF	0	2
64	AG	0	4
65	AH	0	1
66	AI	0	1
67	AJ	0	1
68	AK	0	2
69	AL	0	2
71	AN	0	2
73	AP	0	1
74	AQ	0	3
75	AR	0	1
76	AS	0	1
78	AU	0	1
80	AW	0	1
81	AX	0	15
84	BA	0	3
All	All	0	143

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P0	77	LEU	C-N	6.31	1.38	1.33

The worst 5 of 112 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	AK	57	ARG	CA-C-N	14.83	141.55	120.49
68	AK	57	ARG	C-N-CA	14.83	141.55	120.49
83	AZ	48	U	C1'-C2'-O2'	-14.36	86.86	108.40
83	AZ	48	U	C2'-C3'-O3'	-13.04	94.13	113.70
84	BA	117	ILE	N-CA-C	-10.36	103.87	113.71

There are no chirality outliers.

5 of 143 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	B	159	ARG	Peptide
8	C	93	MET	Peptide
4	P0	16	ARG	Peptide
4	P0	38	MET	Peptide
5	P2	77	ALA	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	1	68931	0	34637	715	0
2	3	2579	0	1304	40	0
3	4	3353	0	1695	39	0
4	P0	1473	0	1514	34	0
5	P2	723	0	774	20	0
6	A	1914	0	1981	49	0
7	B	3075	0	3142	49	0
8	C	2748	0	2859	46	0
9	D	2375	0	2325	38	0
10	E	1239	0	1326	20	0
11	F	1784	0	1862	39	0
12	G	1804	0	1877	26	0
13	H	1518	0	1587	31	0
14	I	1705	0	1736	23	0
15	J	1353	0	1383	38	0
16	L	1543	0	1608	38	0
17	M	1053	0	1149	20	0
18	N	1720	0	1779	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	O	1555	0	1659	23	0
20	P	1420	0	1437	16	0
21	Q	1441	0	1543	30	0
22	R	1521	0	1617	27	0
23	S	1445	0	1487	23	0
24	T	1276	0	1323	19	0
25	U	796	0	812	6	0
26	V	997	0	1037	18	0
27	W	513	0	540	7	0
28	X	964	0	1025	15	0
29	Y	993	0	1081	22	0
30	Z	1092	0	1155	22	0
31	a	1173	0	1215	25	0
32	b	462	0	491	9	0
33	c	743	0	797	12	0
34	d	883	0	918	19	0
35	e	1020	0	1090	16	0
36	f	850	0	880	15	0
37	g	880	0	941	20	0
38	h	969	0	1078	10	0
39	i	771	0	849	19	0
40	j	681	0	683	15	0
41	k	612	0	682	23	0
42	l	436	0	475	8	0
43	m	417	0	455	9	0
44	n	233	0	284	9	0
45	o	847	0	916	12	0
46	p	694	0	736	18	0
47	2	37845	0	19040	604	0
48	q	1577	0	1567	29	0
49	r	1709	0	1784	32	0
50	s	1635	0	1723	39	0
51	t	1734	0	1817	45	0
52	u	2068	0	2154	54	0
53	v	1609	0	1675	42	0
54	w	1790	0	1881	63	0
55	x	1481	0	1572	35	0
56	y	1489	0	1525	47	0
57	z	1494	0	1573	34	0
58	AA	772	0	727	20	0
59	AB	1220	0	1281	15	0
60	AC	890	0	887	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	AD	1192	0	1255	24	0
62	AE	891	0	883	21	0
63	AF	977	0	1002	26	0
64	AG	1105	0	1166	30	0
65	AH	926	0	930	21	0
66	AI	1192	0	1222	30	0
67	AJ	1112	0	1124	28	0
68	AK	855	0	917	26	0
69	AL	684	0	672	15	0
70	AM	1021	0	1060	19	0
71	AN	1121	0	1196	24	0
72	AO	1073	0	1132	29	0
73	AP	563	0	603	17	0
74	AQ	769	0	815	20	0
75	AR	610	0	633	12	0
76	AS	497	0	535	13	0
77	AT	442	0	430	13	0
78	AU	475	0	525	11	0
79	AV	2437	0	2386	74	0
80	AW	287	0	285	8	0
81	AX	6523	0	6581	161	0
82	AY	1626	0	820	16	0
83	AZ	144	0	74	5	0
84	BA	1609	0	1701	40	0
85	AQ	1	0	0	0	0
85	AR	1	0	0	0	0
85	AT	1	0	0	0	0
85	AW	1	0	0	0	0
85	j	1	0	0	0	0
85	m	1	0	0	0	0
85	o	1	0	0	0	0
85	p	1	0	0	0	0
86	AX	32	0	14	3	0
All	All	212058	0	158911	2901	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 8.

The worst 5 of 2901 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)
81:AX:699:DDE:HAC2	83:AZ:49:U:O2'	1.45	1.13
1:1:3231:U:H3	1:1:3256:G:H1	1.05	1.04
47:2:142:G:H5''	54:w:142:ARG:HH22	1.20	1.01
47:2:142:G:N1	47:2:173:A:H2	1.59	1.00
1:1:88:A:H62	1:1:98:G:N2	1.58	0.99

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	P0	187/189 (99%)	145 (78%)	42 (22%)	0	100	100
5	P2	92/94 (98%)	64 (70%)	28 (30%)	0	100	100
6	A	250/252 (99%)	217 (87%)	33 (13%)	0	100	100
7	B	384/386 (100%)	335 (87%)	48 (12%)	1 (0%)	36	70
8	C	359/361 (99%)	305 (85%)	52 (14%)	2 (1%)	21	57
9	D	294/296 (99%)	248 (84%)	43 (15%)	3 (1%)	12	45
10	E	152/175 (87%)	137 (90%)	15 (10%)	0	100	100
11	F	220/222 (99%)	194 (88%)	25 (11%)	1 (0%)	24	60
12	G	231/233 (99%)	204 (88%)	27 (12%)	0	100	100
13	H	189/191 (99%)	168 (89%)	20 (11%)	1 (0%)	24	60
14	I	207/220 (94%)	178 (86%)	29 (14%)	0	100	100
15	J	167/169 (99%)	130 (78%)	34 (20%)	3 (2%)	6	34
16	L	191/193 (99%)	166 (87%)	23 (12%)	2 (1%)	12	45
17	M	134/136 (98%)	121 (90%)	12 (9%)	1 (1%)	18	54
18	N	201/203 (99%)	172 (86%)	29 (14%)	0	100	100
19	O	195/197 (99%)	171 (88%)	21 (11%)	3 (2%)	8	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	P	181/183 (99%)	161 (89%)	20 (11%)	0	100	100
21	Q	183/185 (99%)	165 (90%)	18 (10%)	0	100	100
22	R	186/188 (99%)	170 (91%)	16 (9%)	0	100	100
23	S	170/172 (99%)	151 (89%)	19 (11%)	0	100	100
24	T	157/159 (99%)	146 (93%)	11 (7%)	0	100	100
25	U	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
26	V	134/136 (98%)	120 (90%)	14 (10%)	0	100	100
27	W	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
28	X	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
29	Y	124/126 (98%)	115 (93%)	9 (7%)	0	100	100
30	Z	133/135 (98%)	115 (86%)	17 (13%)	1 (1%)	16	52
31	a	146/148 (99%)	118 (81%)	25 (17%)	3 (2%)	5	32
32	b	56/58 (97%)	46 (82%)	10 (18%)	0	100	100
33	c	95/97 (98%)	90 (95%)	5 (5%)	0	100	100
34	d	107/109 (98%)	95 (89%)	12 (11%)	0	100	100
35	e	125/127 (98%)	103 (82%)	22 (18%)	0	100	100
36	f	104/106 (98%)	90 (86%)	11 (11%)	3 (3%)	3	26
37	g	110/112 (98%)	98 (89%)	10 (9%)	2 (2%)	6	34
38	h	117/119 (98%)	100 (86%)	17 (14%)	0	100	100
39	i	97/99 (98%)	75 (77%)	21 (22%)	1 (1%)	12	45
40	j	85/87 (98%)	67 (79%)	16 (19%)	2 (2%)	4	30
41	k	75/77 (97%)	54 (72%)	19 (25%)	2 (3%)	4	28
42	l	48/50 (96%)	36 (75%)	11 (23%)	1 (2%)	5	32
43	m	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
44	n	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
45	o	103/105 (98%)	78 (76%)	25 (24%)	0	100	100
46	p	89/91 (98%)	78 (88%)	11 (12%)	0	100	100
48	q	204/206 (99%)	162 (79%)	39 (19%)	3 (2%)	8	38
49	r	212/214 (99%)	167 (79%)	41 (19%)	4 (2%)	6	34
50	s	215/217 (99%)	187 (87%)	27 (13%)	1 (0%)	24	60
51	t	221/223 (99%)	182 (82%)	37 (17%)	2 (1%)	14	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	u	258/260 (99%)	195 (76%)	61 (24%)	2 (1%)	16	52
53	v	204/206 (99%)	162 (79%)	41 (20%)	1 (0%)	24	60
54	w	221/223 (99%)	167 (76%)	47 (21%)	7 (3%)	3	25
55	x	182/184 (99%)	145 (80%)	34 (19%)	3 (2%)	7	37
56	y	184/199 (92%)	148 (80%)	36 (20%)	0	100	100
57	z	183/185 (99%)	147 (80%)	36 (20%)	0	100	100
58	AA	94/105 (90%)	76 (81%)	17 (18%)	1 (1%)	11	44
59	AB	151/153 (99%)	131 (87%)	18 (12%)	2 (1%)	9	41
60	AC	122/124 (98%)	93 (76%)	27 (22%)	2 (2%)	7	37
61	AD	148/150 (99%)	118 (80%)	27 (18%)	3 (2%)	6	33
62	AE	125/127 (98%)	104 (83%)	21 (17%)	0	100	100
63	AF	122/124 (98%)	89 (73%)	33 (27%)	0	100	100
64	AG	139/141 (99%)	111 (80%)	27 (19%)	1 (1%)	18	54
65	AH	116/125 (93%)	98 (84%)	17 (15%)	1 (1%)	14	48
66	AI	143/145 (99%)	117 (82%)	24 (17%)	2 (1%)	9	39
67	AJ	141/143 (99%)	126 (89%)	15 (11%)	0	100	100
68	AK	105/107 (98%)	90 (86%)	15 (14%)	0	100	100
69	AL	85/87 (98%)	64 (75%)	19 (22%)	2 (2%)	4	30
70	AM	127/129 (98%)	115 (91%)	11 (9%)	1 (1%)	16	52
71	AN	142/144 (99%)	108 (76%)	34 (24%)	0	100	100
72	AO	132/134 (98%)	115 (87%)	17 (13%)	0	100	100
73	AP	68/70 (97%)	52 (76%)	15 (22%)	1 (2%)	8	38
74	AQ	95/97 (98%)	70 (74%)	25 (26%)	0	100	100
75	AR	79/81 (98%)	58 (73%)	21 (27%)	0	100	100
76	AS	61/63 (97%)	49 (80%)	12 (20%)	0	100	100
77	AT	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
78	AU	58/60 (97%)	42 (72%)	16 (28%)	0	100	100
79	AV	316/318 (99%)	252 (80%)	64 (20%)	0	100	100
80	AW	35/37 (95%)	21 (60%)	14 (40%)	0	100	100
81	AX	834/837 (100%)	676 (81%)	155 (19%)	3 (0%)	30	65
84	BA	202/204 (99%)	153 (76%)	47 (23%)	2 (1%)	12	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	12203/12421 (98%)	10189 (84%)	1938 (16%)	76 (1%)	23	57

5 of 76 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	i	98	ARG
40	j	65	ARG
42	l	30	ARG
48	q	113	ARG
54	w	68	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	P0	160/160 (100%)	158 (99%)	2 (1%)	61	72
5	P2	81/81 (100%)	80 (99%)	1 (1%)	63	73
6	A	193/194 (100%)	190 (98%)	3 (2%)	55	70
7	B	321/322 (100%)	319 (99%)	2 (1%)	78	81
8	C	288/288 (100%)	285 (99%)	3 (1%)	68	76
9	D	244/244 (100%)	243 (100%)	1 (0%)	84	84
10	E	134/152 (88%)	131 (98%)	3 (2%)	45	65
11	F	186/186 (100%)	183 (98%)	3 (2%)	55	70
12	G	187/191 (98%)	185 (99%)	2 (1%)	65	74
13	H	171/171 (100%)	169 (99%)	2 (1%)	63	73
14	I	177/186 (95%)	177 (100%)	0	100	100
15	J	147/147 (100%)	143 (97%)	4 (3%)	39	60
16	L	154/154 (100%)	150 (97%)	4 (3%)	40	61
17	M	107/107 (100%)	106 (99%)	1 (1%)	70	76
18	N	175/175 (100%)	172 (98%)	3 (2%)	53	68
19	O	160/160 (100%)	159 (99%)	1 (1%)	78	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	P	140/145 (97%)	139 (99%)	1 (1%)	76	79
21	Q	150/150 (100%)	150 (100%)	0	100	100
22	R	153/153 (100%)	153 (100%)	0	100	100
23	S	156/156 (100%)	152 (97%)	4 (3%)	40	61
24	T	136/136 (100%)	134 (98%)	2 (2%)	57	70
25	U	87/87 (100%)	85 (98%)	2 (2%)	44	64
26	V	103/104 (99%)	102 (99%)	1 (1%)	68	76
27	W	54/54 (100%)	54 (100%)	0	100	100
28	X	104/105 (99%)	104 (100%)	0	100	100
29	Y	109/109 (100%)	109 (100%)	0	100	100
30	Z	115/115 (100%)	113 (98%)	2 (2%)	53	68
31	a	118/118 (100%)	118 (100%)	0	100	100
32	b	46/46 (100%)	46 (100%)	0	100	100
33	c	81/81 (100%)	79 (98%)	2 (2%)	42	62
34	d	94/96 (98%)	94 (100%)	0	100	100
35	e	109/109 (100%)	109 (100%)	0	100	100
36	f	90/90 (100%)	90 (100%)	0	100	100
37	g	95/95 (100%)	94 (99%)	1 (1%)	65	74
38	h	104/104 (100%)	103 (99%)	1 (1%)	68	76
39	i	81/81 (100%)	79 (98%)	2 (2%)	42	62
40	j	70/70 (100%)	70 (100%)	0	100	100
41	k	68/68 (100%)	68 (100%)	0	100	100
42	l	45/45 (100%)	45 (100%)	0	100	100
43	m	47/47 (100%)	47 (100%)	0	100	100
44	n	23/23 (100%)	23 (100%)	0	100	100
45	o	90/90 (100%)	89 (99%)	1 (1%)	65	74
46	p	71/71 (100%)	70 (99%)	1 (1%)	59	71
48	q	164/173 (95%)	161 (98%)	3 (2%)	51	68
49	r	191/191 (100%)	186 (97%)	5 (3%)	40	61
50	s	176/176 (100%)	175 (99%)	1 (1%)	78	81
51	t	182/182 (100%)	179 (98%)	3 (2%)	55	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	u	221/221 (100%)	217 (98%)	4 (2%)	51	68
53	v	173/173 (100%)	173 (100%)	0	100	100
54	w	189/191 (99%)	186 (98%)	3 (2%)	55	70
55	x	165/165 (100%)	165 (100%)	0	100	100
56	y	150/160 (94%)	149 (99%)	1 (1%)	76	79
57	z	158/158 (100%)	157 (99%)	1 (1%)	78	81
58	AA	77/98 (79%)	76 (99%)	1 (1%)	61	72
59	AB	133/134 (99%)	133 (100%)	0	100	100
60	AC	88/100 (88%)	88 (100%)	0	100	100
61	AD	127/127 (100%)	124 (98%)	3 (2%)	43	63
62	AE	81/96 (84%)	78 (96%)	3 (4%)	30	52
63	AF	101/104 (97%)	99 (98%)	2 (2%)	48	66
64	AG	117/117 (100%)	117 (100%)	0	100	100
65	AH	94/113 (83%)	91 (97%)	3 (3%)	34	56
66	AI	128/128 (100%)	128 (100%)	0	100	100
67	AJ	115/115 (100%)	115 (100%)	0	100	100
68	AK	100/100 (100%)	99 (99%)	1 (1%)	68	76
69	AL	74/74 (100%)	74 (100%)	0	100	100
70	AM	110/110 (100%)	109 (99%)	1 (1%)	70	76
71	AN	119/119 (100%)	117 (98%)	2 (2%)	53	68
72	AO	112/112 (100%)	112 (100%)	0	100	100
73	AP	61/61 (100%)	61 (100%)	0	100	100
74	AQ	83/83 (100%)	80 (96%)	3 (4%)	31	53
75	AR	70/70 (100%)	70 (100%)	0	100	100
76	AS	56/56 (100%)	56 (100%)	0	100	100
77	AT	47/47 (100%)	47 (100%)	0	100	100
78	AU	51/51 (100%)	50 (98%)	1 (2%)	48	66
79	AV	259/261 (99%)	257 (99%)	2 (1%)	73	77
80	AW	31/31 (100%)	31 (100%)	0	100	100
81	AX	708/709 (100%)	694 (98%)	14 (2%)	48	66
84	BA	185/185 (100%)	182 (98%)	3 (2%)	55	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	10320/10457 (99%)	10205 (99%)	115 (1%)	63 74

5 of 115 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	q	188	LEU
81	AX	647	ILE
54	w	18	ILE
81	AX	646	VAL
81	AX	156	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 196 such sidechains are listed below:

Mol	Chain	Res	Type
49	r	153	HIS
57	z	176	ASN
49	r	211	HIS
53	v	128	ASN
59	AB	14	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3220/3396 (94%)	1076 (33%)	33 (1%)
2	3	120/121 (99%)	28 (23%)	3 (2%)
3	4	157/158 (99%)	48 (30%)	5 (3%)
47	2	1774/1797 (98%)	779 (43%)	38 (2%)
82	AY	75/76 (98%)	29 (38%)	0
83	AZ	6/7 (85%)	5 (83%)	2 (33%)
All	All	5352/5555 (96%)	1965 (36%)	81 (1%)

5 of 1965 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	4	U
1	1	6	A
1	1	14	U
1	1	15	C
1	1	17	G

5 of 81 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	2	706	A
47	2	1481	C
47	2	740	A
47	2	1181	U
47	2	1680	G

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

1 non-standard protein/DNA/RNA residue is 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
81	DDE	AX	699	81	18,20,21	2.04	6 (33%)	17,28,30	1.31	2 (11%)

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
81	DDE	AX	699	81	-	6/20/21/23	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	AX	699	DDE	CBI-NAD	5.97	1.46	1.32
81	AX	699	DDE	CAT-CE1	2.96	1.54	1.49
81	AX	699	DDE	CG-ND1	-2.80	1.33	1.38
81	AX	699	DDE	OAG-CBI	-2.35	1.19	1.23
81	AX	699	DDE	CBW-NCB	-2.16	1.49	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	AX	699	DDE	OAG-CBI-NAD	-2.89	117.94	123.04
81	AX	699	DDE	CAC-NCB-CAB	2.75	118.43	107.99

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	AX	699	DDE	N-CA-CB-CG
81	AX	699	DDE	C-CA-CB-CG
81	AX	699	DDE	CAT-CAU-CBW-CBI
81	AX	699	DDE	OAG-CBI-CBW-CAU
81	AX	699	DDE	NAD-CBI-CBW-CAU

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	AX	699	DDE	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 8 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
86	GCP	AX	901	-	32,34,34	0.72	2 (6%)	49,54,54	0.96	3 (6%)

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
86	GCP	AX	901	-	-	5/19/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	AX	901	GCP	PG-O1G	2.28	1.54	1.50
86	AX	901	GCP	PG-O3G	-2.18	1.50	1.55

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	AX	901	GCP	O1B-PB-C3B	4.09	119.81	109.05
86	AX	901	GCP	O1G-PG-C3B	-2.73	105.42	111.37
86	AX	901	GCP	O3G-PG-C3B	2.51	112.48	106.40

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	AX	901	GCP	C5'-O5'-PA-O3A
86	AX	901	GCP	C5'-O5'-PA-O1A
86	AX	901	GCP	C5'-O5'-PA-O2A
86	AX	901	GCP	C4'-C5'-O5'-PA
86	AX	901	GCP	C3'-C4'-C5'-O5'

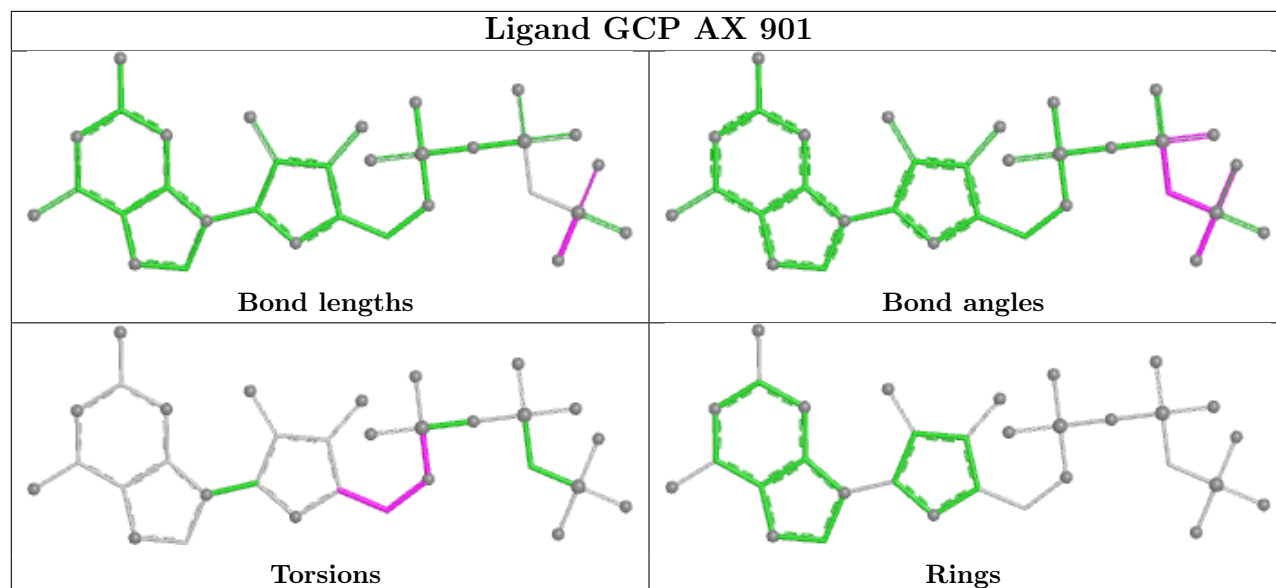
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	AX	901	GCP	3	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.

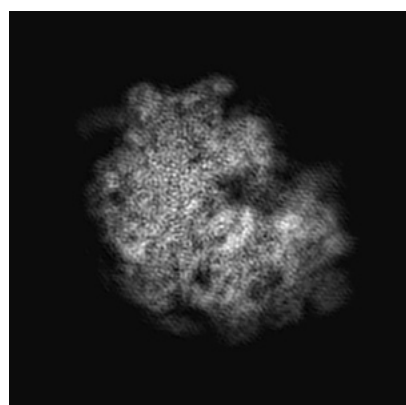
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0049. These allow visual inspection of the internal detail of the map and identification of artifacts.

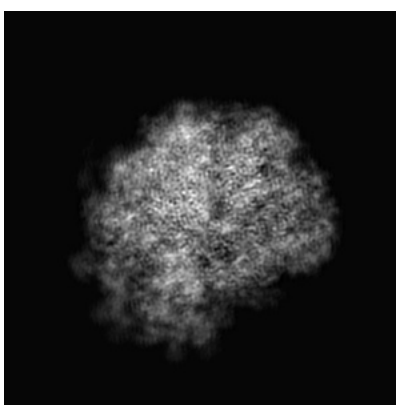
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

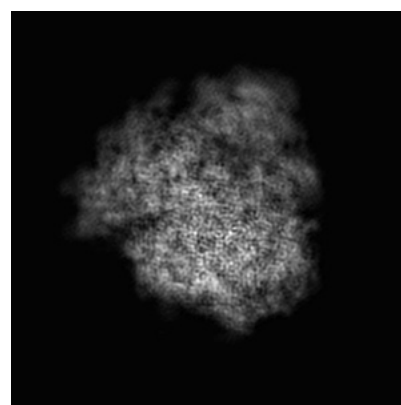
6.1.1 Primary map



X



Y

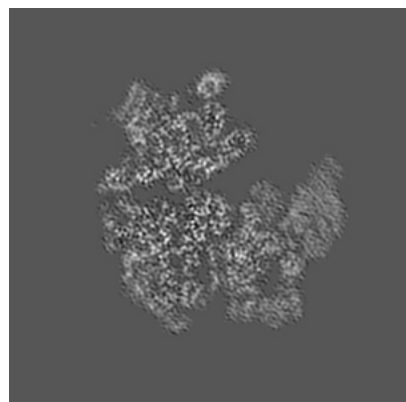


Z

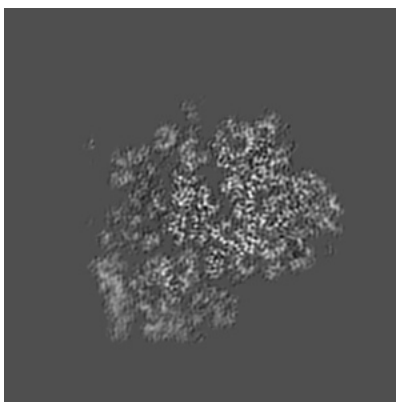
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

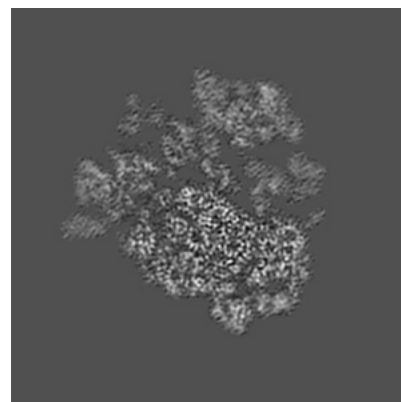
6.2.1 Primary map



X Index: 180



Y Index: 180

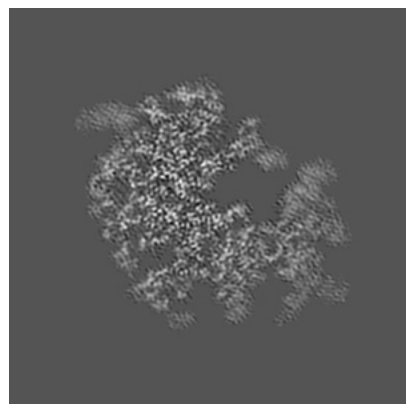


Z Index: 180

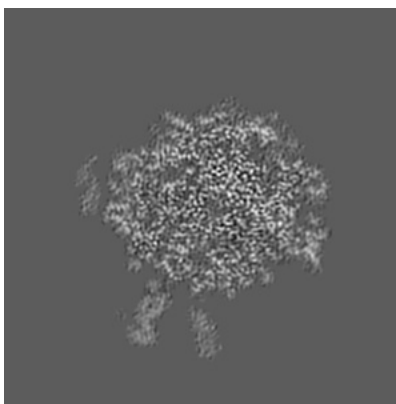
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

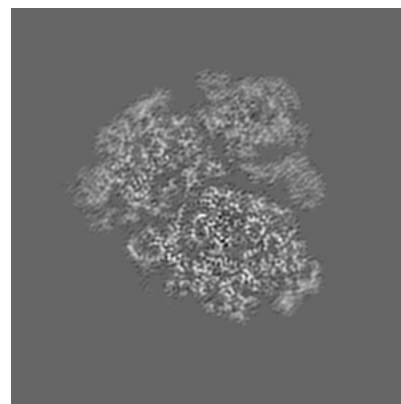
6.3.1 Primary map



X Index: 194



Y Index: 158

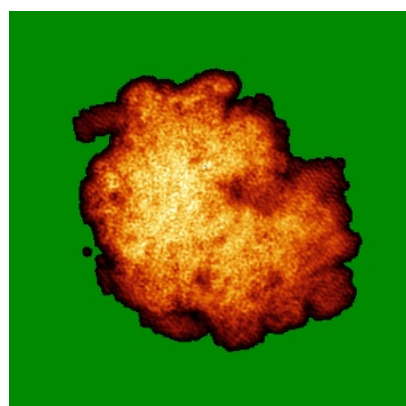


Z Index: 166

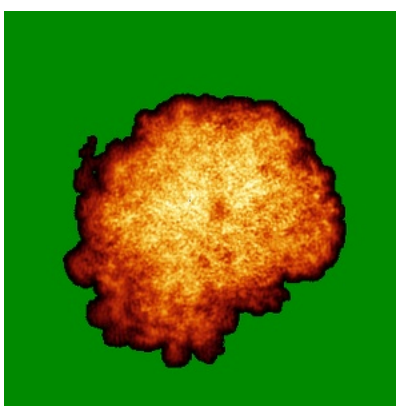
The images above show the largest variance slices of the map in three orthogonal directions.

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

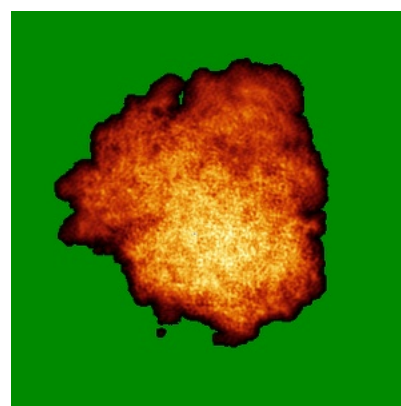
6.4.1 Primary map



X



Y

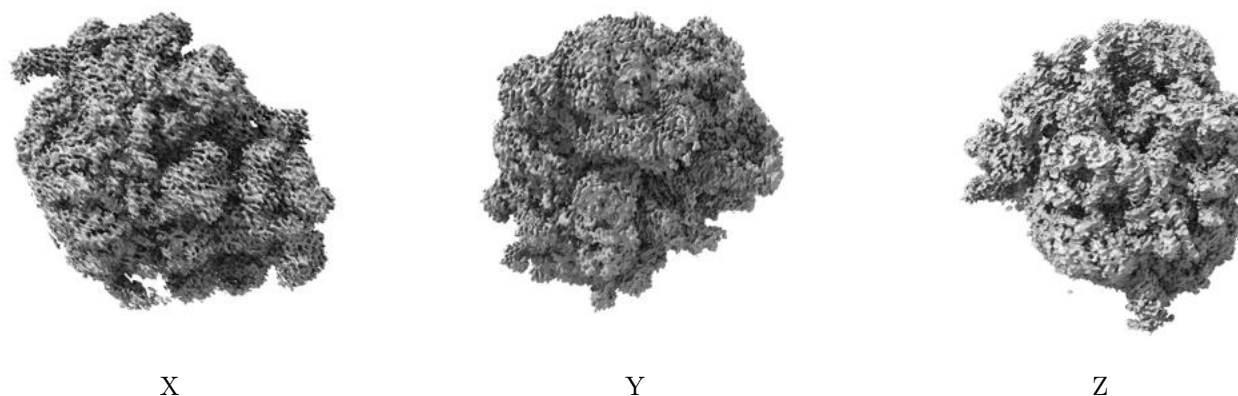


Z

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 0.033. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

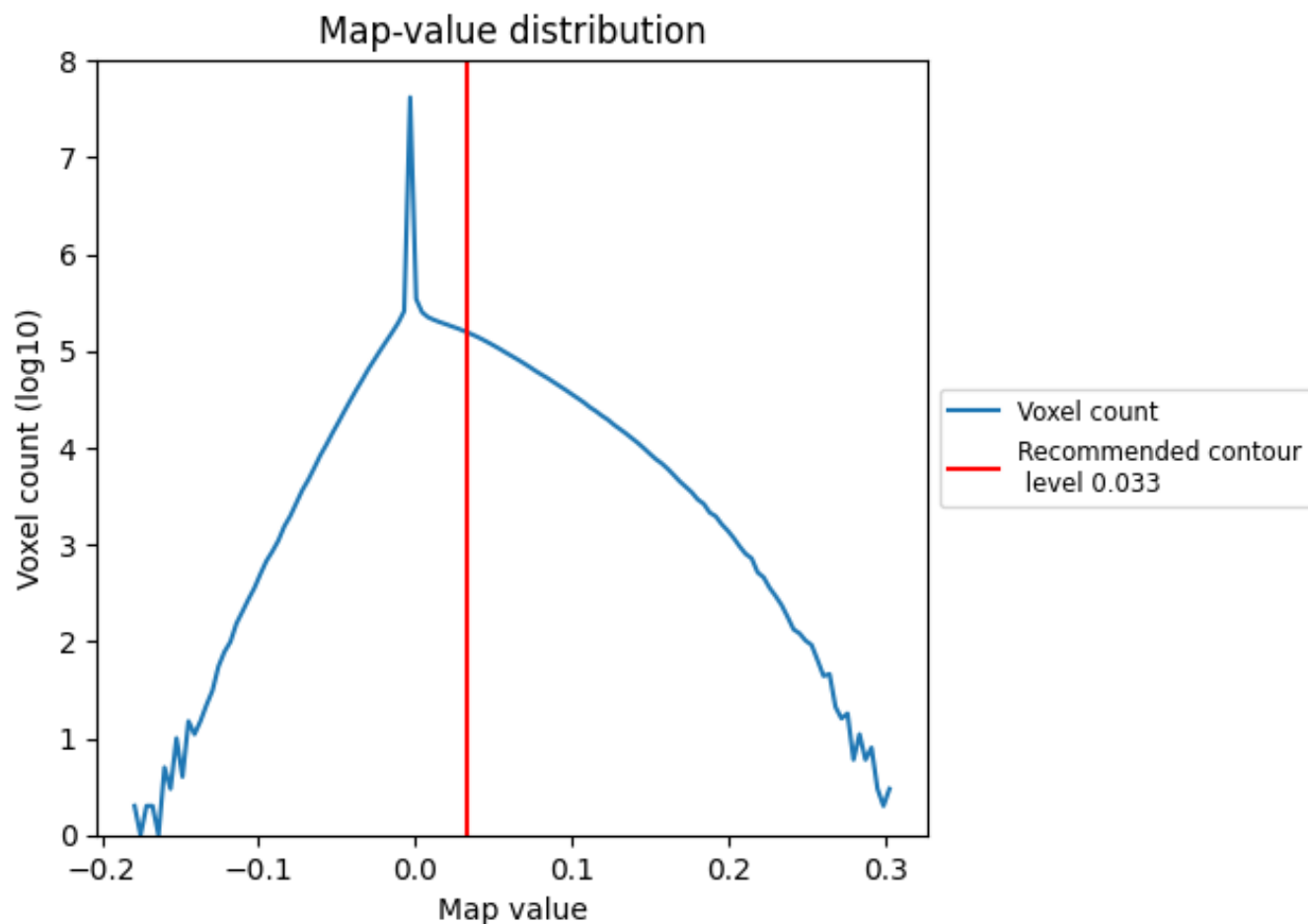
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

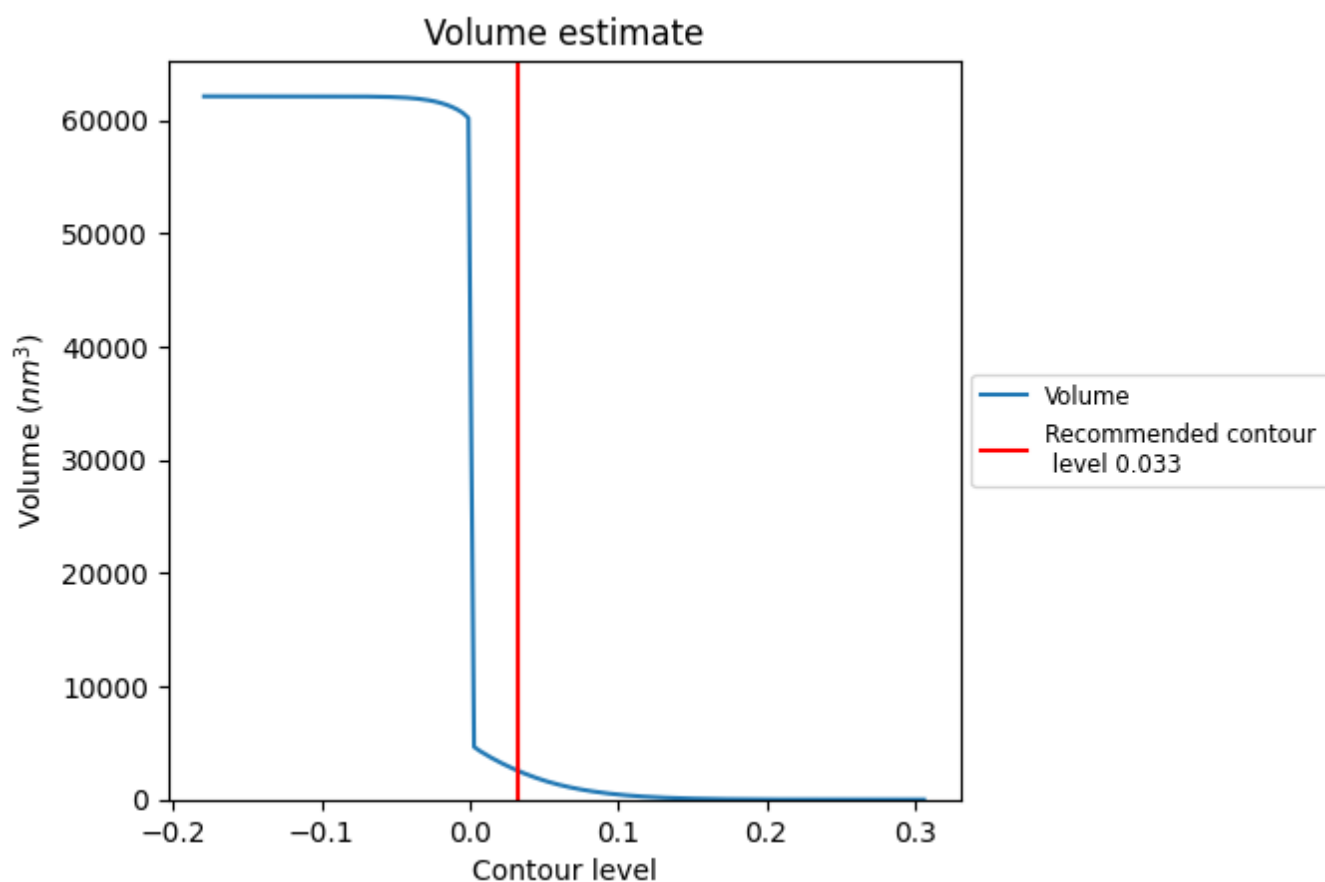
This section contains the results of statistical analysis of the map.

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.

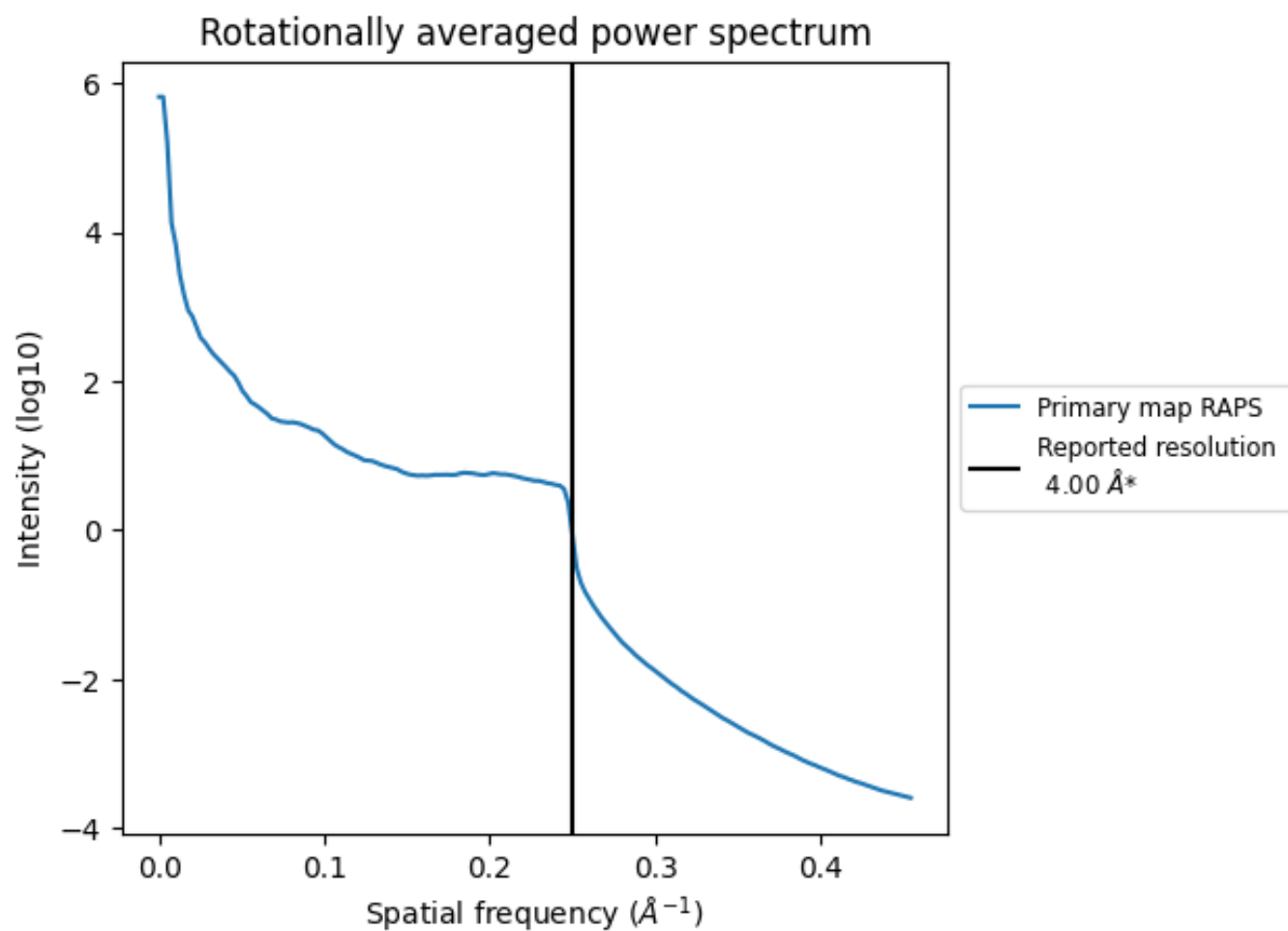
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2513 nm³; this corresponds to an approximate mass of 2270 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 0.250 Å⁻¹

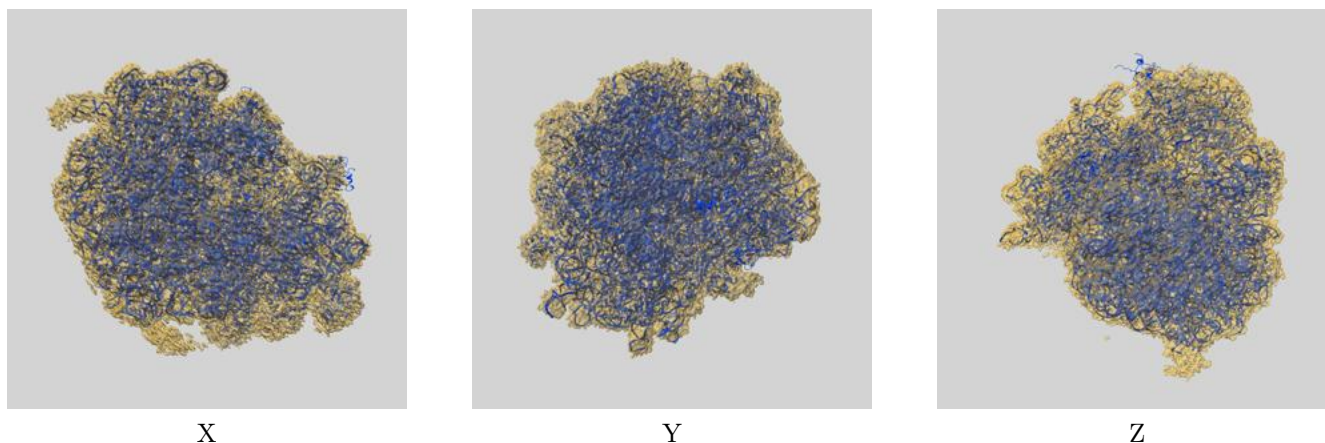
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

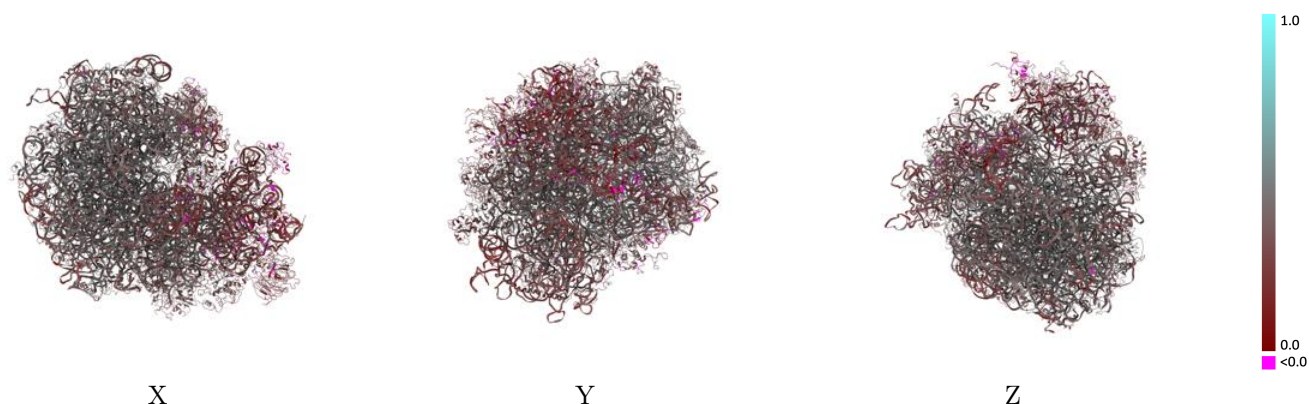
This section contains information regarding the fit between EMDB map EMD-0049 and PDB model 6GQV. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



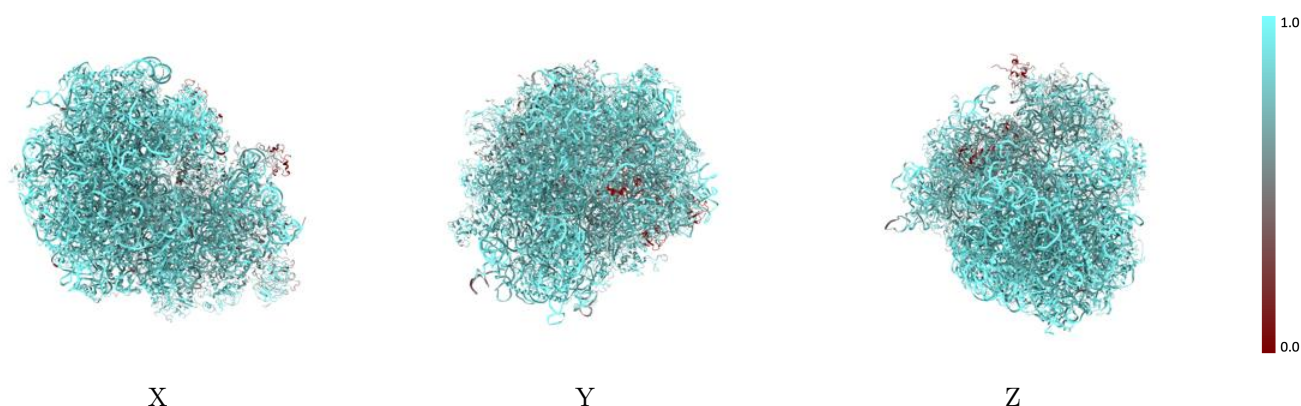
The images above show the 3D surface view of the map at the recommended contour level 0.033 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



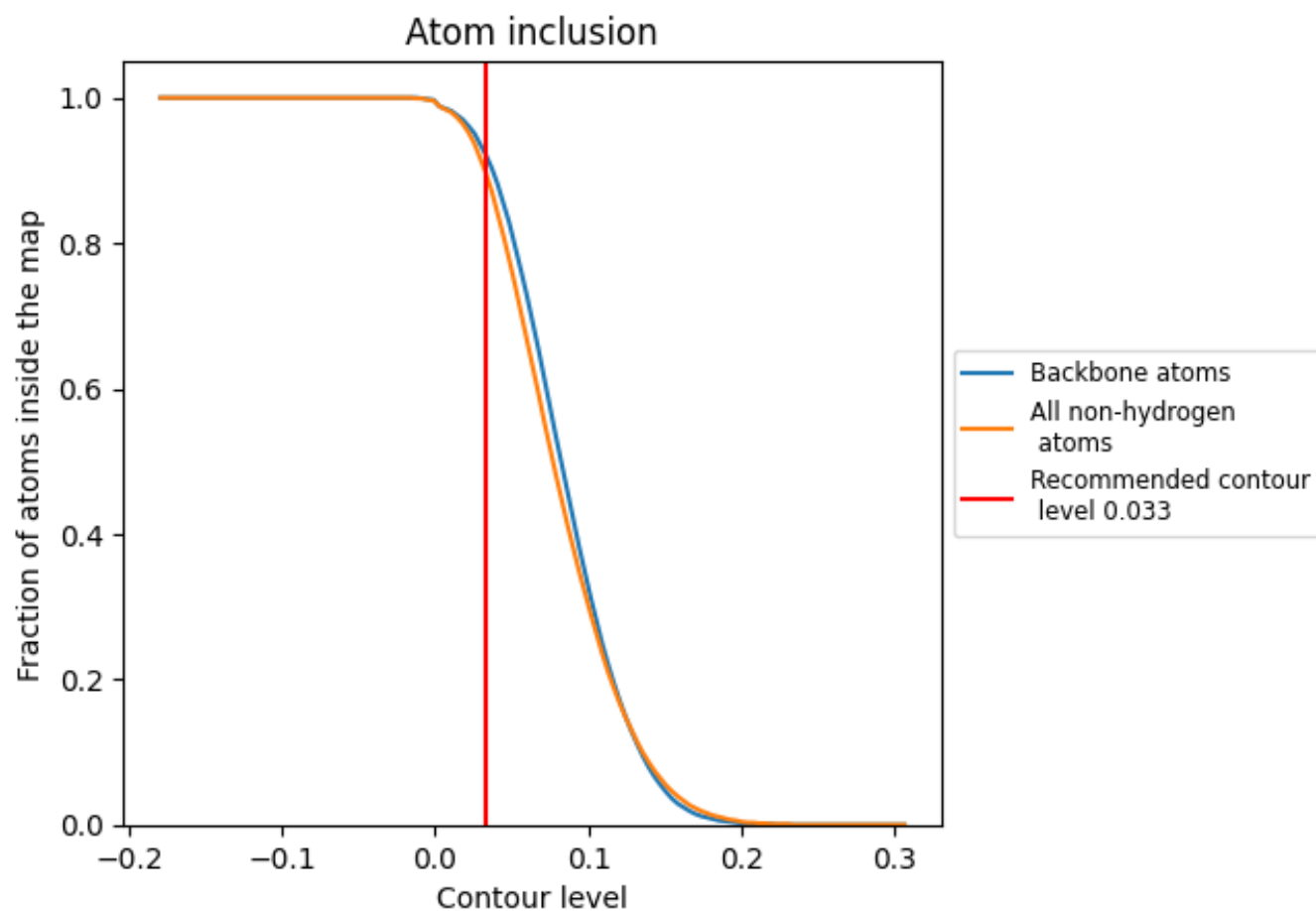
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.033).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.033) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8970	 0.3780
1	 0.9620	 0.4060
2	 0.9300	 0.3390
3	 0.9810	 0.3960
4	 0.9710	 0.4200
A	 0.8630	 0.4620
AA	 0.8670	 0.2720
AB	 0.7910	 0.3950
AC	 0.2450	 0.1250
AD	 0.8670	 0.3920
AE	 0.8890	 0.3890
AF	 0.8080	 0.2840
AG	 0.7620	 0.2500
AH	 0.7470	 0.2820
AI	 0.7790	 0.2900
AJ	 0.8080	 0.2680
AK	 0.6880	 0.2810
AL	 0.8280	 0.3480
AM	 0.8550	 0.4190
AN	 0.8110	 0.4140
AO	 0.8750	 0.3220
AP	 0.6250	 0.2320
AQ	 0.8550	 0.3750
AR	 0.8740	 0.3780
AS	 0.6370	 0.2470
AT	 0.8700	 0.3180
AU	 0.8100	 0.3710
AV	 0.7500	 0.2590
AW	 0.6640	 0.2630
AX	 0.7640	 0.3440
AY	 0.8380	 0.2940
AZ	 0.4440	 0.3240
B	 0.9000	 0.4470
BA	 0.6630	 0.2530
C	 0.9280	 0.4430



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Chain	Atom inclusion	Q-score
D	 0.9010	 0.3750
E	 0.9090	 0.4020
F	 0.9020	 0.4280
G	 0.9020	 0.4100
H	 0.8780	 0.4080
I	 0.8960	 0.4300
J	 0.8660	 0.3700
L	 0.9230	 0.4270
M	 0.9100	 0.4030
N	 0.9070	 0.4580
O	 0.9000	 0.4250
P	 0.8980	 0.4500
P0	 0.2760	 0.1750
P2	 0.3050	 0.1930
Q	 0.9150	 0.4480
R	 0.9010	 0.4200
S	 0.9070	 0.4280
T	 0.8930	 0.4360
U	 0.8980	 0.3800
V	 0.8320	 0.4470
W	 0.8490	 0.4290
X	 0.8920	 0.4150
Y	 0.9170	 0.4220
Z	 0.9050	 0.4140
a	 0.9260	 0.4490
b	 0.8920	 0.4260
c	 0.8960	 0.4210
d	 0.8820	 0.4400
e	 0.8930	 0.4460
f	 0.9000	 0.4490
g	 0.8810	 0.4480
h	 0.8910	 0.4170
i	 0.9060	 0.4080
j	 0.9280	 0.4760
k	 0.8610	 0.3850
l	 0.8840	 0.4430
m	 0.8940	 0.4490
n	 0.7880	 0.4600
o	 0.8770	 0.4430
p	 0.8480	 0.4440
q	 0.8610	 0.3510
r	 0.8990	 0.3770

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Chain	Atom inclusion	Q-score
s	 0.8630	 0.4010
t	 0.7250	 0.2790
u	 0.8770	 0.3550
v	 0.7480	 0.2720
w	 0.8770	 0.3310
x	 0.8420	 0.3220
y	 0.8420	 0.3460
z	 0.8880	 0.3620