



wwPDB EM Validation Summary Report ⓘ

Sep 21, 2026 – 12:45 PM EDT

PDB ID : 9YDE / pdb_00009yde
EMDB ID : EMD-72802
Title : Eukaryotic 80S ribosome with P/P tRNA from uL16 P-site loop mutants in bypass condition
Authors : Guan, K.; Taylor, D.W.
Deposited on : 2025-09-22
Resolution : 2.82 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:

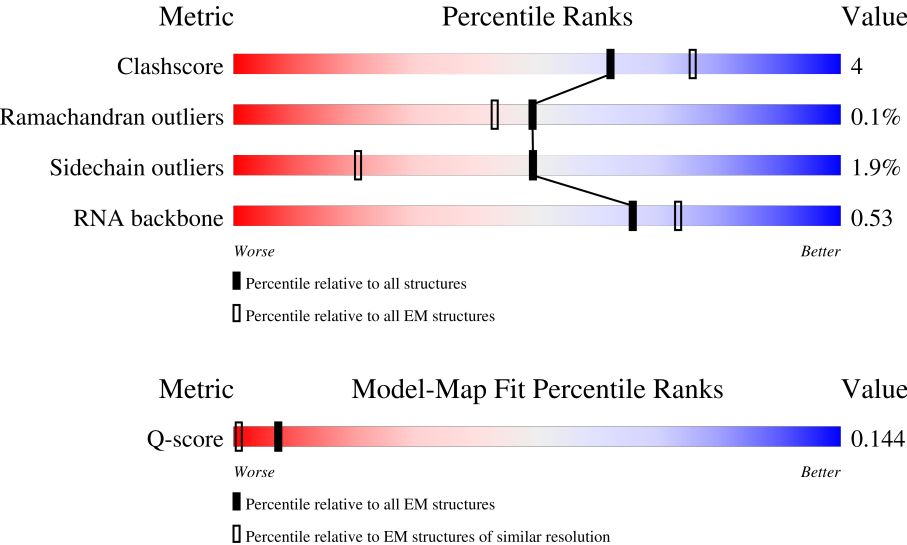
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.82 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	11795 (2.32 - 3.32)

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	A	3396	12% 66% 22% 10%
2	B	121	18% 81% 17% •
3	C	158	8% 78% 20% •

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Mol	Chain	Length	Quality of chain
4	D	10	
5	E	1800	
6	LD	254	
7	LE	387	
8	LF	362	
9	LG	297	
10	LH	176	
11	LI	244	
12	LJ	256	
13	LK	191	
14	LL	210	
15	LM	174	
16	LN	199	
17	LO	138	
18	LP	204	
19	LQ	199	
20	LR	184	
21	LS	186	
22	LT	189	
23	LU	172	
24	LV	160	
25	LW	121	
26	LX	137	
27	LY	155	
28	LZ	142	

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Mol	Chain	Length	Quality of chain
29	La	127	
30	Lb	136	
31	Lc	149	
32	Ld	59	
33	Le	105	
34	Lf	113	
35	Lg	130	
36	Lh	107	
37	Li	121	
38	Lj	120	
39	Lk	100	
40	Ll	88	
41	Lm	78	
42	Ln	51	
43	Lo	128	
44	Lp	25	
45	Lq	106	
46	Lr	92	
47	SA	240	
48	SB	225	
49	SC	105	
50	SD	143	
51	SE	142	
52	SF	143	
53	SG	136	

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Mol	Chain	Length	Quality of chain
54	SH	146	
55	SI	144	
56	SJ	121	
57	SK	108	
58	SL	67	
59	SM	56	
60	SN	152	
61	SO	319	
62	SP	252	
63	SQ	255	
64	SR	254	
65	SS	261	
66	ST	236	
67	SU	190	
68	SV	200	
69	SW	197	
70	SX	156	
71	SY	151	
72	SZ	138	
73	Sa	87	
74	Sb	130	
75	Sc	145	
76	Sd	135	
77	Se	119	
78	Sf	82	

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Mol	Chain	Length	Quality of chain
79	Sg	63	54% 67% 19% • 13%
80	n	75	73% 36% 43% 9% 12%

2 Entry composition [i](#)

There are 81 unique types of molecules in this entry. The entry contains 192549 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 RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3041	Total	C	N	O	P	0	0
			65056	29059	11741	21215	3041		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	493	U	G	conflict	GB 831416132

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

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

- Molecule 3 is a RNA chain called 8S RNA.

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

- Molecule 4 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	10	Total	C	N	O	P	0	0
			218	98	44	66	10		

- Molecule 5 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	1583	Total	C	N	O	P	0	0
			33767	15095	6008	11081	1583		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LE	386	Total	C	N	O	S	0	0
			3079	1954	584	533	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LF	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

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

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

- Molecule 10 is a protein called Large ribosomal subunit protein eL6B.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	LH	156	Total	C	N	O	0	0
			1243	803	222	218		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LI	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	LJ	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	LK	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 14 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	207	Total	C	N	O	S	0	0
			1686	1071	319	291	5		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LL	?	-	MET	deletion	UNP P41805
LL	?	-	LEU	deletion	UNP P41805
LL	?	-	SER	deletion	UNP P41805
LL	?	-	CYS	deletion	UNP P41805
LL	?	-	ALA	deletion	UNP P41805
LL	?	-	GLY	deletion	UNP P41805
LL	?	-	ALA	deletion	UNP P41805
LL	?	-	ASP	deletion	UNP P41805
LL	?	-	ARG	deletion	UNP P41805
LL	?	-	LEU	deletion	UNP P41805
LL	?	-	GLN	deletion	UNP P41805

- Molecule 15 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	168	Total	C	N	O	S	0	0
			1337	837	250	246	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LN	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	LO	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	LP	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	LQ	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	LR	172	Total	C	N	O	S	0	0
			1361	846	273	242			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	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	LT	174	Total	C	N	O	S	0	0
			1409	867	304	238			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
25	LW	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	LX	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	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	LZ	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
29	La	125	Total	C	N	O	0	0
			984	620	191	173		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Lb	133	Total	C	N	O	0	0
			1066	692	196	178		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Ld	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	Le	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	105	Total	C	N	O	S	0	0
			856	544	163	148	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	126	Total	C	N	O	S	0	0
			1008	638	203	166	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	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	Li	110	Total	C	N	O	S	0	0
			866	536	176	150	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lj	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	Lk	98	Total	C	N	O	S	0	0
			761	475	153	131	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	77	Total	C	N	O	S	0	0
			608	388	114	106			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	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	Lo	51	Total	C	N	O	S	0	0
			409	253	85	66	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lp	24	Total	C	N	O	S	0	0
			224	136	61	26	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lq	100	Total	C	N	O	S	0	0
			805	506	163	131	5		

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

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

- Molecule 47 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SA	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 48 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SB	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 49 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SC	83	Total	C	N	O	S	0	0
			708	461	113	132	2		

- Molecule 50 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SD	97	Total	C	N	O	S	0	0
			736	466	127	141	2		

- Molecule 51 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE	116	Total	C	N	O	S	0	0
			905	577	167	154	7		

- Molecule 52 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	SF	141	Total	C	N	O	0	0
			1095	702	199	194		

- Molecule 53 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SG	114	Total	C	N	O	S	0	0
			908	573	169	164	2		

- Molecule 54 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SH	145	Total	C	N	O	S	0	0
			1188	741	237	208	2		

- Molecule 55 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 56 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SJ	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 57 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	SK	69	Total	C	N	O	0	0
			558	357	103	98		

- Molecule 58 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SL	62	Total	C	N	O	S	0	0
			486	300	95	90	1		

- Molecule 59 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SM	53	Total	C	N	O	S	0	0
			443	275	92	72	4		

- Molecule 60 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SN	56	Total	C	N	O	S	0	0
			429	271	84	70	4		

- Molecule 61 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SO	311	Total	C	N	O	S	0	0
			2375	1509	408	451	7		

- Molecule 62 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SP	205	Total	C	N	O	S	0	0
			1596	1025	283	286	2		

- Molecule 63 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SQ	225	Total	C	N	O	S	0	0
			1787	1131	328	324	4		

- Molecule 64 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SR	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 65 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SS	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 66 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	ST	218	Total	C	N	O	S	0	0
			1755	1102	337	313	3		

- Molecule 67 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
67	SU	180	Total	C	N	O		
			1451	932	259	260	0	0

- Molecule 68 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	SV	186	Total	C	N	O	S	
			1471	913	294	262	2	0

- Molecule 69 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	SW	184	Total	C	N	O	S	
			1479	935	285	258	1	0

- Molecule 70 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	SX	141	Total	C	N	O	S	
			1137	730	216	188	3	0

- Molecule 71 is a protein called 40S ribosomal protein S13.

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

- Molecule 72 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	SZ	127	Total	C	N	O	S	
			923	568	185	167	3	0

- Molecule 73 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	Sa	87	Total	C	N	O	S	
			673	415	125	131	2	0

- Molecule 74 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 75 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 76 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sd	131	Total	C	N	O	S	0	0
			1016	642	192	182			

- Molecule 77 is a protein called Small ribosomal subunit protein eS26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Se	97	Total	C	N	O	S	0	0
			765	473	160	127	5		

- Molecule 78 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sf	74	Total	C	N	O	S	0	0
			562	353	101	105	3		

- Molecule 79 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sg	55	Total	C	N	O	S	0	0
			437	276	89	71	1		

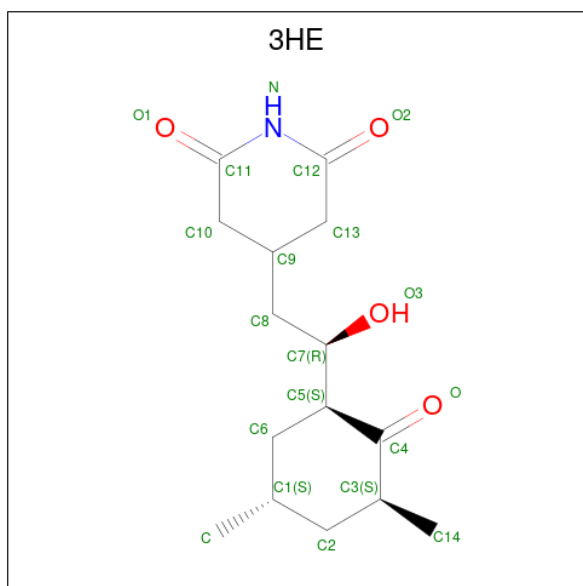
- Molecule 80 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	n	66	Total	C	N	O	P	0	0
			1409	628	257	458	66		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	10	A	G	conflict	GB 176433

- Molecule 81 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: $C_{15}H_{23}NO_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
81	A	1	Total	C	N	O	0
			20	15	1	4	

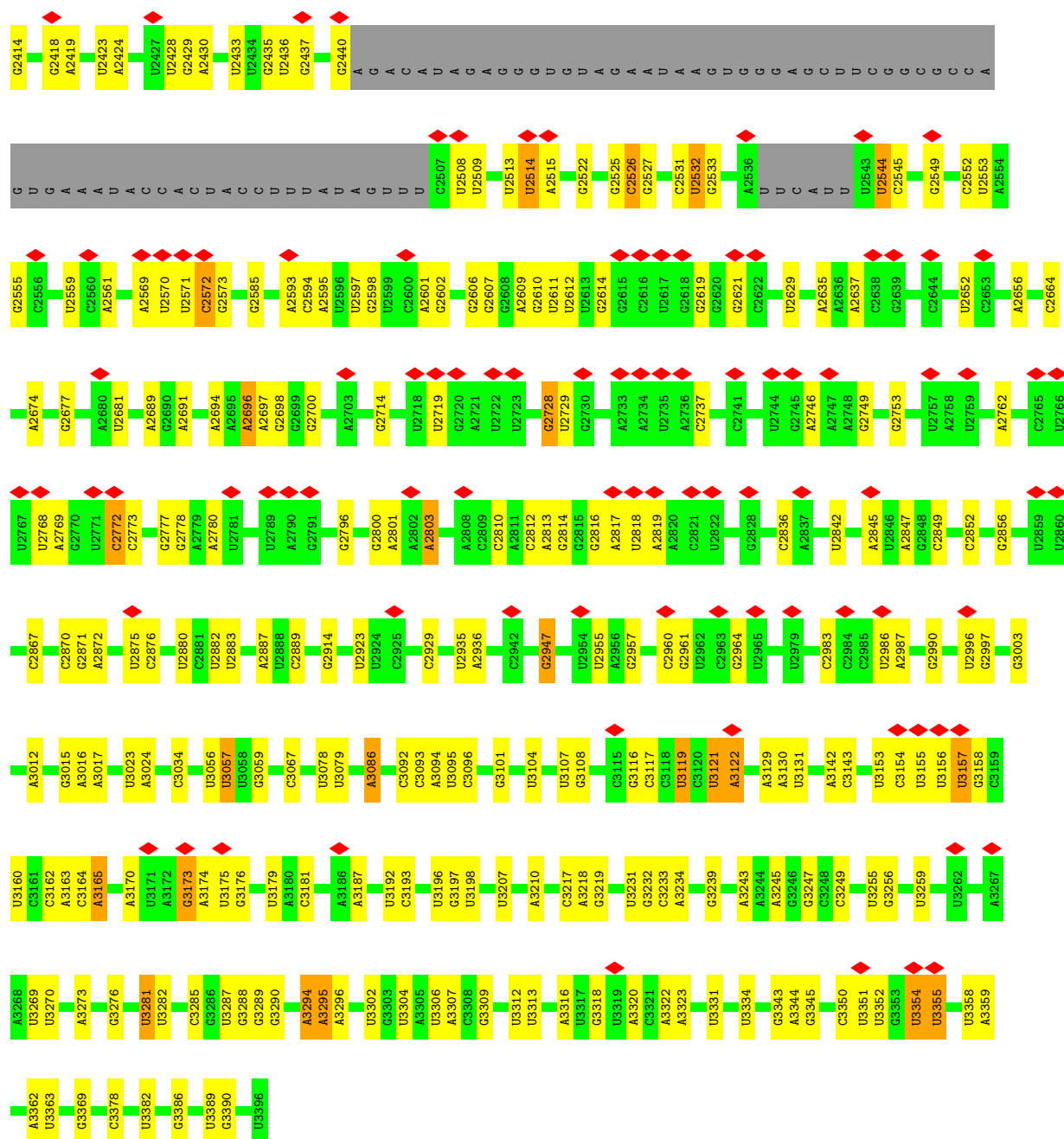
3 Residue-property plots

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.

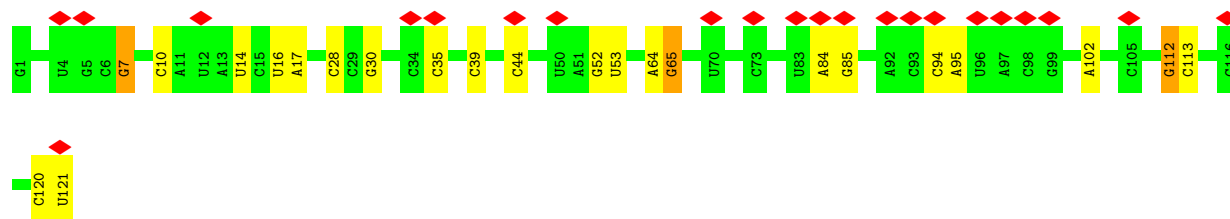
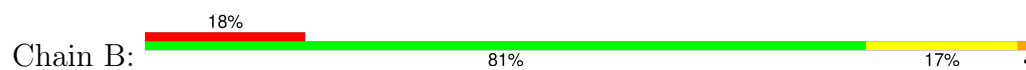
• Molecule 1: 25S RNA



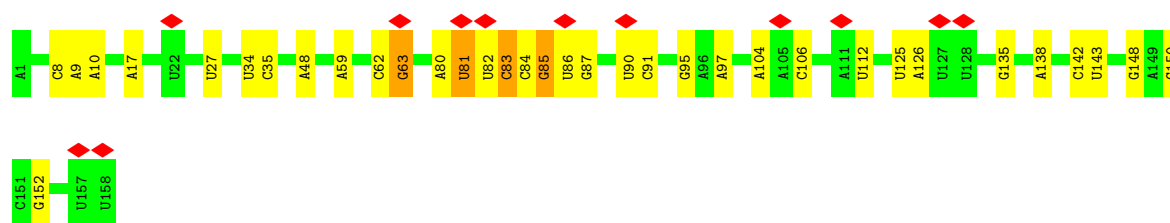


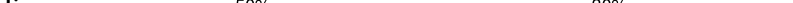


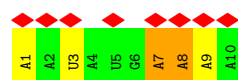
• Molecule 2: 5S RNA

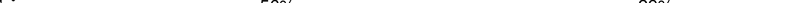


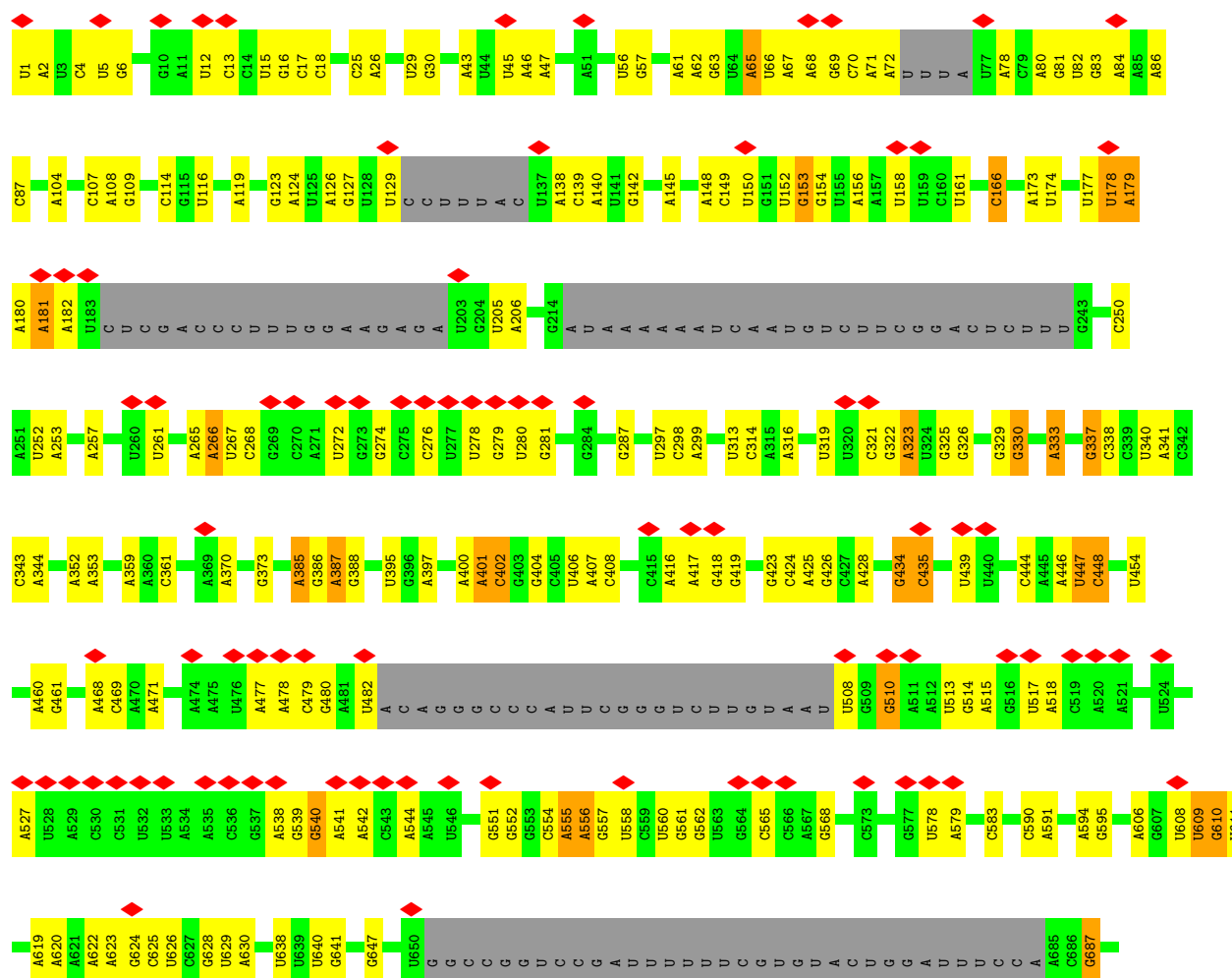
• Molecule 3: 8S RNA



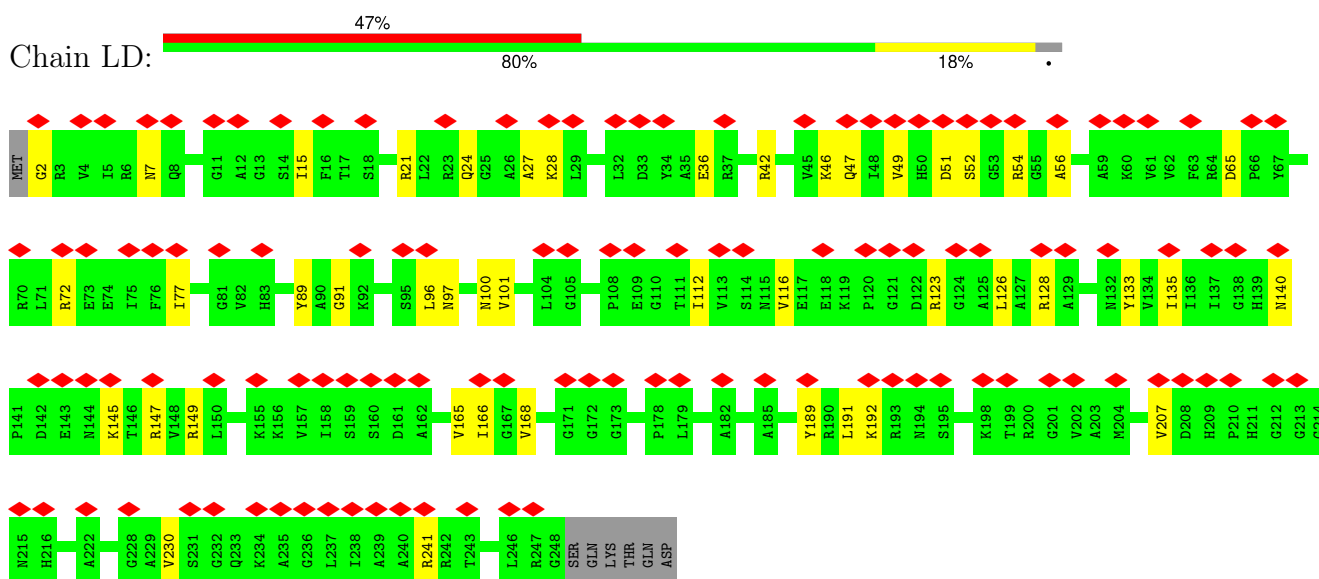
- Chain D:  80% 50% 30% 20%



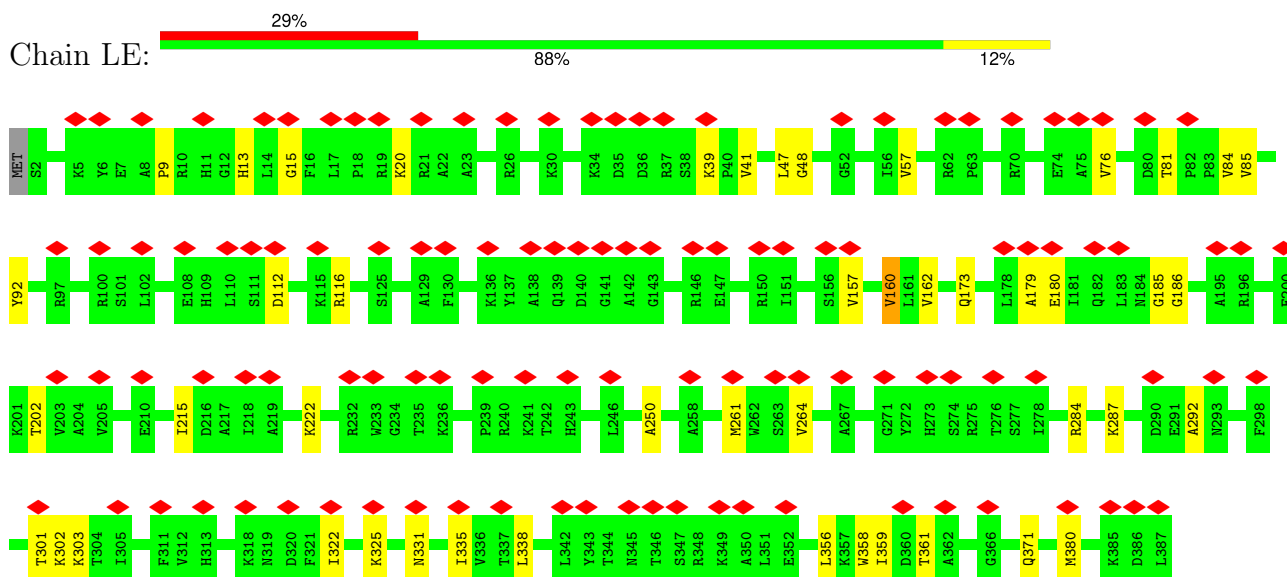
- Chain E:  12% 56% 29% 12%





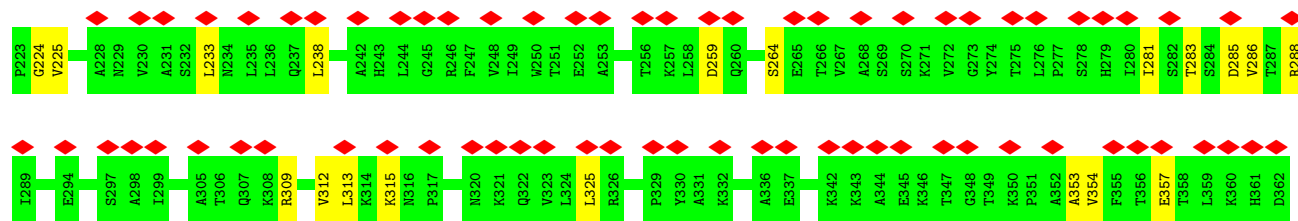


• Molecule 7: 60S ribosomal protein L3

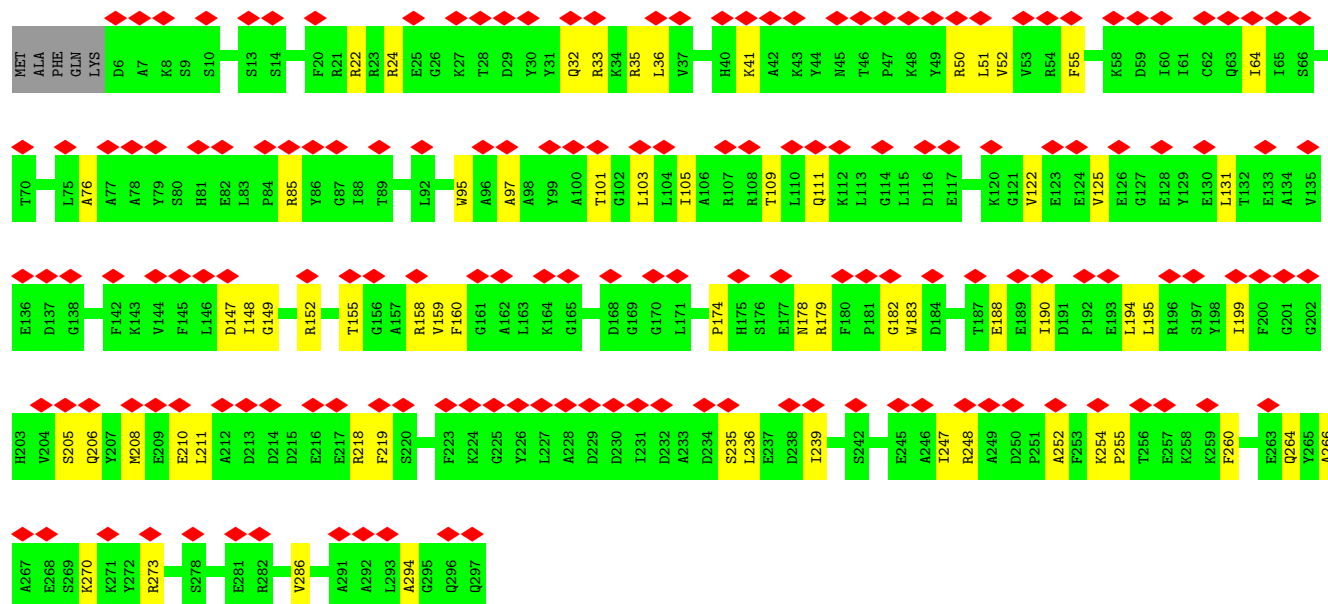
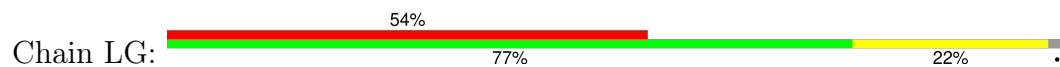


• Molecule 8: 60S ribosomal protein L4-A

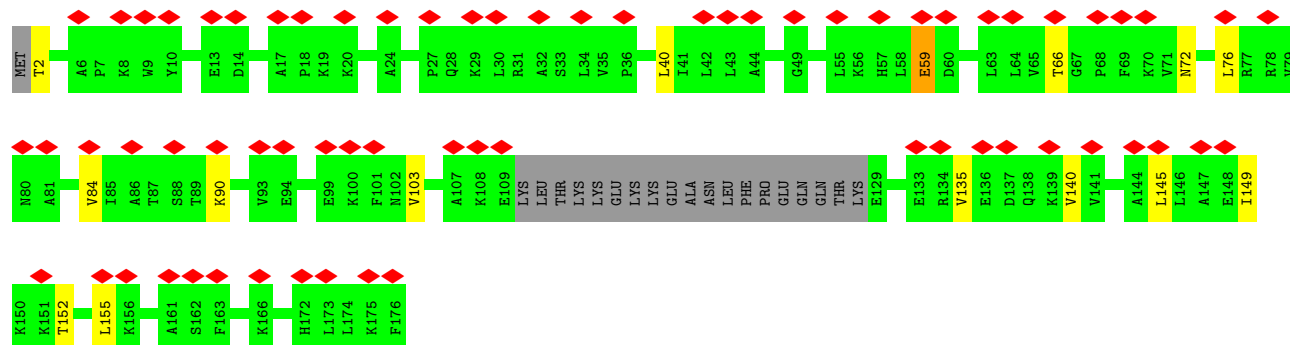
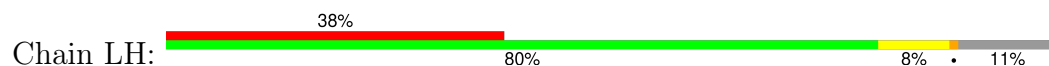




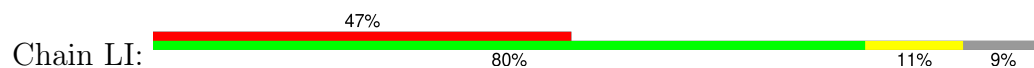
• Molecule 9: 60S ribosomal protein L5

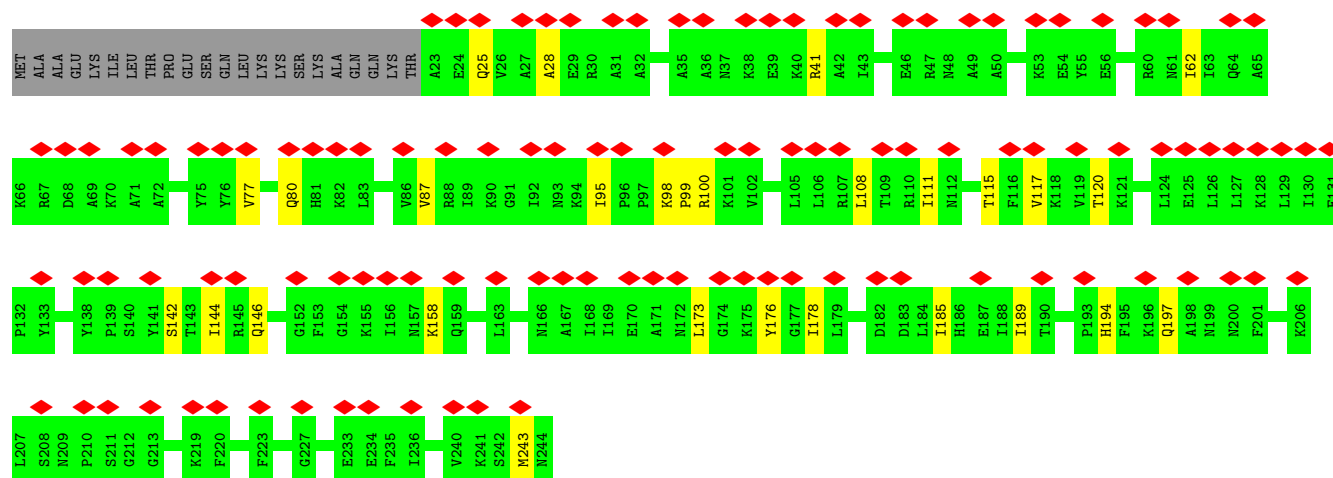


• Molecule 10: Large ribosomal subunit protein eL6B

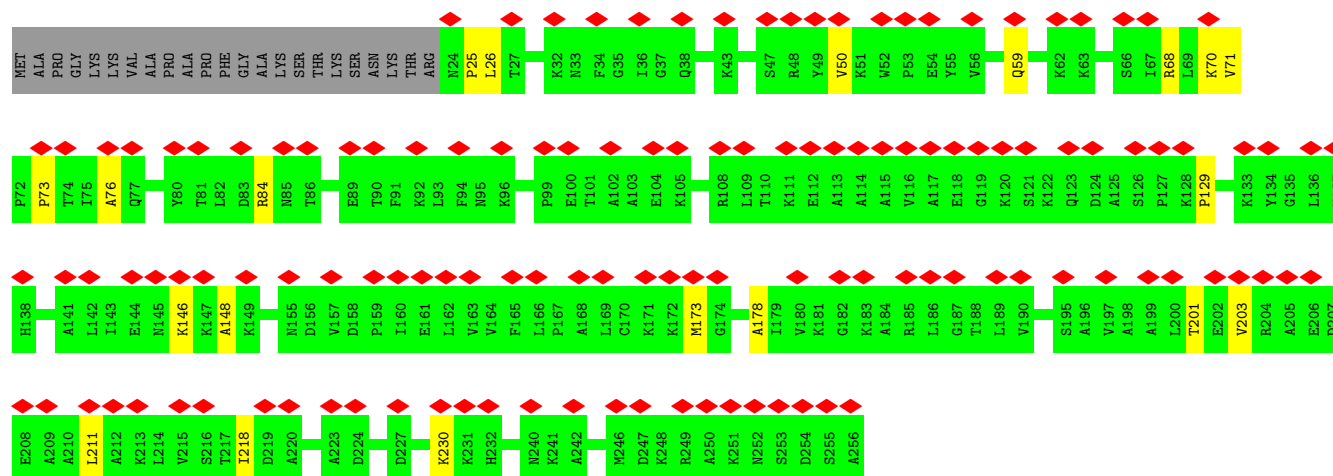
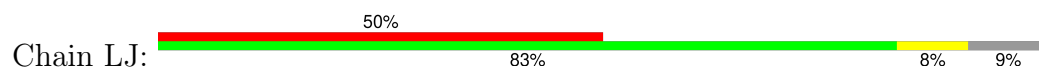


• Molecule 11: 60S ribosomal protein L7-A

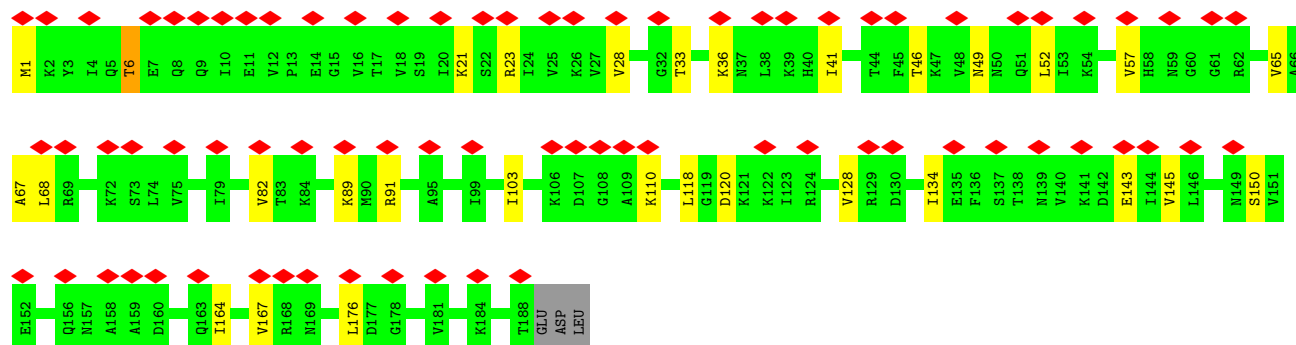
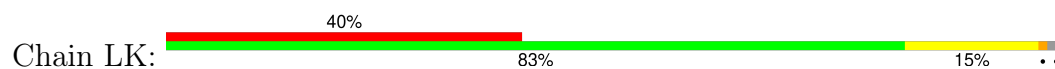




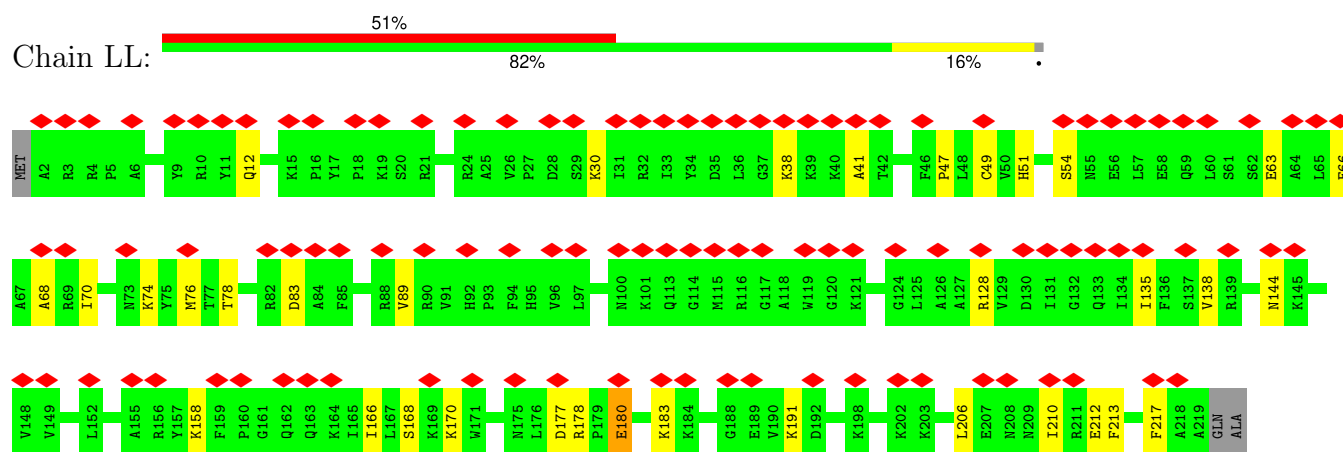
• Molecule 12: 60S ribosomal protein L8-A



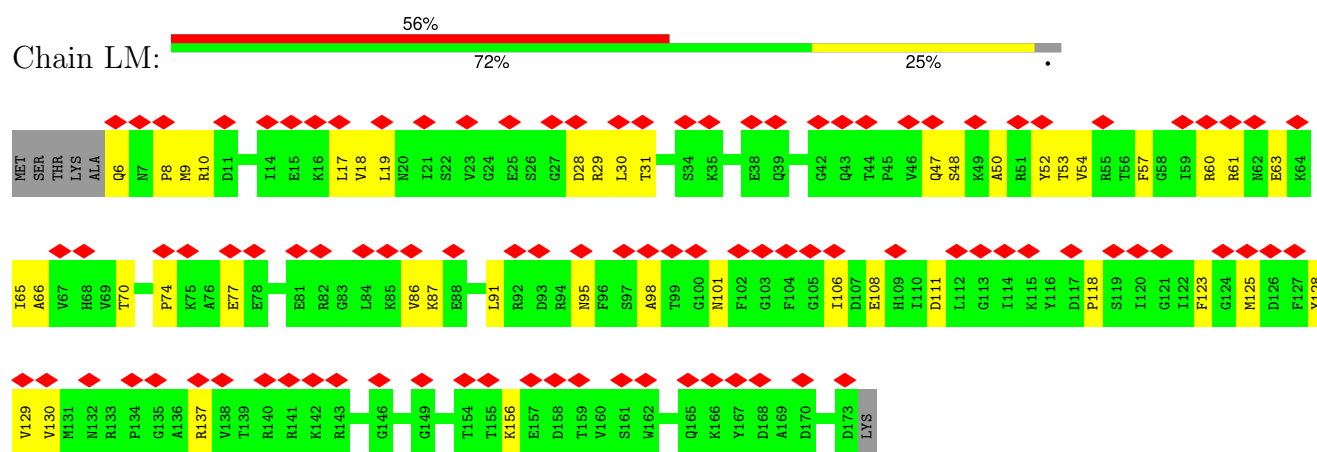
• Molecule 13: 60S ribosomal protein L9-A



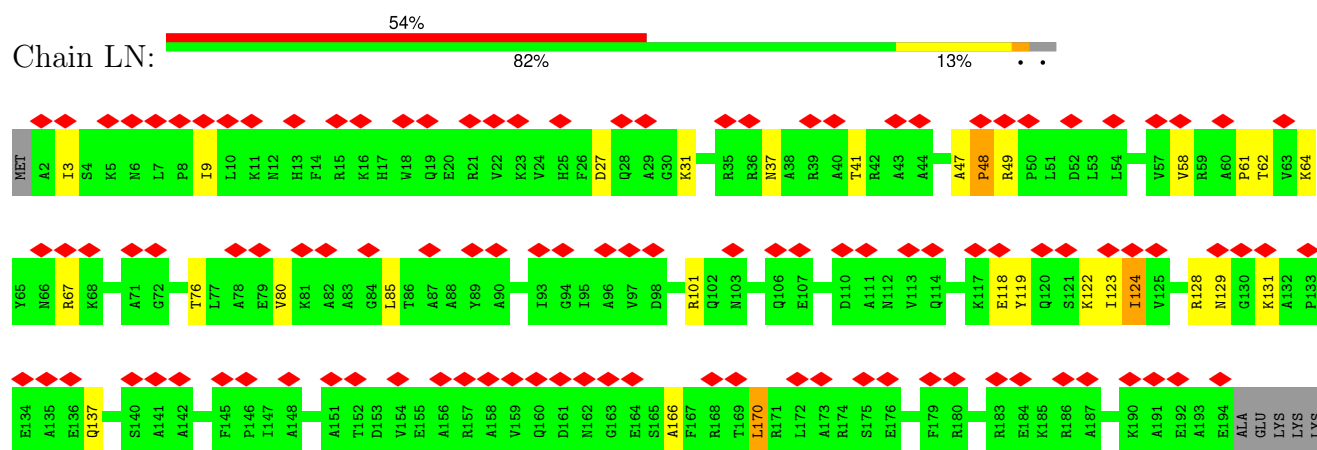
• Molecule 14: Large ribosomal subunit protein uL16



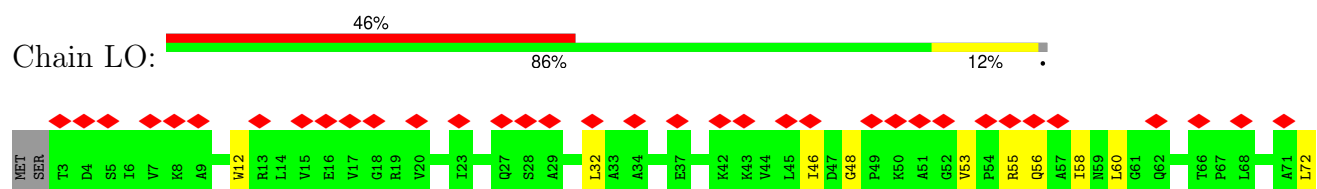
• Molecule 15: Large ribosomal subunit protein uL5B

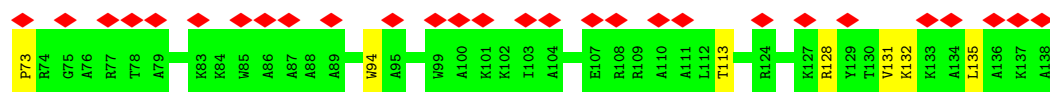


• Molecule 16: 60S ribosomal protein L13-A

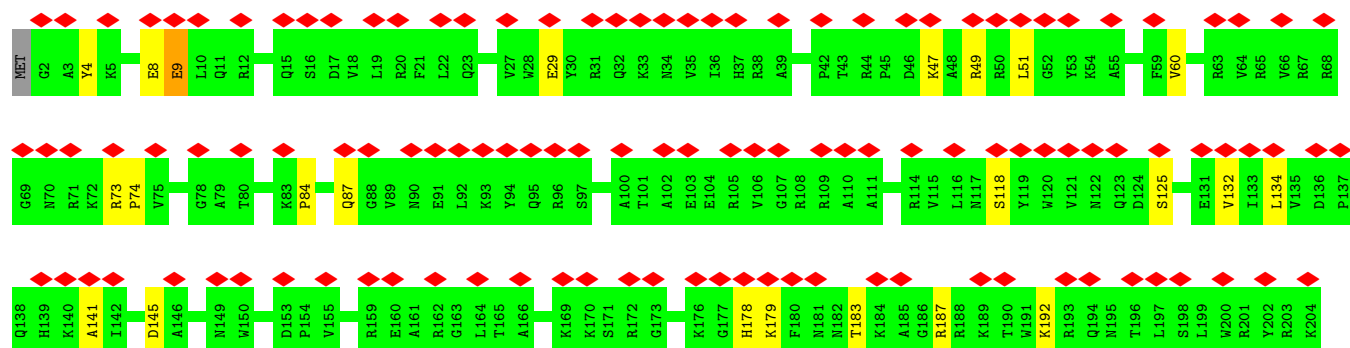
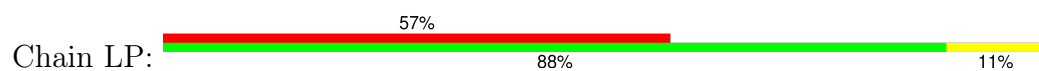


• Molecule 17: 60S ribosomal protein L14-A

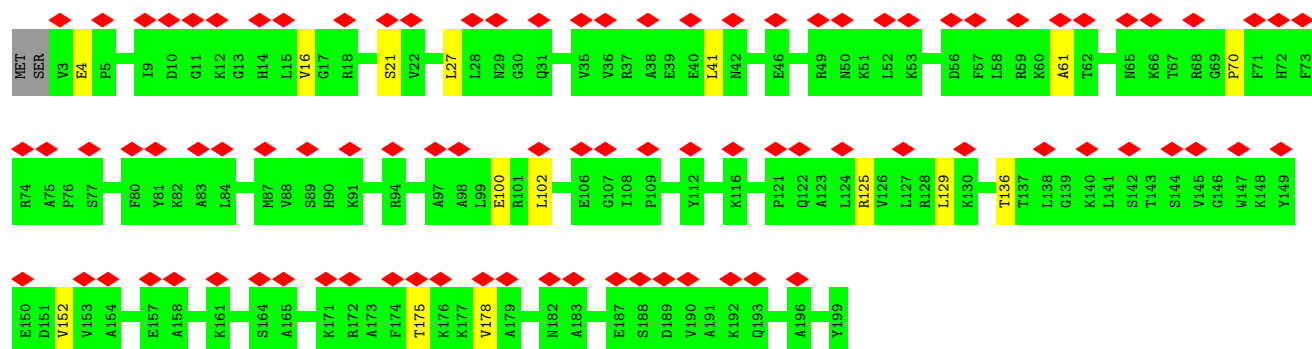
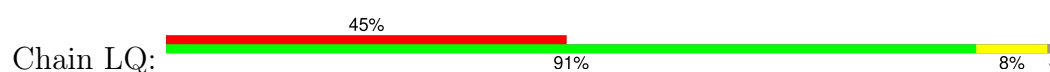




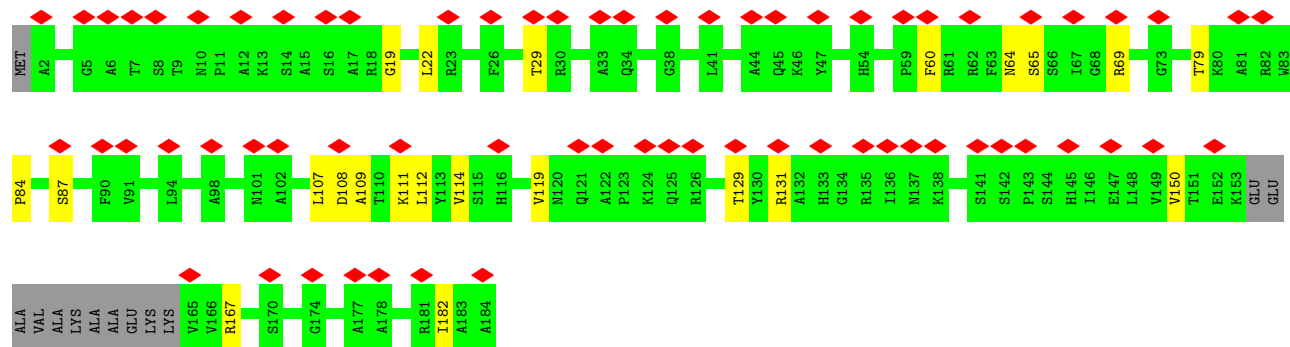
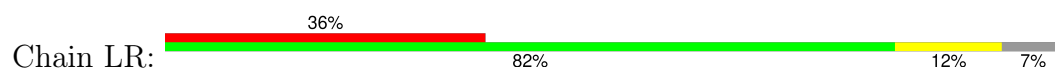
• Molecule 18: 60S ribosomal protein L15-A



• Molecule 19: 60S ribosomal protein L16-A

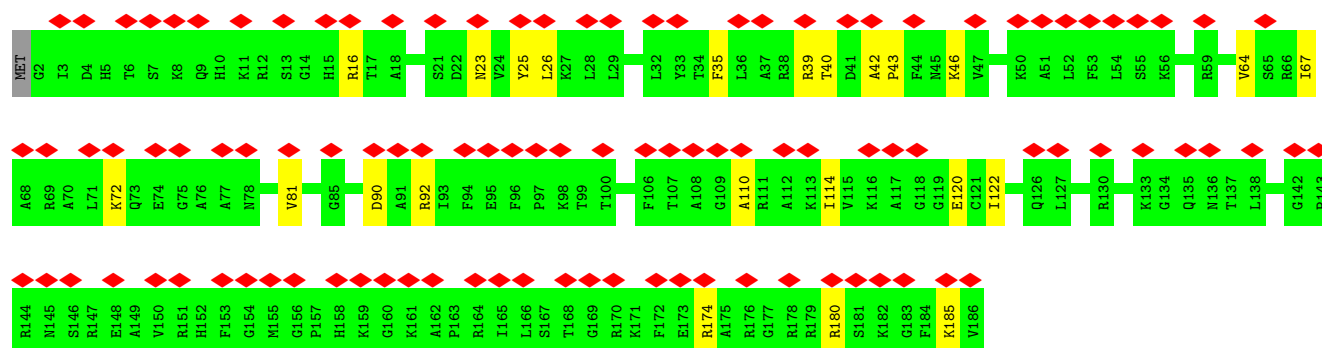


• Molecule 20: 60S ribosomal protein L17-A



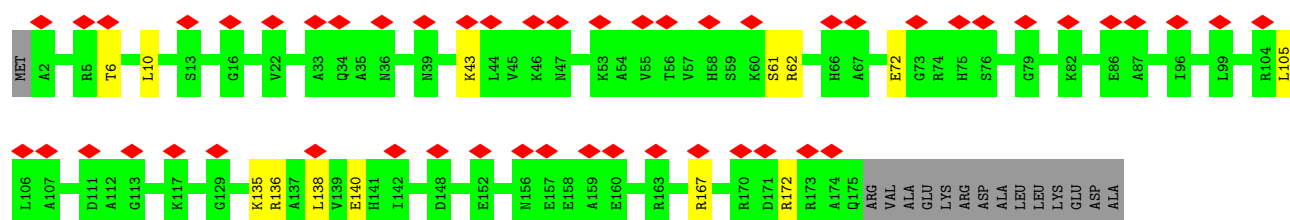
• Molecule 21: 60S ribosomal protein L18-A

Chain LS: 



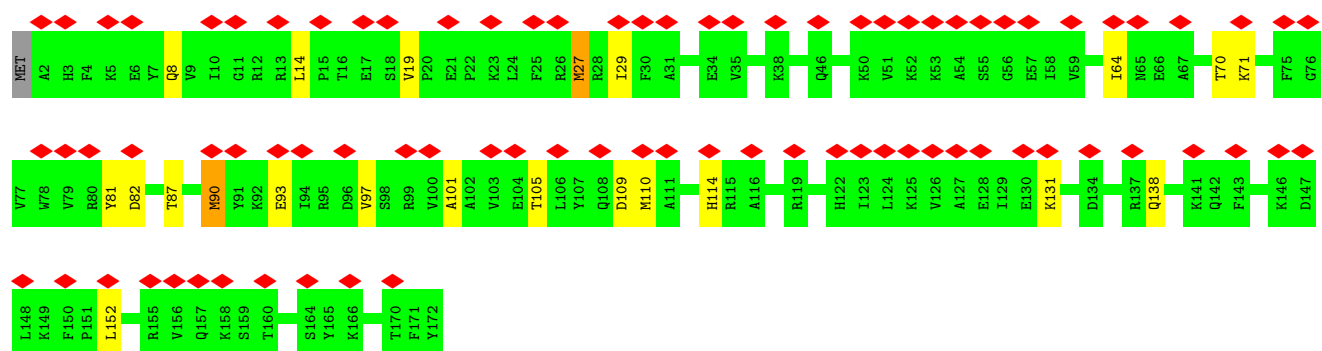
• Molecule 22: 60S ribosomal protein L19-A

Chain LT: 



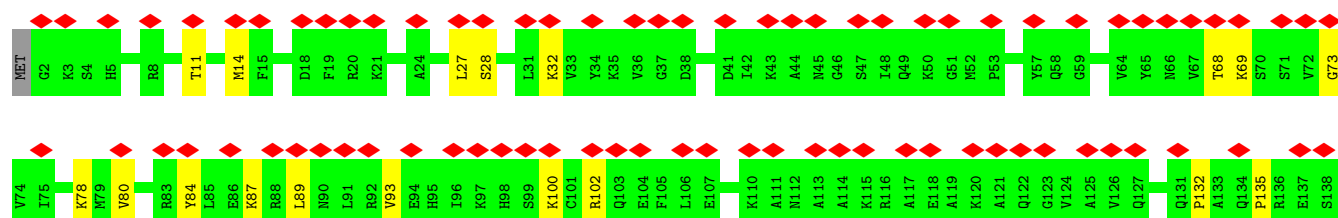
• Molecule 23: 60S ribosomal protein L20-A

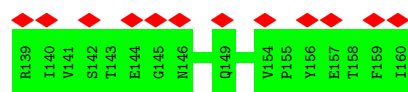
Chain LU: 



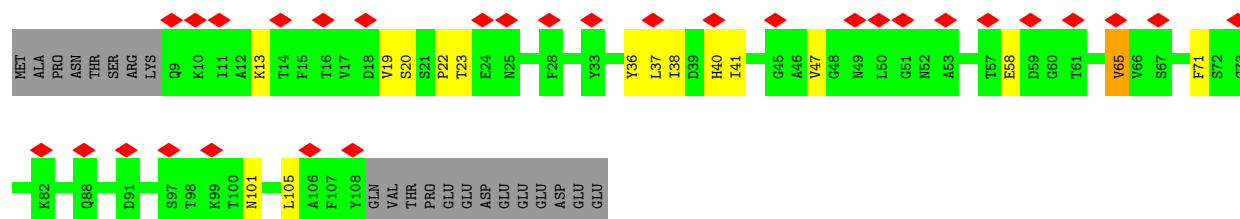
• Molecule 24: 60S ribosomal protein L21-A

Chain LV: 

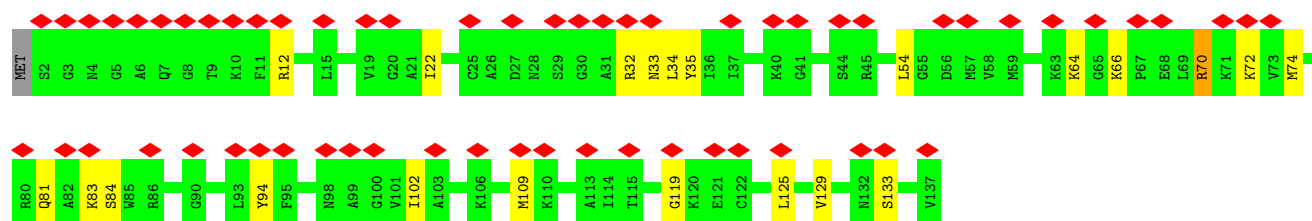
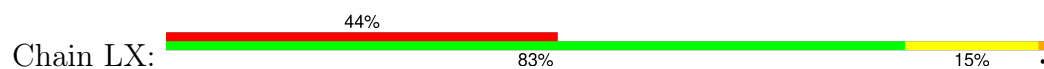




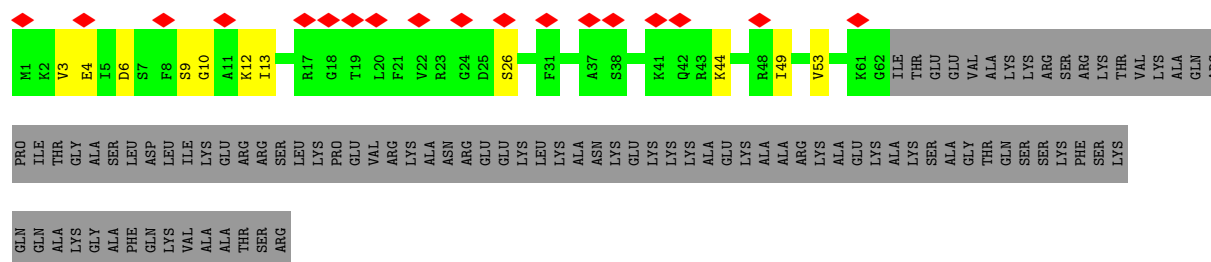
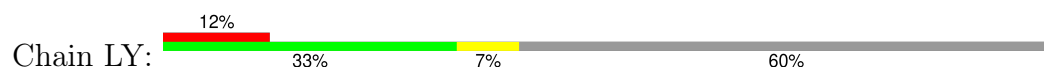
• Molecule 25: 60S ribosomal protein L22-A



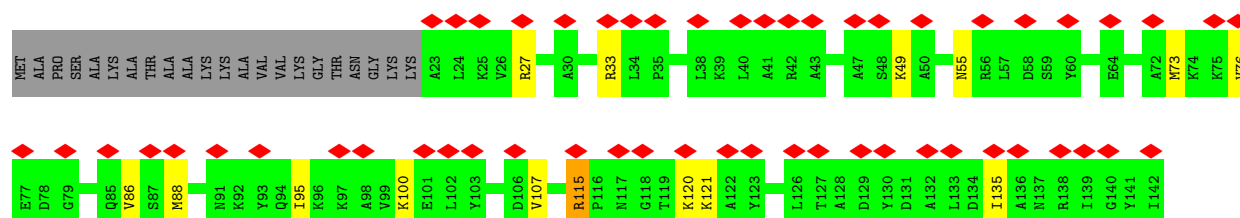
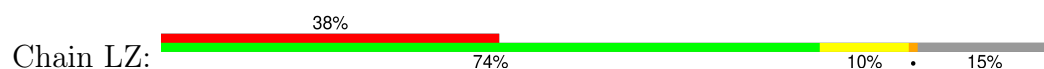
• Molecule 26: 60S ribosomal protein L23-A



• Molecule 27: 60S ribosomal protein L24-A

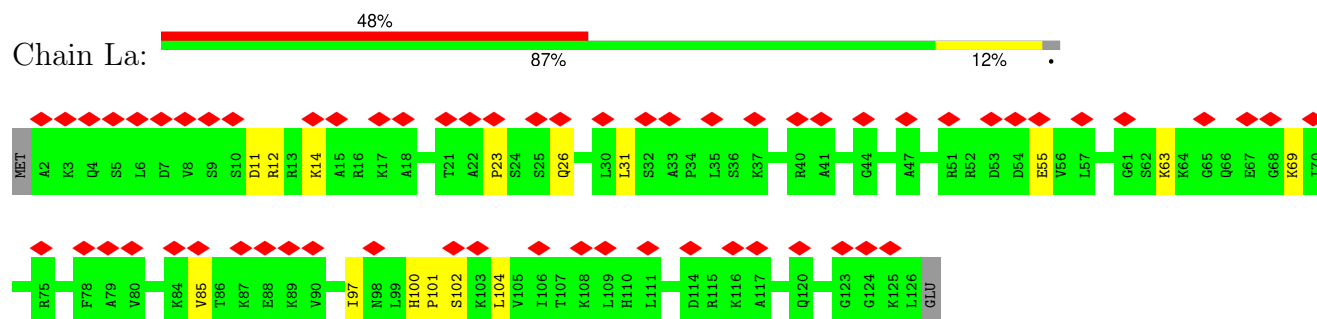


• Molecule 28: 60S ribosomal protein L25



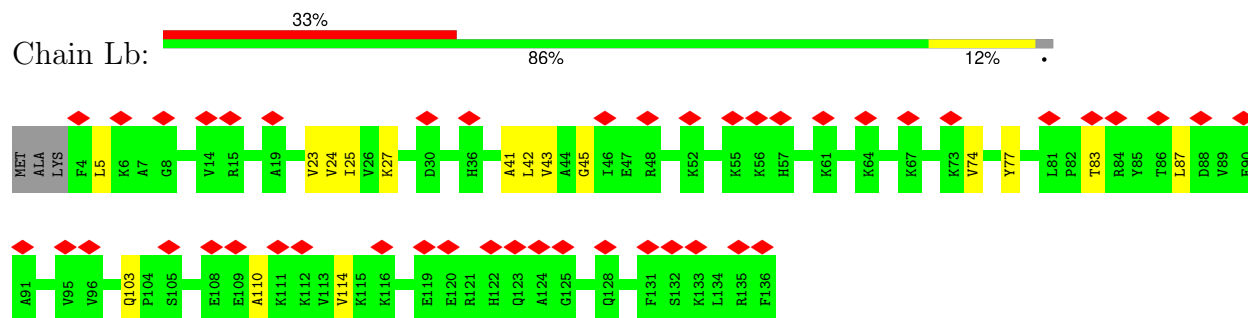
- Molecule 29: 60S ribosomal protein L26-A

Chain La:



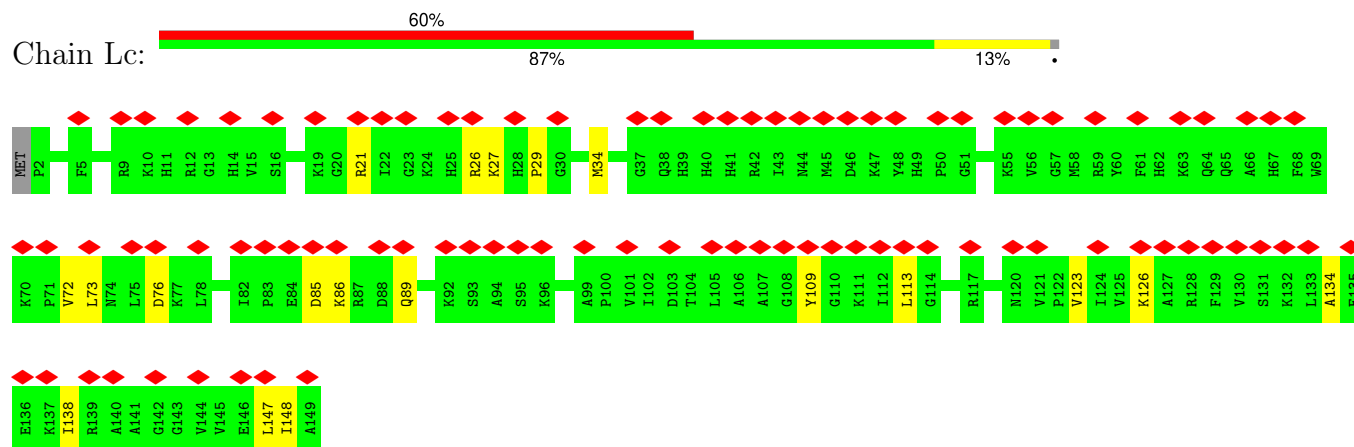
- Molecule 30: 60S ribosomal protein L27-A

Chain Lb:



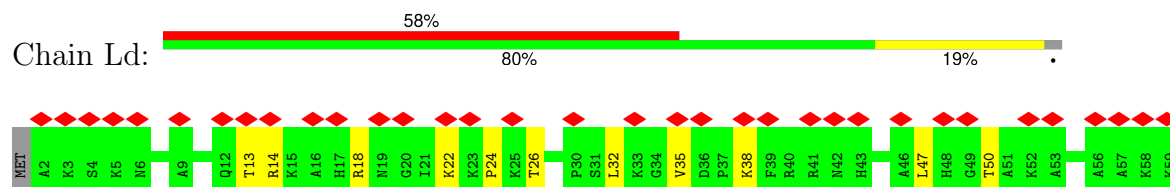
- Molecule 31: 60S ribosomal protein L28

Chain Lc:



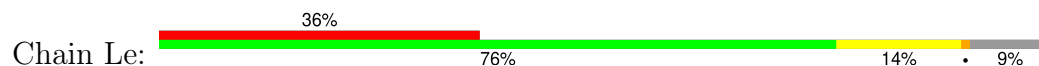
- Molecule 32: 60S ribosomal protein L29

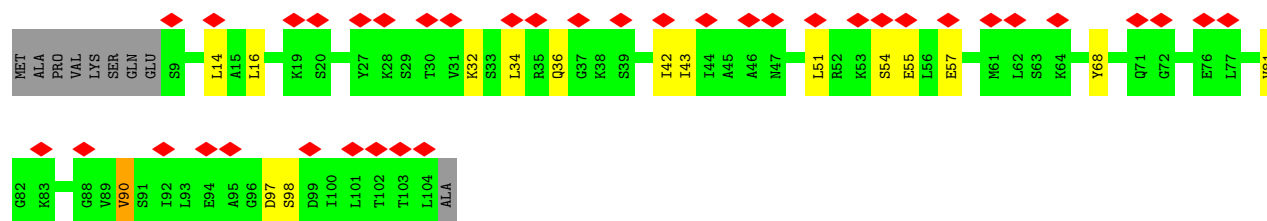
Chain Ld:



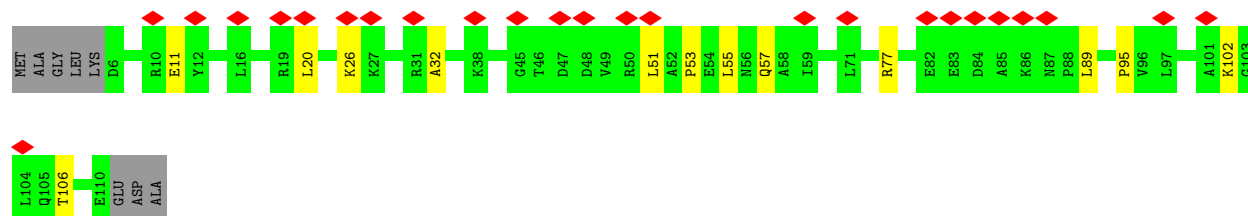
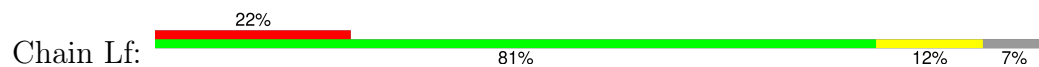
- Molecule 33: 60S ribosomal protein L30

Chain Le:

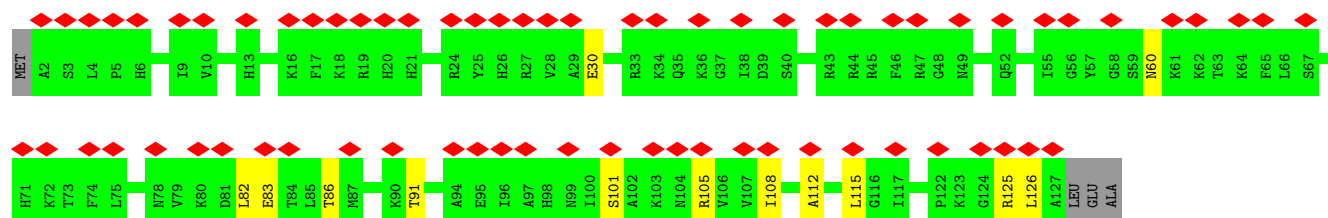
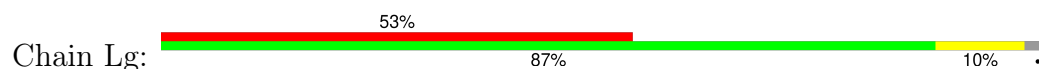




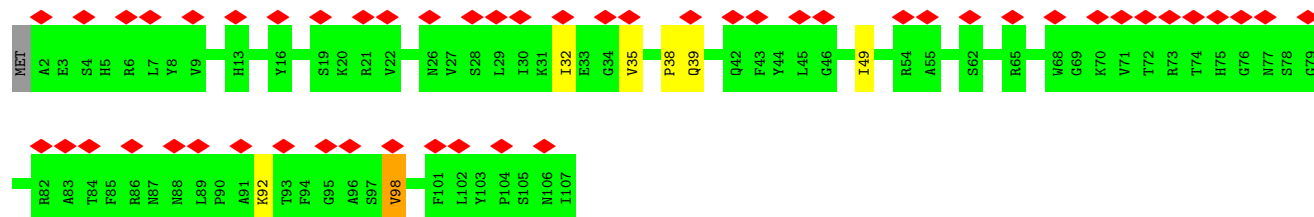
• Molecule 34: 60S ribosomal protein L31-A



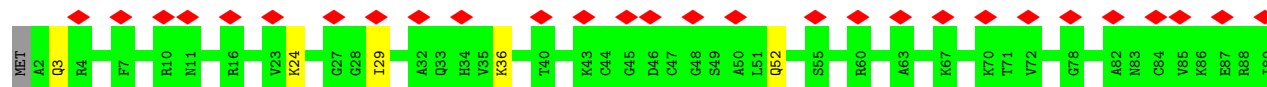
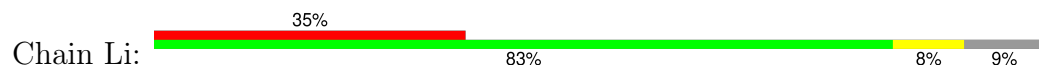
• Molecule 35: 60S ribosomal protein L32

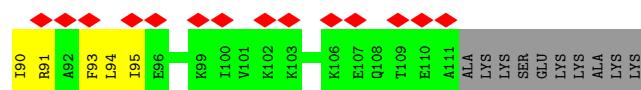


• Molecule 36: 60S ribosomal protein L33-A

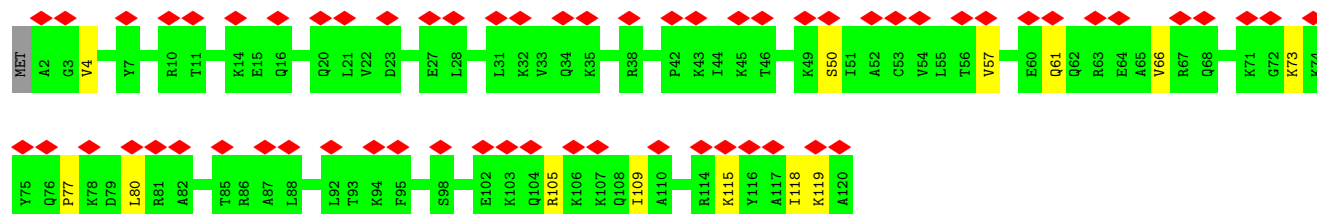
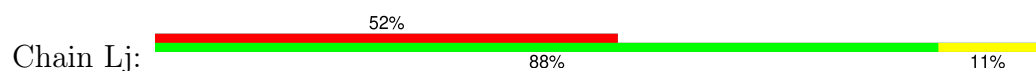


• Molecule 37: 60S ribosomal protein L34-A

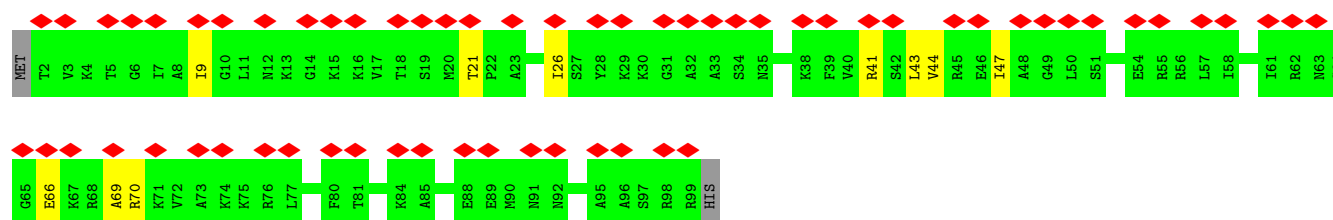
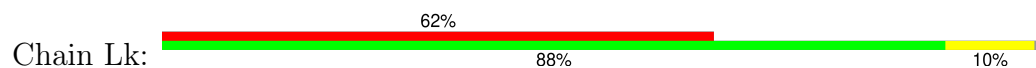




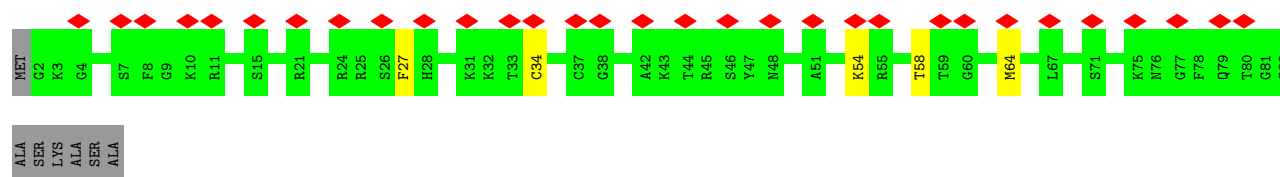
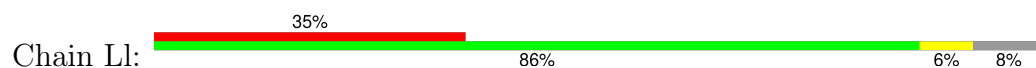
- Molecule 38: 60S ribosomal protein L35-A



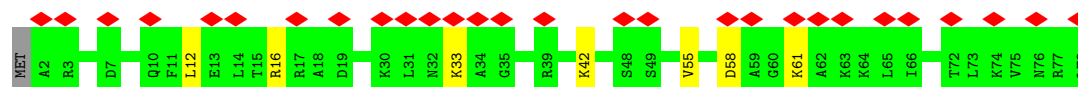
- Molecule 39: 60S ribosomal protein L36-A



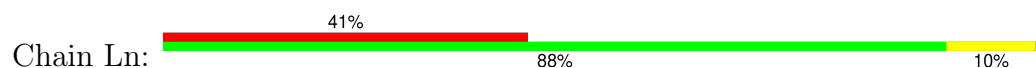
- Molecule 40: 60S ribosomal protein L37-A



- Molecule 41: 60S ribosomal protein L38



- Molecule 42: 60S ribosomal protein L39

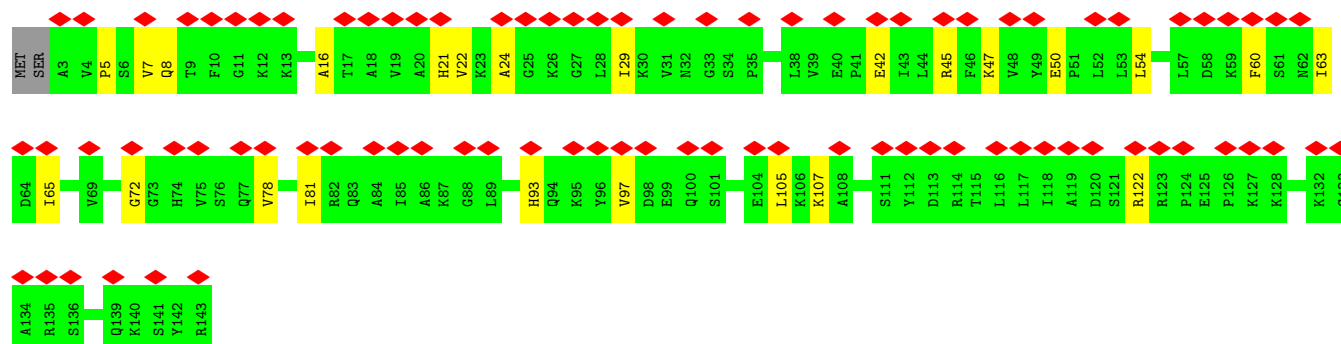
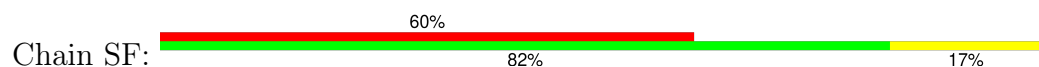




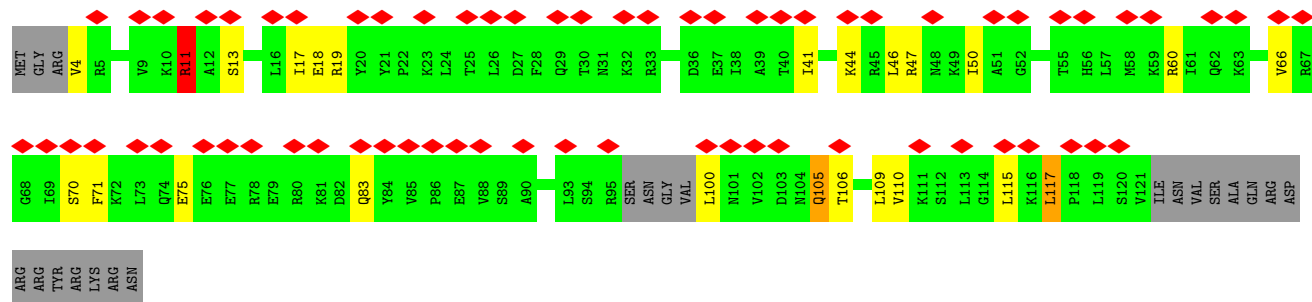
• Molecule 51: 40S ribosomal protein S15



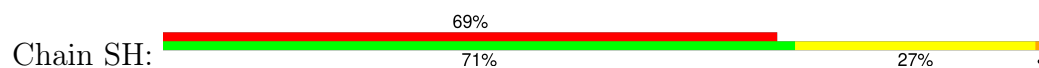
• Molecule 52: 40S ribosomal protein S16-A

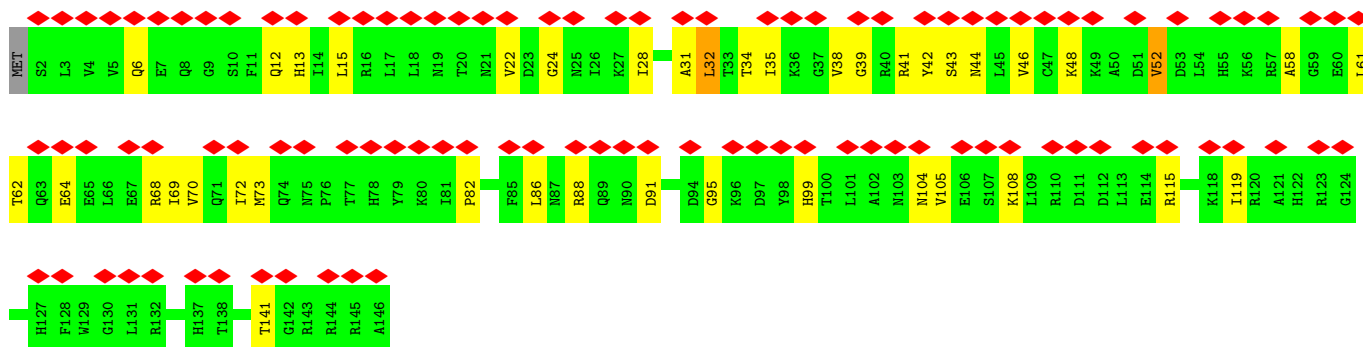


• Molecule 53: 40S ribosomal protein S17-B

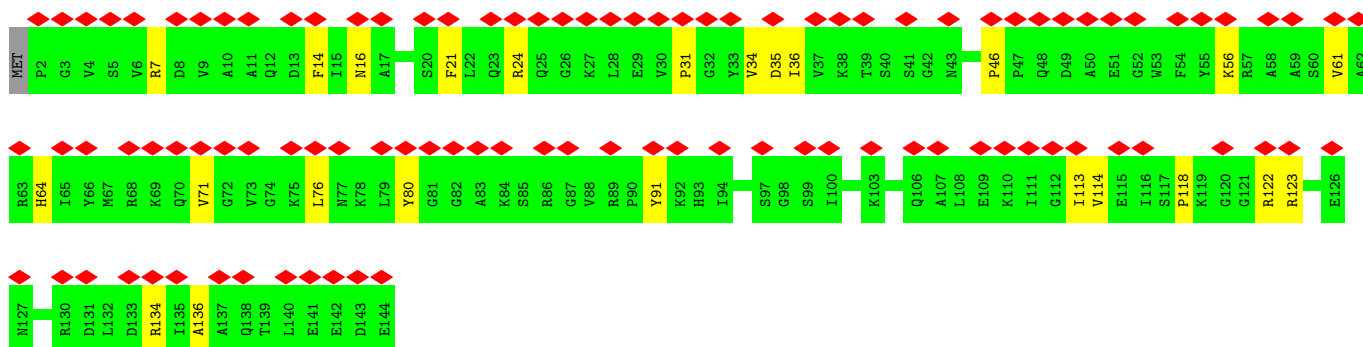
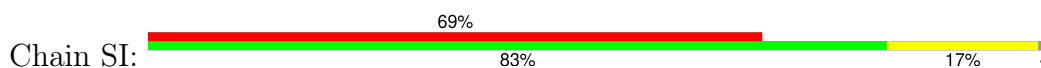


• Molecule 54: 40S ribosomal protein S18-A

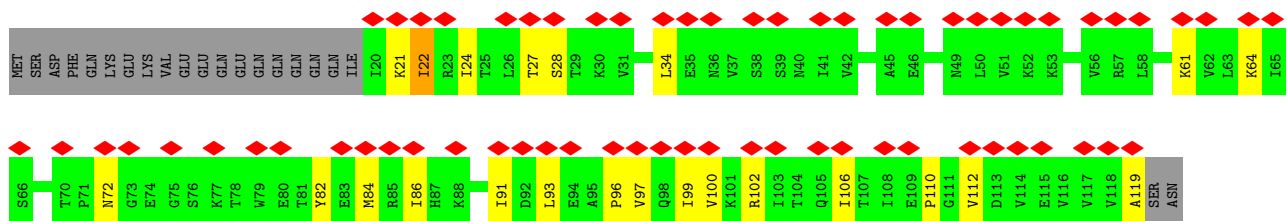




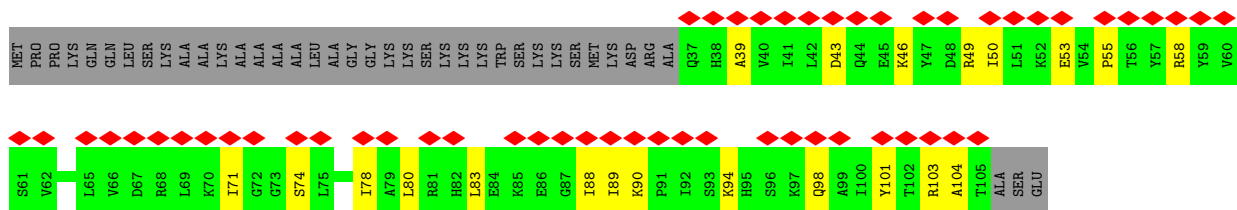
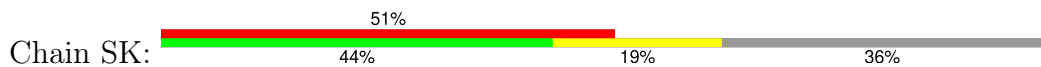
• Molecule 55: 40S ribosomal protein S19-A



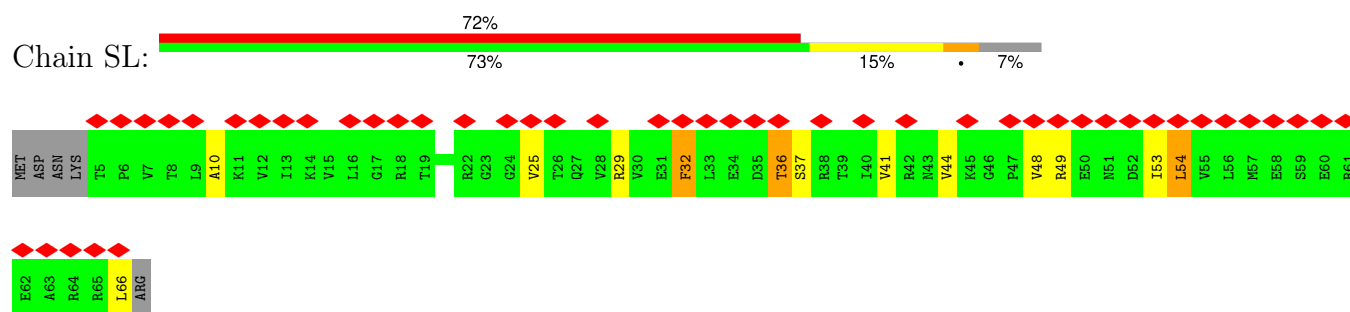
• Molecule 56: 40S ribosomal protein S20



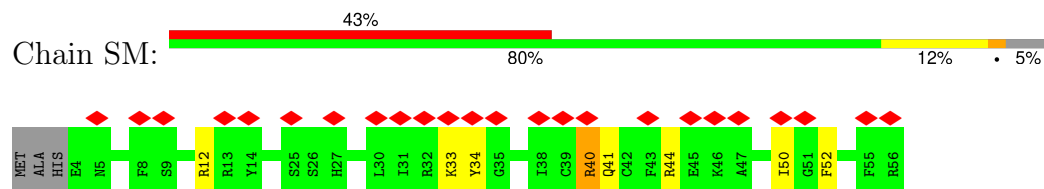
• Molecule 57: 40S ribosomal protein S25-A



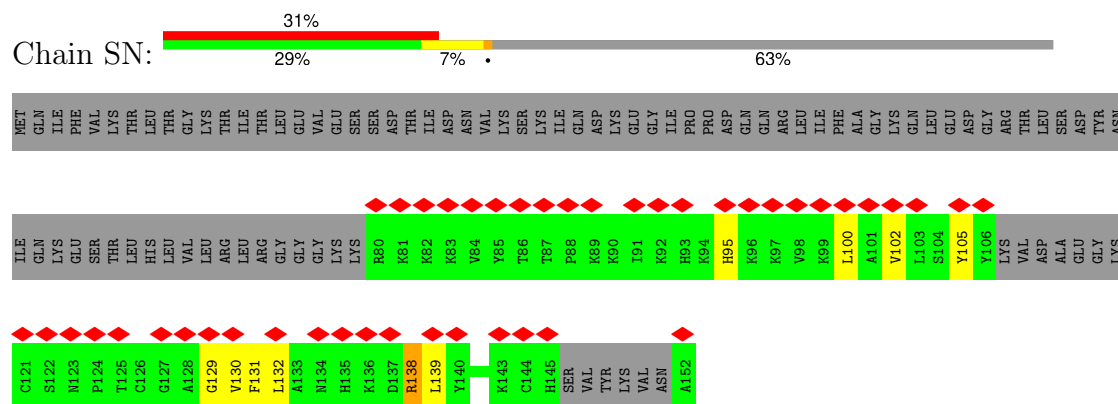
• Molecule 58: 40S ribosomal protein S28-A



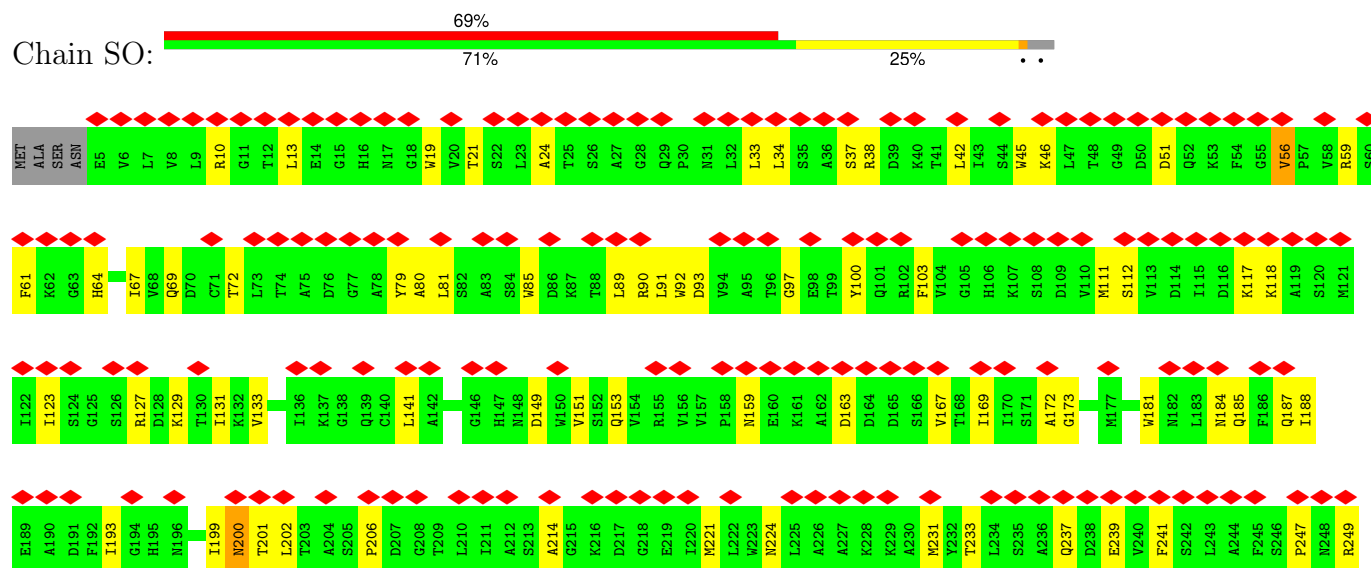
- Molecule 59: 40S ribosomal protein S29-A



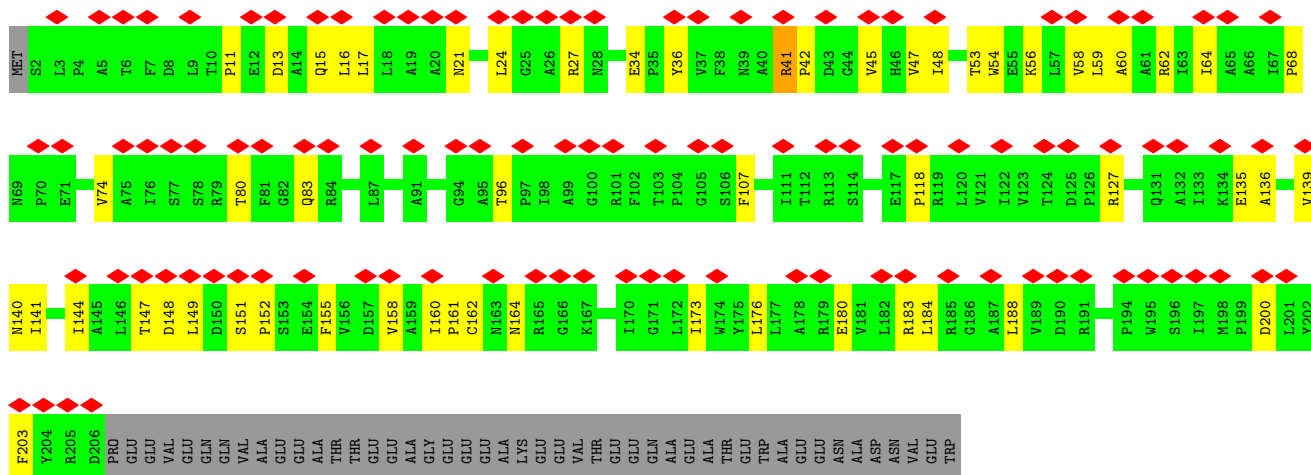
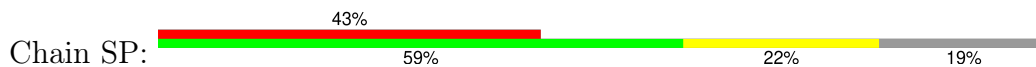
- Molecule 60: Ubiquitin-40S ribosomal protein S31



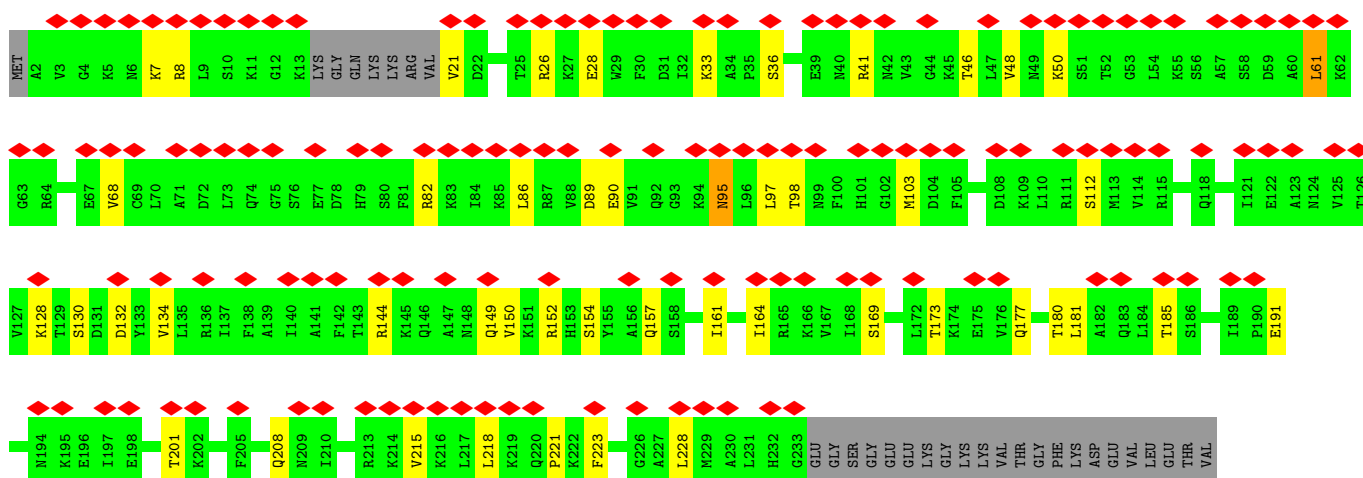
- Molecule 61: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 62: 40S ribosomal protein S0-A

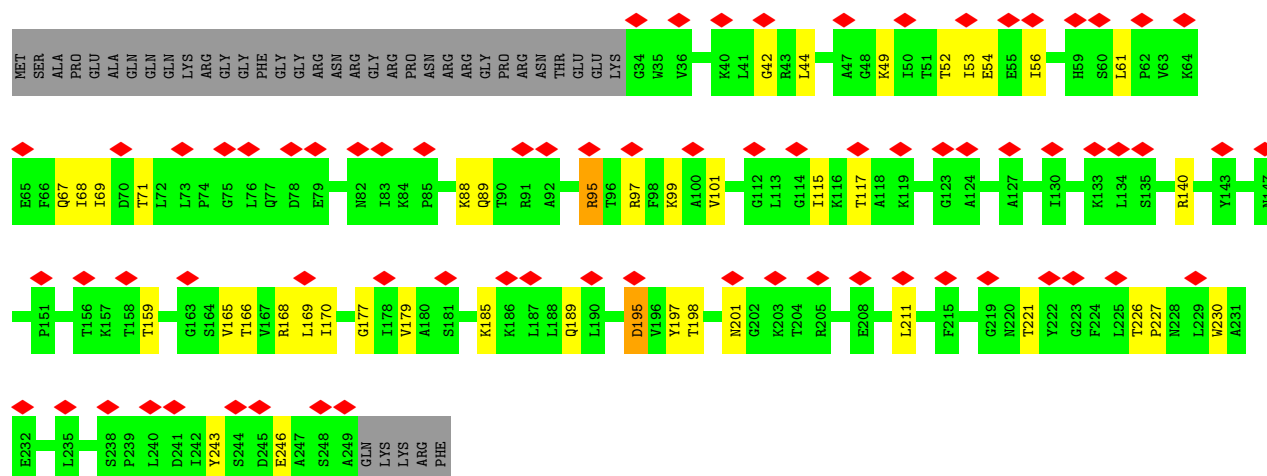


- Molecule 63: Small ribosomal subunit protein eS1A

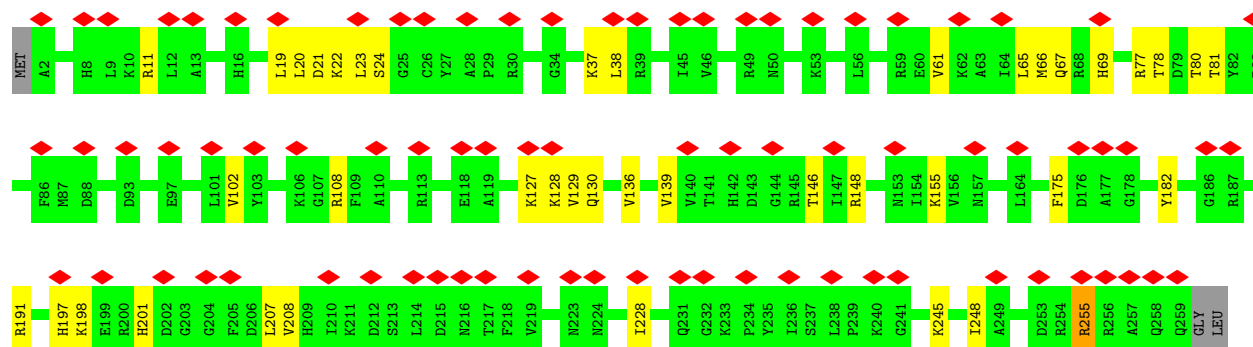
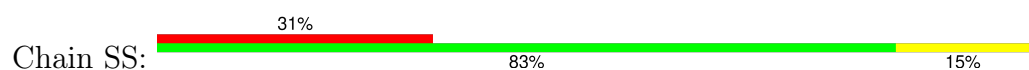


- Molecule 64: 40S ribosomal protein S2

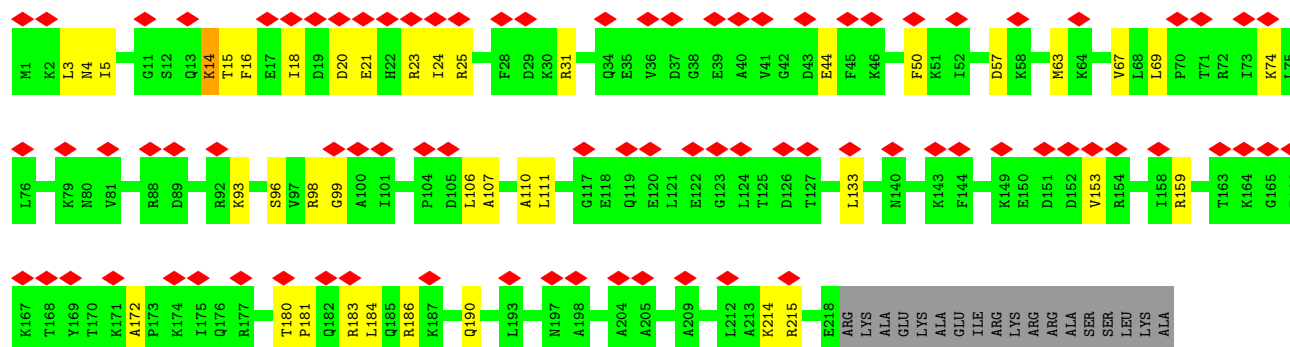
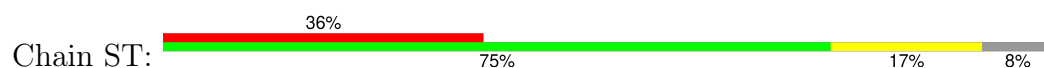




• Molecule 65: 40S ribosomal protein S4-A

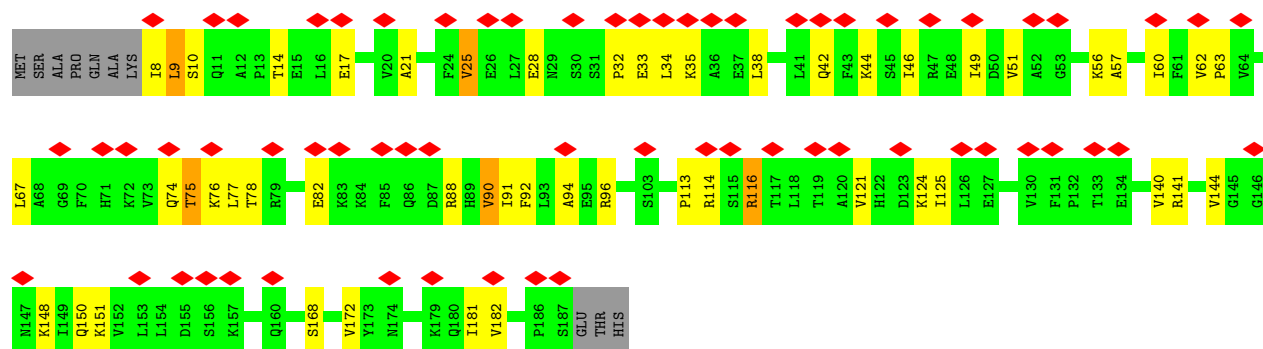


• Molecule 66: 40S ribosomal protein S6-A

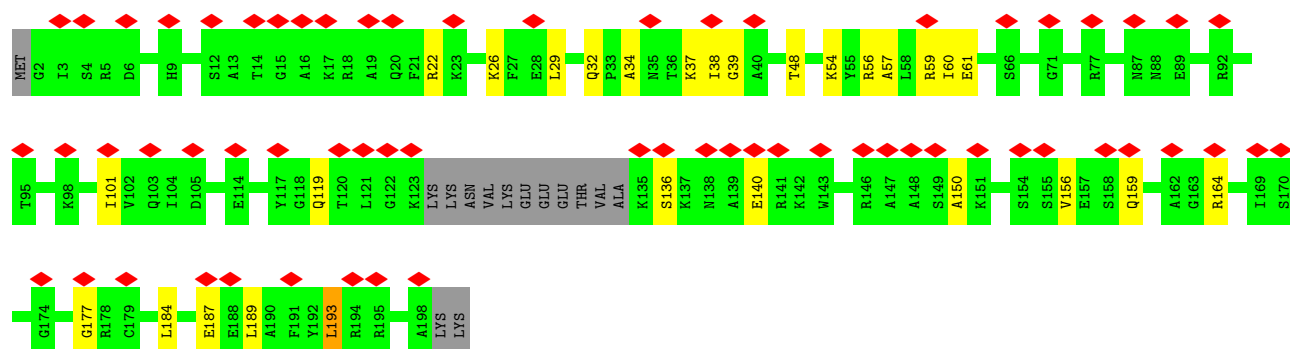
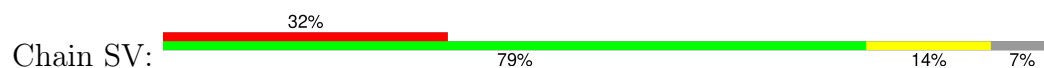


• Molecule 67: 40S ribosomal protein S7-A

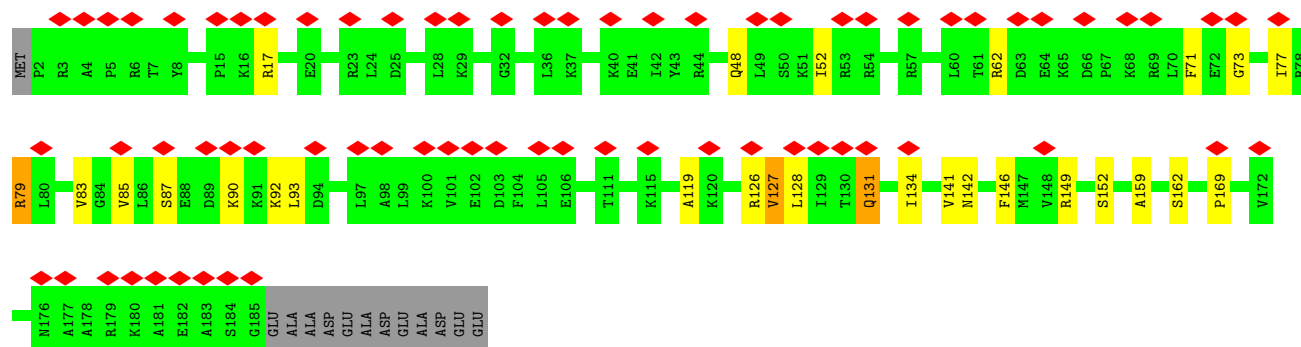
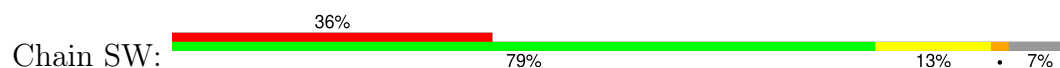




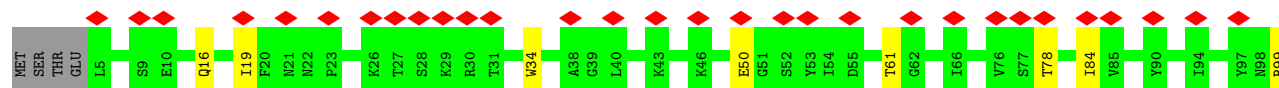
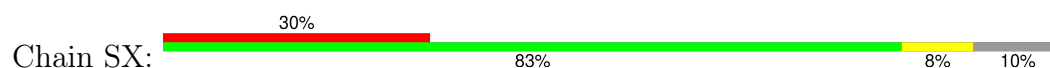
• Molecule 68: 40S ribosomal protein S8-A

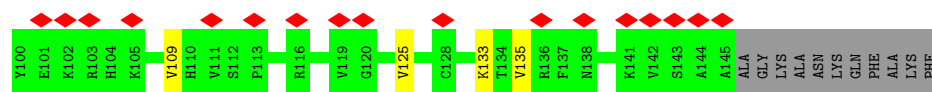


• Molecule 69: 40S ribosomal protein S9-A

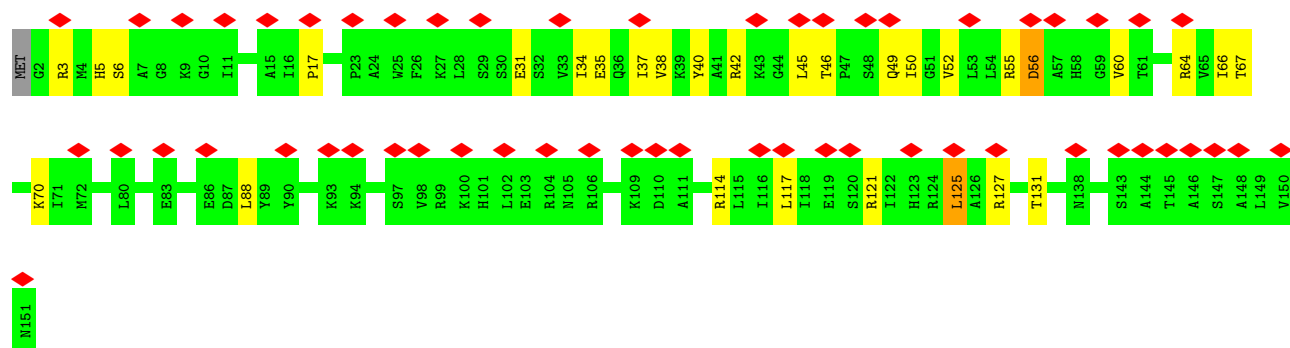
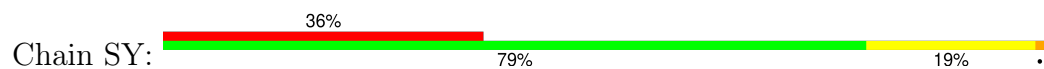


• Molecule 70: 40S ribosomal protein S11-A

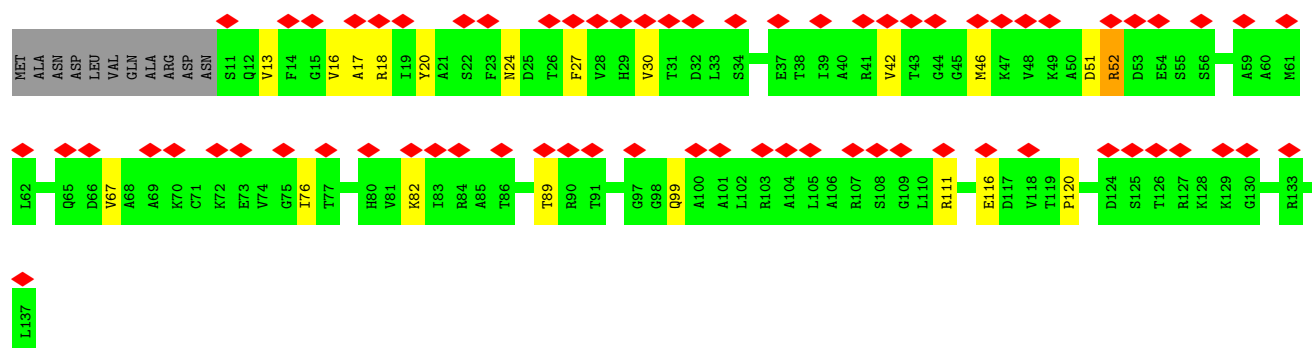
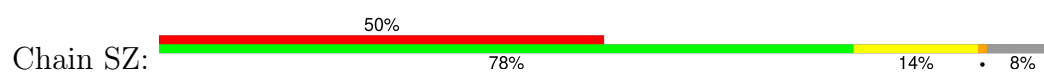




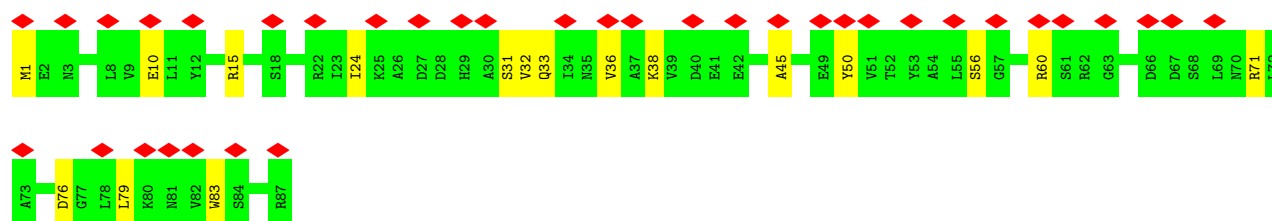
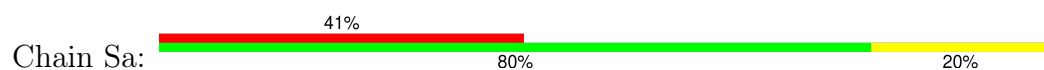
- Molecule 71: 40S ribosomal protein S13



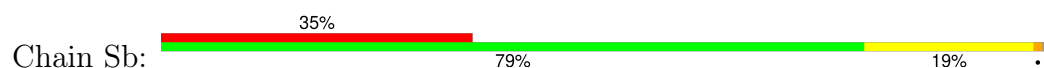
- Molecule 72: 40S ribosomal protein S14-B

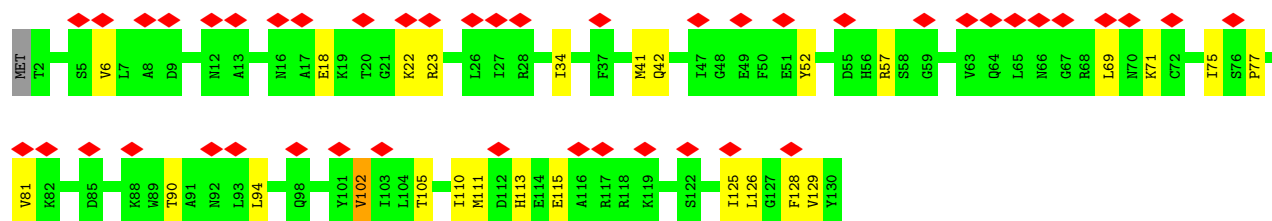


- Molecule 73: 40S ribosomal protein S21-A

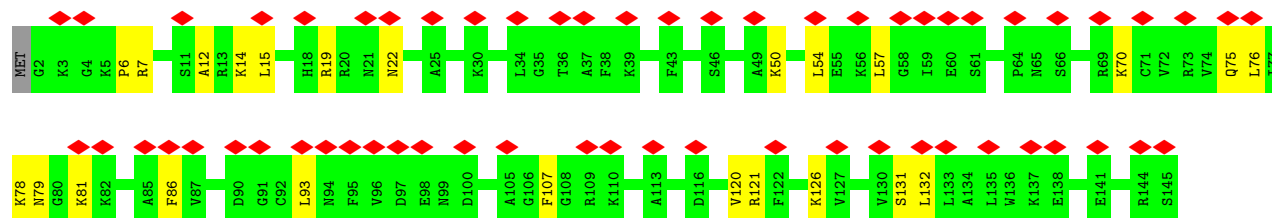
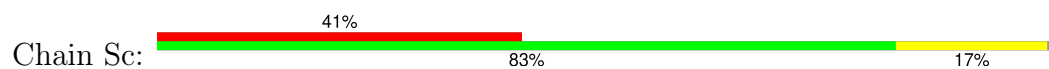


- Molecule 74: 40S ribosomal protein S22-A

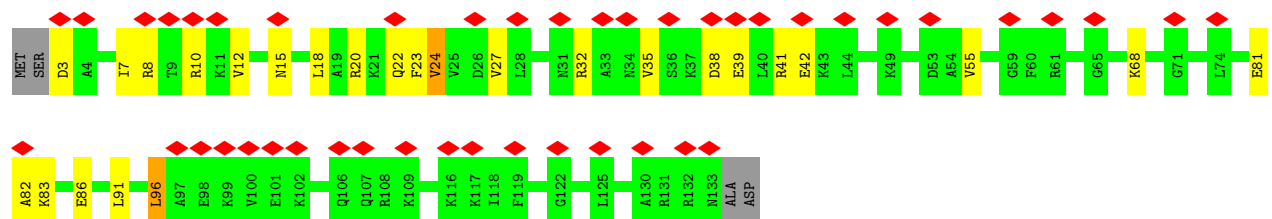
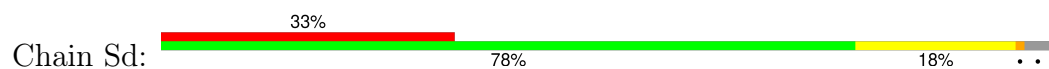




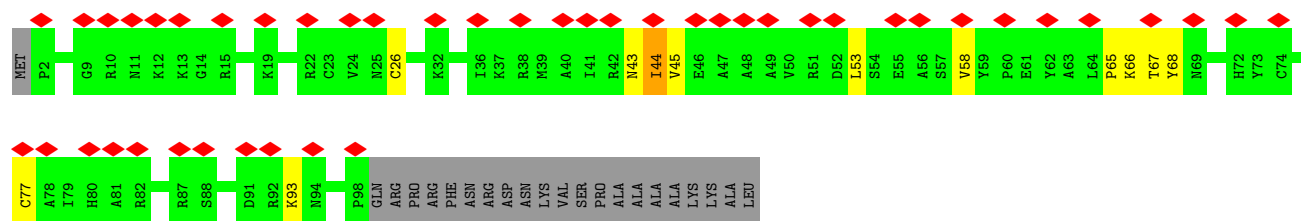
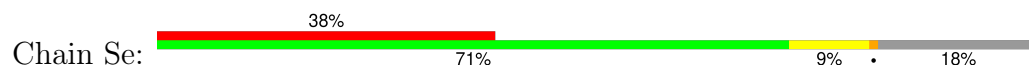
• Molecule 75: 40S ribosomal protein S23-A



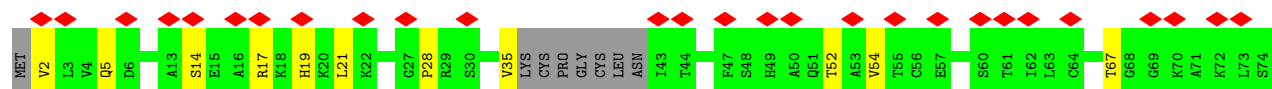
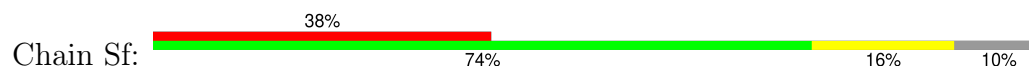
• Molecule 76: 40S ribosomal protein S24-A



• Molecule 77: Small ribosomal subunit protein eS26B

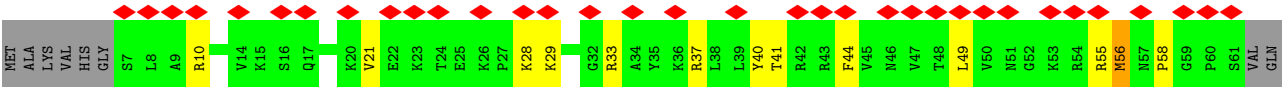


• Molecule 78: 40S ribosomal protein S27-A

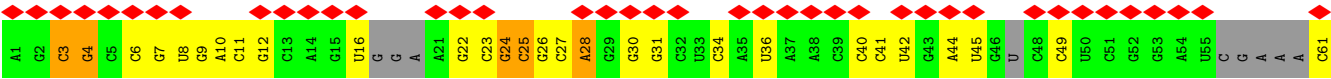




• Molecule 79: 40S ribosomal protein S30-A



• Molecule 80: P site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35555	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.782	Depositor
Minimum map value	-0.311	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	498.0, 498.0, 498.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3HE

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	A	0.25	0/72816	0.37	0/113508
2	B	0.22	0/2883	0.35	0/4491
3	C	0.25	0/3746	0.36	0/5832
4	D	0.24	0/245	0.52	0/378
5	E	0.23	0/37769	0.44	0/58836
6	LD	0.28	0/1912	0.58	0/2569
7	LE	0.26	0/3150	0.49	0/4236
8	LF	0.26	0/2801	0.53	0/3792
9	LG	0.28	0/2390	0.64	2/3225 (0.1%)
10	LH	0.30	0/1265	0.68	0/1706
11	LI	0.28	0/1821	0.55	0/2451
12	LJ	0.26	0/1836	0.58	0/2481
13	LK	0.27	0/1514	0.65	0/2039
14	LL	0.28	0/1723	0.62	0/2312
15	LM	0.31	0/1358	0.80	0/1823
16	LN	0.29	0/1568	0.58	0/2106
17	LO	0.28	0/1068	0.61	0/1438
18	LP	0.28	0/1757	0.53	0/2354
19	LQ	0.29	0/1585	0.55	0/2128
20	LR	0.26	0/1383	0.53	0/1858
21	LS	0.26	0/1465	0.55	0/1965
22	LT	0.27	0/1426	0.53	0/1901
23	LU	0.28	0/1473	0.59	0/1980
24	LV	0.28	0/1296	0.59	0/1739
25	LW	0.28	0/812	0.68	0/1099
26	LX	0.28	0/1018	0.55	0/1369
27	LY	0.30	0/525	0.61	0/696
28	LZ	0.27	0/974	0.65	0/1314
29	La	0.23	0/995	0.48	0/1329
30	Lb	0.28	0/1092	0.61	0/1467
31	Lc	0.27	0/1200	0.56	0/1607
32	Ld	0.23	0/473	0.49	0/629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.30	0/745	0.61	0/1001
34	Lf	0.25	0/870	0.54	0/1168
35	Lg	0.24	0/1029	0.48	0/1379
36	Lh	0.26	0/868	0.55	0/1168
37	Li	0.30	0/876	0.60	0/1171
38	Lj	0.28	0/978	0.60	0/1301
39	Lk	0.28	0/767	0.69	0/1019
40	Ll	0.25	0/660	0.48	0/875
41	Lm	0.27	0/614	0.58	0/822
42	Ln	0.29	0/443	0.54	0/588
43	Lo	0.26	0/415	0.55	0/551
44	Lp	0.25	0/225	0.49	0/289
45	Lq	0.23	0/817	0.54	0/1078
46	Lr	0.25	0/701	0.51	0/934
47	SA	0.31	0/1754	0.71	0/2361
48	SB	0.28	0/1625	0.71	1/2197 (0.0%)
49	SC	0.36	0/725	0.94	0/978
50	SD	0.34	0/742	0.77	0/1005
51	SE	0.34	0/925	0.78	1/1245 (0.1%)
52	SF	0.26	0/1115	0.64	0/1499
53	SG	0.31	0/917	0.75	1/1229 (0.1%)
54	SH	0.31	0/1207	0.71	0/1623
55	SI	0.31	0/1130	0.80	0/1517
56	SJ	0.35	0/807	0.81	0/1091
57	SK	0.27	0/566	0.72	0/761
58	SL	0.27	0/488	0.70	0/656
59	SM	0.26	0/453	0.70	0/602
60	SN	0.53	0/437	0.74	0/585
61	SO	0.29	0/2428	0.78	1/3308 (0.0%)
62	SP	0.29	0/1636	0.68	0/2237
63	SQ	0.28	0/1812	0.68	0/2433
64	SR	0.30	0/1656	0.66	0/2251
65	SS	0.29	0/2097	0.74	1/2823 (0.0%)
66	ST	0.28	0/1779	0.69	0/2379
67	SU	0.31	0/1475	0.73	0/1987
68	SV	0.27	0/1496	0.61	0/1999
69	SW	0.30	0/1504	0.78	2/2016 (0.1%)
70	SX	0.27	0/1163	0.60	0/1568
71	SY	0.31	0/1215	0.68	0/1638
72	SZ	0.30	0/934	0.71	0/1257
73	Sa	0.26	0/682	0.59	0/921
74	Sb	0.33	0/1038	0.62	0/1395
75	Sc	0.24	0/1139	0.58	0/1518

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sd	0.27	0/1030	0.66	0/1379
77	Se	0.26	0/778	0.59	0/1042
78	Sf	0.26	0/570	0.63	0/769
79	Sg	0.28	0/444	0.78	0/591
80	n	0.24	0/1571	0.52	0/2440
All	All	0.26	0/206685	0.50	9/303302 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	LD	0	1
9	LG	0	2
13	LK	0	1
16	LN	0	2
21	LS	0	1
22	LT	0	1
26	LX	0	2
39	Lk	0	1
45	Lq	0	1
47	SA	0	4
48	SB	0	2
49	SC	0	1
50	SD	0	1
53	SG	0	2
54	SH	0	1
55	SI	0	2
56	SJ	0	1
57	SK	0	1
59	SM	0	2
60	SN	0	1
61	SO	0	1
62	SP	0	1
63	SQ	0	1
64	SR	0	1
66	ST	0	1
67	SU	0	1
69	SW	0	3
72	SZ	0	1
74	Sb	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
78	Sf	0	2
79	Sg	0	1
All	All	0	44

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	LG	188	GLU	CB-CG-CD	7.81	125.88	112.60
9	LG	188	GLU	CA-CB-CG	7.26	128.62	114.10
51	SE	61	ARG	CB-CG-CD	6.95	127.27	111.30
53	SG	11	ARG	CG-CD-NE	6.17	125.56	112.00
61	SO	237	GLN	CA-CB-CG	5.74	125.58	114.10

There are no chirality outliers.

5 of 44 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	LD	241	ARG	Sidechain
9	LG	218	ARG	Sidechain
9	LG	85	ARG	Sidechain
13	LK	23	ARG	Sidechain
16	LN	49	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	65056	0	32701	255	0
2	B	2579	0	1304	9	0
3	C	3353	0	1695	13	0
4	D	218	0	109	3	0
5	E	33767	0	16988	218	0
6	LD	1878	0	1946	27	0
7	LE	3079	0	3158	30	0
8	LF	2749	0	2863	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	LG	2341	0	2290	43	0
10	LH	1243	0	1327	7	0
11	LI	1784	0	1862	15	0
12	LJ	1804	0	1877	15	0
13	LK	1493	0	1566	18	0
14	LL	1686	0	1725	21	0
15	LM	1337	0	1357	25	0
16	LN	1543	0	1608	18	0
17	LO	1053	0	1149	10	0
18	LP	1720	0	1779	14	0
19	LQ	1555	0	1659	7	0
20	LR	1361	0	1398	12	0
21	LS	1441	0	1543	15	0
22	LT	1409	0	1499	8	0
23	LU	1437	0	1475	12	0
24	LV	1272	0	1312	15	0
25	LW	796	0	812	8	0
26	LX	1003	0	1048	12	0
27	LY	513	0	540	5	0
28	LZ	959	0	1023	11	0
29	La	984	0	1075	8	0
30	Lb	1066	0	1104	9	0
31	Lc	1169	0	1211	13	0
32	Ld	462	0	491	7	0
33	Le	737	0	792	11	0
34	Lf	856	0	904	8	0
35	Lg	1008	0	1068	6	0
36	Lh	850	0	880	5	0
37	Li	866	0	927	10	0
38	Lj	969	0	1078	9	0
39	Lk	761	0	842	6	0
40	Ll	645	0	649	3	0
41	Lm	608	0	671	4	0
42	Ln	436	0	475	2	0
43	Lo	409	0	448	4	0
44	Lp	224	0	271	2	0
45	Lq	805	0	877	2	0
46	Lr	694	0	738	5	0
47	SA	1729	0	1812	23	0
48	SB	1605	0	1669	36	0
49	SC	708	0	701	16	0
50	SD	736	0	771	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	SE	905	0	928	18	0
52	SF	1095	0	1144	13	0
53	SG	908	0	961	13	0
54	SH	1188	0	1218	25	0
55	SI	1112	0	1124	13	0
56	SJ	797	0	863	17	0
57	SK	558	0	598	12	0
58	SL	486	0	522	11	0
59	SM	443	0	436	5	0
60	SN	429	0	412	6	0
61	SO	2375	0	2323	44	0
62	SP	1596	0	1603	34	0
63	SQ	1787	0	1870	27	0
64	SR	1626	0	1715	24	0
65	SS	2056	0	2140	28	0
66	ST	1755	0	1846	24	0
67	SU	1451	0	1538	33	0
68	SV	1471	0	1499	20	0
69	SW	1479	0	1556	13	0
70	SX	1137	0	1207	7	0
71	SY	1192	0	1255	17	0
72	SZ	923	0	948	14	0
73	Sa	673	0	662	11	0
74	Sb	1021	0	1060	15	0
75	Sc	1121	0	1196	15	0
76	Sd	1016	0	1032	15	0
77	Se	765	0	811	8	0
78	Sf	562	0	582	7	0
79	Sg	437	0	484	9	0
80	n	1409	0	721	15	0
81	A	20	0	23	0	0
All	All	192549	0	143344	1428	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 4.

The worst 5 of 1428 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)
5:E:628:G:N2	5:E:971:A:H62	1.59	1.00
80:n:10:A:H61	80:n:25:C:H42	1.13	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:628:G:H21	5:E:971:A:N6	1.67	0.92
5:E:868:G:H1	5:E:960:U:H3	1.18	0.90
69:SW:127:VAL:O	69:SW:131:GLN:HB2	1.76	0.85

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	
6	LD	245/254 (96%)	238 (97%)	7 (3%)	0	100	100
7	LE	384/387 (99%)	372 (97%)	12 (3%)	0	100	100
8	LF	359/362 (99%)	346 (96%)	12 (3%)	1 (0%)	36	64
9	LG	290/297 (98%)	286 (99%)	4 (1%)	0	100	100
10	LH	152/176 (86%)	143 (94%)	8 (5%)	1 (1%)	18	45
11	LI	220/244 (90%)	218 (99%)	2 (1%)	0	100	100
12	LJ	231/256 (90%)	224 (97%)	7 (3%)	0	100	100
13	LK	186/191 (97%)	178 (96%)	8 (4%)	0	100	100
14	LL	205/210 (98%)	197 (96%)	8 (4%)	0	100	100
15	LM	166/174 (95%)	164 (99%)	2 (1%)	0	100	100
16	LN	191/199 (96%)	184 (96%)	6 (3%)	1 (0%)	24	53
17	LO	134/138 (97%)	133 (99%)	1 (1%)	0	100	100
18	LP	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
19	LQ	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
20	LR	168/184 (91%)	163 (97%)	5 (3%)	0	100	100
21	LS	183/186 (98%)	179 (98%)	4 (2%)	0	100	100
22	LT	172/189 (91%)	169 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	LU	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
24	LV	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
25	LW	98/121 (81%)	94 (96%)	4 (4%)	0	100	100
26	LX	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
27	LY	60/155 (39%)	60 (100%)	0	0	100	100
28	LZ	118/142 (83%)	116 (98%)	2 (2%)	0	100	100
29	La	123/127 (97%)	123 (100%)	0	0	100	100
30	Lb	131/136 (96%)	127 (97%)	4 (3%)	0	100	100
31	Lc	146/149 (98%)	140 (96%)	6 (4%)	0	100	100
32	Ld	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
33	Le	94/105 (90%)	94 (100%)	0	0	100	100
34	Lf	103/113 (91%)	101 (98%)	2 (2%)	0	100	100
35	Lg	124/130 (95%)	123 (99%)	1 (1%)	0	100	100
36	Lh	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
37	Li	108/121 (89%)	103 (95%)	5 (5%)	0	100	100
38	Lj	117/120 (98%)	116 (99%)	1 (1%)	0	100	100
39	Lk	96/100 (96%)	91 (95%)	4 (4%)	1 (1%)	12	36
40	Ll	79/88 (90%)	77 (98%)	2 (2%)	0	100	100
41	Lm	75/78 (96%)	75 (100%)	0	0	100	100
42	Ln	48/51 (94%)	48 (100%)	0	0	100	100
43	Lo	49/128 (38%)	49 (100%)	0	0	100	100
44	Lp	22/25 (88%)	22 (100%)	0	0	100	100
45	Lq	98/106 (92%)	96 (98%)	2 (2%)	0	100	100
46	Lr	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
47	SA	220/240 (92%)	213 (97%)	7 (3%)	0	100	100
48	SB	204/225 (91%)	189 (93%)	14 (7%)	1 (0%)	24	53
49	SC	81/105 (77%)	75 (93%)	6 (7%)	0	100	100
50	SD	93/143 (65%)	86 (92%)	7 (8%)	0	100	100
51	SE	114/142 (80%)	111 (97%)	3 (3%)	0	100	100
52	SF	139/143 (97%)	133 (96%)	6 (4%)	0	100	100
53	SG	110/136 (81%)	107 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	SH	143/146 (98%)	137 (96%)	6 (4%)	0	100	100
55	SI	141/144 (98%)	140 (99%)	1 (1%)	0	100	100
56	SJ	98/121 (81%)	97 (99%)	1 (1%)	0	100	100
57	SK	67/108 (62%)	64 (96%)	3 (4%)	0	100	100
58	SL	60/67 (90%)	55 (92%)	5 (8%)	0	100	100
59	SM	51/56 (91%)	47 (92%)	4 (8%)	0	100	100
60	SN	51/152 (34%)	47 (92%)	3 (6%)	1 (2%)	6	19
61	SO	309/319 (97%)	298 (96%)	11 (4%)	0	100	100
62	SP	203/252 (81%)	194 (96%)	8 (4%)	1 (0%)	24	53
63	SQ	221/255 (87%)	215 (97%)	6 (3%)	0	100	100
64	SR	214/254 (84%)	210 (98%)	4 (2%)	0	100	100
65	SS	256/261 (98%)	241 (94%)	15 (6%)	0	100	100
66	ST	216/236 (92%)	214 (99%)	2 (1%)	0	100	100
67	SU	178/190 (94%)	170 (96%)	8 (4%)	0	100	100
68	SV	182/200 (91%)	172 (94%)	10 (6%)	0	100	100
69	SW	182/197 (92%)	168 (92%)	12 (7%)	2 (1%)	11	34
70	SX	139/156 (89%)	134 (96%)	5 (4%)	0	100	100
71	SY	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
72	SZ	125/138 (91%)	121 (97%)	4 (3%)	0	100	100
73	Sa	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
74	Sb	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
75	Sc	142/145 (98%)	140 (99%)	2 (1%)	0	100	100
76	Sd	129/135 (96%)	127 (98%)	2 (2%)	0	100	100
77	Se	95/119 (80%)	92 (97%)	3 (3%)	0	100	100
78	Sf	70/82 (85%)	66 (94%)	4 (6%)	0	100	100
79	Sg	53/63 (84%)	44 (83%)	7 (13%)	2 (4%)	2	8
All	All	10726/11870 (90%)	10385 (97%)	330 (3%)	11 (0%)	49	75

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	48	PRO
60	SN	95	HIS

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Mol	Chain	Res	Type
48	SB	100	ASN
62	SP	68	PRO
69	SW	93	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	
6	LD	189/196 (96%)	189 (100%)	0	100	100
7	LE	321/323 (99%)	318 (99%)	3 (1%)	70	89
8	LF	288/289 (100%)	284 (99%)	4 (1%)	59	84
9	LG	241/245 (98%)	240 (100%)	1 (0%)	84	94
10	LH	136/155 (88%)	132 (97%)	4 (3%)	37	71
11	LI	186/205 (91%)	182 (98%)	4 (2%)	45	77
12	LJ	187/208 (90%)	186 (100%)	1 (0%)	81	93
13	LK	168/171 (98%)	164 (98%)	4 (2%)	43	75
14	LL	177/179 (99%)	174 (98%)	3 (2%)	53	81
15	LM	144/151 (95%)	141 (98%)	3 (2%)	47	78
16	LN	154/159 (97%)	151 (98%)	3 (2%)	50	79
17	LO	107/109 (98%)	105 (98%)	2 (2%)	50	79
18	LP	175/176 (99%)	173 (99%)	2 (1%)	65	86
19	LQ	160/162 (99%)	156 (98%)	4 (2%)	42	74
20	LR	138/146 (94%)	136 (99%)	2 (1%)	59	84
21	LS	150/151 (99%)	148 (99%)	2 (1%)	61	85
22	LT	142/154 (92%)	140 (99%)	2 (1%)	59	84
23	LU	155/156 (99%)	146 (94%)	9 (6%)	18	47
24	LV	135/137 (98%)	135 (100%)	0	100	100
25	LW	87/107 (81%)	84 (97%)	3 (3%)	32	66
26	LX	104/105 (99%)	103 (99%)	1 (1%)	68	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	LY	54/129 (42%)	53 (98%)	1 (2%)	50	79
28	LZ	104/118 (88%)	101 (97%)	3 (3%)	37	71
29	La	108/110 (98%)	107 (99%)	1 (1%)	70	89
30	Lb	111/116 (96%)	110 (99%)	1 (1%)	70	89
31	Lc	117/119 (98%)	115 (98%)	2 (2%)	53	81
32	Ld	46/47 (98%)	45 (98%)	1 (2%)	45	77
33	Le	81/88 (92%)	79 (98%)	2 (2%)	42	74
34	Lf	92/97 (95%)	92 (100%)	0	100	100
35	Lg	107/111 (96%)	103 (96%)	4 (4%)	30	63
36	Lh	90/91 (99%)	89 (99%)	1 (1%)	65	86
37	Li	94/103 (91%)	93 (99%)	1 (1%)	65	86
38	Lj	104/105 (99%)	104 (100%)	0	100	100
39	Lk	80/82 (98%)	80 (100%)	0	100	100
40	Ll	67/71 (94%)	67 (100%)	0	100	100
41	Lm	67/69 (97%)	66 (98%)	1 (2%)	57	83
42	Ln	45/46 (98%)	44 (98%)	1 (2%)	45	77
43	Lo	46/116 (40%)	45 (98%)	1 (2%)	45	77
44	Lp	22/23 (96%)	22 (100%)	0	100	100
45	Lq	86/91 (94%)	84 (98%)	2 (2%)	44	76
46	Lr	71/72 (99%)	71 (100%)	0	100	100
47	SA	182/195 (93%)	178 (98%)	4 (2%)	45	77
48	SB	172/191 (90%)	170 (99%)	2 (1%)	63	86
49	SC	77/98 (79%)	76 (99%)	1 (1%)	61	85
50	SD	80/119 (67%)	79 (99%)	1 (1%)	61	85
51	SE	94/118 (80%)	92 (98%)	2 (2%)	47	78
52	SF	115/119 (97%)	113 (98%)	2 (2%)	53	81
53	SG	100/124 (81%)	95 (95%)	5 (5%)	22	53
54	SH	127/129 (98%)	121 (95%)	6 (5%)	23	55
55	SI	115/116 (99%)	113 (98%)	2 (2%)	53	81
56	SJ	93/114 (82%)	91 (98%)	2 (2%)	45	77
57	SK	61/89 (68%)	60 (98%)	1 (2%)	55	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	SL	55/60 (92%)	52 (94%)	3 (6%)	19	49
59	SM	47/49 (96%)	46 (98%)	1 (2%)	47	78
60	SN	42/135 (31%)	37 (88%)	5 (12%)	5	16
61	SO	249/262 (95%)	245 (98%)	4 (2%)	55	82
62	SP	169/210 (80%)	166 (98%)	3 (2%)	51	80
63	SQ	198/224 (88%)	193 (98%)	5 (2%)	42	74
64	SR	175/205 (85%)	172 (98%)	3 (2%)	53	81
65	SS	220/222 (99%)	218 (99%)	2 (1%)	70	89
66	ST	187/201 (93%)	185 (99%)	2 (1%)	65	86
67	SU	162/170 (95%)	156 (96%)	6 (4%)	30	63
68	SV	148/161 (92%)	145 (98%)	3 (2%)	48	79
69	SW	156/166 (94%)	153 (98%)	3 (2%)	50	79
70	SX	126/137 (92%)	124 (98%)	2 (2%)	55	82
71	SY	127/128 (99%)	123 (97%)	4 (3%)	35	69
72	SZ	90/105 (86%)	88 (98%)	2 (2%)	45	77
73	Sa	71/74 (96%)	68 (96%)	3 (4%)	26	59
74	Sb	110/111 (99%)	107 (97%)	3 (3%)	39	72
75	Sc	119/120 (99%)	116 (98%)	3 (2%)	42	74
76	Sd	101/113 (89%)	96 (95%)	5 (5%)	22	53
77	Se	82/100 (82%)	80 (98%)	2 (2%)	43	75
78	Sf	64/71 (90%)	62 (97%)	2 (3%)	35	69
79	Sg	47/54 (87%)	47 (100%)	0	100	100
All	All	9097/9978 (91%)	8924 (98%)	173 (2%)	49	79

5 of 173 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
60	SN	138	ARG
68	SV	193	LEU
61	SO	239	GLU
64	SR	246	GLU
71	SY	67	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 180 such sidechains are listed below:

Mol	Chain	Res	Type
54	SH	104	ASN
65	SS	69	HIS
55	SI	106	GLN
61	SO	299	GLN
67	SU	161	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3029/3396 (89%)	473 (15%)	23 (0%)
2	B	120/121 (99%)	11 (9%)	2 (1%)
3	C	157/158 (99%)	25 (15%)	1 (0%)
4	D	9/10 (90%)	3 (33%)	1 (11%)
5	E	1571/1800 (87%)	340 (21%)	44 (2%)
80	n	62/75 (82%)	28 (45%)	0
All	All	4948/5560 (88%)	880 (17%)	71 (1%)

5 of 880 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	14	U
1	A	26	A
1	A	40	A
1	A	43	A

5 of 71 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	E	1362	U
5	E	1430	U
5	E	1572	G
2	B	120	C
2	B	52	G

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

1 ligand 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	3HE	A	3401	-	21,21,21	0.53	0	23,30,30	0.86	0

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	3HE	A	3401	-	-	2/8/36/36	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

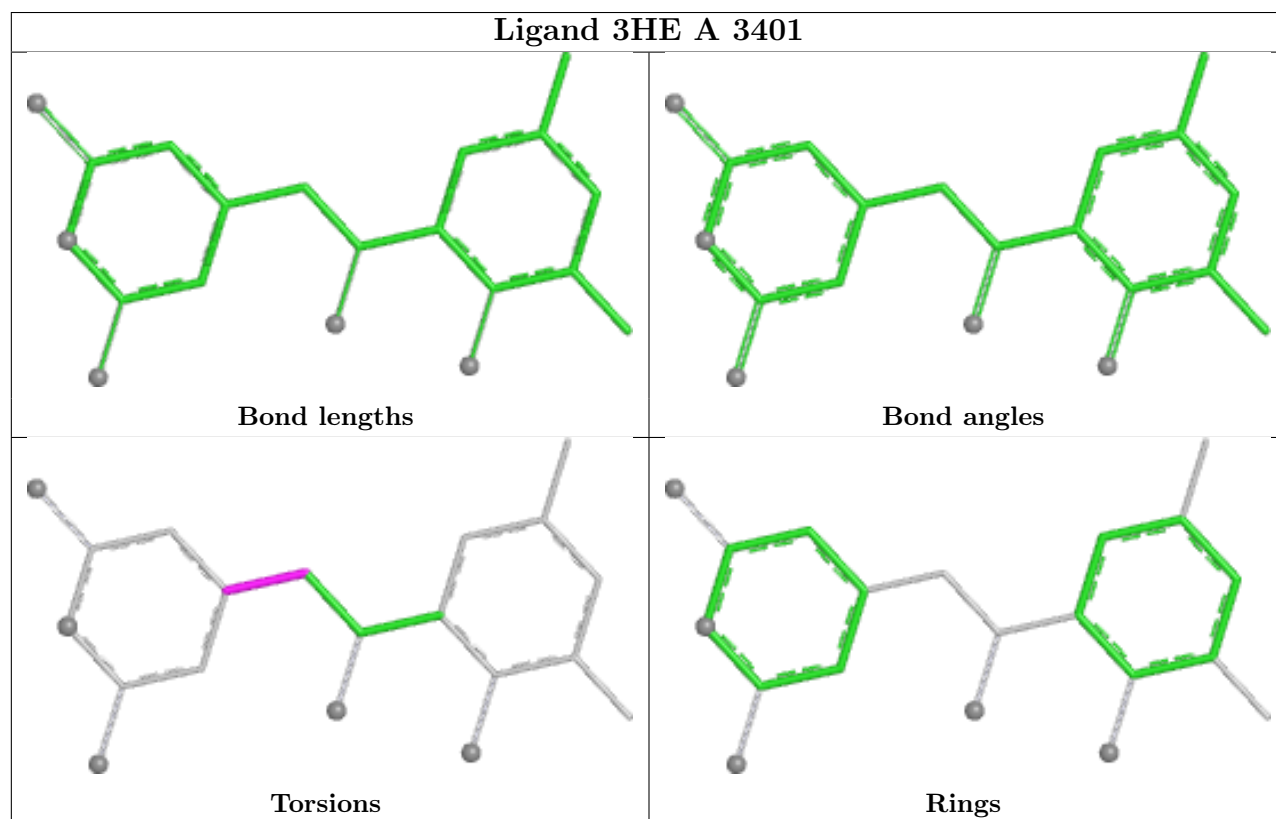
Mol	Chain	Res	Type	Atoms
81	A	3401	3HE	C7-C8-C9-C10
81	A	3401	3HE	C7-C8-C9-C13

There are no ring outliers.

No monomer is involved in short contacts.

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.

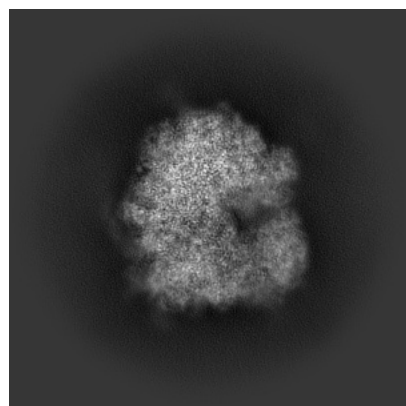
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72802. These allow visual inspection of the internal detail of the map and identification of artifacts.

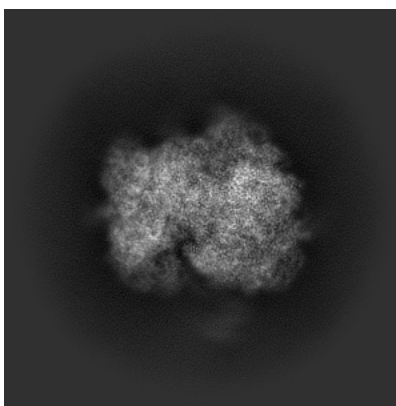
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

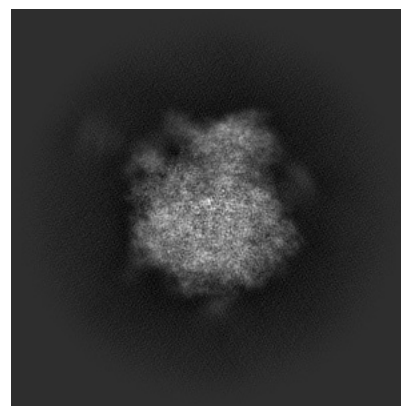
6.1.1 Primary map



X

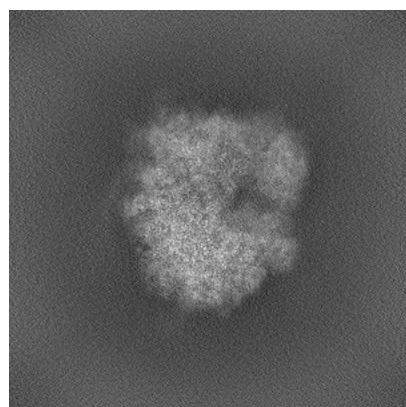


Y

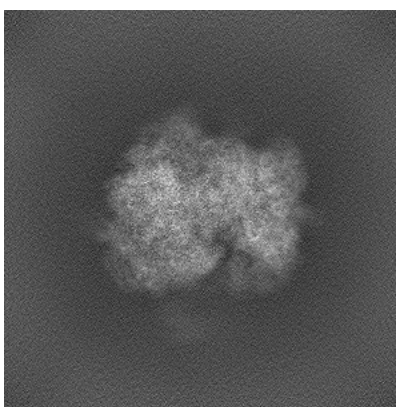


Z

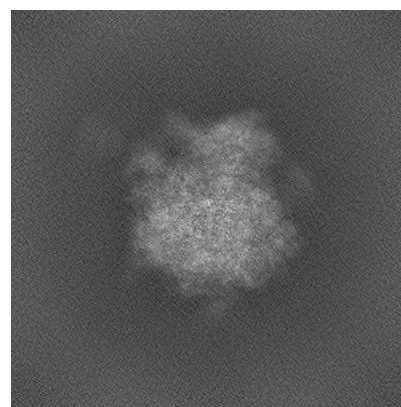
6.1.2 Raw map



X



Y

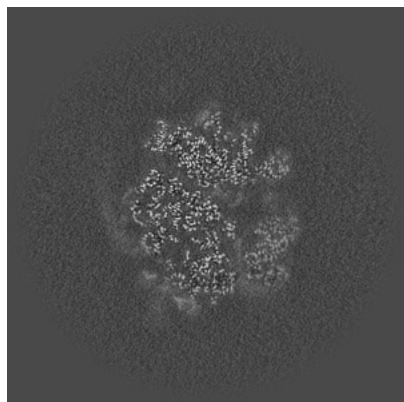


Z

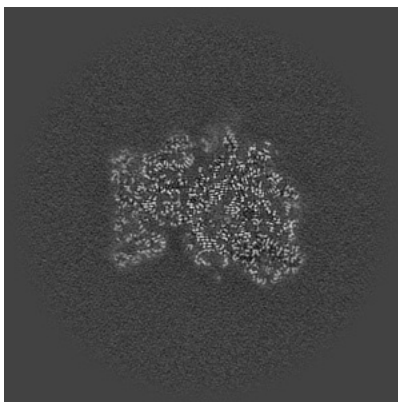
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

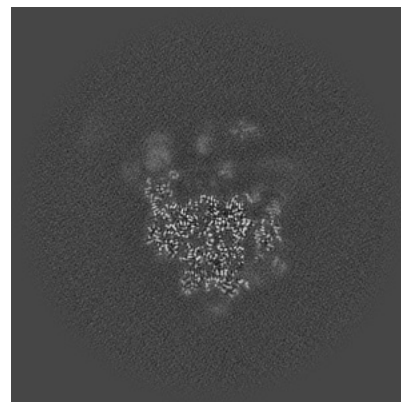
6.2.1 Primary map



X Index: 300

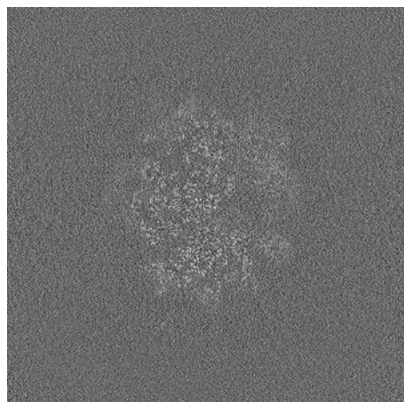


Y Index: 300

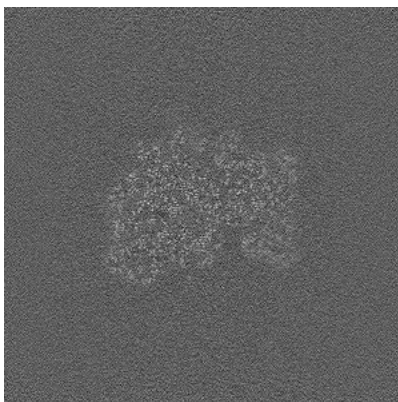


Z Index: 300

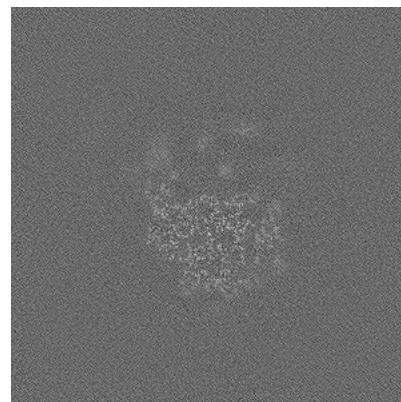
6.2.2 Raw map



X Index: 300



Y Index: 300

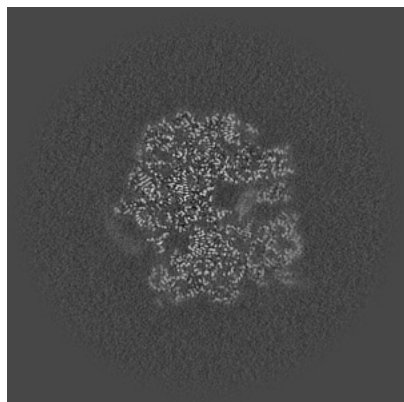


Z Index: 300

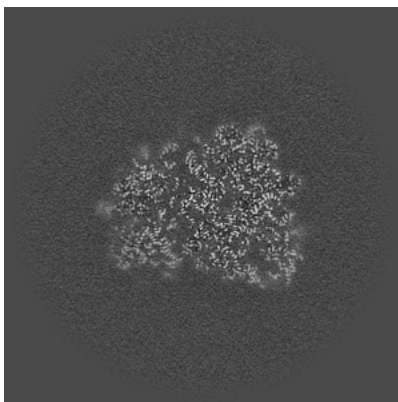
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

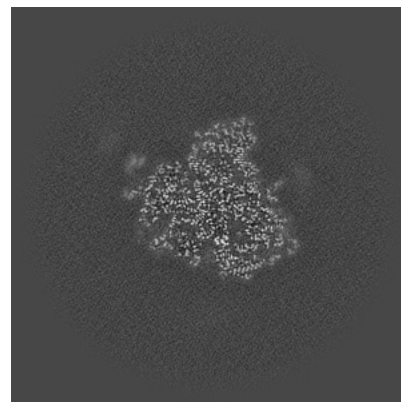
6.3.1 Primary map



X Index: 326

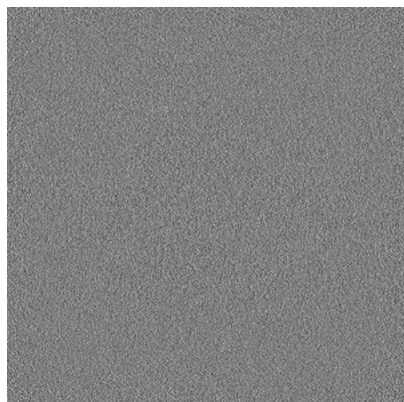


Y Index: 277

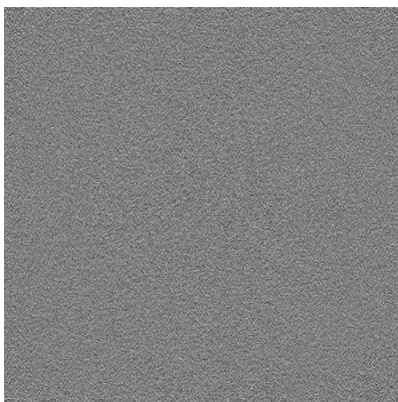


Z Index: 364

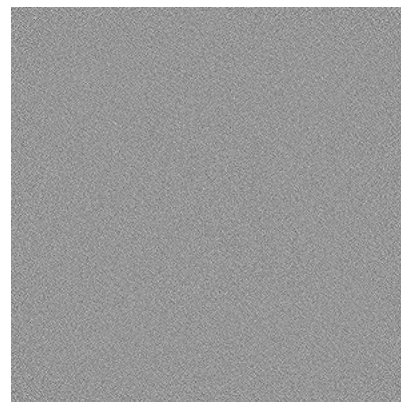
6.3.2 Raw map



X Index: 0



Y Index: 0

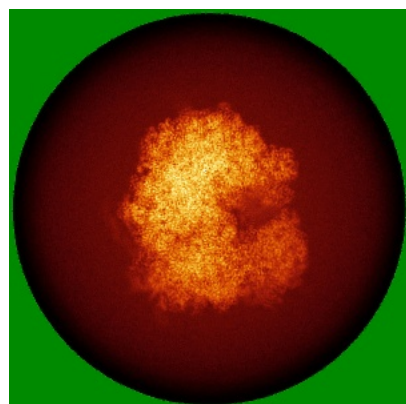


Z Index: 0

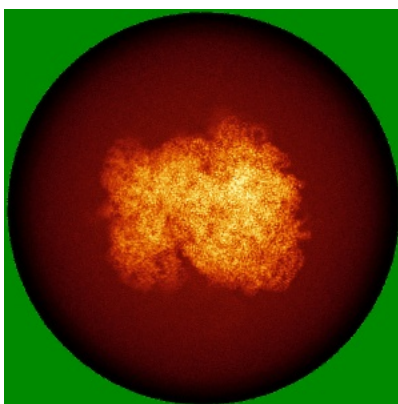
The images above show the largest variance slices of the map in three orthogonal directions.

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

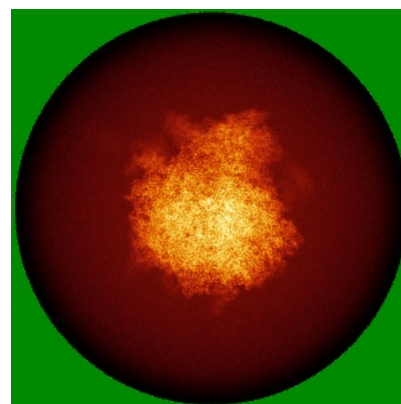
6.4.1 Primary map



X

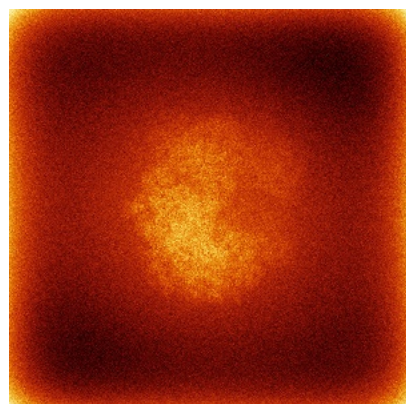


Y

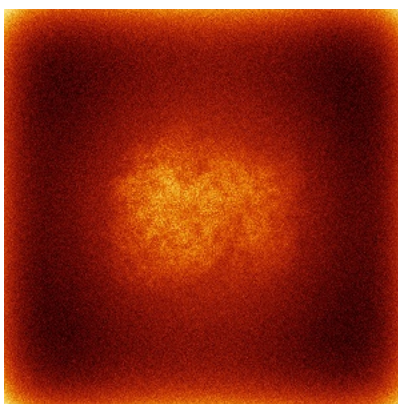


Z

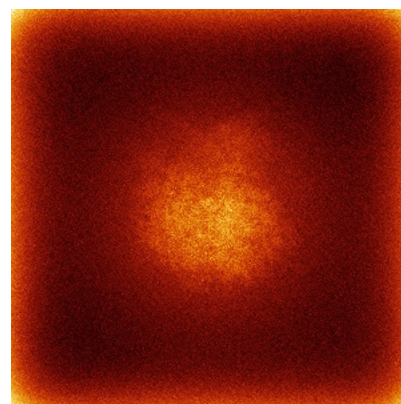
6.4.2 Raw map



X



Y

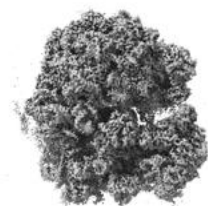


Z

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

6.5 Orthogonal surface views [i](#)

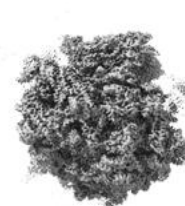
6.5.1 Primary map



X



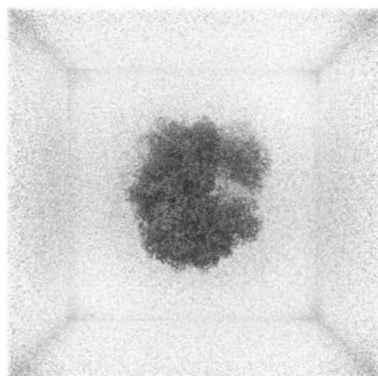
Y



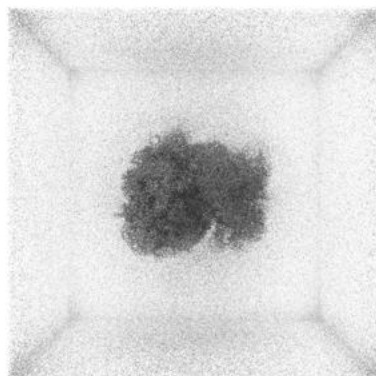
Z

The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

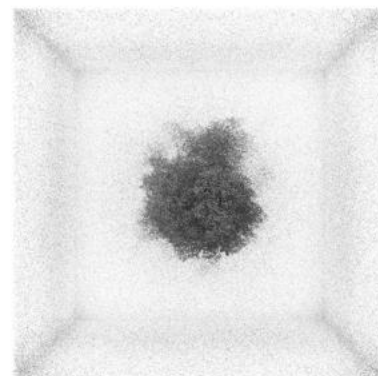
6.5.2 Raw map



X



Y



Z

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

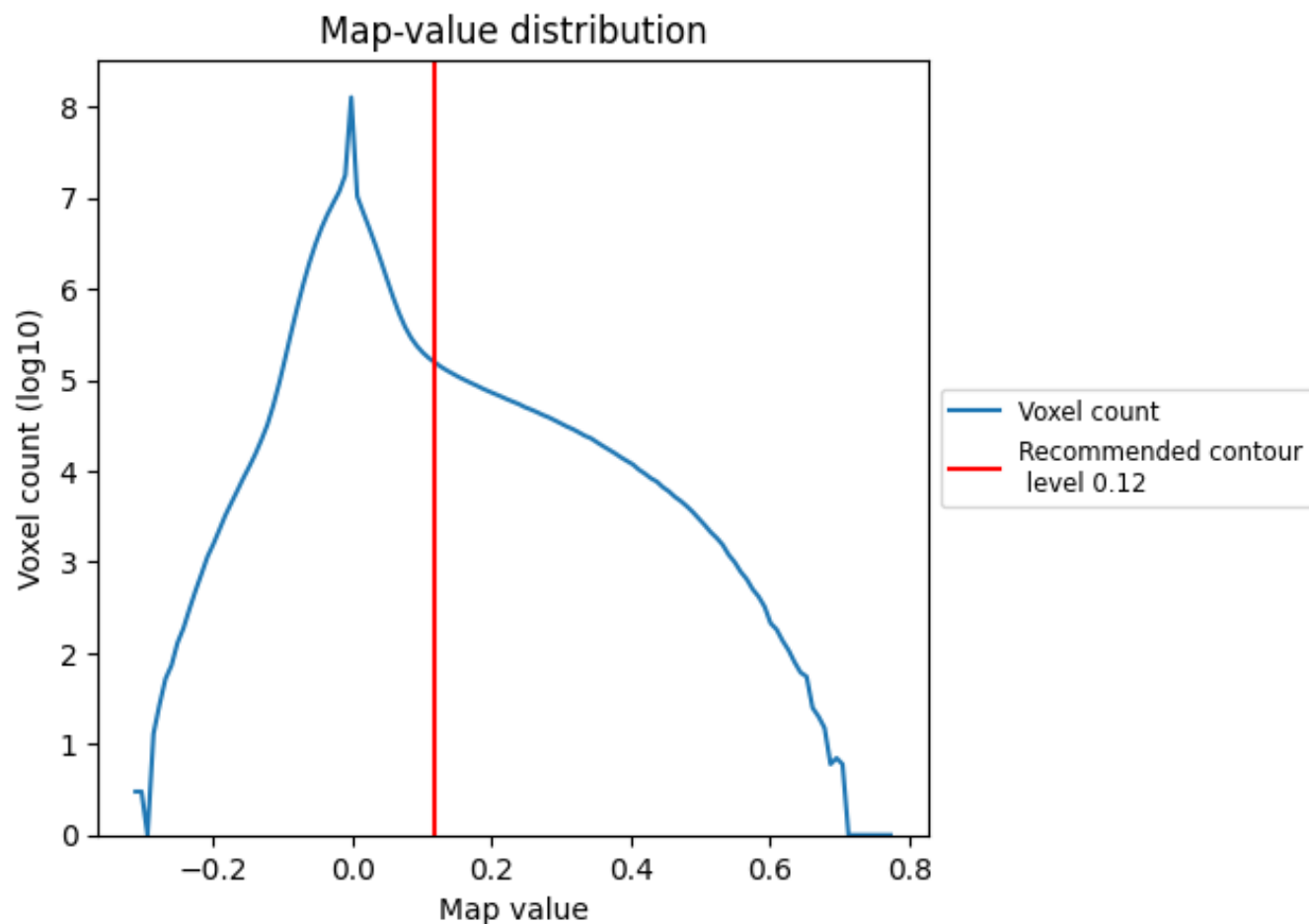
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

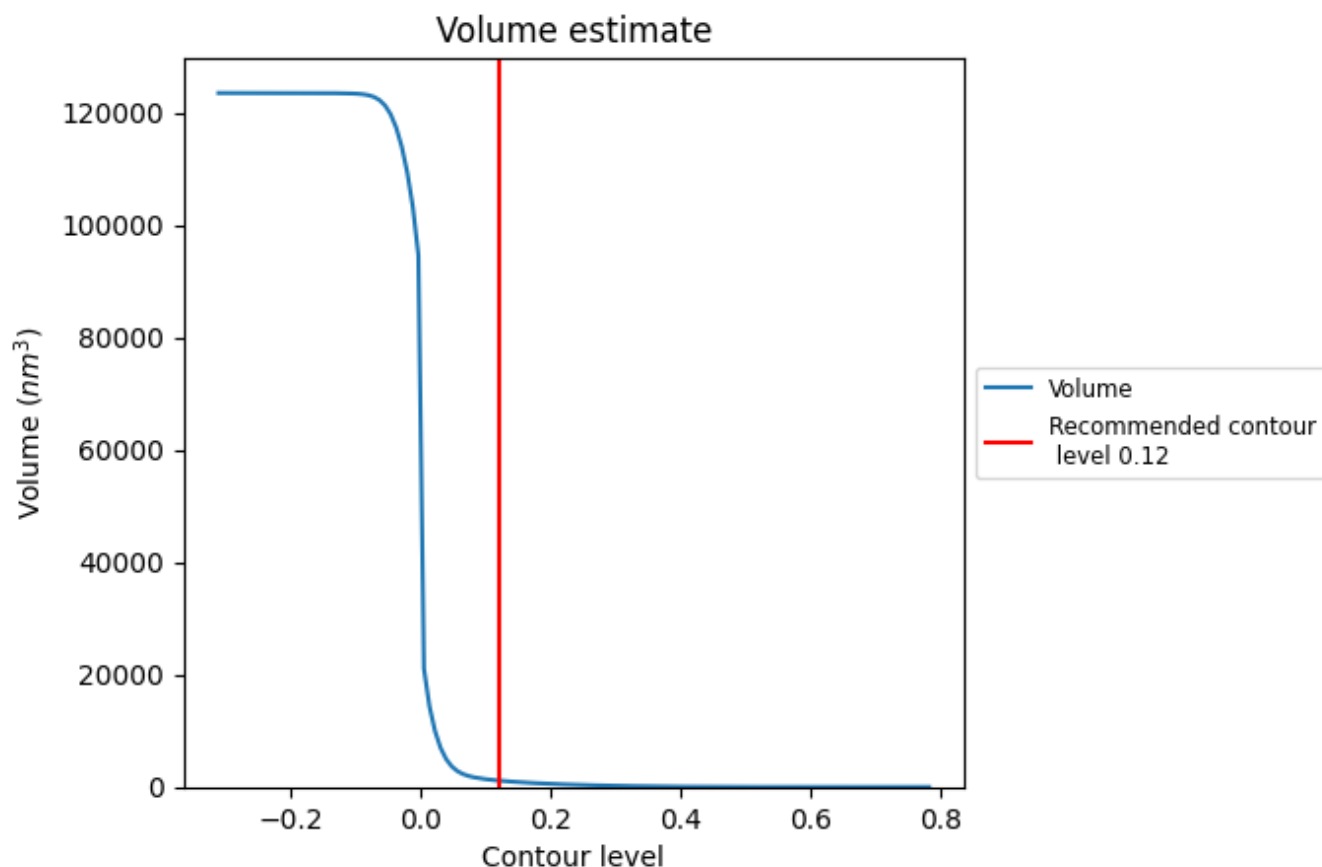
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

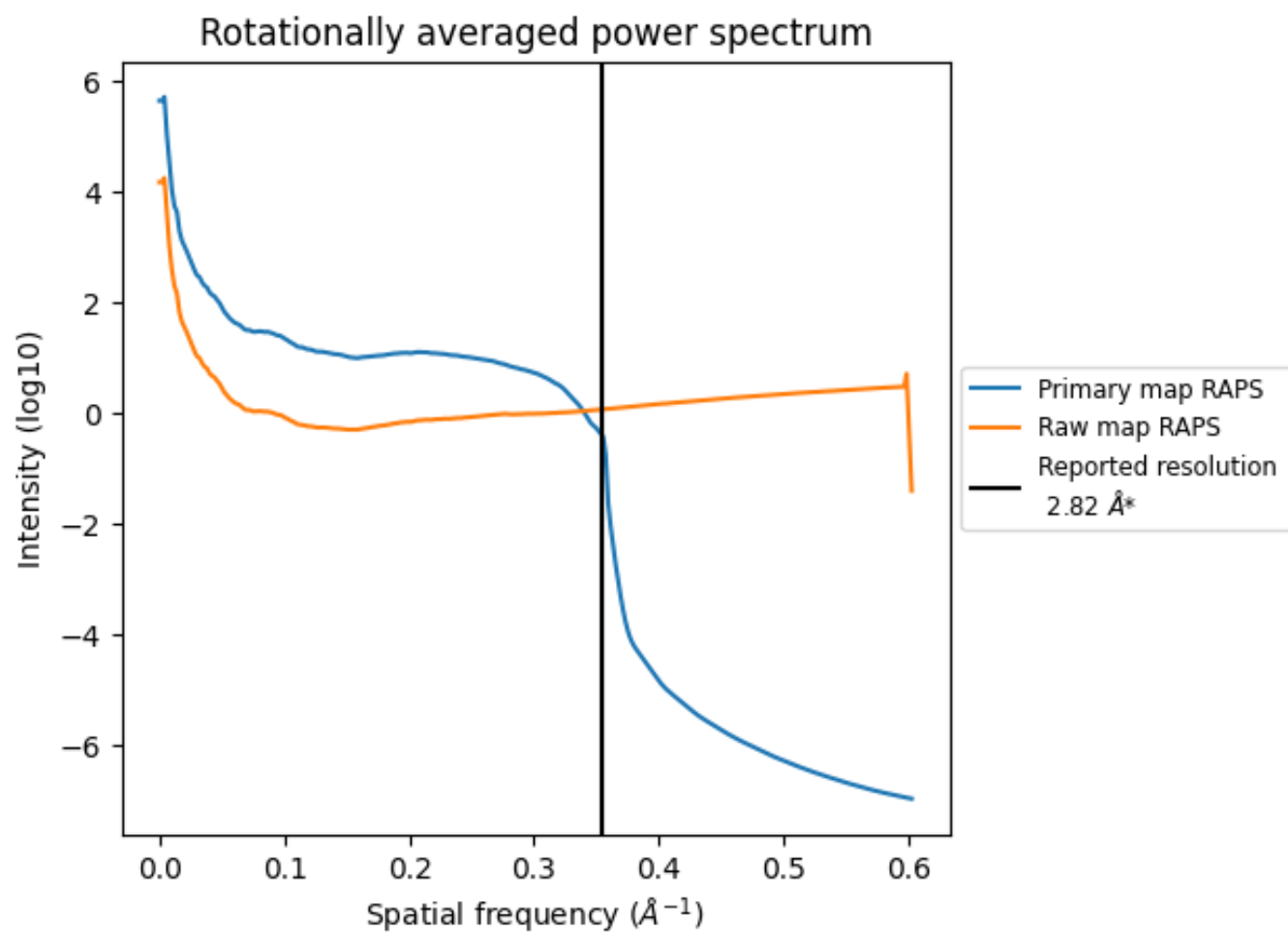
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1138 nm^3 ; this corresponds to an approximate mass of 1028 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 ⓘ

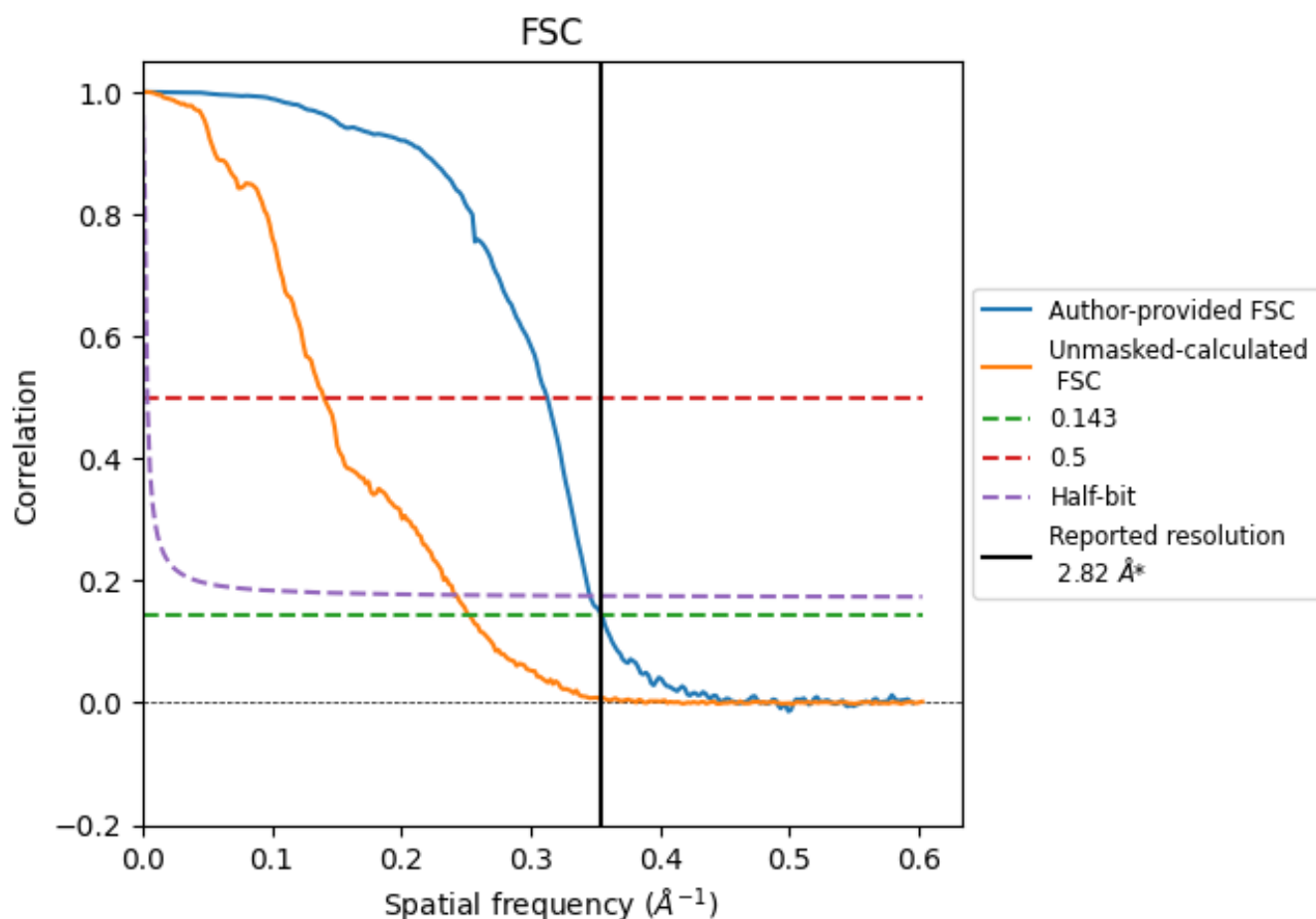


*Reported resolution corresponds to spatial frequency of 0.355 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.355 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

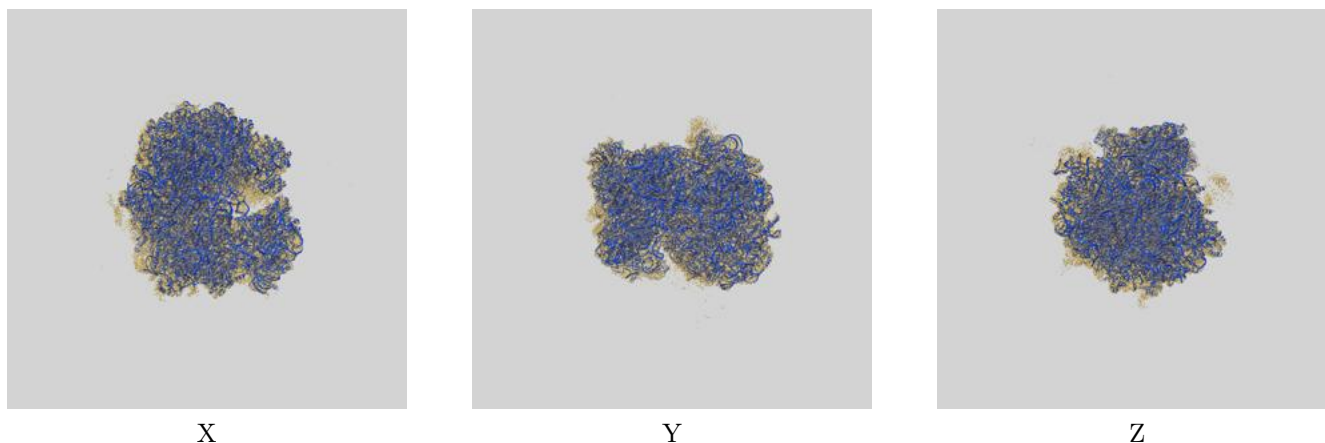
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.82	-	-
Author-provided FSC curve	2.82	3.20	2.89
Unmasked-calculated*	3.95	7.13	4.15

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.95 differs from the reported value 2.82 by more than 10 %

9 Map-model fit [i](#)

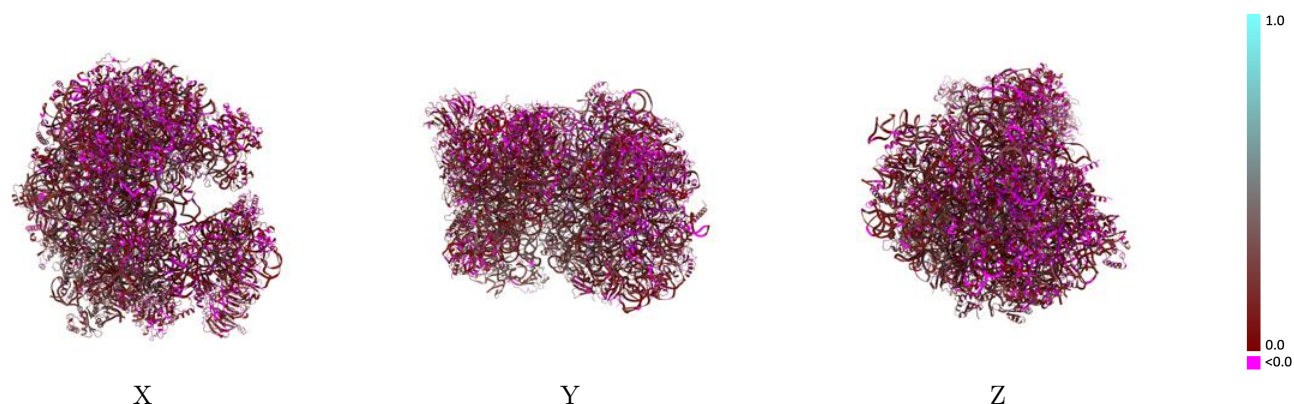
This section contains information regarding the fit between EMDB map EMD-72802 and PDB model 9YDE. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



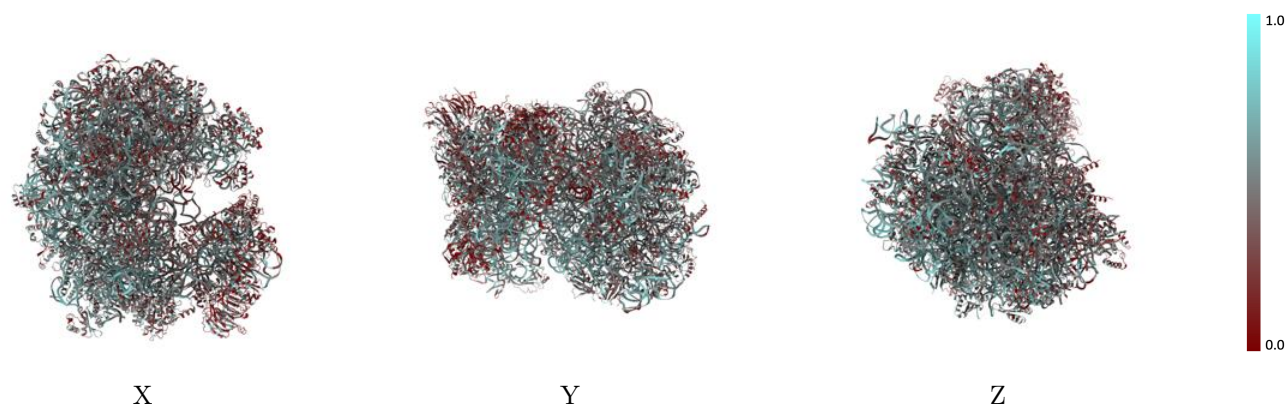
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



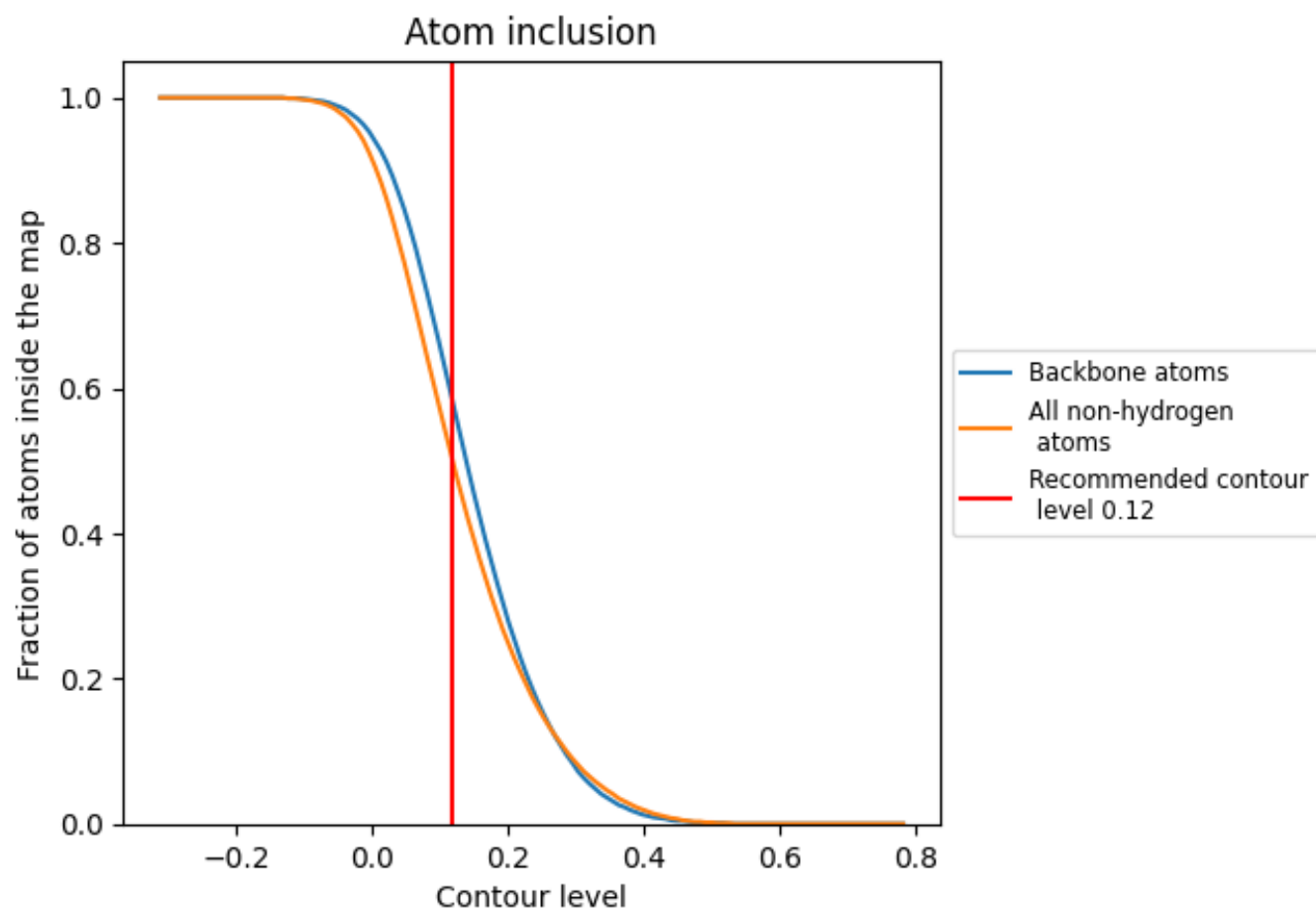
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 50% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4970	 0.1440
A	 0.5560	 0.1420
B	 0.5490	 0.0640
C	 0.5610	 0.1430
D	 0.2660	 0.0790
E	 0.5700	 0.1580
LD	 0.4400	 0.1270
LE	 0.5340	 0.2140
LF	 0.4200	 0.0860
LG	 0.3770	 0.0720
LH	 0.4430	 0.1380
LI	 0.4120	 0.0990
LJ	 0.4020	 0.1000
LK	 0.4660	 0.1680
LL	 0.3850	 0.1250
LM	 0.3700	 0.1240
LN	 0.3820	 0.0520
LO	 0.4600	 0.1290
LP	 0.3870	 0.0670
LQ	 0.4580	 0.1420
LR	 0.4750	 0.1420
LS	 0.3790	 0.0580
LT	 0.5480	 0.2420
LU	 0.4300	 0.1280
LV	 0.3720	 0.0820
LW	 0.5010	 0.2200
LX	 0.4680	 0.2190
LY	 0.5330	 0.2360
LZ	 0.4650	 0.1440
La	 0.4530	 0.1060
Lb	 0.4770	 0.1590
Lc	 0.3890	 0.0700
Ld	 0.3890	 0.1000
Le	 0.4590	 0.1510
Lf	 0.5350	 0.2230



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Chain	Atom inclusion	Q-score
Lg	 0.4020	 0.0940
Lh	 0.4400	 0.1150
Li	 0.4840	 0.1520
Lj	 0.4070	 0.0770
Lk	 0.3590	 0.0730
Ll	 0.4620	 0.1100
Lm	 0.4860	 0.2160
Ln	 0.5230	 0.1890
Lo	 0.4630	 0.1640
Lp	 0.4040	 0.1700
Lq	 0.3700	 0.0780
Lr	 0.4540	 0.1470
SA	 0.3430	 0.1290
SB	 0.3070	 0.0800
SC	 0.4210	 0.1970
SD	 0.1350	 0.1150
SE	 0.3220	 0.1430
SF	 0.3480	 0.1010
SG	 0.3610	 0.1170
SH	 0.2910	 0.0820
SI	 0.2950	 0.0670
SJ	 0.3180	 0.1200
SK	 0.2660	 0.0330
SL	 0.2760	 0.0760
SM	 0.4460	 0.1760
SN	 0.2210	 0.1400
SO	 0.2890	 0.1200
SP	 0.4130	 0.1130
SQ	 0.3400	 0.0880
SR	 0.4960	 0.2000
SS	 0.5240	 0.2760
ST	 0.4710	 0.2570
SU	 0.4900	 0.2570
SV	 0.5070	 0.2580
SW	 0.4740	 0.2130
SX	 0.5040	 0.2600
SY	 0.4940	 0.2080
SZ	 0.3760	 0.0980
Sa	 0.4660	 0.1670
Sb	 0.5020	 0.2130
Sc	 0.4530	 0.2190
Sd	 0.5040	 0.2540

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Chain	Atom inclusion	Q-score
Se	 0.4490	 0.1590
Sf	 0.4560	 0.1650
Sg	 0.3470	 0.1390
n	 0.2470	 0.0820