



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:07 AM UTC

PDB ID : 4V4N / pdb_00004v4n
EMDB ID : EMD-5691
Title : Structure of the Methanococcus jannaschii ribosome-SecYEBeta channel complex
Authors : Menetret, J.F.; Park, E.; Gumbart, J.C.; Ludtke, S.J.; Li, W.; Whynot, A.; Rapoport, T.A.; Akey, C.W.
Deposited on : 2013-06-17
Resolution : 9.00 Å (reported)
Based on initial models : 3J21, 3J2L, 3J20, 1RHZ

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:

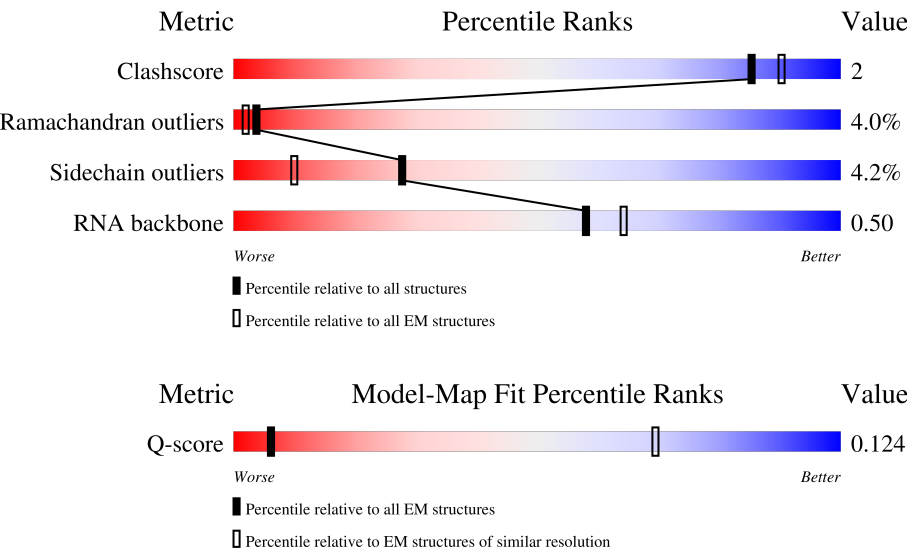
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.00 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	257 (8.50 - 9.50)

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	A7	67	7% 45% 48% ...
2	A8	52	27% 31% 38%
3	Af	51	65% 31% 53% 16%

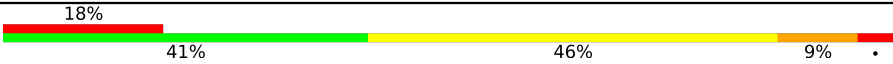
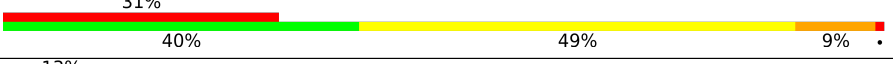
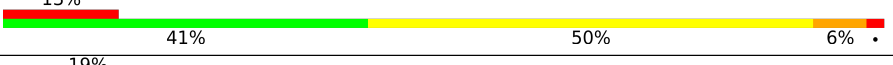
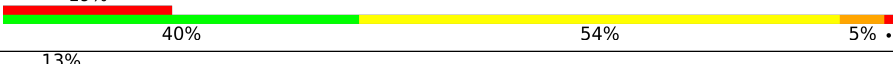
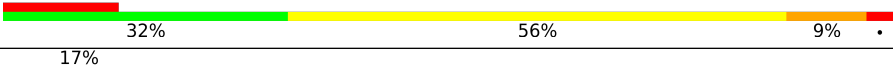
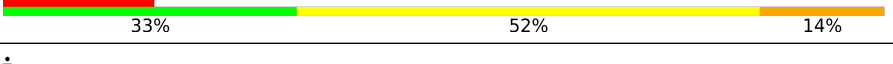
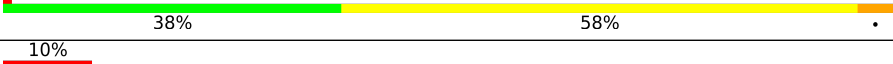
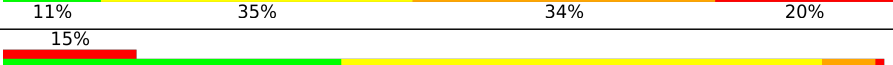
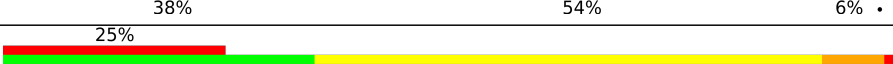
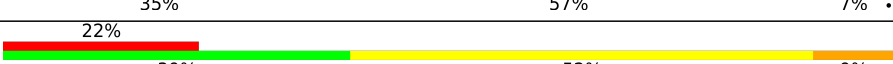
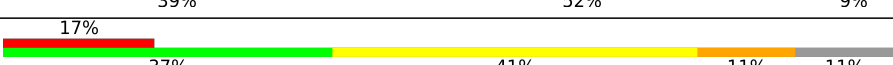
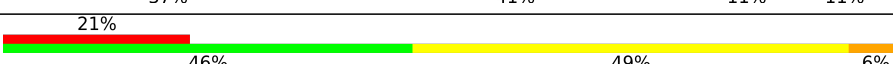
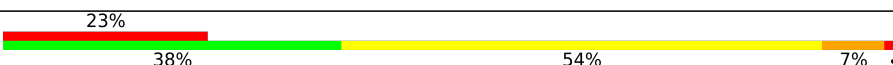
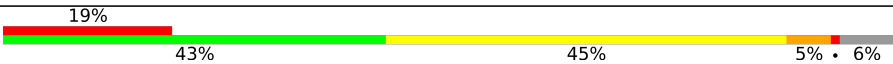
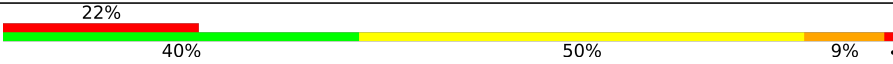
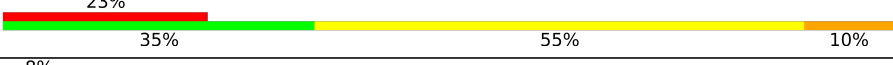
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Mol	Chain	Length	Quality of chain
4	AQ	150	
5	AS	150	
6	AT	84	
7	AU	121	
8	AW	72	
9	AX	436	
10	B1	77	
11	B2	1495	
12	AG	123	
12	B3	123	
13	BA	190	
14	BB	202	
15	BC	186	
16	BD	172	
17	BE	241	
18	BF	217	
19	BG	125	
20	BH	215	
21	BI	129	
22	BJ	127	
23	BK	135	
24	BL	102	
25	BM	133	
26	BN	145	
27	BO	148	

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Mol	Chain	Length	Quality of chain
28	BP	56	
29	BQ	158	
30	BR	113	
31	BS	67	
32	BT	111	
33	BU	144	
34	BV	99	
35	BW	63	
36	BX	71	
37	BY	50	
38	A1	3049	
39	A3	126	
40	A5	81	
40	AK	81	
41	AA	216	
42	Aa	92	
43	AB	239	
44	Ab	127	
45	AC	365	
46	AD	255	
47	Ad	89	
48	AE	186	
49	Ae	62	
50	AF	184	
51	Ag	45	

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Mol	Chain	Length	Quality of chain
52	AH	134	
53	Ah	24	
54	AI	142	
55	Ai	78	
56	AJ	132	
57	Aj	94	
58	Ak	212	
59	AL	147	
60	AM	194	
61	AN	168	
62	AO	197	
63	AP	120	
64	AR	95	
65	AV	66	
66	AY	155	
67	AZ	99	

2 Entry composition [i](#)

There are 67 unique types of molecules in this entry. The entry contains 171094 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 Preprotein translocase subunit SecE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A7	65	Total	C	N	O	S	0	0
			525	348	85	91	1		

- Molecule 2 is a protein called Preprotein translocase subunit SecG.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	A8	32	Total	C	N	O	0	0
			258	172	42	44		

- Molecule 3 is a protein called 50S ribosomal protein L39E.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Af	51	Total	C	N	O	S	0	0
			445	284	98	62	1		

- Molecule 4 is a protein called 50S ribosomal protein L19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AQ	150	Total	C	N	O	S	0	0
			1256	794	255	202	5		

- Molecule 5 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AS	150	Total	C	N	O	S	0	0
			1200	764	230	202	4		

- Molecule 6 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	AT	84	Total	C	N	O	0	0
			680	440	118	122		

- Molecule 7 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AU	121	Total	C	N	O	S	0	0
			1008	637	195	172	4		

- Molecule 8 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AW	66	Total	C	N	O	S	0	0
			546	338	105	99	4		

- Molecule 9 is a protein called Protein translocase subunit SecY.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AX	432	Total	C	N	O	S	0	0
			3309	2210	521	559	19		

- Molecule 10 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B1	77	Total	C	N	O	P	0	0
			1646	734	303	533	76		

- Molecule 11 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B2	1495	Total	C	N	O	P	0	0
			32132	14297	5954	10387	1494		

- Molecule 12 is a protein called 30S ribosomal protein L7AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	B3	123	Total	C	N	O	S	0	0
			939	599	155	181	4		
12	AG	123	Total	C	N	O	S	0	0
			939	599	155	181	4		

- Molecule 13 is a protein called 30S ribosomal protein S3AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BA	190	Total	C	N	O	S	0	0
			1559	1007	273	274	5		

- Molecule 14 is a protein called 30S ribosomal protein S2P.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BB	202	Total	C	N	O	S	0	0
			1623	1046	282	290	5		

- Molecule 15 is a protein called 30S ribosomal protein S3P.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BC	186	Total	C	N	O	S	0	0
			1460	933	271	252	4		

- Molecule 16 is a protein called 30S ribosomal protein S4P.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BD	172	Total	C	N	O	S	0	0
			1434	902	273	255	4		

- Molecule 17 is a protein called 30S ribosomal protein S4E.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BE	241	Total	C	N	O	S	0	0
			1976	1277	355	339	5		

- Molecule 18 is a protein called 30S ribosomal protein S5P.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BF	217	Total	C	N	O	S	0	0
			1717	1084	319	306	8		

- Molecule 19 is a protein called 30S ribosomal protein S6E.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BG	125	Total	C	N	O	S	0	0
			984	623	180	179	2		

- Molecule 20 is a protein called 30S ribosomal protein S7P.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BH	215	Total	C	N	O	S	0	0
			1736	1100	326	302	8		

- Molecule 21 is a protein called 30S ribosomal protein S8P.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BI	129	Total	C	N	O	S	0	0
			1028	668	178	180	2		

- Molecule 22 is a protein called 30S ribosomal protein S8E.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BJ	127	Total	C	N	O	S	0	0
			1004	622	207	174	1		

- Molecule 23 is a protein called 30S ribosomal protein S9P.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BK	135	Total	C	N	O	S	0	0
			1072	671	205	190	6		

- Molecule 24 is a protein called 30S ribosomal protein S10P.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BL	102	Total	C	N	O	S	0	0
			822	507	159	152	4		

- Molecule 25 is a protein called 30S ribosomal protein S11P.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BM	133	Total	C	N	O	S	0	0
			1004	623	200	179	2		

- Molecule 26 is a protein called 30S ribosomal protein S12P.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BN	145	Total	C	N	O	S	0	0
			1141	722	223	193	3		

- Molecule 27 is a protein called 30S ribosomal protein S13P.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BO	148	Total	C	N	O	S	0	0
			1189	746	237	200	6		

- Molecule 28 is a protein called 30S ribosomal protein S14P.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BP	56	Total	C	N	O	S	0	0
			462	292	95	69	6		

- Molecule 29 is a protein called 30S ribosomal protein S15P/S13E.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BQ	158	Total	C	N	O	S	0	0
			1310	834	250	221	5		

- Molecule 30 is a protein called 30S ribosomal protein S17P.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BR	113	Total	C	N	O	S	0	0
			934	592	177	160	5		

- Molecule 31 is a protein called 30S ribosomal protein S17E.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BS	67	Total	C	N	O	S	0	0
			556	353	105	95	3		

- Molecule 32 is a protein called 30S ribosomal protein S19P.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BT	111	Total	C	N	O	S	0	0
			924	594	173	151	6		

- Molecule 33 is a protein called 30S ribosomal protein S19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BU	144	Total	C	N	O	S	0	0
			1176	758	212	205	1		

- Molecule 34 is a protein called 30S ribosomal protein S24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BV	99	Total	C	N	O	S	0	0
			823	532	134	154	3		

- Molecule 35 is a protein called 30S ribosomal protein S27E.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BW	63	Total	C	N	O	S	0	0
			478	306	85	81	6		

- Molecule 36 is a protein called 30S ribosomal protein S28E.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BX	71	Total	C	N	O	S	0	0
			568	345	115	107	1		

- Molecule 37 is a protein called 30S ribosomal protein S27AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BY	50	Total	C	N	O	S	0	0
			409	262	75	66	6		

- Molecule 38 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	2969	Total	C	N	O	P	0	0
			63885	28427	11905	20589	2964		

- Molecule 39 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A3	126	Total	C	N	O	P	0	0
			2691	1199	492	875	125		

- Molecule 40 is a protein called 50S ribosomal protein L14E.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A5	81	Total	C	N	O	S	0	0
			614	386	119	108	1		
40	AK	81	Total	C	N	O	S	0	0
			614	386	119	108	1		

- Molecule 41 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AA	216	Total	C	N	O	S	0	0
			1677	1068	300	304	5		

- Molecule 42 is a protein called 50S ribosomal protein L31E.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	Aa	82	Total	C	N	O		
			677	444	126	107	0	0

- Molecule 43 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AB	239	Total	C	N	O	S		
			1838	1169	347	317	5	0	0

- Molecule 44 is a protein called 50S ribosomal protein L32E.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ab	127	Total	C	N	O	S		
			1075	689	217	168	1	0	0

- Molecule 45 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AC	342	Total	C	N	O	S		
			2717	1741	495	467	14	0	0

- Molecule 46 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AD	255	Total	C	N	O	S		
			2026	1288	391	342	5	0	0

- Molecule 47 is a protein called 50S ribosomal protein L34E.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ad	89	Total	C	N	O	S		
			740	463	158	108	11	0	0

- Molecule 48 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AE	186	Total	C	N	O	S		
			1489	937	278	265	9	0	0

- Molecule 49 is a protein called 50S ribosomal protein L37E.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ae	62	Total	C	N	O	S	0	0
			506	312	111	78	5		

- Molecule 50 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AF	184	Total	C	N	O	S	0	0
			1476	956	252	266	2		

- Molecule 51 is a protein called 50S ribosomal protein L40E.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ag	45	Total	C	N	O	S	0	0
			372	236	76	56	4		

- Molecule 52 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AH	134	Total	C	N	O	S	0	0
			989	635	164	184	6		

- Molecule 53 is a protein called 50S ribosomal protein L41E.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ah	24	Total	C	N	O	S	0	0
			230	147	54	28	1		

- Molecule 54 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AI	142	Total	C	N	O	S	0	0
			1150	737	215	195	3		

- Molecule 55 is a protein called 50S ribosomal protein L37AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Ai	78	Total	C	N	O	S	0	0
			590	368	122	95	5		

- Molecule 56 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AJ	132	Total	C	N	O	S	0	0
			1014	631	204	176	3		

- Molecule 57 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Aj	94	Total	C	N	O	S	0	0
			788	499	162	122	5		

- Molecule 58 is a protein called 50S ribosomal protein P0/L10E.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ak	212	Total	C	N	O	S	0	0
			1633	1051	272	304	6		

- Molecule 59 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AL	147	Total	C	N	O	S	0	0
			1154	727	227	195	5		

- Molecule 60 is a protein called 50S ribosomal protein L15E.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AM	194	Total	C	N	O	S	0	0
			1595	1020	316	253	6		

- Molecule 61 is a protein called 50S ribosomal protein L10E/L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AN	168	Total	C	N	O	S	0	0
			1379	872	268	233	6		

- Molecule 62 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AO	197	Total	C	N	O	S	0	0
			1598	1021	299	275	3		

- Molecule 63 is a protein called 50S ribosomal protein L18E.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AP	120	Total	C	N	O	S	0	0
			966	606	186	171	3		

- Molecule 64 is a protein called 50S ribosomal protein L21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AR	95	Total	C	N	O	S	0	0
			787	501	160	125	1		

- Molecule 65 is a protein called 50S ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AV	66	Total	C	N	O	S	0	0
			555	351	106	91	7		

- Molecule 66 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AY	155	Total	C	N	O	S	0	0
			1243	788	235	213	7		

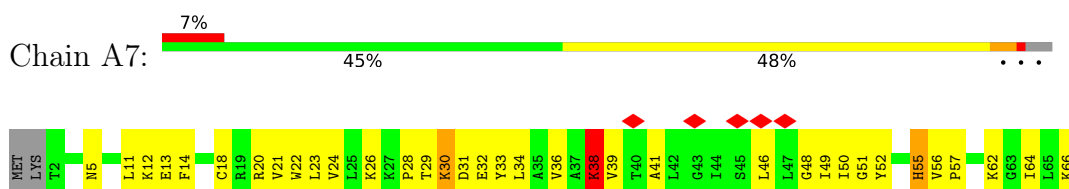
- Molecule 67 is a protein called 50S ribosomal protein L30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AZ	99	Total	C	N	O	S	0	0
			754	489	121	142	2		

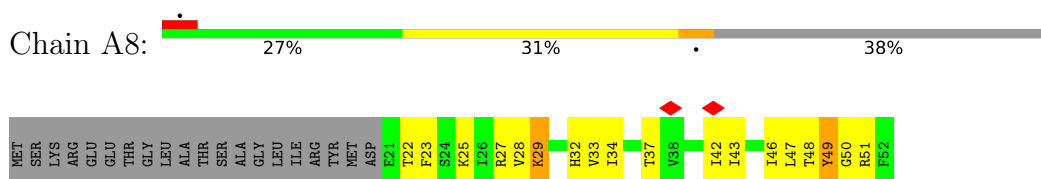
3 Residue-property plots [i](#)

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

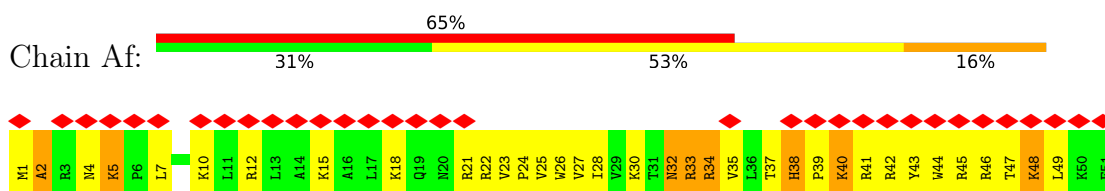
- Molecule 1: Preprotein translocase subunit SecE



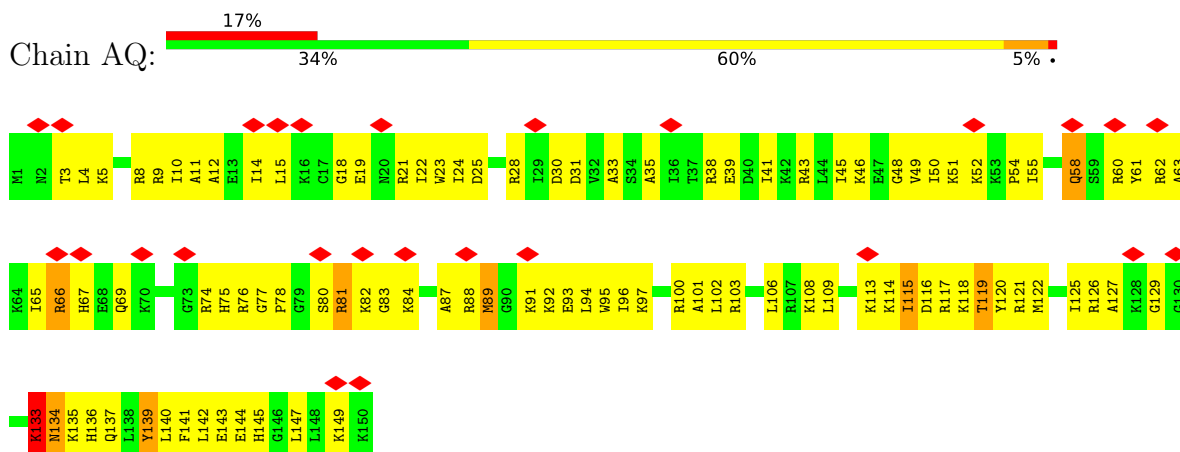
- Molecule 2: Preprotein translocase subunit SecG



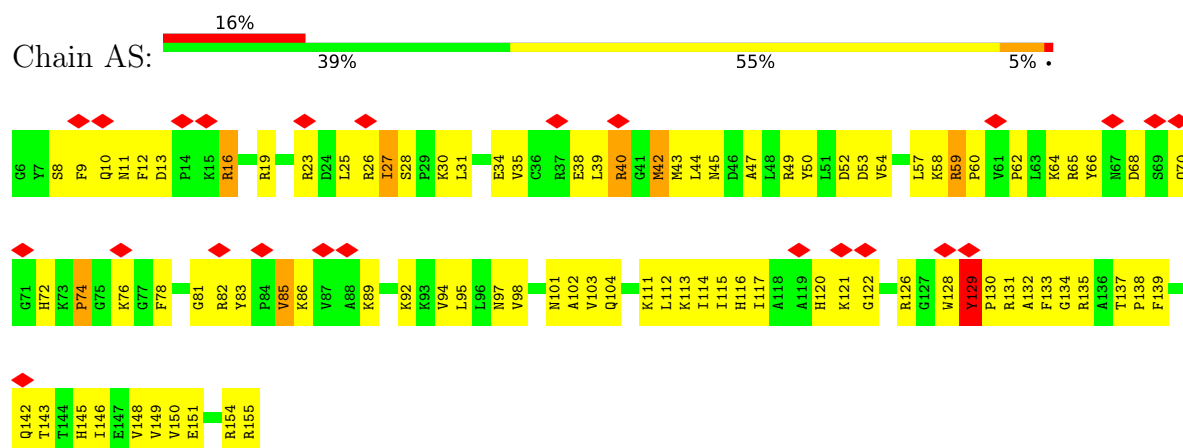
- Molecule 3: 50S ribosomal protein L39E



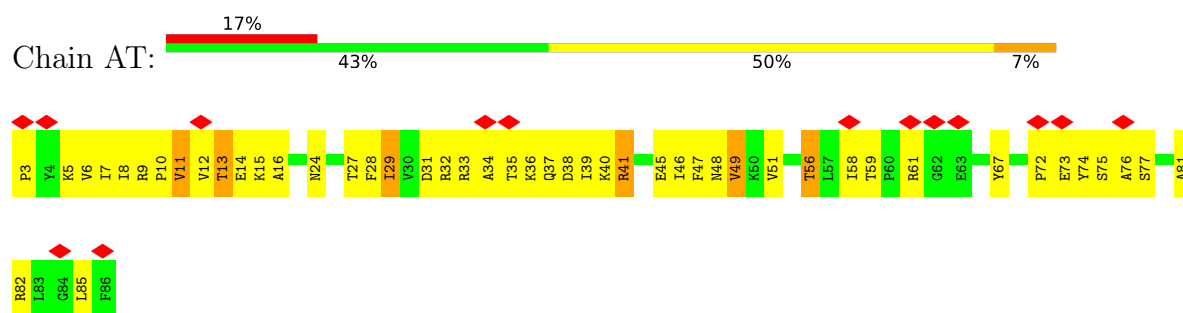
- Molecule 4: 50S ribosomal protein L19E



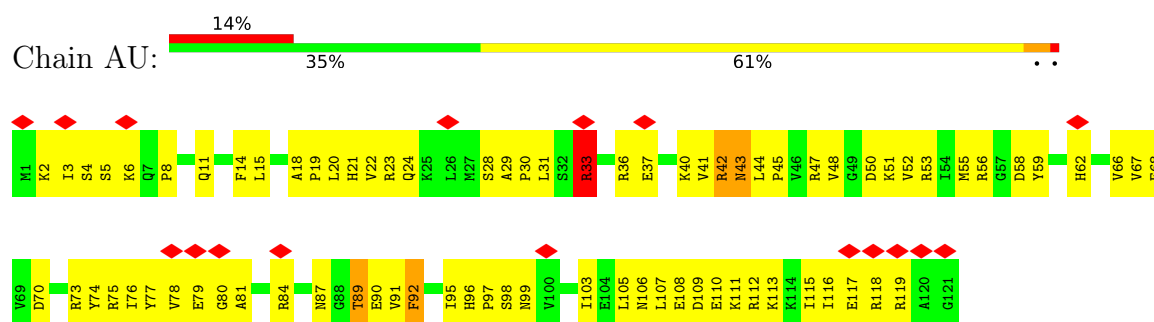
- Molecule 5: 50S ribosomal protein L22P



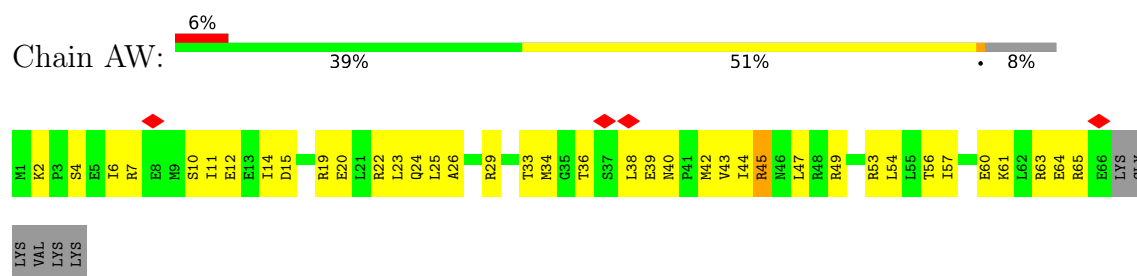
- Molecule 6: 50S ribosomal protein L23P



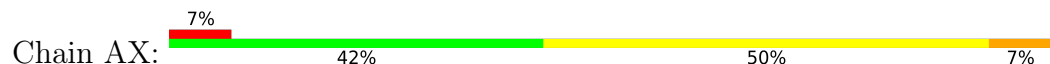
- Molecule 7: 50S ribosomal protein L24P

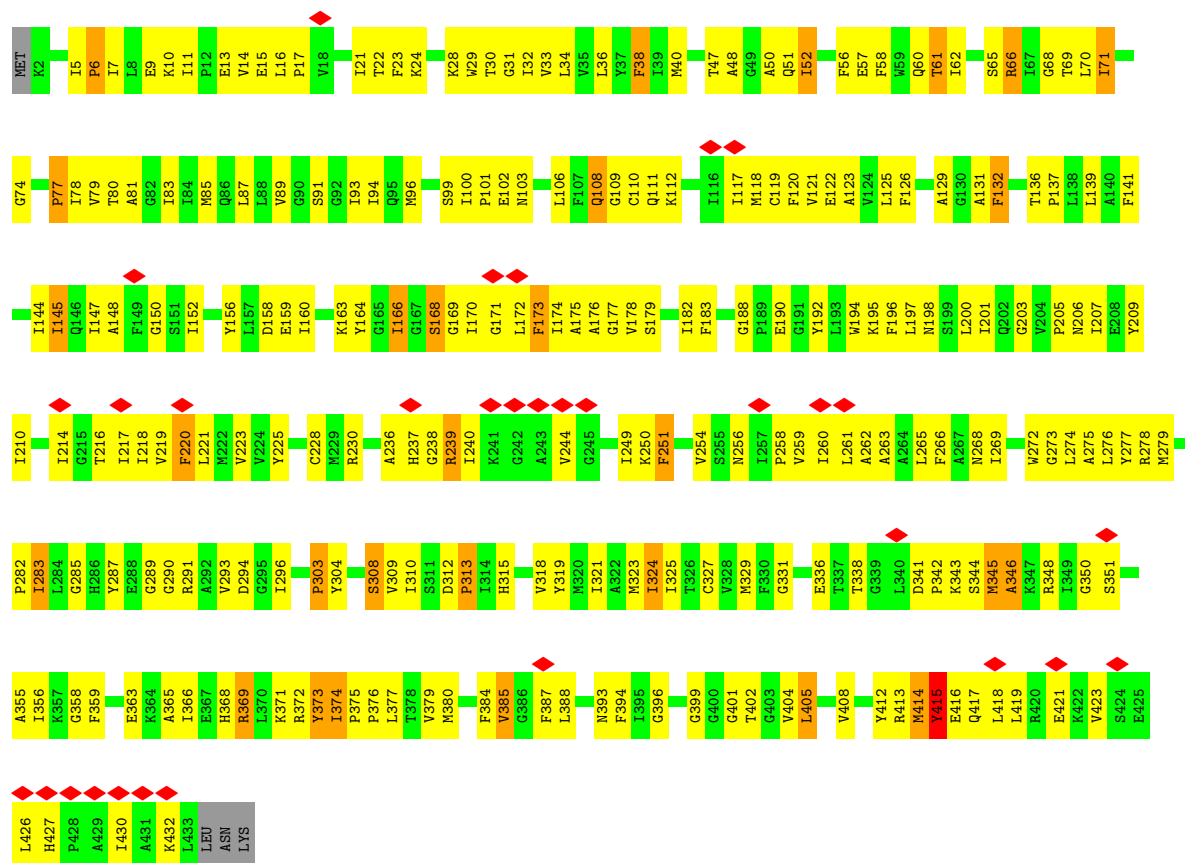


- Molecule 8: 50S ribosomal protein L29P

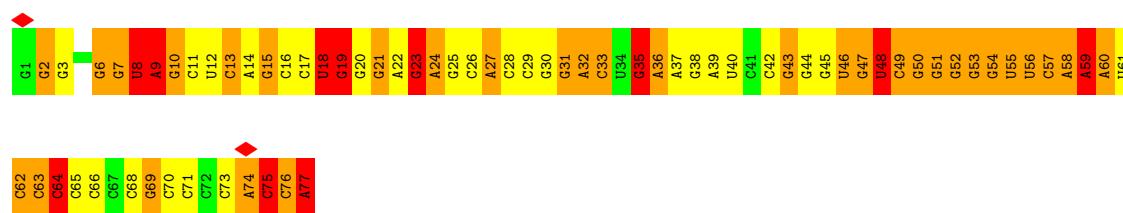


- Molecule 9: Protein translocase subunit SecY

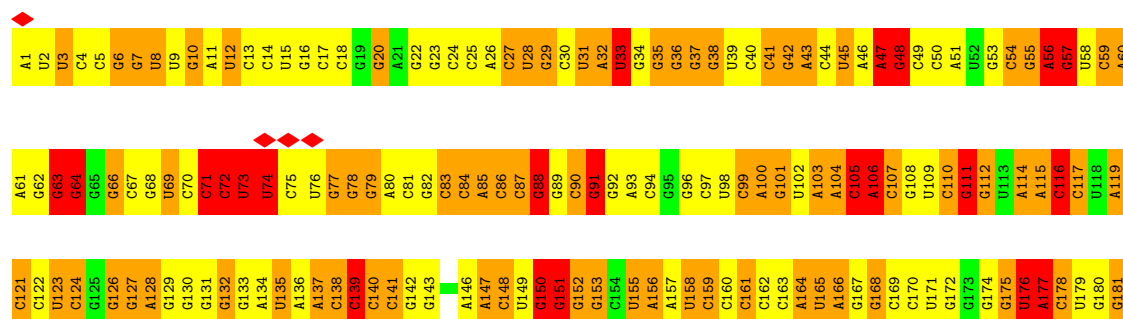




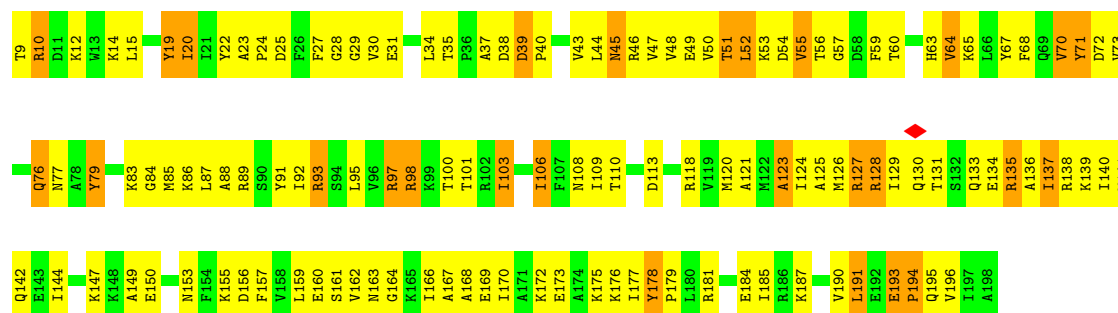
• Molecule 10: E-tRNA



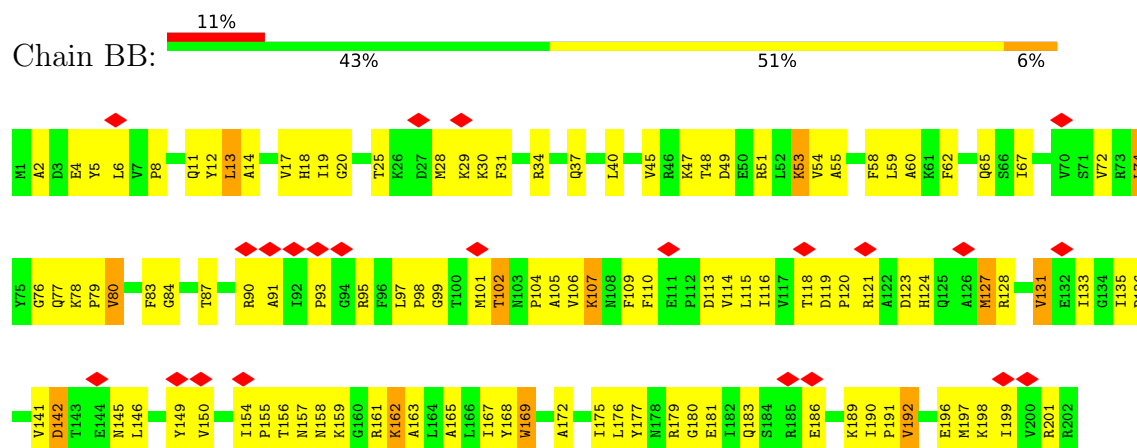
• Molecule 11: 16S ribosomal RNA



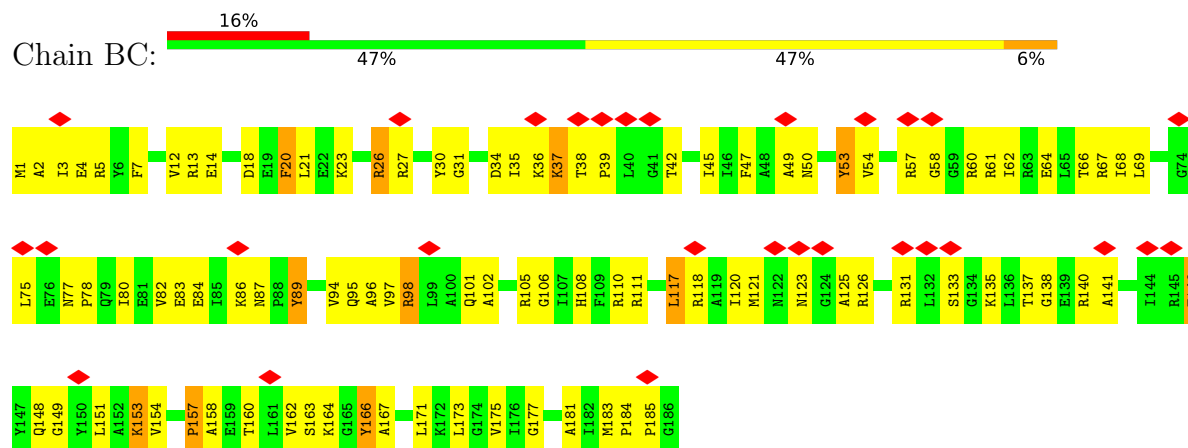
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C1038	A976	U915	C854	G791	G730	A669	U607	C545	A485	C425	C365	C304	G243	A183
A1040	G977	U916	C855	G792	A731	C670	G608		A486	C426	C366	C305	G244	G185
C1041	G978	A917	G856	G793	G732	C671	G609	A548	U487	G427	C367	C306	U245	G186
U1042	G979	A918	C857	A794	C733	C672	G610	A549	A488	G428	C368	G307	A246	U187
U1043	U979	U919	A858	G795	G734	C673	A611	G550	C489	A429	C369	G308	G247	C187
U1044	U982	U920	A859	G796	A735	C674	G612	U551	C490	G430	A370	A309	U248	C188
A1045	G983	G921	C860	U797	A736	A675	G613	C552	G492	U431	U371		U249	C189
C984	C984	G922	C861	U798	G737	G676	G614		U555	U432	G372	U312	G250	C190
U1046	C985	A923	C862	U799	G738	U677	G615	G556	G493	U433	G373	G314	G251	A191
U1047	G986	U924	U863	G800	G739	U678	G616	G557	G494	A434	G374	G315	U252	G192
G1048	G987	U925		A801	G740	G679	A617	G558	G495	A435	G375	G316	G253	G193
U1049	A988	U926	A866	G802	A741	C680	G618	C559	C496	A436	G376	C317	G254	C194
G1050	C989	A927	A867	C803	U742	G681	A619	G559	C497	A437	A377	A317	G255	C195
G1051	G990	A928	C868	U804	U743	A682	G620		U498	A438	A378	C318	G256	G196
U1052	C991	C929	U869	A805	A744	A683	G621	A561	G499	A439	A379	U319	U257	A197
A1053	G992	G930	U870	G806	G745	G684	C622	A562	G500	C440	C380	G320	A258	A198
A1054	C993	C931	A871	G807	A746	G685	C623	U563	G501	U441	C381	A421	A259	A199
C1055	C994		A872	C808	U747	C686	G624	C564	U502	C442	G382	G322	C260	G200
G1056	G995	G932	A873	C809	U748	G687	G625	C565	G503	C443	C383	A323	G261	G201
A1057	A996	G934	G874	G810	A749	C688	G626	C566	G504	G444	G384	C324	G262	G202
G1058	G997	G935	G875	G811		C689	G627	A567	U505	G445	A385	A325	C263	A203
C1059	A998	A936	U812	G812	G752	C690	G628	C568	G506	G446	C386	C326	C264	G204
G1060	G999	A937	A877	G813	G753	G691	U629	G569	G507	A447	G387	G327	C265	C205
	G1000	C938	U878	G822	G754	G692		G570	C568	A448	G388	G328	A266	C206
A1063	A1001	C939	U879	G823	U755	G693	C632	C571	C509	U449	G389	G329	C267	G207
C1064	G1002	U940	G880	U817	A756	G694	C633	U572	A510	A450	G390	U330	C268	U208
C1065	C1003	C941	G881	A818	G757	G695	C634	C573	A511	A451	G391	C331	A269	A209
C1066	U1004	A942	C882	G819	G758	G696	C635	A574	U512	G452	G392	C332	A270	A210
G1067	G1005	G943	G883	G820	C759	A697	G636	A575	A513	G453	A393	G333	G271	G211
C1068	C1006	C944	G884	G821	C760			C576	U514	G454	C394	G334	C272	G212
G1069	A1007	G945	C885	A822	U761		G639	C577	U515	C455	C395	G335	G273	G213
C1070	U1008	G946	G886	G823	G762	G700	U640	G578	A516	U456	C396	G336	G274	C214
C1071	G1009	G947	G887	G824	G763	G701	A641	U579	U517	G457	C397	C337	A275	C215
C1072	G1010	G948	A888	C825	C764	G702	G642	G580	U518	G458	C398	C338	G276	G216
G1073	C1011	G949	G889	C826	U765	C704	G643	G581	G519	G459	A399	U339	G277	C217
C1074	C1012	C950	G890	G827	G766	G705	G644	G582	G520	C460	A400	A340	A278	C218
A1075	G1013	G951	A891	U828	U767	G706	G645	G583	G521	A461	U401	C341	U279	C219
G1076	C1014	A952	C892		A768	A707	U646	G584	G522	A462	G402	G342	C280	G220
U1077	C953	C953	U893	G832	A769	C708	G647	U835	U523	G463	C403	G343	G281	A221
U1078	G1015	A954	C833	A818	A770	G709	A648	C586	U524	G464	C404	G344	G282	G222
G1079	U1016	G955	C834	C834	G771	G710	A649	G587	A525	C465	G405	G345	U283	G223
C1080	C1018	C956	G835	G835	G772	U711	A650	G588	A526	C466	U406	C346	A284	G224
C1081	A1019	A957	A896	G836	A773	G712	U651	C589	A527	G467	G407	C347	C285	A224
A1082	G1020	G958	G896	C837	U774	A713	C652	U589	G528	G468	C408	G348	G286	U225
G1083	C1021	G959	G897	C838	G775	G714	C653	G591	C529	U469	C409	A349	G287	G226
U1084	U1022	A960	G899	G839	C776	G715	U654	G592	G530	G470	U410	G350	G288	G227
C1085	C1023	U961	G901	C840	G777	G716	A655	G593	G531	G471	C411	C351	C289	G228
C1086	G1024	G962	U902	C841	G778	G717	U656	G594	C532	C472	U412	A352	C290	G229
		A963	G903	U842	G779	G718	A657	U595	C533	A473	G413	G353	G291	C230
U1087	C1027	A964	G904	G843	C780	G719	A658	A596	G534	G474	G414	G354	U292	G231
U1088	G1028	G965	A905	G844	A781	A720	U659	C597	U535	C475	G415	C355	G293	G232
C1089	U1029	G966	G906	G845	A782	A721	C660	U598	A536	C476	C416	G356	A294	G233
C1090	U1030	C967	C907	G846	G722	G722	C661	G599	G537	G477	C417	C357	G295	G234
C1091	G1031		G908	A847	G723	G724	G662	G600	C538	G478	G418	G358	G296	G235
G1092	U1032		U909	G848	U785	C724	G663	G601	C539	C479	G419	A359	C297	G236
C1093	G1033		G910	U849	G786	C725	G664	G602	G540	C480	C420	A360	G298	G237
U1094	U1034		G911	A850	U787	A726	G665	G603	G541	C481	G421	A361	G300	G238
C1095	C1035		G912	C851	G788	G727	G666	G604	G542	U422	U422	C362	G301	A239
G1096	U1036		G913	G852	G789	G728	G667	C605	C543	G483	U423	C363	A302	U241



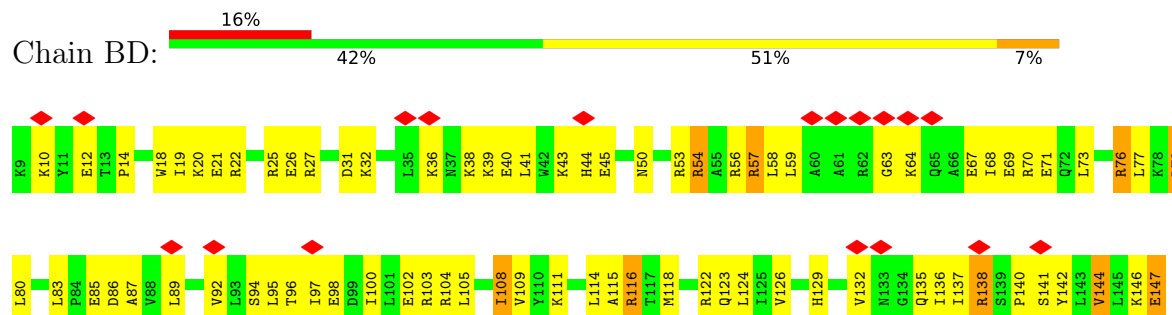
• Molecule 14: 30S ribosomal protein S2P

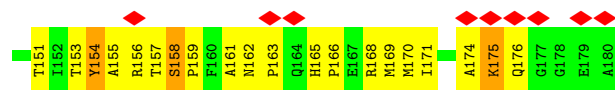


• Molecule 15: 30S ribosomal protein S3P

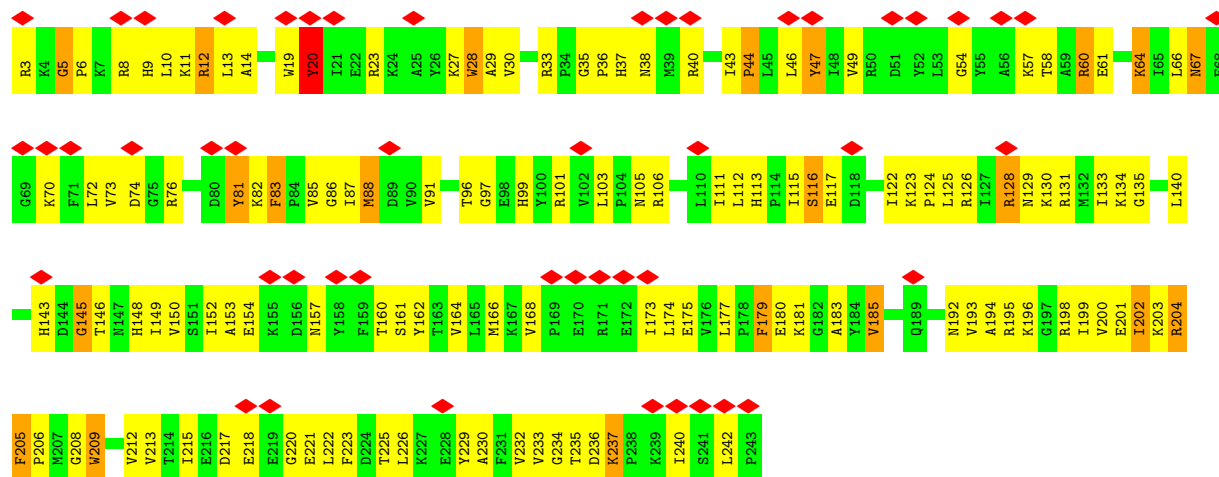
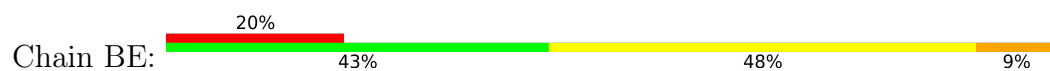


• Molecule 16: 30S ribosomal protein S4P

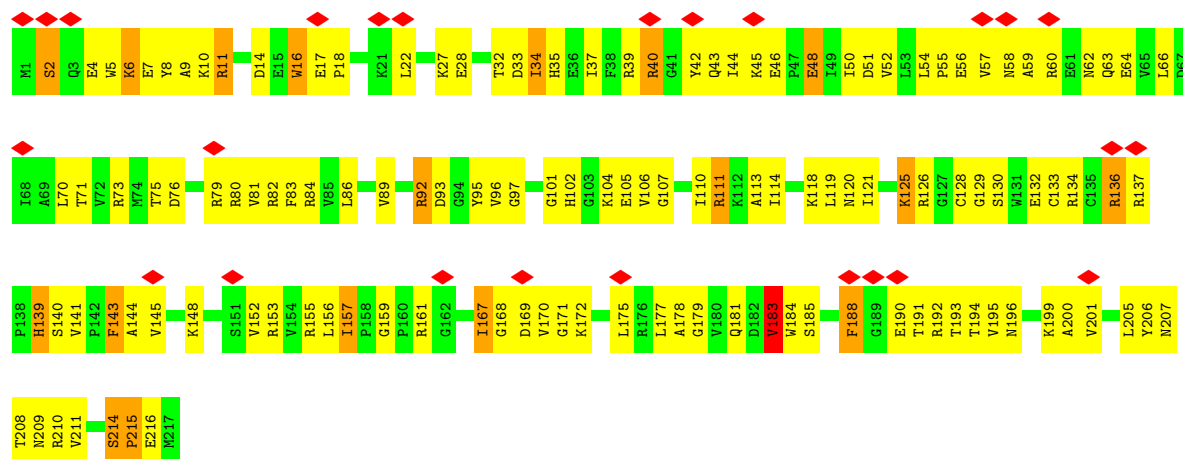




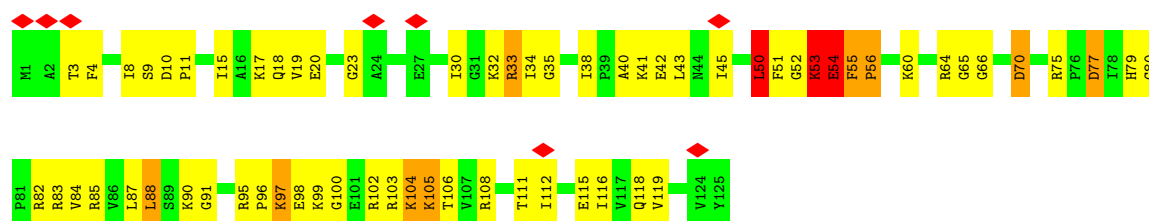
• Molecule 17: 30S ribosomal protein S4E



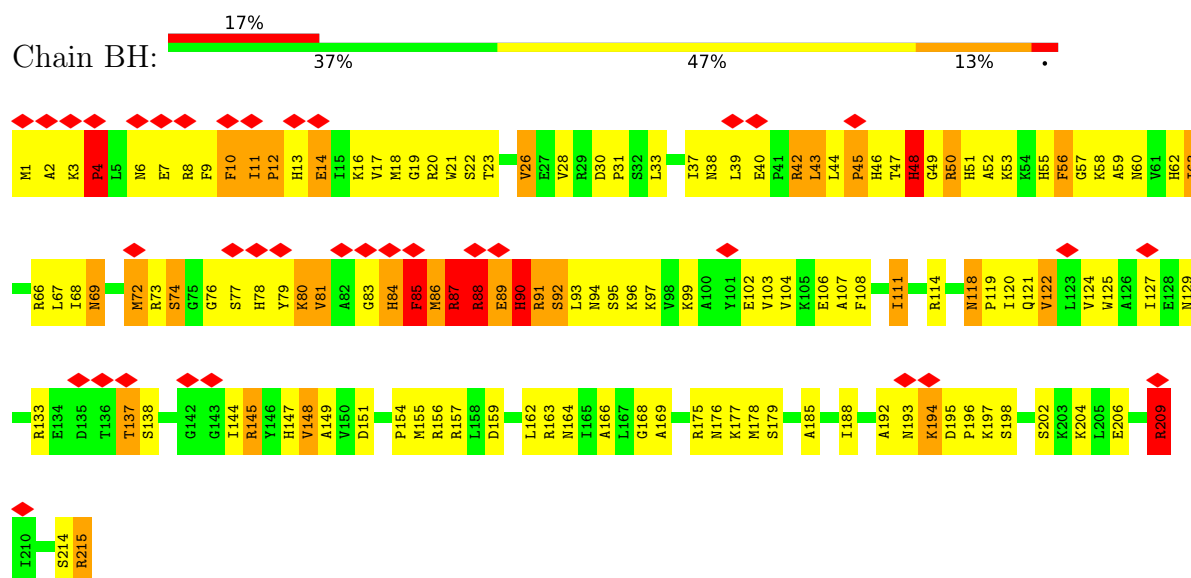
• Molecule 18: 30S ribosomal protein S5P



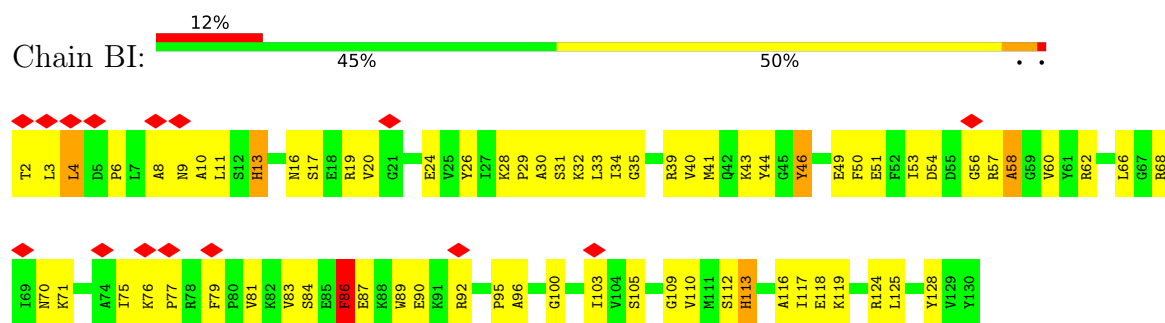
• Molecule 19: 30S ribosomal protein S6E



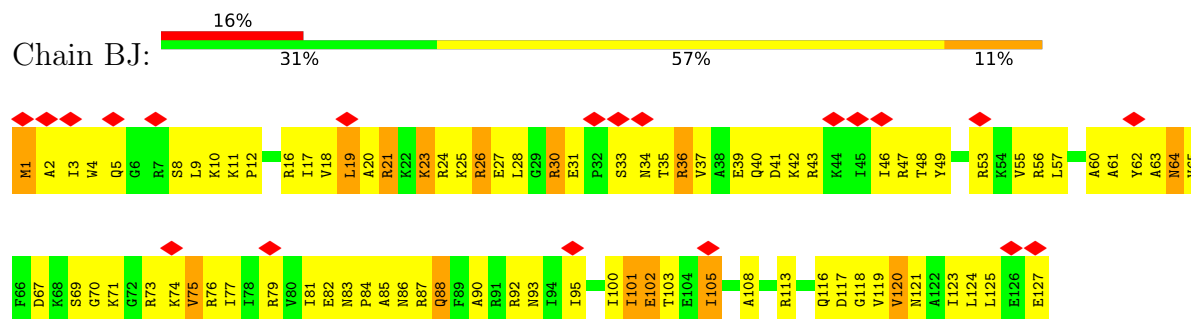
- Molecule 20: 30S ribosomal protein S7P



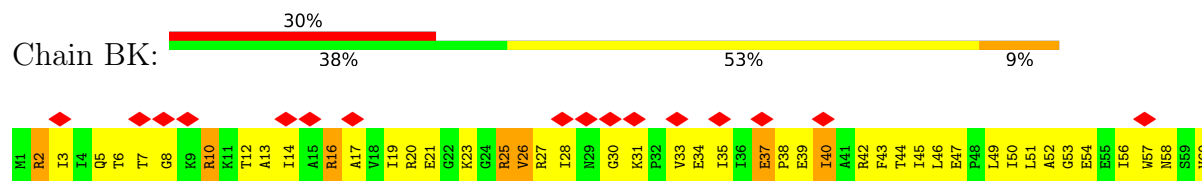
- Molecule 21: 30S ribosomal protein S8P

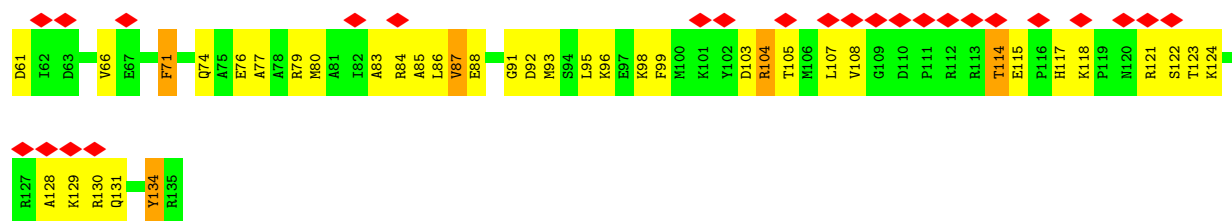


- Molecule 22: 30S ribosomal protein S8E

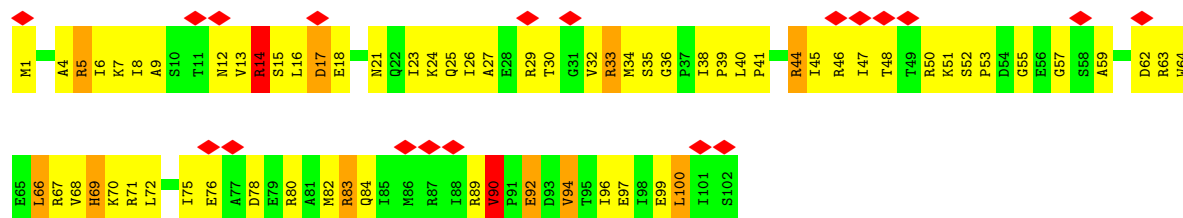


- Molecule 23: 30S ribosomal protein S9P

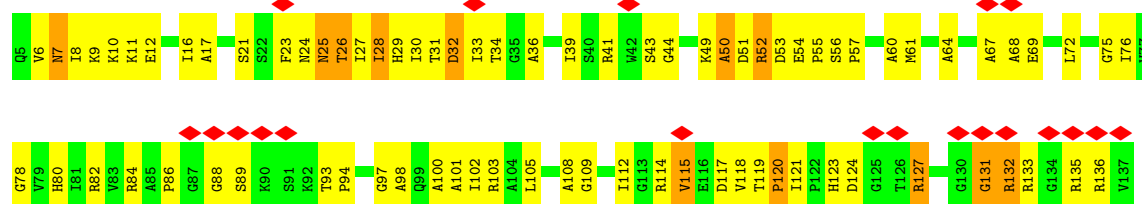




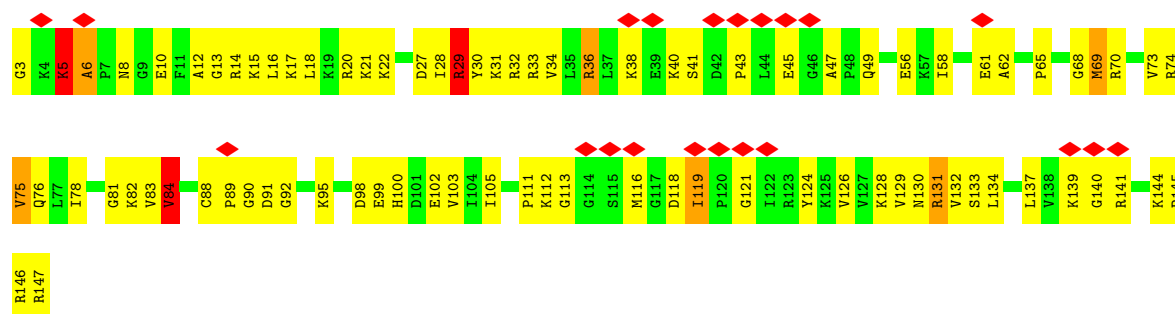
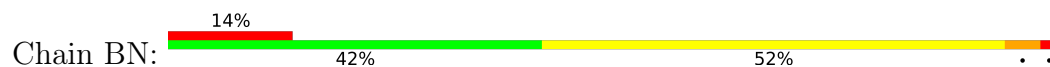
• Molecule 24: 30S ribosomal protein S10P



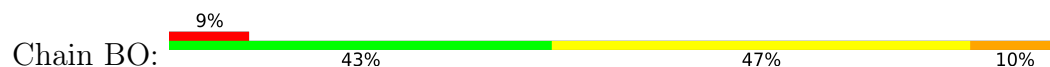
• Molecule 25: 30S ribosomal protein S11P

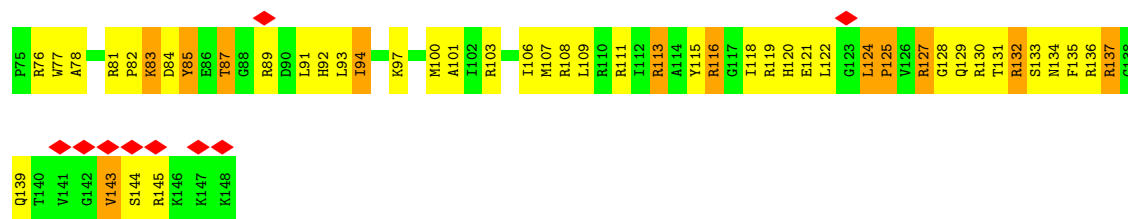


• Molecule 26: 30S ribosomal protein S12P

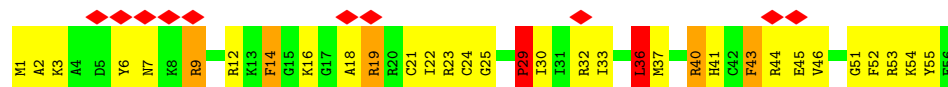
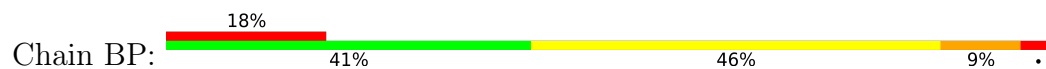


• Molecule 27: 30S ribosomal protein S13P

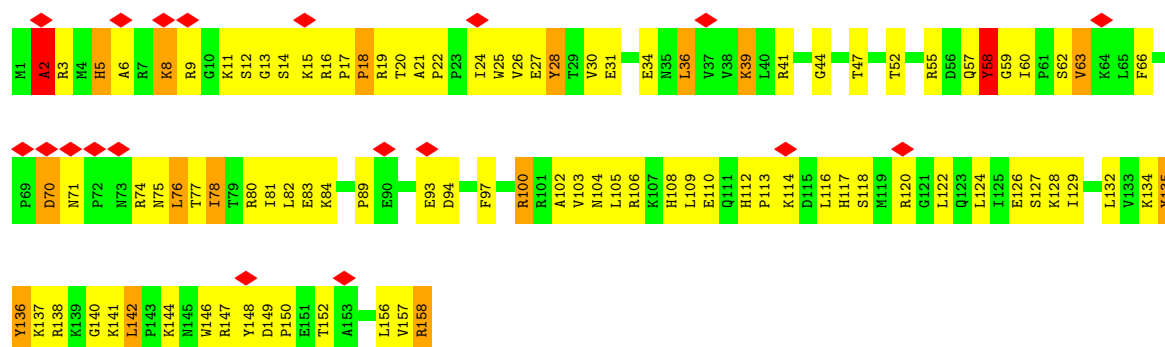
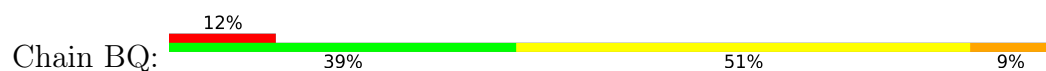




• Molecule 28: 30S ribosomal protein S14P

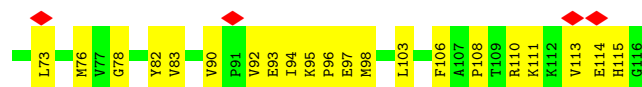
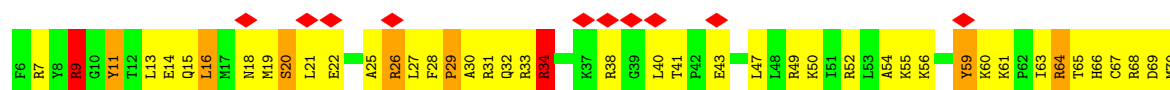
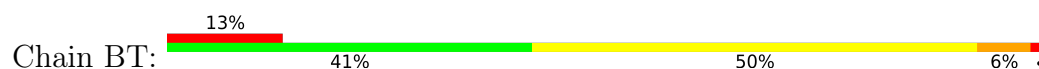


• Molecule 29: 30S ribosomal protein S15P/S13E

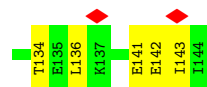
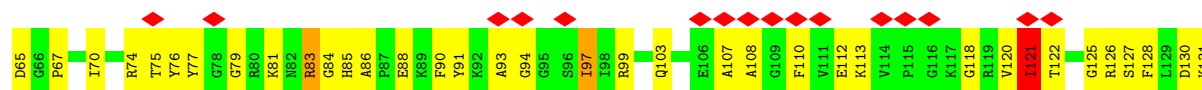
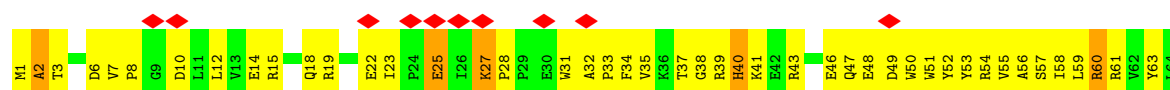




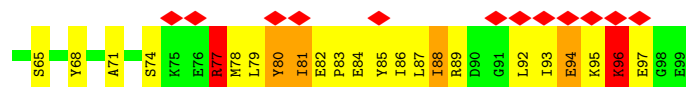
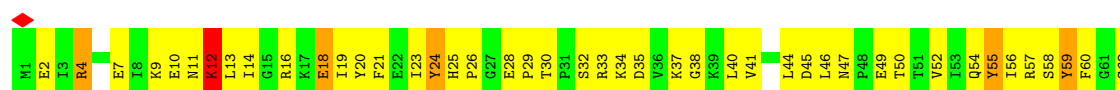
- Molecule 32: 30S ribosomal protein S19P



- Molecule 33: 30S ribosomal protein S19E



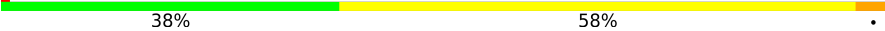
- Molecule 34: 30S ribosomal protein S24E

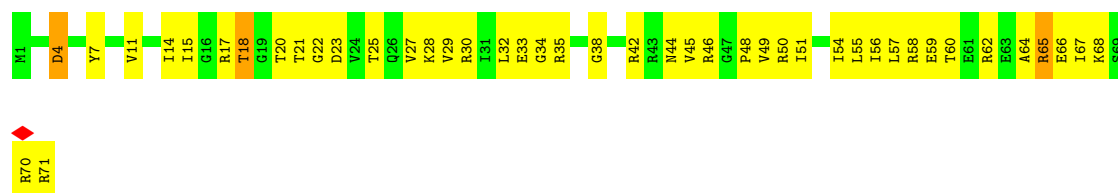


- Molecule 35: 30S ribosomal protein S27E



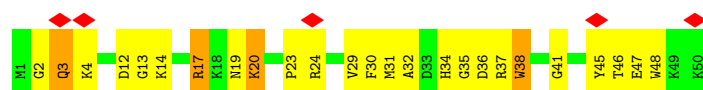
- Molecule 36: 30S ribosomal protein S28E

Chain BX: 



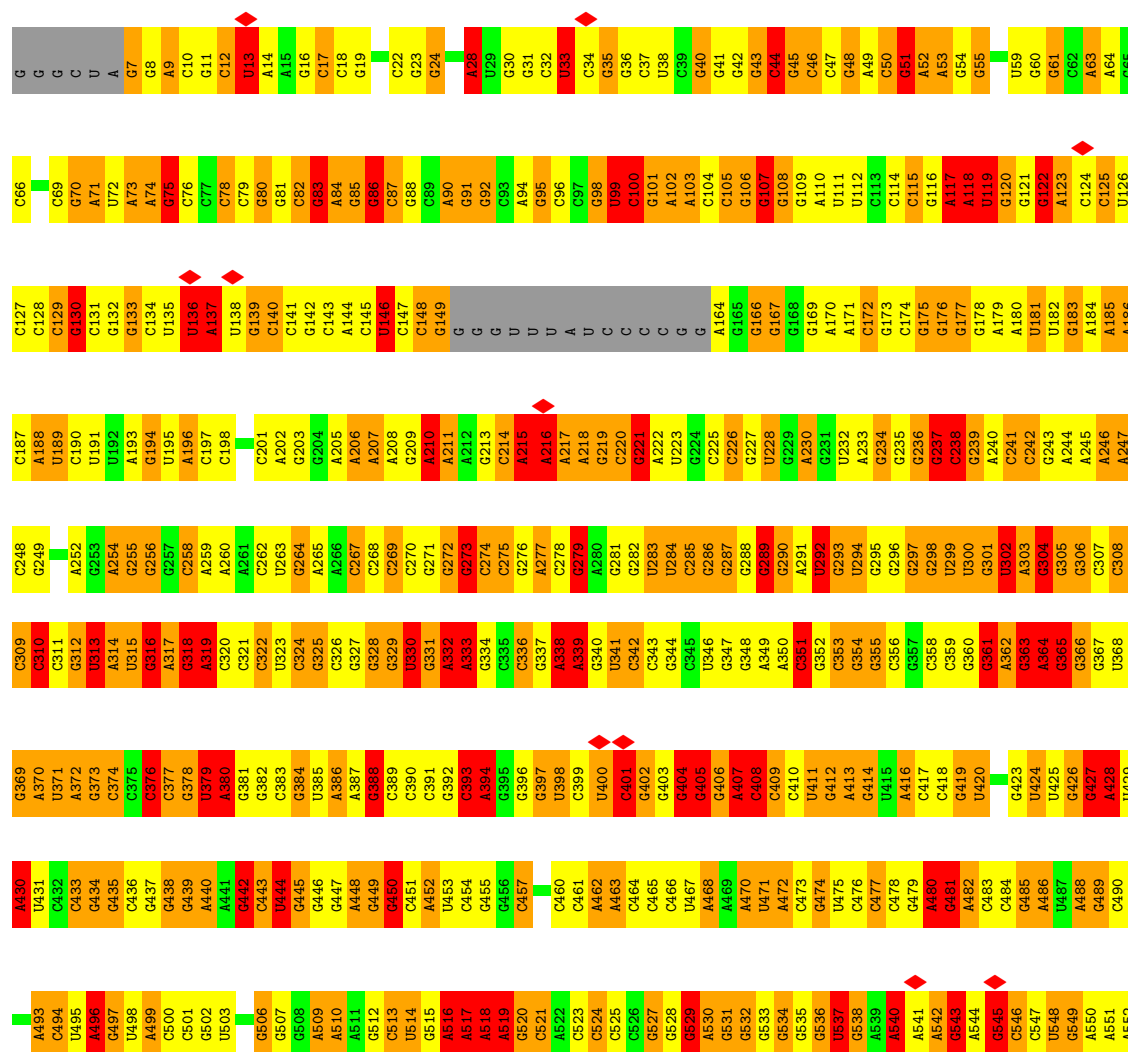
- Molecule 37: 30S ribosomal protein S27AE

Chain BY: 



- Molecule 38: 23S ribosomal RNA

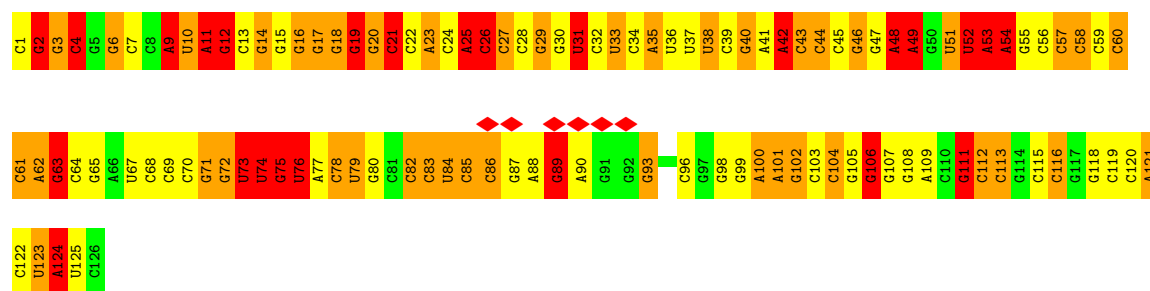
Chain A1: 



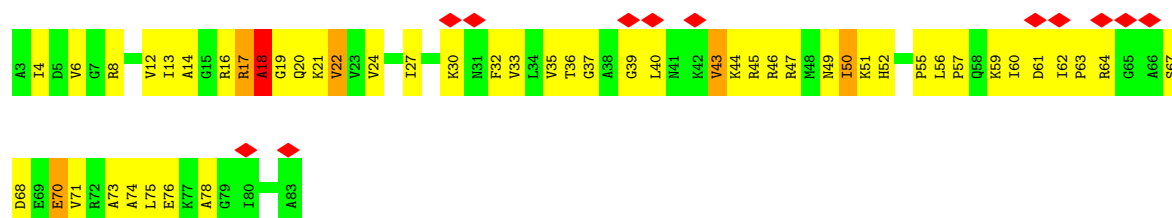
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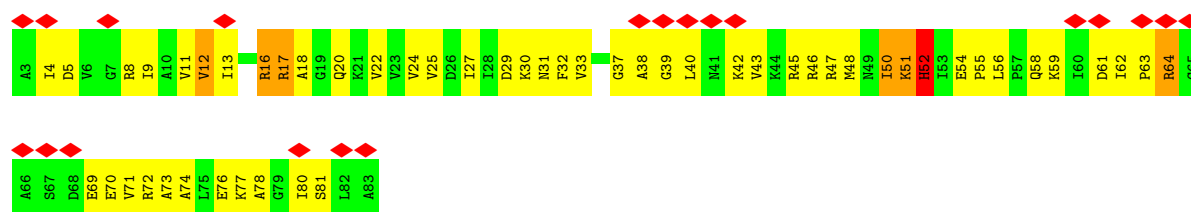




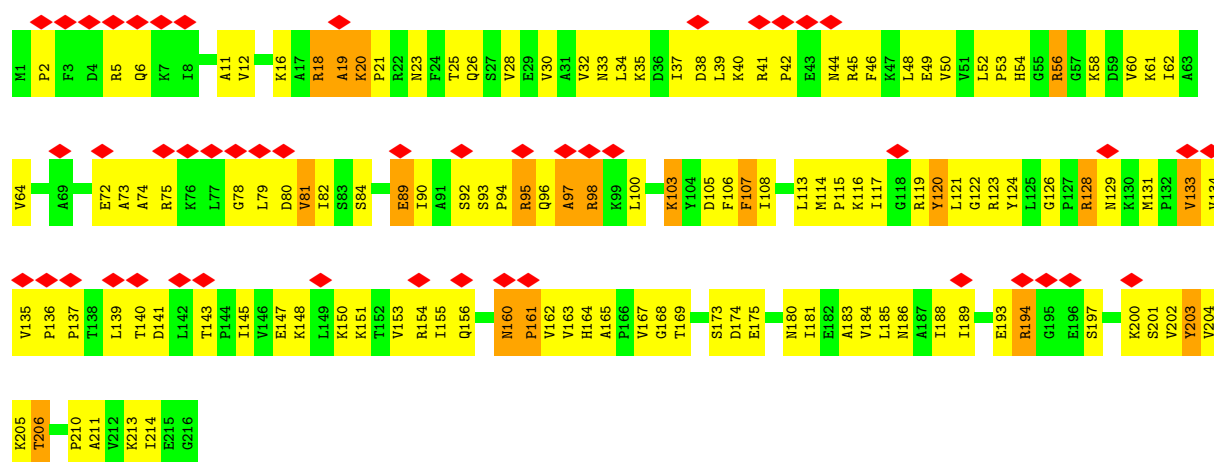
- Molecule 40: 50S ribosomal protein L14E



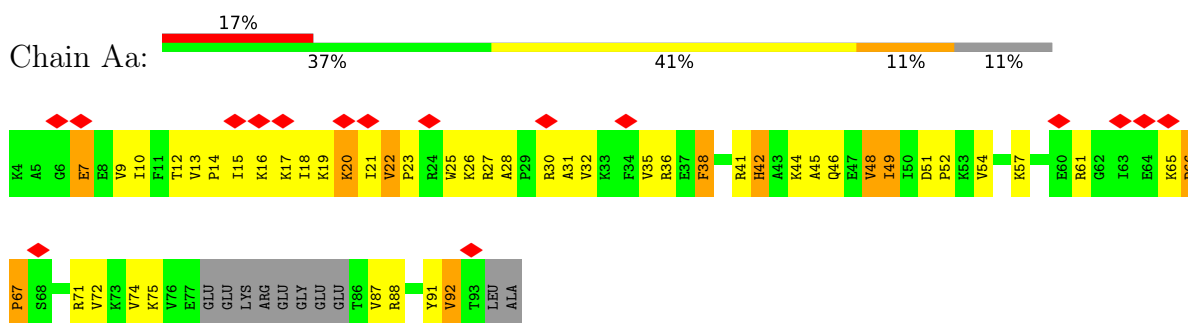
- Molecule 40: 50S ribosomal protein L14E



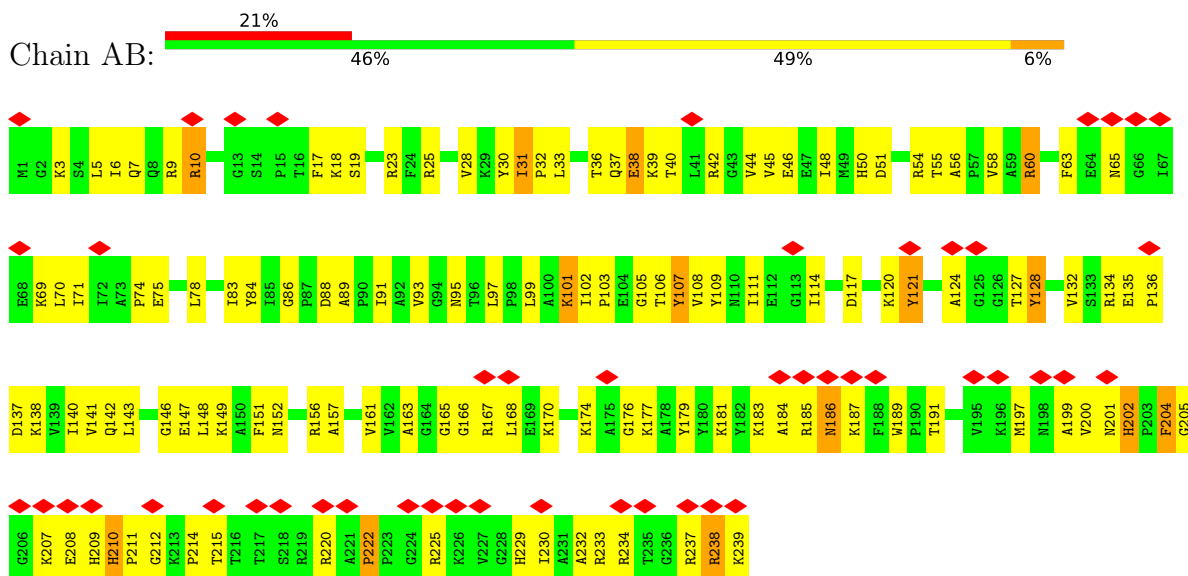
- Molecule 41: 50S ribosomal protein L1P



- Molecule 42: 50S ribosomal protein L31E



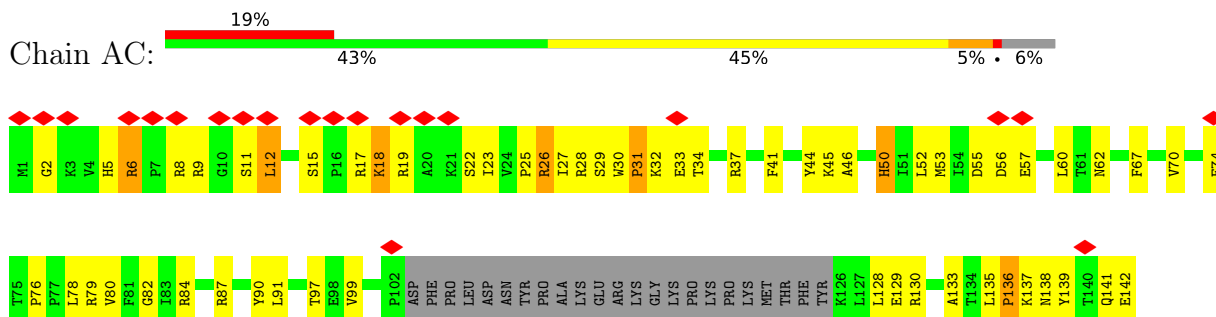
• Molecule 43: 50S ribosomal protein L2

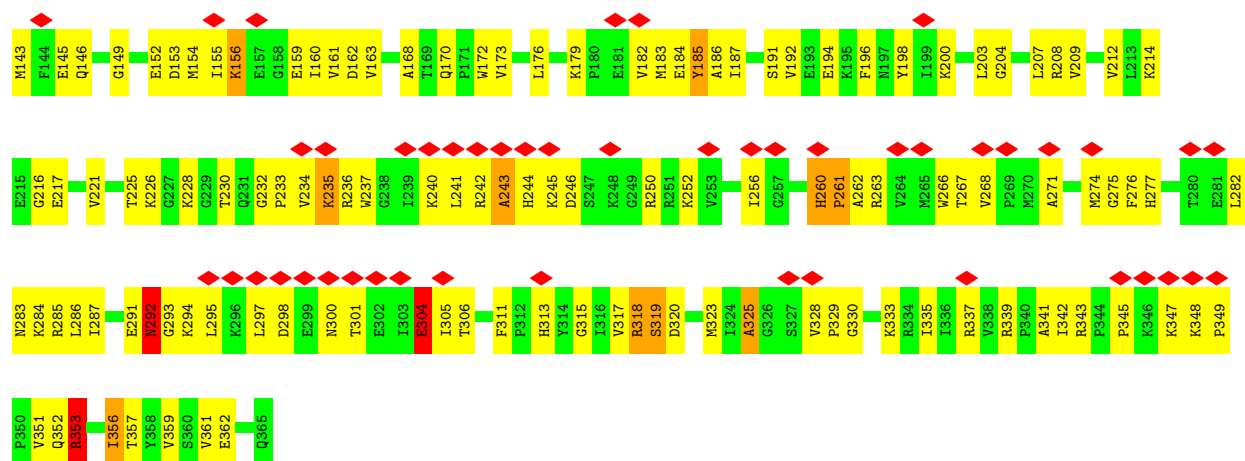


• Molecule 44: 50S ribosomal protein L32E

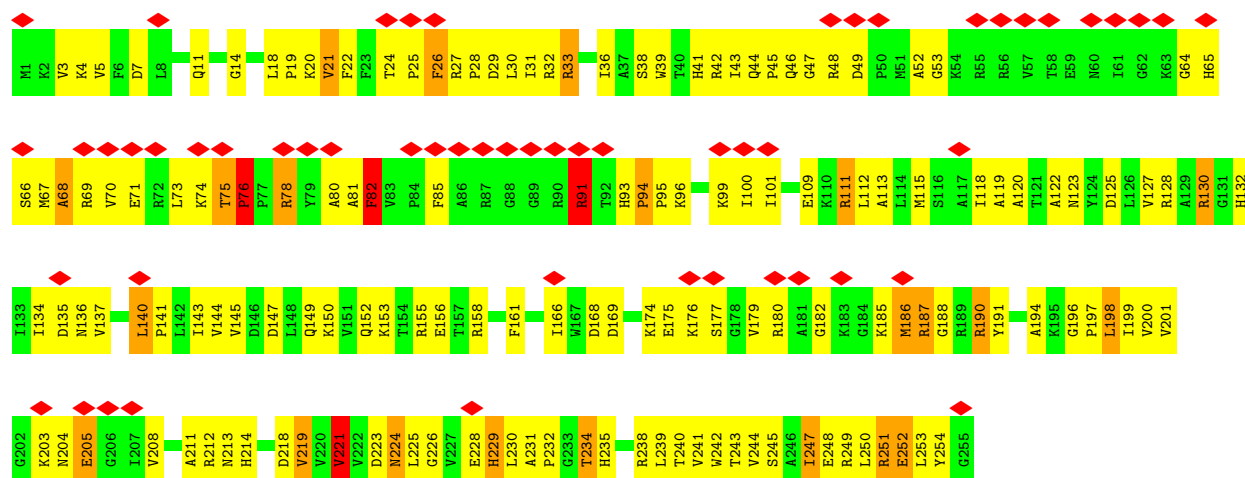


• Molecule 45: 50S ribosomal protein L3P

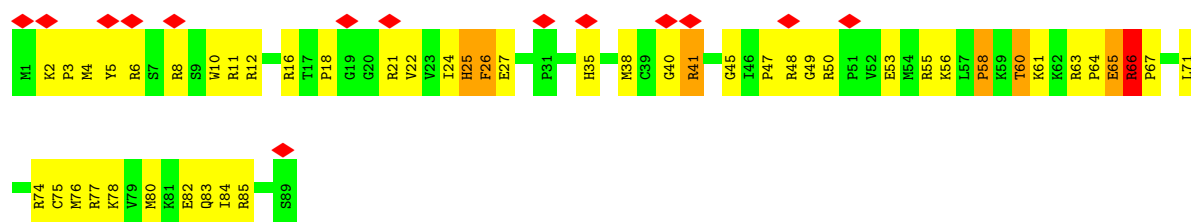




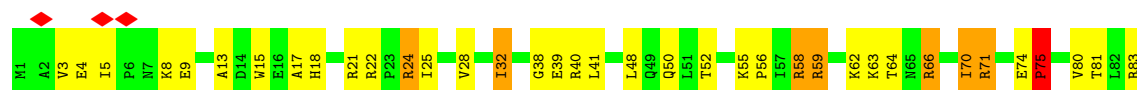
• Molecule 46: 50S ribosomal protein L4P

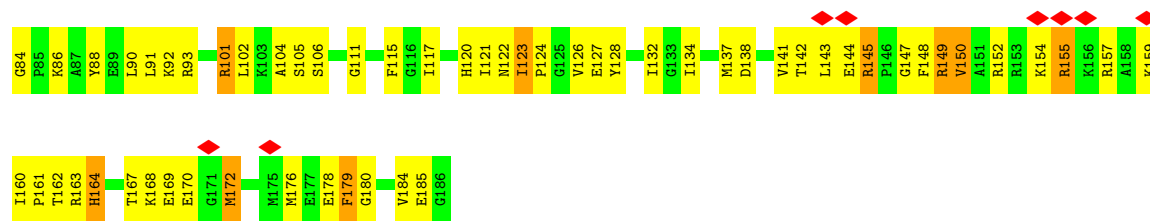


• Molecule 47: 50S ribosomal protein L34E

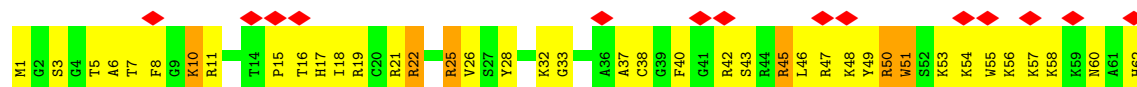


• Molecule 48: 50S ribosomal protein L5P

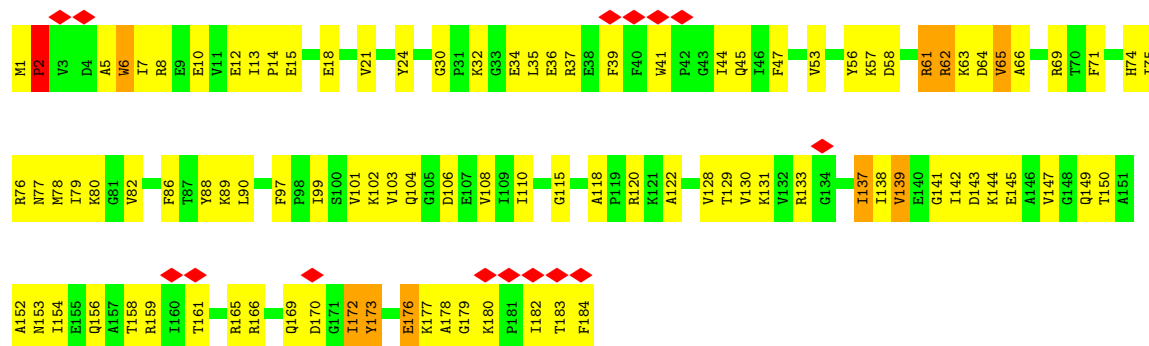




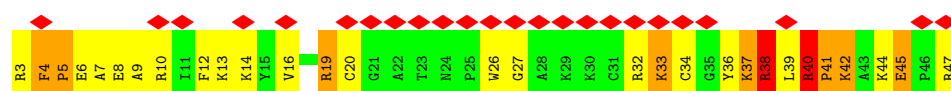
• Molecule 49: 50S ribosomal protein L37E



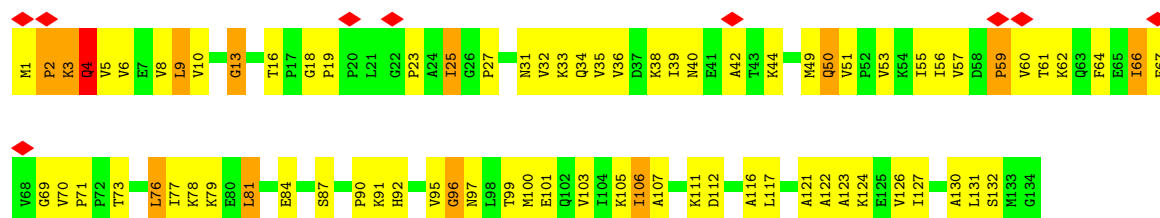
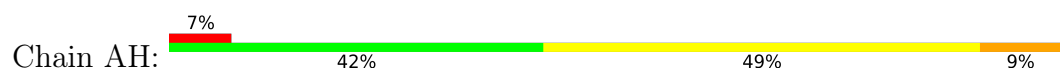
• Molecule 50: 50S ribosomal protein L6P



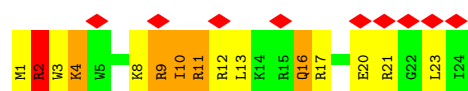
• Molecule 51: 50S ribosomal protein L40E



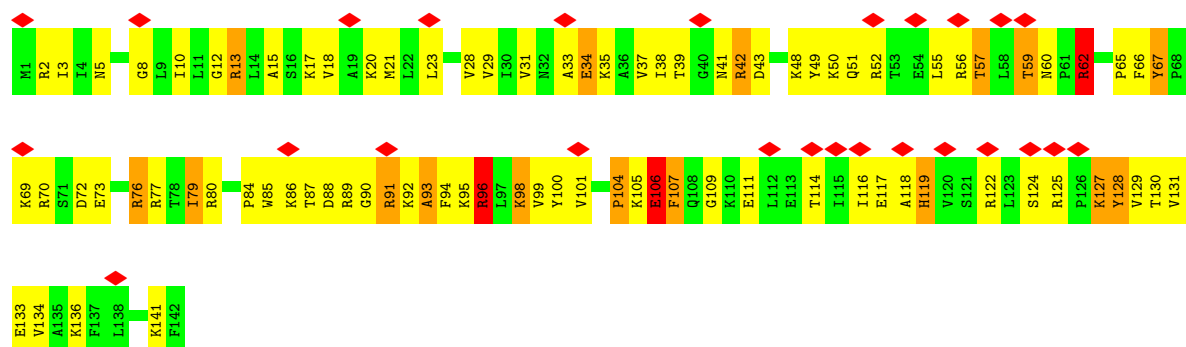
• Molecule 52: 50S ribosomal protein L11P



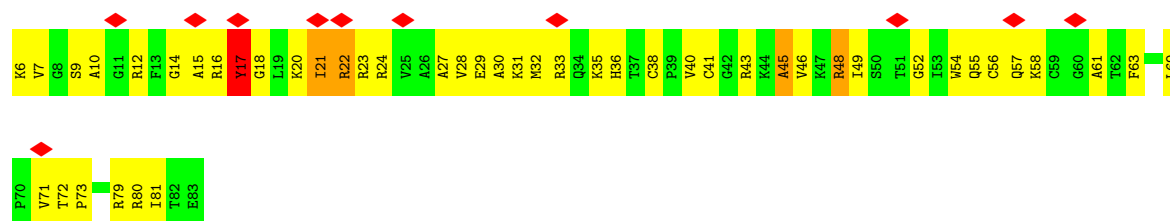
• Molecule 53: 50S ribosomal protein L41E



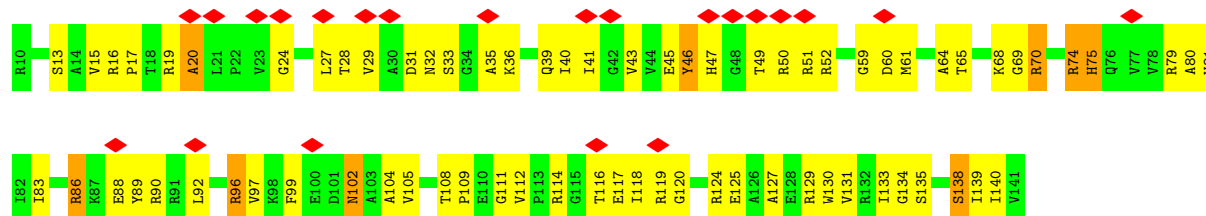
• Molecule 54: 50S ribosomal protein L13P



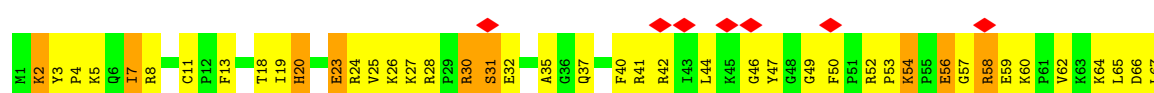
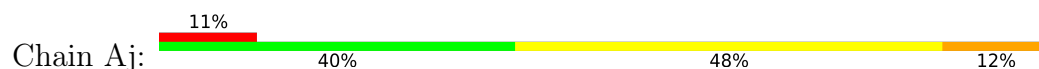
• Molecule 55: 50S ribosomal protein L37AE



• Molecule 56: 50S ribosomal protein L14P

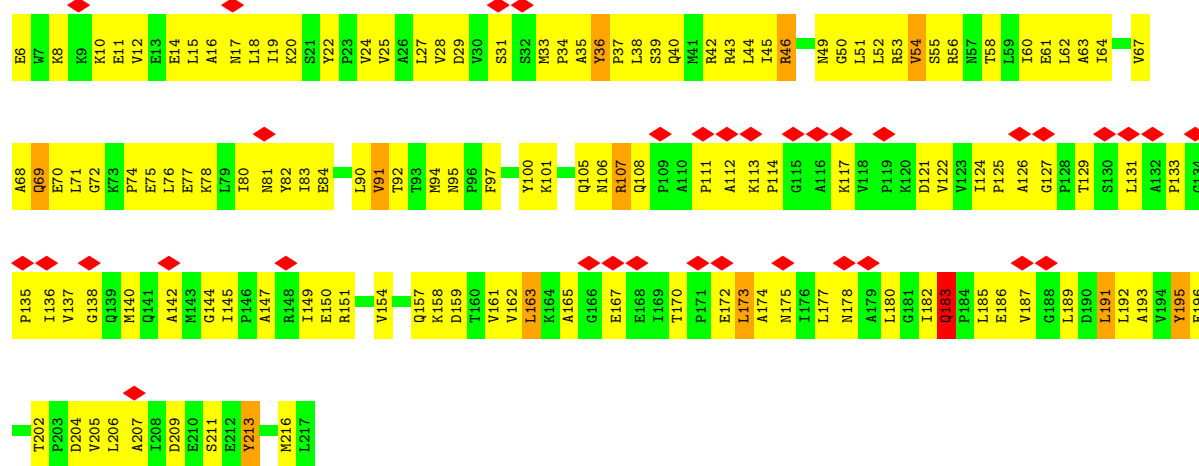


• Molecule 57: 50S ribosomal protein L44E

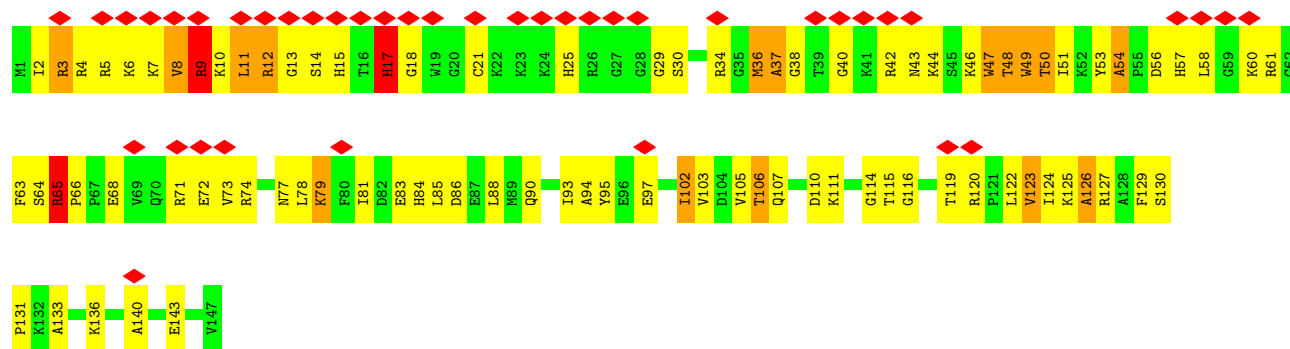




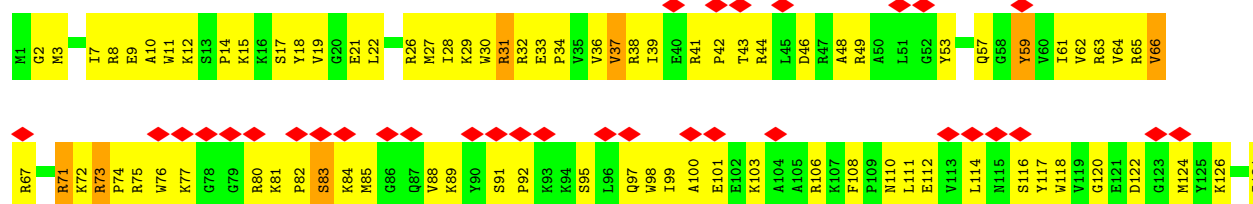
• Molecule 58: 50S ribosomal protein P0/L10E

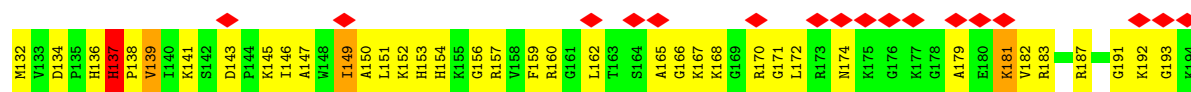


• Molecule 59: 50S ribosomal protein L15P

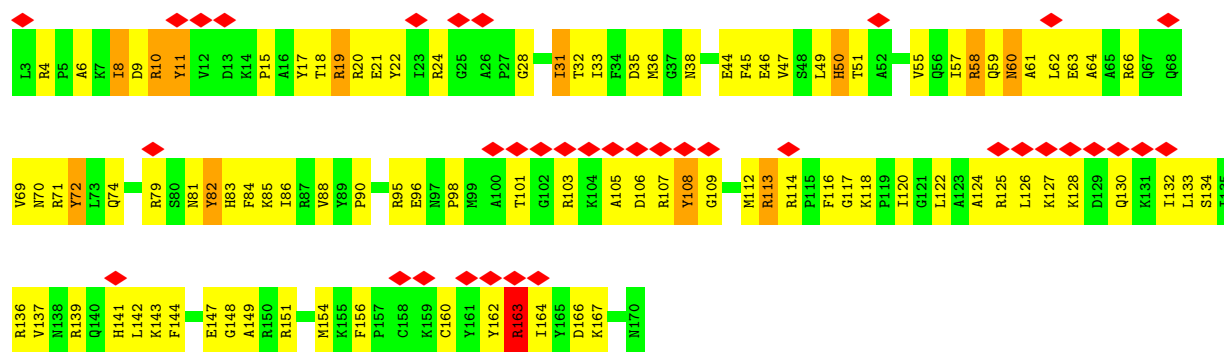
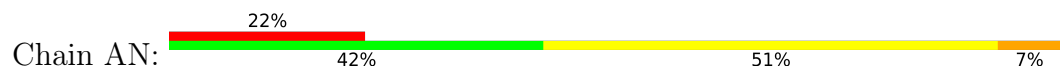


• Molecule 60: 50S ribosomal protein L15E

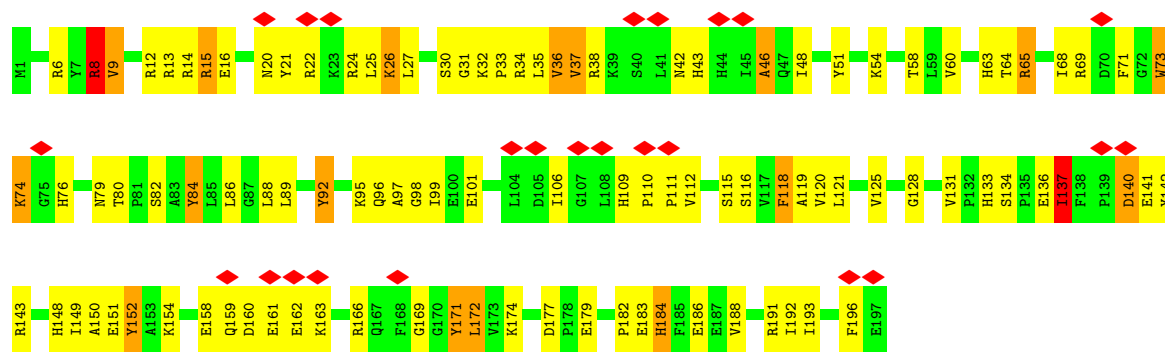




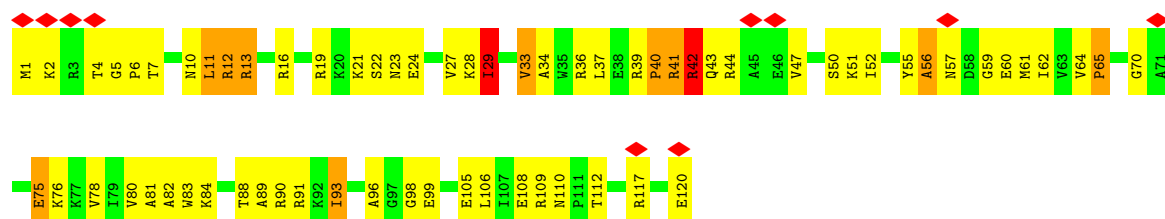
• Molecule 61: 50S ribosomal protein L10E/L16



• Molecule 62: 50S ribosomal protein L18P

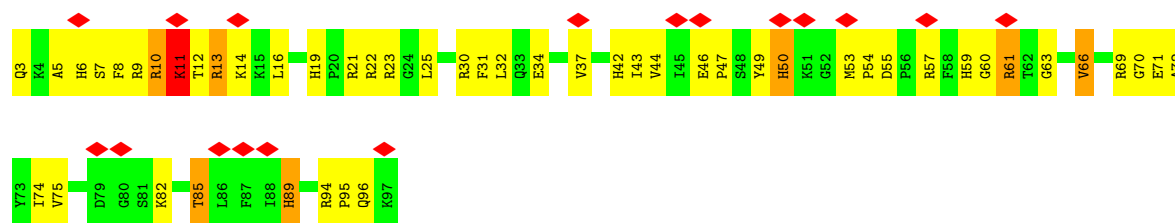


• Molecule 63: 50S ribosomal protein L18E

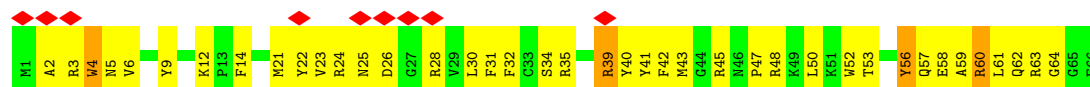


• Molecule 64: 50S ribosomal protein L21E





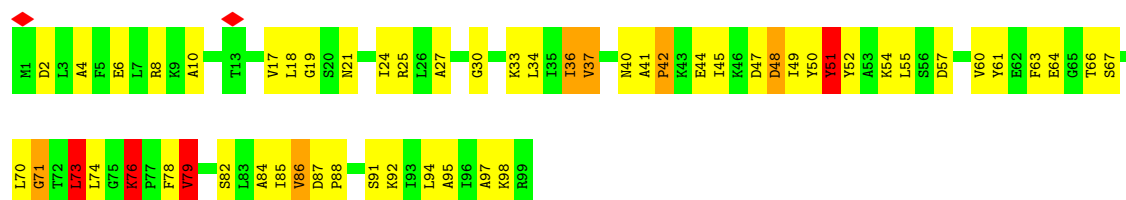
- Molecule 65: 50S ribosomal protein L24E



- Molecule 66: 50S ribosomal protein L30P



- Molecule 67: 50S ribosomal protein L30E



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	37000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	per micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	51000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	3.556	Depositor
Minimum map value	-0.752	Depositor
Average map value	0.060	Depositor
Map value standard deviation	0.270	Depositor
Recommended contour level	0.93	Depositor
Map size ($\text{\AA}$)	444.99, 444.99, 442.26	wwPDB
Map dimensions	163, 163, 162	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.73, 2.73, 2.73	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	A7	2.22	15/534 (2.8%)	2.54	33/719 (4.6%)
2	A8	2.38	15/263 (5.7%)	2.51	20/354 (5.6%)
3	Af	2.47	24/453 (5.3%)	2.54	46/603 (7.6%)
4	AQ	2.35	57/1272 (4.5%)	2.64	108/1676 (6.4%)
5	AS	2.41	60/1226 (4.9%)	2.54	103/1649 (6.2%)
6	AT	2.12	15/689 (2.2%)	2.48	50/924 (5.4%)
7	AU	2.34	46/1024 (4.5%)	2.42	75/1365 (5.5%)
8	AW	2.35	26/547 (4.8%)	2.47	35/725 (4.8%)
9	AX	2.28	126/3383 (3.7%)	2.59	273/4593 (5.9%)
10	B1	2.02	35/1840 (1.9%)	1.92	69/2869 (2.4%)
11	B2	2.02	719/35963 (2.0%)	1.88	1249/56134 (2.2%)
12	AG	2.34	41/951 (4.3%)	2.46	59/1281 (4.6%)
12	B3	2.24	42/951 (4.4%)	2.35	46/1281 (3.6%)
13	BA	2.24	60/1585 (3.8%)	2.50	122/2124 (5.7%)
14	BB	2.27	60/1654 (3.6%)	2.52	126/2233 (5.6%)
15	BC	2.38	64/1481 (4.3%)	2.43	94/1985 (4.7%)
16	BD	2.32	58/1457 (4.0%)	2.55	102/1953 (5.2%)
17	BE	2.26	68/2025 (3.4%)	2.44	132/2732 (4.8%)
18	BF	2.37	85/1746 (4.9%)	2.51	124/2350 (5.3%)
19	BG	2.27	30/999 (3.0%)	2.37	52/1337 (3.9%)
20	BH	2.35	68/1773 (3.8%)	2.69	163/2381 (6.8%)
21	BI	2.30	42/1049 (4.0%)	2.44	67/1408 (4.8%)
22	BJ	2.42	55/1013 (5.4%)	2.49	67/1349 (5.0%)
23	BK	2.33	49/1088 (4.5%)	2.51	84/1455 (5.8%)
24	BL	2.38	40/830 (4.8%)	2.48	53/1113 (4.8%)
25	BM	2.47	52/1022 (5.1%)	2.43	68/1375 (4.9%)
26	BN	2.30	49/1157 (4.2%)	2.51	84/1536 (5.5%)
27	BO	2.29	42/1208 (3.5%)	2.55	95/1619 (5.9%)
28	BP	2.38	22/471 (4.7%)	2.46	33/620 (5.3%)
29	BQ	2.30	57/1338 (4.3%)	2.54	91/1797 (5.1%)
30	BR	2.28	34/956 (3.6%)	2.46	66/1287 (5.1%)
31	BS	2.19	16/562 (2.8%)	2.68	50/744 (6.7%)
32	BT	2.29	36/943 (3.8%)	2.64	79/1257 (6.3%)
33	BU	2.33	43/1204 (3.6%)	2.44	74/1621 (4.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	BV	2.30	38/839 (4.5%)	2.50	59/1122 (5.3%)
35	BW	2.24	20/485 (4.1%)	2.38	25/651 (3.8%)
36	BX	2.41	29/570 (5.1%)	2.41	30/760 (3.9%)
37	BY	2.06	10/421 (2.4%)	2.41	25/558 (4.5%)
38	A1	2.01	1404/71524 (2.0%)	1.86	2313/111652 (2.1%)
39	A3	2.03	64/3007 (2.1%)	1.95	115/4689 (2.5%)
40	A5	2.52	45/618 (7.3%)	2.45	34/829 (4.1%)
40	AK	2.20	20/618 (3.2%)	2.61	54/829 (6.5%)
41	AA	2.25	60/1702 (3.5%)	2.55	146/2293 (6.4%)
42	Aa	2.19	22/690 (3.2%)	2.61	58/926 (6.3%)
43	AB	2.36	83/1883 (4.4%)	2.43	107/2540 (4.2%)
44	Ab	2.39	50/1100 (4.5%)	2.55	81/1466 (5.5%)
45	AC	2.26	88/2774 (3.2%)	2.44	175/3727 (4.7%)
46	AD	2.31	87/2068 (4.2%)	2.51	153/2787 (5.5%)
47	Ad	2.27	26/758 (3.4%)	2.53	54/1007 (5.4%)
48	AE	2.27	57/1513 (3.8%)	2.38	88/2026 (4.3%)
49	Ae	2.34	24/517 (4.6%)	2.42	30/681 (4.4%)
50	AF	2.23	50/1507 (3.3%)	2.37	85/2033 (4.2%)
51	Ag	2.33	15/381 (3.9%)	2.45	23/504 (4.6%)
52	AH	2.25	44/1002 (4.4%)	2.65	93/1351 (6.9%)
53	Ah	2.33	8/233 (3.4%)	2.51	18/301 (6.0%)
54	AI	2.31	52/1168 (4.5%)	2.48	84/1561 (5.4%)
55	Ai	2.43	30/599 (5.0%)	2.60	51/798 (6.4%)
56	AJ	2.47	53/1027 (5.2%)	2.42	54/1385 (3.9%)
57	Aj	2.32	34/806 (4.2%)	2.50	47/1065 (4.4%)
58	Ak	2.32	66/1660 (4.0%)	2.53	132/2253 (5.9%)
59	AL	2.36	51/1175 (4.3%)	2.52	95/1563 (6.1%)
60	AM	2.30	66/1634 (4.0%)	2.64	144/2179 (6.6%)
61	AN	2.33	60/1410 (4.3%)	2.51	106/1890 (5.6%)
62	AO	2.27	61/1636 (3.7%)	2.48	98/2196 (4.5%)
63	AP	2.29	31/980 (3.2%)	2.49	74/1313 (5.6%)
64	AR	2.39	41/808 (5.1%)	2.48	52/1080 (4.8%)
65	AV	2.31	24/570 (4.2%)	2.52	40/758 (5.3%)
66	AY	2.27	50/1262 (4.0%)	2.49	100/1687 (5.9%)
67	AZ	2.29	34/764 (4.5%)	2.45	49/1028 (4.8%)
All	All	2.13	5148/184366 (2.8%)	2.12	8884/271937 (3.3%)

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
2	A8	0	1
3	Af	0	6
4	AQ	0	5
5	AS	0	5
6	AT	0	2
7	AU	0	4
9	AX	0	9
10	B1	0	35
11	B2	0	725
12	AG	0	2
13	BA	0	11
14	BB	0	2
15	BC	0	8
16	BD	0	7
17	BE	0	9
18	BF	0	3
19	BG	1	4
20	BH	4	13
21	BI	0	3
22	BJ	0	6
23	BK	0	7
24	BL	0	8
25	BM	0	2
26	BN	0	4
27	BO	0	5
28	BP	0	1
29	BQ	0	7
30	BR	0	3
31	BS	0	2
32	BT	0	5
33	BU	0	4
34	BV	0	12
35	BW	0	1
36	BX	0	3
37	BY	0	3
38	A1	2	1412
39	A3	0	55
40	A5	0	2
40	AK	0	2
41	AA	0	4
42	Aa	0	2
43	AB	0	8
44	Ab	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
45	AC	0	7
46	AD	0	9
47	Ad	0	1
48	AE	0	6
49	Ae	1	9
50	AF	0	3
51	Ag	1	5
52	AH	1	2
53	Ah	0	2
54	AI	0	7
55	Ai	0	2
56	AJ	0	4
57	Aj	0	7
58	Ak	0	4
59	AL	2	10
60	AM	0	4
61	AN	0	7
62	AO	0	10
63	AP	0	4
64	AR	0	1
65	AV	0	5
66	AY	0	2
67	AZ	0	1
All	All	12	2533

The worst 5 of 5148 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	BC	177	GLY	CA-C	-14.95	1.41	1.52
7	AU	108	GLU	N-CA	-14.54	1.33	1.46
16	BD	161	ALA	C-N	13.67	1.43	1.33
41	AA	135	VAL	CA-CB	13.41	1.60	1.54
9	AX	65	SER	CA-C	-12.71	1.36	1.52

The worst 5 of 8884 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	129	C	P-O3'-C3'	19.35	149.23	120.20
38	A1	1226	G	P-O3'-C3'	19.21	149.01	120.20
38	A1	1200	A	P-O3'-C3'	18.92	148.58	120.20
39	A3	52	U	P-O3'-C3'	18.61	148.12	120.20
39	A3	19	G	P-O3'-C3'	18.46	147.89	120.20

5 of 12 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
19	BG	53	LYS	CA
20	BH	85	PHE	CA
20	BH	86	MET	CA
20	BH	87	ARG	CA
20	BH	96	LYS	CA

5 of 2533 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A8	49	TYR	Sidechain
3	Af	2	ALA	Peptide
3	Af	33	ARG	Peptide
3	Af	34	ARG	Sidechain
3	Af	37	THR	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	A7	525	0	567	3	0
2	A8	258	0	272	0	0
3	Af	445	0	510	1	0
4	AQ	1256	0	1390	2	0
5	AS	1200	0	1255	2	0
6	AT	680	0	739	4	0
7	AU	1008	0	1077	3	0
8	AW	546	0	601	1	0
9	AX	3309	0	3523	6	0
10	B1	1646	0	835	75	0
11	B2	32132	0	16199	155	0
12	AG	939	0	994	3	0
12	B3	939	0	994	3	0
13	BA	1559	0	1648	4	0
14	BB	1623	0	1685	6	0
15	BC	1460	0	1549	1	0
16	BD	1434	0	1498	3	0
17	BE	1976	0	2046	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	BF	1717	0	1770	4	0
19	BG	984	0	1044	5	0
20	BH	1736	0	1787	15	0
21	BI	1028	0	1065	3	0
22	BJ	1004	0	1088	5	0
23	BK	1072	0	1128	8	0
24	BL	822	0	870	6	0
25	BM	1004	0	1041	1	0
26	BN	1141	0	1240	2	0
27	BO	1189	0	1248	6	0
28	BP	462	0	492	5	0
29	BQ	1310	0	1392	12	0
30	BR	934	0	960	2	0
31	BS	556	0	604	4	0
32	BT	924	0	986	3	0
33	BU	1176	0	1216	5	0
34	BV	823	0	847	6	0
35	BW	478	0	524	5	0
36	BX	568	0	600	0	0
37	BY	409	0	410	4	0
38	A1	63885	0	32208	260	0
39	A3	2691	0	1371	13	0
40	A5	614	0	670	5	0
40	AK	614	0	670	1	0
41	AA	1677	0	1796	13	0
42	Aa	677	0	749	5	0
43	AB	1838	0	1914	4	0
44	Ab	1075	0	1168	0	0
45	AC	2717	0	2875	9	0
46	AD	2026	0	2137	11	0
47	Ad	740	0	809	3	0
48	AE	1489	0	1550	5	0
49	Ae	506	0	529	1	0
50	AF	1476	0	1518	7	0
51	Ag	372	0	395	3	0
52	AH	989	0	1077	4	0
53	Ah	230	0	270	50	0
54	AI	1150	0	1240	6	0
55	Ai	590	0	631	3	0
56	AJ	1014	0	1072	5	0
57	Aj	788	0	842	5	0
58	Ak	1633	0	1726	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	AL	1154	0	1219	10	0
60	AM	1595	0	1695	1	0
61	AN	1379	0	1405	3	0
62	AO	1598	0	1639	4	0
63	AP	966	0	1019	3	0
64	AR	787	0	827	4	0
65	AV	555	0	548	1	0
66	AY	1243	0	1326	4	0
67	AZ	754	0	804	12	0
All	All	171094	0	125393	640	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 2.

The worst 5 of 640 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)
11:B2:849:U:H4'	53:Ah:9:ARG:CZ	1.28	1.61
11:B2:849:U:C5'	53:Ah:9:ARG:HD2	1.39	1.51
10:B1:77:A:H5''	38:A1:2513:C:C2'	1.48	1.40
29:BQ:158:ARG:OXT	67:AZ:73:LEU:CD2	1.69	1.40
11:B2:849:U:H4'	53:Ah:9:ARG:NH1	1.38	1.35

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	A7	63/67 (94%)	43 (68%)	16 (25%)	4 (6%)	1	13
2	A8	30/52 (58%)	22 (73%)	7 (23%)	1 (3%)	3	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Af	49/51 (96%)	40 (82%)	6 (12%)	3 (6%)	1	13
4	AQ	148/150 (99%)	139 (94%)	5 (3%)	4 (3%)	4	25
5	AS	148/150 (99%)	135 (91%)	10 (7%)	3 (2%)	6	31
6	AT	82/84 (98%)	75 (92%)	4 (5%)	3 (4%)	2	20
7	AU	119/121 (98%)	113 (95%)	5 (4%)	1 (1%)	16	54
8	AW	64/72 (89%)	64 (100%)	0	0	100	100
9	AX	430/436 (99%)	322 (75%)	77 (18%)	31 (7%)	1	11
12	AG	121/123 (98%)	114 (94%)	4 (3%)	3 (2%)	4	26
12	B3	121/123 (98%)	100 (83%)	14 (12%)	7 (6%)	1	14
13	BA	188/190 (99%)	164 (87%)	12 (6%)	12 (6%)	1	12
14	BB	200/202 (99%)	182 (91%)	12 (6%)	6 (3%)	3	23
15	BC	184/186 (99%)	171 (93%)	9 (5%)	4 (2%)	5	29
16	BD	170/172 (99%)	148 (87%)	20 (12%)	2 (1%)	10	44
17	BE	239/241 (99%)	207 (87%)	20 (8%)	12 (5%)	1	16
18	BF	215/217 (99%)	188 (87%)	16 (7%)	11 (5%)	1	15
19	BG	123/125 (98%)	103 (84%)	13 (11%)	7 (6%)	1	14
20	BH	213/215 (99%)	186 (87%)	14 (7%)	13 (6%)	1	13
21	BI	127/129 (98%)	118 (93%)	8 (6%)	1 (1%)	16	54
22	BJ	125/127 (98%)	107 (86%)	15 (12%)	3 (2%)	4	27
23	BK	133/135 (98%)	116 (87%)	10 (8%)	7 (5%)	1	15
24	BL	100/102 (98%)	90 (90%)	7 (7%)	3 (3%)	3	23
25	BM	131/133 (98%)	112 (86%)	9 (7%)	10 (8%)	1	10
26	BN	143/145 (99%)	128 (90%)	7 (5%)	8 (6%)	1	14
27	BO	146/148 (99%)	122 (84%)	16 (11%)	8 (6%)	1	15
28	BP	54/56 (96%)	44 (82%)	8 (15%)	2 (4%)	2	20
29	BQ	156/158 (99%)	137 (88%)	9 (6%)	10 (6%)	1	12
30	BR	111/113 (98%)	105 (95%)	5 (4%)	1 (1%)	14	51
31	BS	65/67 (97%)	60 (92%)	5 (8%)	0	100	100
32	BT	109/111 (98%)	102 (94%)	5 (5%)	2 (2%)	6	34
33	BU	142/144 (99%)	123 (87%)	11 (8%)	8 (6%)	1	14
34	BV	97/99 (98%)	88 (91%)	5 (5%)	4 (4%)	2	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	BW	61/63 (97%)	52 (85%)	6 (10%)	3 (5%)	1	16
36	BX	69/71 (97%)	62 (90%)	6 (9%)	1 (1%)	9	40
37	BY	48/50 (96%)	41 (85%)	5 (10%)	2 (4%)	2	17
40	A5	79/81 (98%)	67 (85%)	9 (11%)	3 (4%)	2	19
40	AK	79/81 (98%)	70 (89%)	4 (5%)	5 (6%)	1	13
41	AA	214/216 (99%)	186 (87%)	19 (9%)	9 (4%)	2	17
42	Aa	78/92 (85%)	69 (88%)	9 (12%)	0	100	100
43	AB	237/239 (99%)	209 (88%)	23 (10%)	5 (2%)	5	30
44	Ab	125/127 (98%)	108 (86%)	11 (9%)	6 (5%)	2	16
45	AC	338/365 (93%)	303 (90%)	21 (6%)	14 (4%)	2	18
46	AD	253/255 (99%)	220 (87%)	23 (9%)	10 (4%)	2	18
47	Ad	87/89 (98%)	78 (90%)	6 (7%)	3 (3%)	3	21
48	AE	184/186 (99%)	161 (88%)	15 (8%)	8 (4%)	2	17
49	Ae	60/62 (97%)	43 (72%)	13 (22%)	4 (7%)	1	12
50	AF	182/184 (99%)	165 (91%)	14 (8%)	3 (2%)	7	38
51	Ag	43/45 (96%)	30 (70%)	8 (19%)	5 (12%)	0	5
52	AH	132/134 (98%)	114 (86%)	11 (8%)	7 (5%)	1	15
53	Ah	22/24 (92%)	21 (96%)	1 (4%)	0	100	100
54	AI	140/142 (99%)	121 (86%)	13 (9%)	6 (4%)	2	17
55	Ai	76/78 (97%)	69 (91%)	4 (5%)	3 (4%)	2	19
56	AJ	130/132 (98%)	121 (93%)	6 (5%)	3 (2%)	5	28
57	Aj	92/94 (98%)	69 (75%)	18 (20%)	5 (5%)	1	15
58	Ak	210/212 (99%)	192 (91%)	11 (5%)	7 (3%)	3	21
59	AL	145/147 (99%)	129 (89%)	11 (8%)	5 (3%)	3	21
60	AM	192/194 (99%)	175 (91%)	11 (6%)	6 (3%)	3	22
61	AN	166/168 (99%)	141 (85%)	19 (11%)	6 (4%)	2	20
62	AO	195/197 (99%)	166 (85%)	20 (10%)	9 (5%)	2	17
63	AP	118/120 (98%)	107 (91%)	5 (4%)	6 (5%)	1	15
64	AR	93/95 (98%)	85 (91%)	3 (3%)	5 (5%)	1	15
65	AV	64/66 (97%)	61 (95%)	3 (5%)	0	100	100
66	AY	153/155 (99%)	137 (90%)	12 (8%)	4 (3%)	4	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	AZ	97/99 (98%)	84 (87%)	9 (9%)	4 (4%)	2	18
All	All	8708/8907 (98%)	7624 (88%)	733 (8%)	351 (4%)	4	18

5 of 351 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A7	30	LYS
4	AQ	134	ASN
9	AX	239	ARG
9	AX	277	TYR
9	AX	346	ALA

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	A7	57/59 (97%)	55 (96%)	2 (4%)	32	53
2	A8	28/44 (64%)	27 (96%)	1 (4%)	31	52
3	Af	47/47 (100%)	47 (100%)	0	100	100
4	AQ	130/130 (100%)	124 (95%)	6 (5%)	24	45
5	AS	126/126 (100%)	120 (95%)	6 (5%)	23	44
6	AT	75/75 (100%)	72 (96%)	3 (4%)	28	49
7	AU	110/110 (100%)	105 (96%)	5 (4%)	24	46
8	AW	61/66 (92%)	61 (100%)	0	100	100
9	AX	351/355 (99%)	343 (98%)	8 (2%)	44	64
12	AG	99/99 (100%)	94 (95%)	5 (5%)	21	42
12	B3	99/99 (100%)	96 (97%)	3 (3%)	36	57
13	BA	166/166 (100%)	154 (93%)	12 (7%)	13	35
14	BB	173/173 (100%)	166 (96%)	7 (4%)	28	49
15	BC	145/145 (100%)	140 (97%)	5 (3%)	32	54
16	BD	153/153 (100%)	150 (98%)	3 (2%)	48	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	BE	212/212 (100%)	200 (94%)	12 (6%)	18	40
18	BF	181/181 (100%)	173 (96%)	8 (4%)	25	47
19	BG	108/108 (100%)	106 (98%)	2 (2%)	50	67
20	BH	184/184 (100%)	168 (91%)	16 (9%)	9	29
21	BI	107/107 (100%)	106 (99%)	1 (1%)	70	79
22	BJ	103/103 (100%)	95 (92%)	8 (8%)	11	32
23	BK	111/111 (100%)	107 (96%)	4 (4%)	31	52
24	BL	91/91 (100%)	85 (93%)	6 (7%)	15	37
25	BM	100/100 (100%)	96 (96%)	4 (4%)	28	49
26	BN	119/119 (100%)	112 (94%)	7 (6%)	18	39
27	BO	122/122 (100%)	119 (98%)	3 (2%)	42	63
28	BP	46/46 (100%)	44 (96%)	2 (4%)	26	47
29	BQ	143/143 (100%)	134 (94%)	9 (6%)	16	37
30	BR	102/102 (100%)	96 (94%)	6 (6%)	18	39
31	BS	61/61 (100%)	59 (97%)	2 (3%)	33	55
32	BT	99/99 (100%)	95 (96%)	4 (4%)	28	49
33	BU	121/121 (100%)	118 (98%)	3 (2%)	42	63
34	BV	89/89 (100%)	86 (97%)	3 (3%)	32	54
35	BW	54/54 (100%)	48 (89%)	6 (11%)	6	20
36	BX	60/60 (100%)	56 (93%)	4 (7%)	15	36
37	BY	41/41 (100%)	41 (100%)	0	100	100
40	A5	64/64 (100%)	63 (98%)	1 (2%)	55	70
40	AK	64/64 (100%)	58 (91%)	6 (9%)	8	26
41	AA	182/182 (100%)	173 (95%)	9 (5%)	22	43
42	Aa	73/81 (90%)	70 (96%)	3 (4%)	27	49
43	AB	189/189 (100%)	183 (97%)	6 (3%)	34	56
44	Ab	114/114 (100%)	106 (93%)	8 (7%)	14	35
45	AC	291/312 (93%)	279 (96%)	12 (4%)	27	49
46	AD	213/213 (100%)	205 (96%)	8 (4%)	29	50
47	Ad	81/81 (100%)	80 (99%)	1 (1%)	63	75
48	AE	158/158 (100%)	152 (96%)	6 (4%)	29	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	Ae	51/51 (100%)	49 (96%)	2 (4%)	28	49
50	AF	156/156 (100%)	150 (96%)	6 (4%)	29	50
51	Ag	37/37 (100%)	36 (97%)	1 (3%)	39	61
52	AH	110/110 (100%)	108 (98%)	2 (2%)	51	68
53	Ah	23/23 (100%)	23 (100%)	0	100	100
54	AI	122/122 (100%)	117 (96%)	5 (4%)	27	49
55	Ai	57/57 (100%)	55 (96%)	2 (4%)	32	53
56	AJ	104/104 (100%)	101 (97%)	3 (3%)	37	58
57	Aj	83/83 (100%)	81 (98%)	2 (2%)	43	64
58	Ak	179/179 (100%)	170 (95%)	9 (5%)	22	43
59	AL	117/117 (100%)	114 (97%)	3 (3%)	40	62
60	AM	162/162 (100%)	155 (96%)	7 (4%)	26	47
61	AN	140/140 (100%)	136 (97%)	4 (3%)	37	58
62	AO	166/166 (100%)	157 (95%)	9 (5%)	20	41
63	AP	101/101 (100%)	96 (95%)	5 (5%)	22	43
64	AR	85/85 (100%)	80 (94%)	5 (6%)	18	39
65	AV	56/56 (100%)	56 (100%)	0	100	100
66	AY	133/133 (100%)	130 (98%)	3 (2%)	44	64
67	AZ	80/80 (100%)	73 (91%)	7 (9%)	9	28
All	All	7465/7521 (99%)	7154 (96%)	311 (4%)	28	48

5 of 311 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	AF	102	LYS
62	AO	74	LYS
51	Ag	40	ARG
58	Ak	31	SER
64	AR	85	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 143 such sidechains are listed below:

Mol	Chain	Res	Type
58	Ak	17	ASN

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Mol	Chain	Res	Type
59	AL	77	ASN
63	AP	23	ASN
24	BL	69	HIS
24	BL	21	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B1	76/77 (98%)	20 (26%)	4 (5%)
11	B2	1494/1495 (99%)	267 (17%)	103 (6%)
38	A1	2964/3049 (97%)	615 (20%)	158 (5%)
39	A3	125/126 (99%)	36 (28%)	11 (8%)
All	All	4659/4747 (98%)	938 (20%)	276 (5%)

5 of 938 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	B1	8	U
10	B1	9	A
10	B1	10	G
10	B1	18	U
10	B1	19	G

5 of 276 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A1	2324	C
38	A1	2401	A
38	A1	2957	G
11	B2	1399	G
11	B2	1322	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

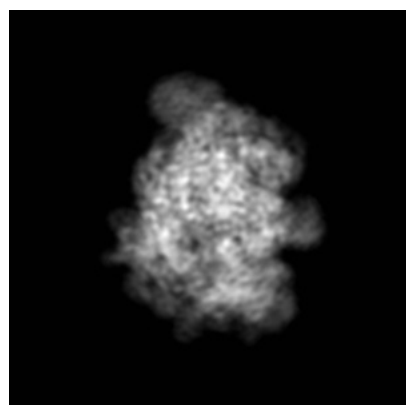
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5691. These allow visual inspection of the internal detail of the map and identification of artifacts.

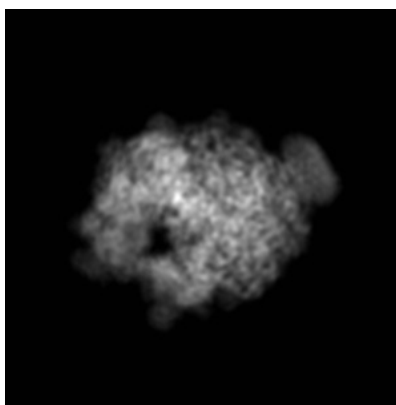
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

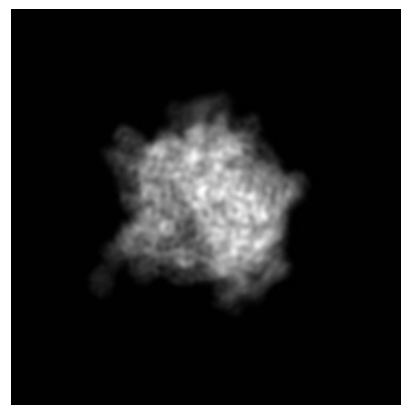
6.1.1 Primary map



X



Y

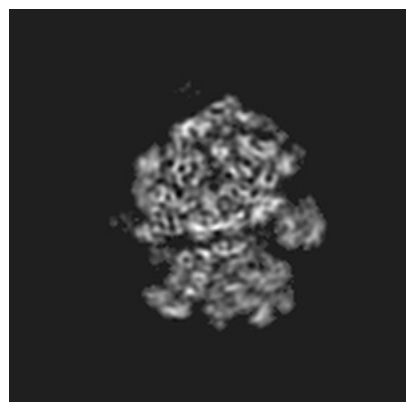


Z

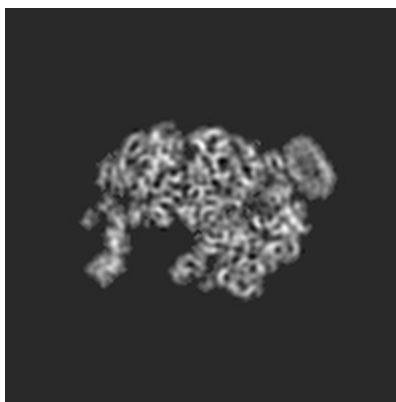
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

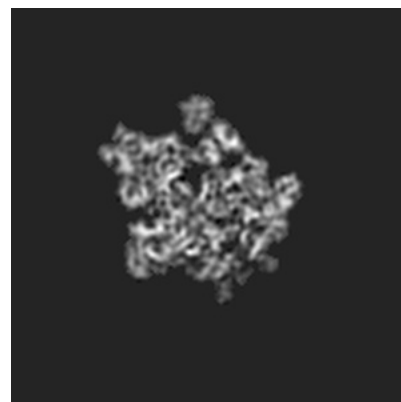
6.2.1 Primary map



X Index: 81



Y Index: 81

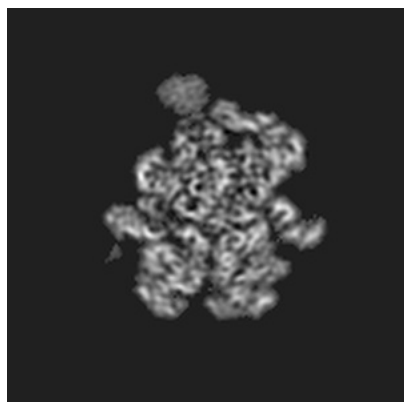


Z Index: 81

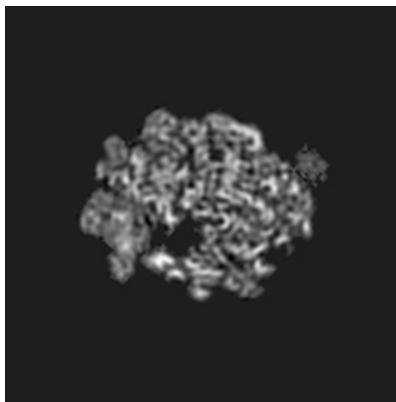
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

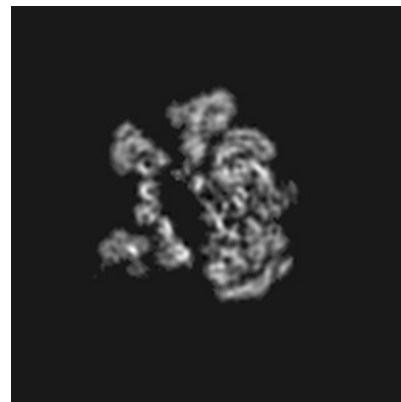
6.3.1 Primary map



X Index: 85



Y Index: 87

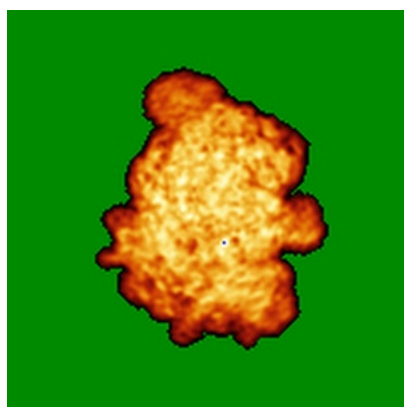


Z Index: 70

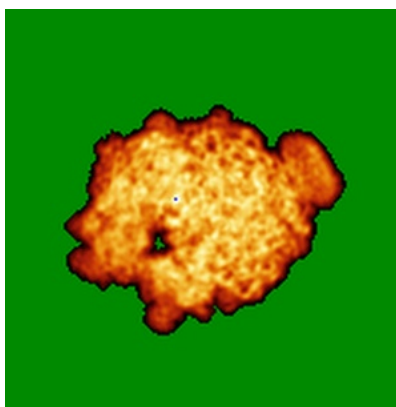
The images above show the largest variance slices of the map in three orthogonal directions.

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

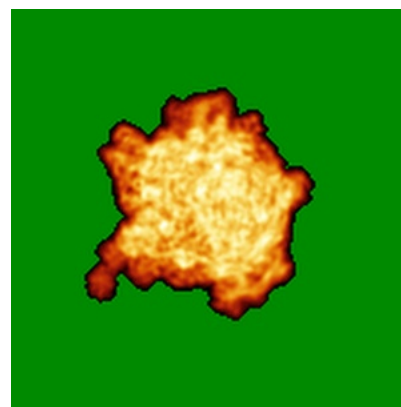
6.4.1 Primary map



X



Y



Z

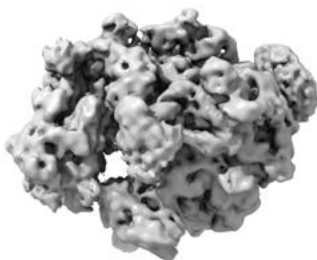
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

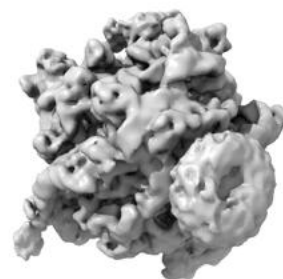
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.93. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

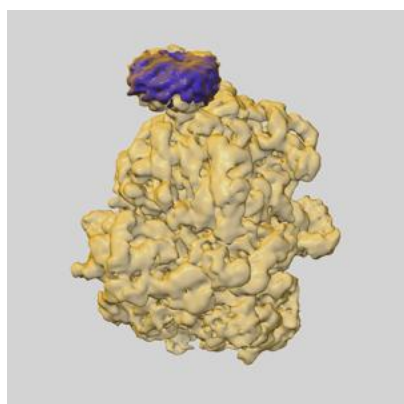
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

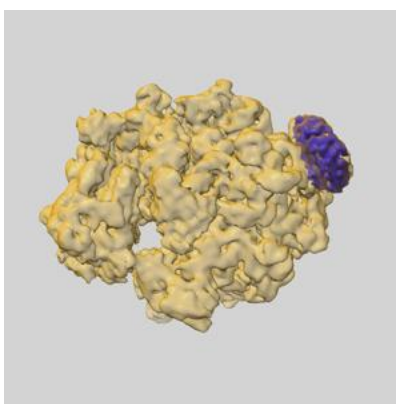
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

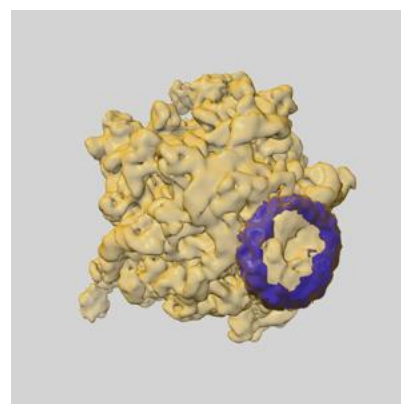
6.6.1 emd_5691_msk_4.map [i](#)



X

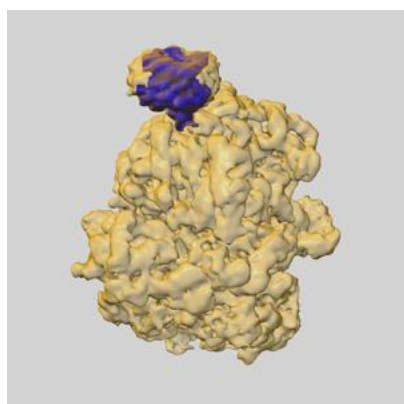


Y

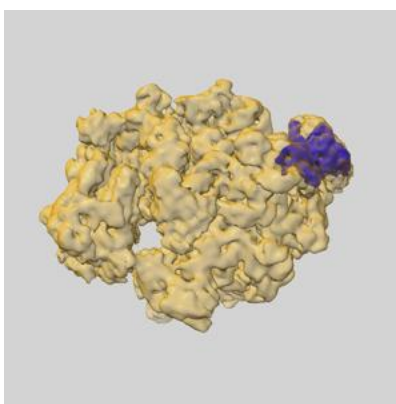


Z

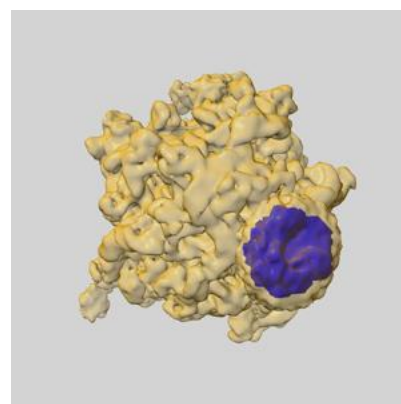
6.6.2 emd_5691_msk_3.map [i](#)



X

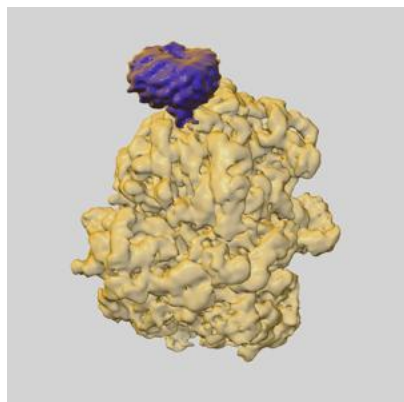


Y

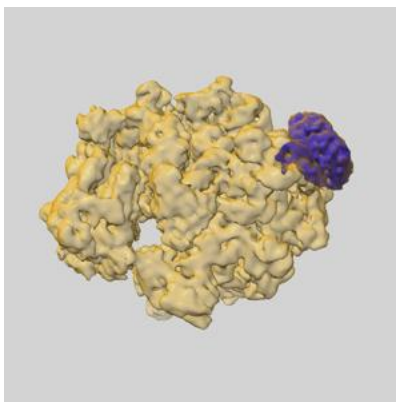


Z

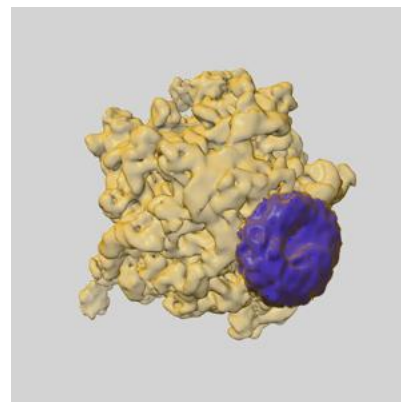
6.6.3 emd_5691_msk_2.map [i](#)



X

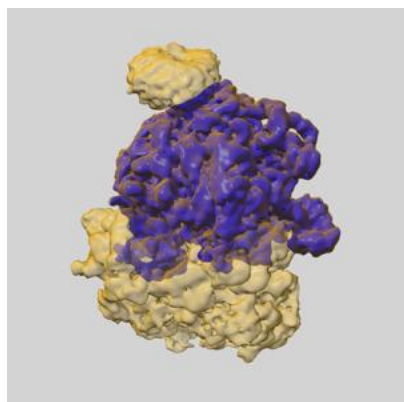


Y

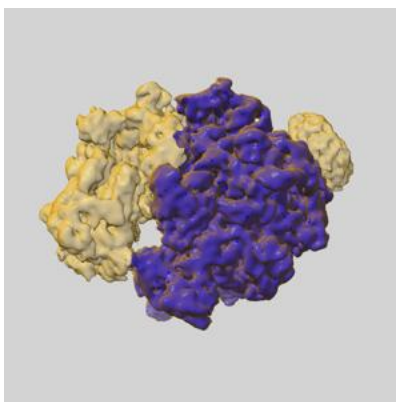


Z

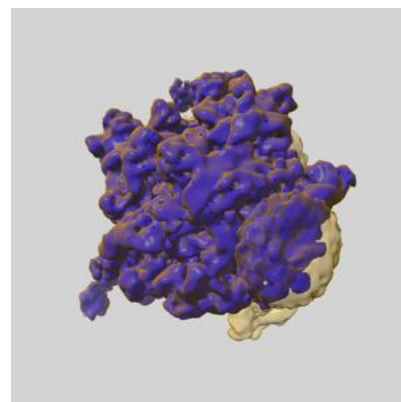
6.6.4 emd_5691_msk_1.map [i](#)



X

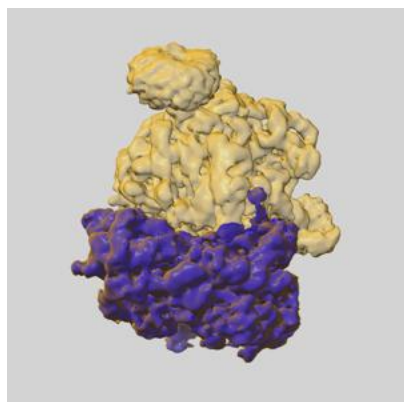


Y

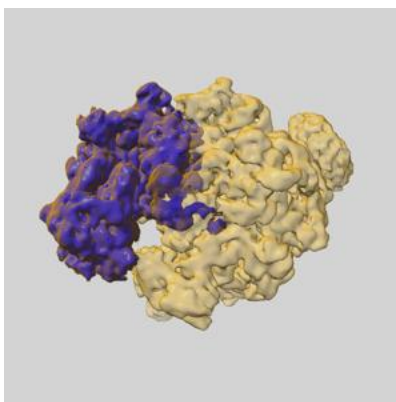


Z

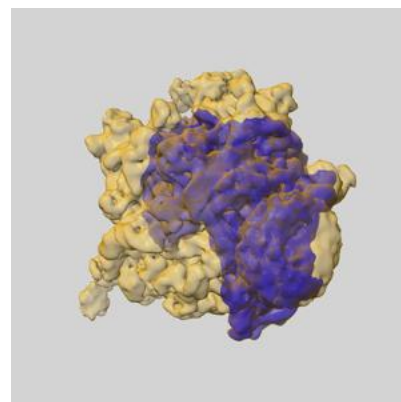
6.6.5 emd_5691_msk_5.map [i](#)



X



Y

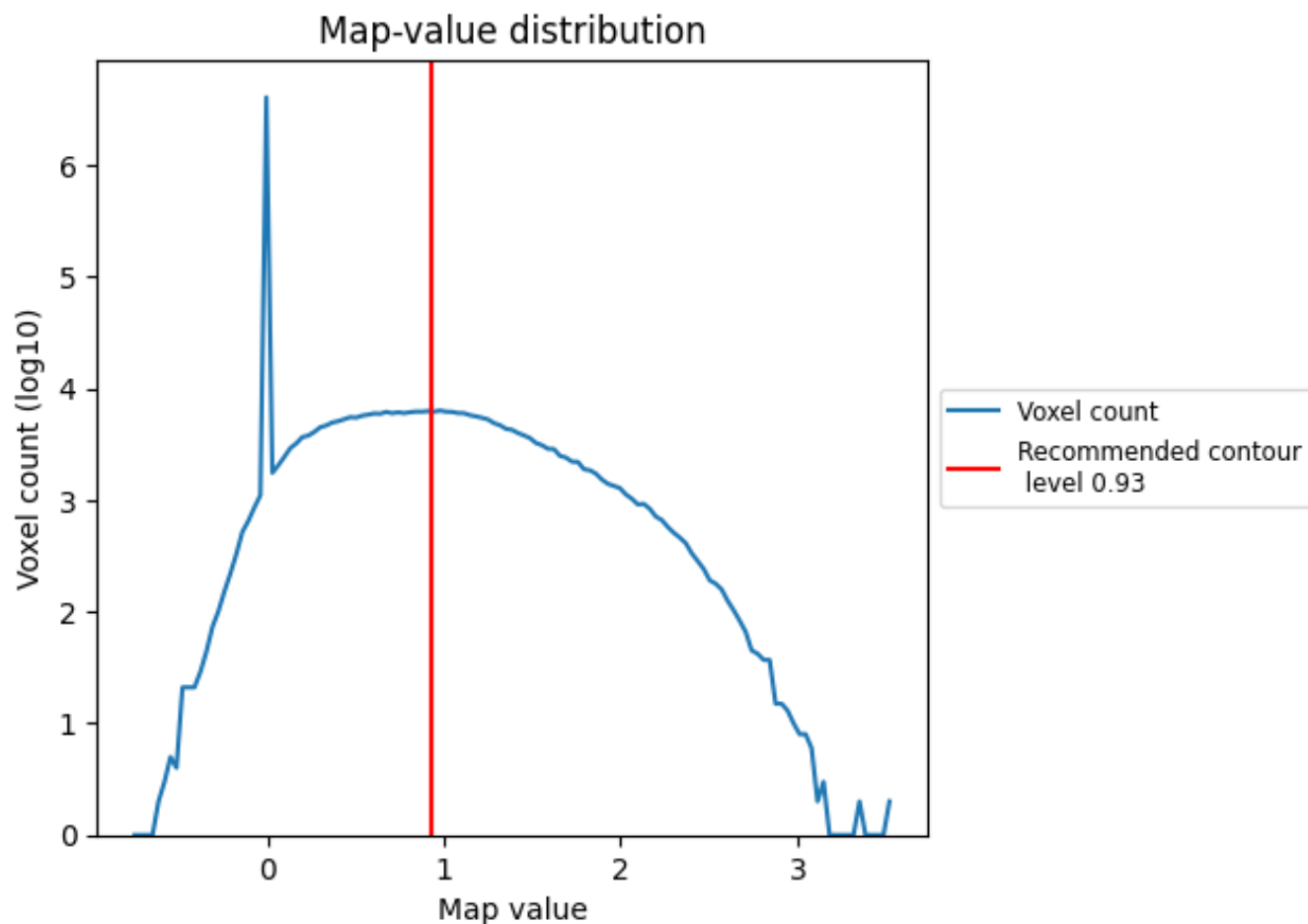


Z

7 Map analysis [i](#)

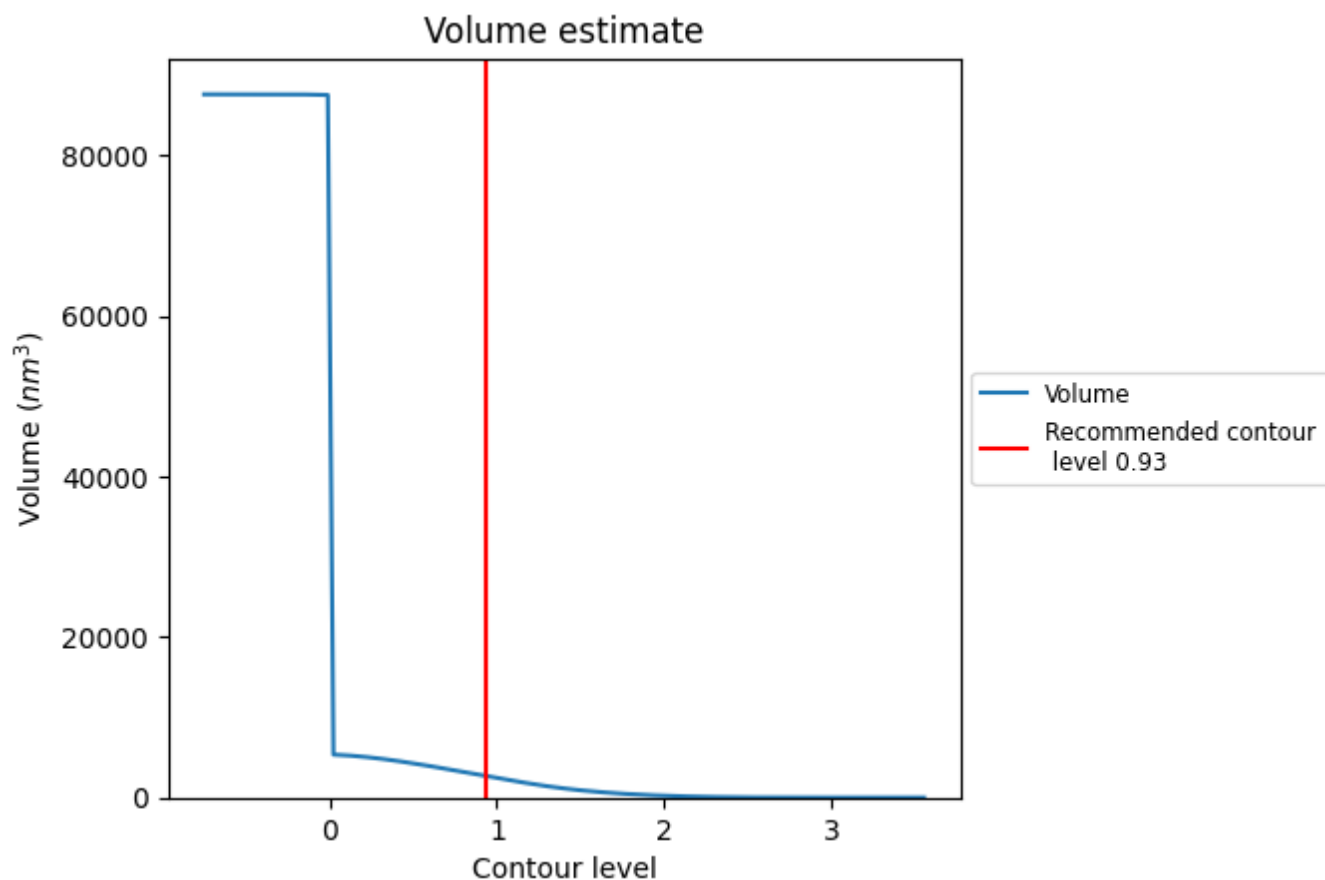
This section contains the results of statistical analysis of the map.

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 2715 nm³; this corresponds to an approximate mass of 2453 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation

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

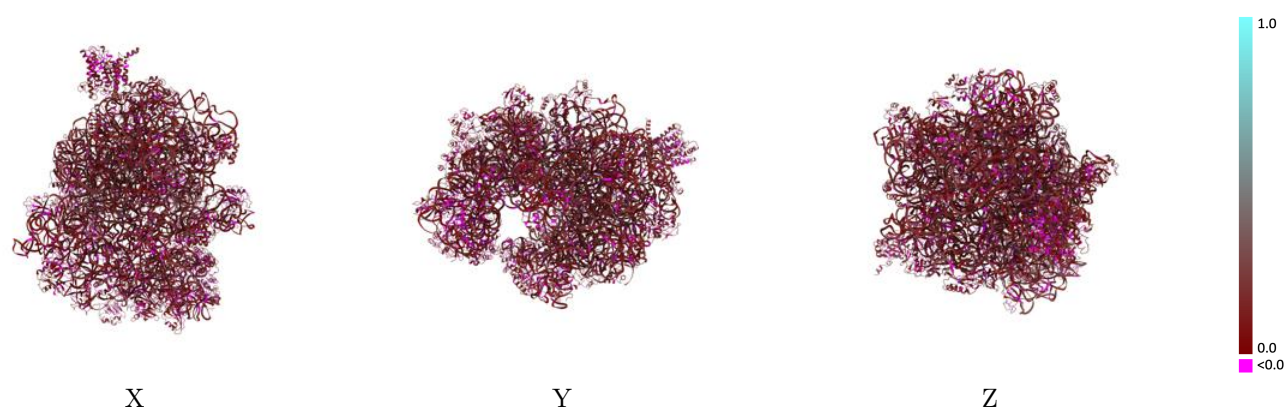
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5691 and PDB model 4V4N. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

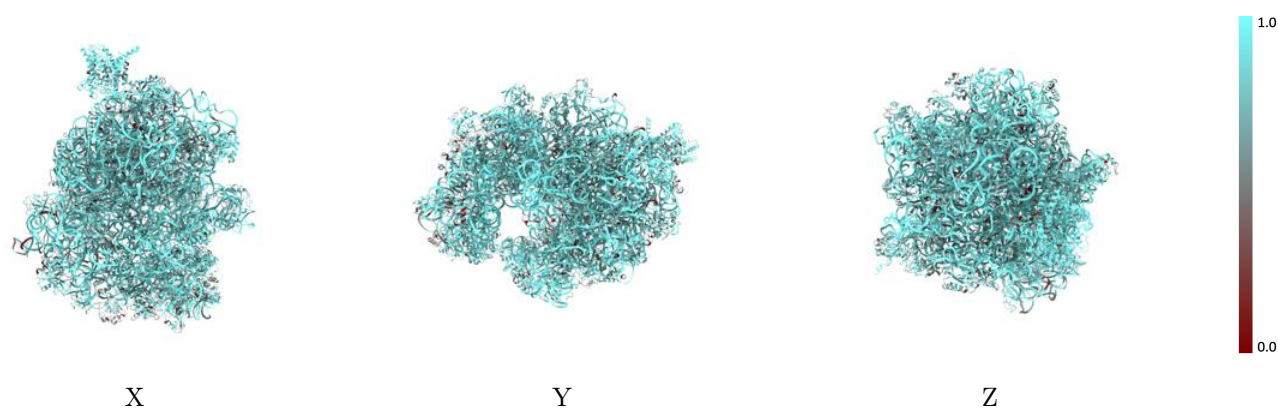
This section was not generated.

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



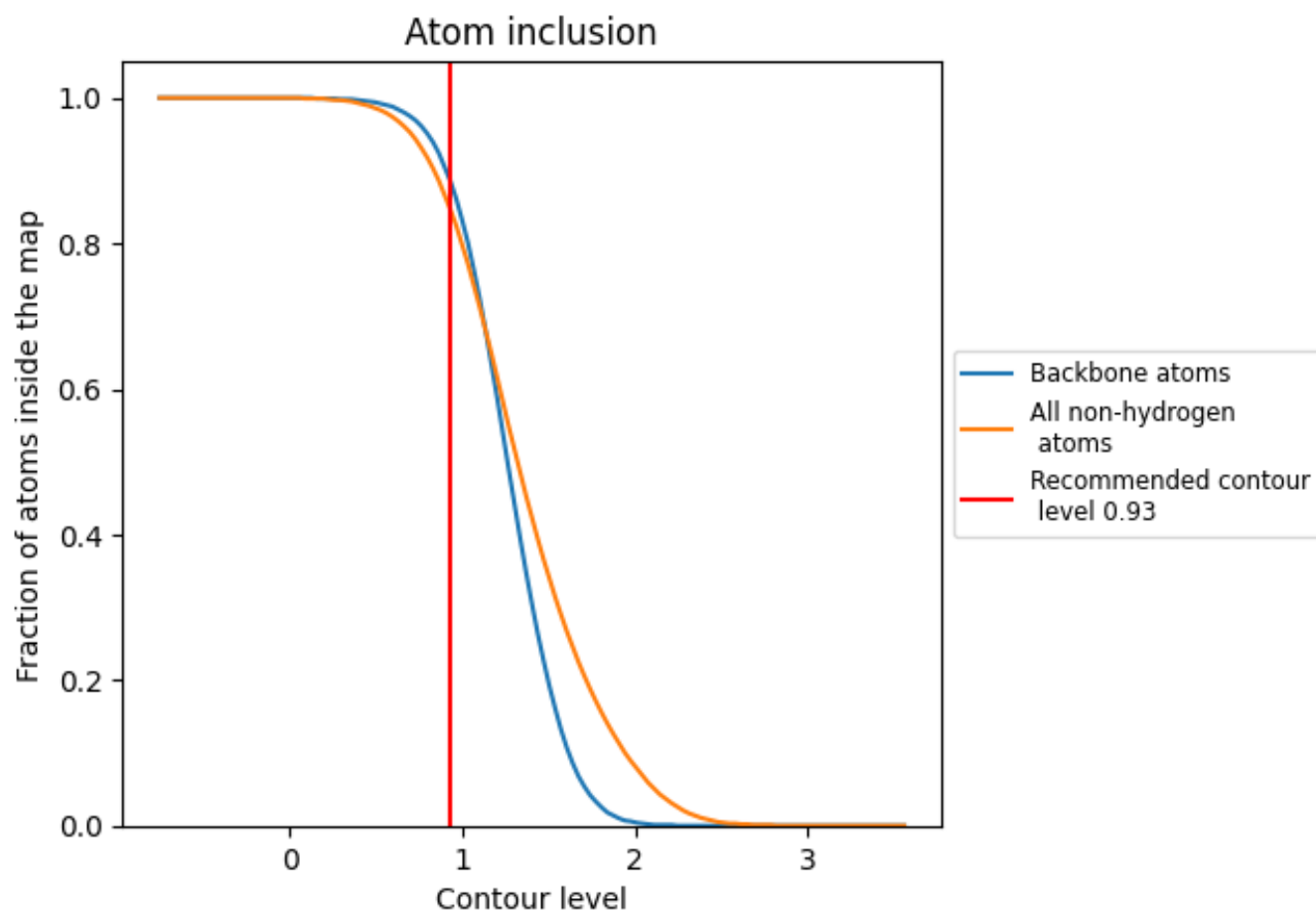
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.93).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.93) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8470	 0.1240
A1	 0.9300	 0.1530
A3	 0.8970	 0.1350
A5	 0.7410	 0.1180
A7	 0.8860	 0.1390
A8	 0.9090	 0.0680
AA	 0.7120	 0.0850
AB	 0.6590	 0.0870
AC	 0.6820	 0.0840
AD	 0.6510	 0.0890
AE	 0.8360	 0.1010
AF	 0.7700	 0.1100
AG	 0.8010	 0.1310
AH	 0.8720	 0.0650
AI	 0.6350	 0.1030
AJ	 0.6970	 0.0860
AK	 0.6620	 0.1130
AL	 0.6150	 0.0750
AM	 0.6090	 0.0770
AN	 0.6760	 0.0960
AO	 0.7420	 0.1000
AP	 0.7630	 0.1130
AQ	 0.6740	 0.0980
AR	 0.6640	 0.0850
AS	 0.7080	 0.0980
AT	 0.6840	 0.1060
AU	 0.7180	 0.1020
AV	 0.7430	 0.0970
AW	 0.7590	 0.1270
AX	 0.8680	 0.1020
AY	 0.6910	 0.1130
AZ	 0.8210	 0.1280
Aa	 0.6630	 0.0790
Ab	 0.6230	 0.0900
Ad	 0.6940	 0.0790



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Chain	Atom inclusion	Q-score
Ae	 0.6110	 0.0430
Af	 0.2890	 0.0250
Ag	 0.4060	 0.0270
Ah	 0.5420	 0.0520
Ai	 0.6860	 0.1150
Aj	 0.7910	 0.0890
Ak	 0.7710	 0.1020
B1	 0.8520	 0.1170
B2	 0.9350	 0.1380
B3	 0.5800	 0.0800
BA	 0.8750	 0.1130
BB	 0.7500	 0.1120
BC	 0.7360	 0.1080
BD	 0.7170	 0.0920
BE	 0.6980	 0.0590
BF	 0.7390	 0.1020
BG	 0.8000	 0.0880
BH	 0.7540	 0.0780
BI	 0.7270	 0.0990
BJ	 0.7290	 0.0740
BK	 0.6320	 0.0360
BL	 0.7110	 0.0710
BM	 0.7710	 0.0910
BN	 0.6860	 0.0930
BO	 0.8360	 0.0850
BP	 0.7530	 0.0550
BQ	 0.7480	 0.0960
BR	 0.7180	 0.0820
BS	 0.5900	 0.0680
BT	 0.8170	 0.0770
BU	 0.7540	 0.0640
BV	 0.7530	 0.0900
BW	 0.7170	 0.0850
BX	 0.8830	 0.0910
BY	 0.7990	 0.0630