



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 10:16 AM UTC

PDB ID : 4D5Y / pdb_00004d5y
EMDB ID : EMD-2810
Title : Cryo-EM structures of ribosomal 80S complexes with termination factors and cricket paralysis virus IRES reveal the IRES in the translocated state
Authors : Muhs, M.; Hilal, T.; Mielke, T.; Skabkin, M.A.; Sanbonmatsu, K.Y.; Pestova, T.V.; Spahn, C.M.T.
Deposited on : 2014-11-07
Resolution : 9.00 Å (reported)
Based on initial model : 4CXD

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:

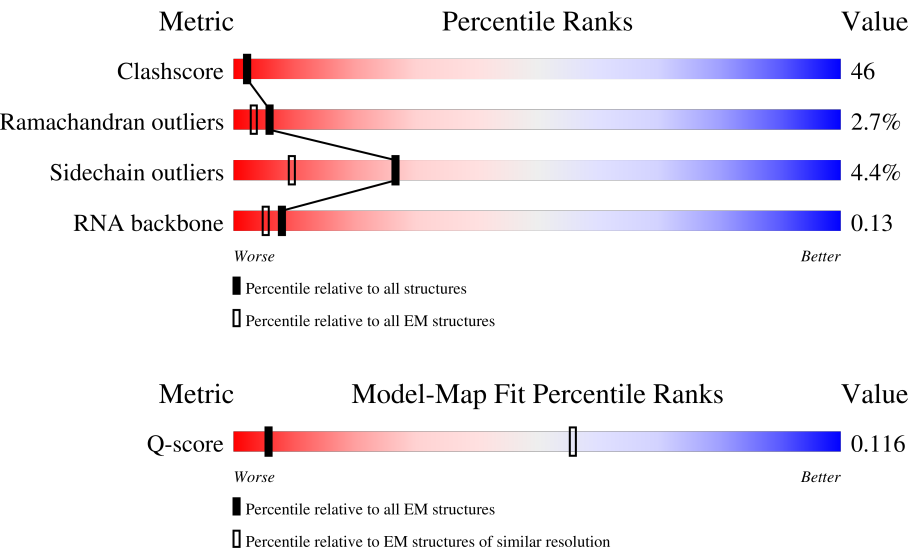
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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	282 (8.20 - 9.20)

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	257	25% 54% 40% • •
2	B	403	17% 54% 38% 5% • •
3	C	427	11% 43% 35% 6% • 15%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	297	
5	E	288	
6	F	248	
7	G	266	
8	H	192	
9	I	214	
10	J	178	
11	L	211	
12	M	215	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	159	
28	c	115	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	117	
33	h	123	
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	128	
39	n	25	
40	o	106	
41	p	92	
42	t	137	
43	u	210	
44	2	5025	
45	3	194	
46	4	119	

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 136495 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 60S RIBOSOMAL PROTEIN UL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	247	Total	C	N	O	S	0	1
			1888	1183	388	311	6		

- Molecule 2 is a protein called 60S RIBOSOMAL PROTEIN UL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	396	Total	C	N	O	S	0	1
			3190	2030	601	545	14		

- Molecule 3 is a protein called 60S RIBOSOMAL PROTEIN UL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	364	Total	C	N	O	S	0	1
			2889	1817	578	480	14		

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN UL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	290	Total	C	N	O	S	0	0
			2361	1489	431	427	14		

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN EL6.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	158	Total	C	N	O	0	0
			1286	834	238	214		

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN UL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	234	Total	C	N	O	S	0	0
			1949	1252	376	312	9		

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN EL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	235	Total	C	N	O	S	0	1
			1881	1197	363	317	4		

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN UL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	192	Total	C	N	O	S	0	0
			1535	965	286	278	6		

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN UL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	196	Total	C	N	O	S	0	0
			1604	1022	308	262	12		

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN UL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN EL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	200	Total	C	N	O	S	0	1
			1617	1013	335	265	4		

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN EL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	140	Total	C	N	O	S	0	1
			1139	730	219	183	7		

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN EL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	204	Total	C	N	O	S	0	0
			1708	1077	360	266	5		

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN UL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	196	Total	C	N	O	S	0	1
			1607	1034	316	252	5		

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN UL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	1
			1234	771	241	213	9		

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN EL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	184	Total	C	N	O	S	0	0
			1493	933	311	244	5		

- Molecule 17 is a protein called 60S RIBOSOMAL PROTEIN UL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	183	Total	C	N	O	S	0	1
			1526	943	331	242	10		

- Molecule 18 is a protein called 60S RIBOSOMAL PROTEIN EL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	173	Total	C	N	O	S	0	0
			1438	916	280	232	10		

- Molecule 19 is a protein called 60S RIBOSOMAL PROTEIN EL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1297	823	252	216	6		

- Molecule 20 is a protein called 60S RIBOSOMAL PROTEIN EL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	102	Total	C	N	O	S	0	1
			827	529	146	150	2		

- Molecule 21 is a protein called 60S RIBOSOMAL PROTEIN UL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	128	Total	C	N	O	S	0	0
			963	610	181	167	5		

- Molecule 22 is a protein called 60S RIBOSOMAL PROTEIN EL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	64	Total	C	N	O	S	0	1
			529	337	104	85	3		

- Molecule 23 is a protein called 60S RIBOSOMAL PROTEIN UL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	119	Total	C	N	O	S	0	0
			975	624	183	167	1		

- Molecule 24 is a protein called 60S RIBOSOMAL PROTEIN UL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	128	Total	C	N	O	S	0	1
			1065	668	217	177	3		

- Molecule 25 is a protein called 60S RIBOSOMAL PROTEIN EL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	136	Total	C	N	O	S	0	0
			1114	719	209	182	4		

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN UL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1161	736	237	185	3		

- Molecule 27 is a protein called 60S RIBOSOMAL PROTEIN EL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	69	Total	C	N	O	S	0	1
			560	344	123	90	3		

- Molecule 28 is a protein called 60S RIBOSOMAL PROTEIN EL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	104	Total	C	N	O	S	0	1
			802	508	142	145	7		

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN EL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	109	Total	C	N	O	S	0	0
			904	570	174	158	2		

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN EL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	1
			1053	664	219	165	5		

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN EL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	107	Total	C	N	O	S	0	0
			865	550	172	140	3		

- Molecule 32 is a protein called 60S RIBOSOMAL PROTEIN EL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	115	Total	C	N	O	S	0	1
			907	566	188	147	6		

- Molecule 33 is a protein called 60S RIBOSOMAL PROTEIN UL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1014	641	205	167	1		

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN EL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	97	Total	C	N	O	S	0	1
			783	488	168	122	5		

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN EL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	85	Total	C	N	O	S	0	1
			690	423	153	109	5		

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN EL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			568	366	103	98	1		

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN EL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			443	281	98	63	1		

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN EL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			428	266	90	66	6		

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN EL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN EL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	106	Total	C	N	O	S	0	0
			870	547	176	140	7		

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN EL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			707	445	136	119	7		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN EL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	t	130	Total	C	N	O	S	0	1
			1043	646	220	172	5		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN UL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	u	210	Total	C	N	O	S	0	0
			1621	990	278	347	6		

- Molecule 44 is a RNA chain called 28S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2	3616	Total	C	N	O	P	0	0
			77488	34508	14153	25212	3615		

- Molecule 45 is a RNA chain called 5.8S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	3	157	Total	C	N	O	P	0	0
			3334	1489	587	1102	156		

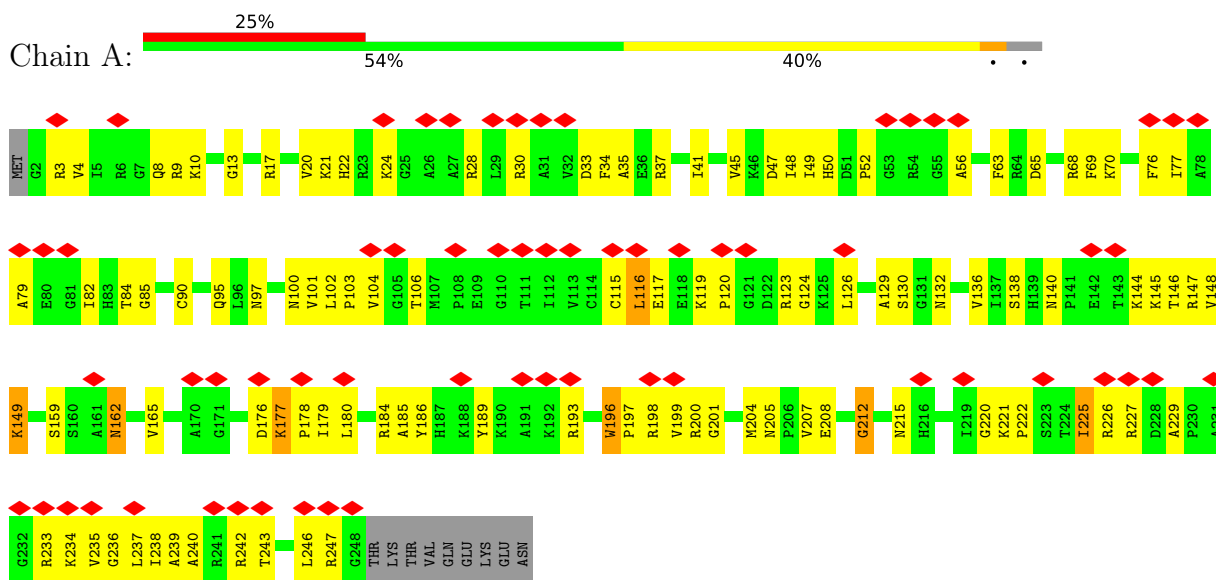
- Molecule 46 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	4	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

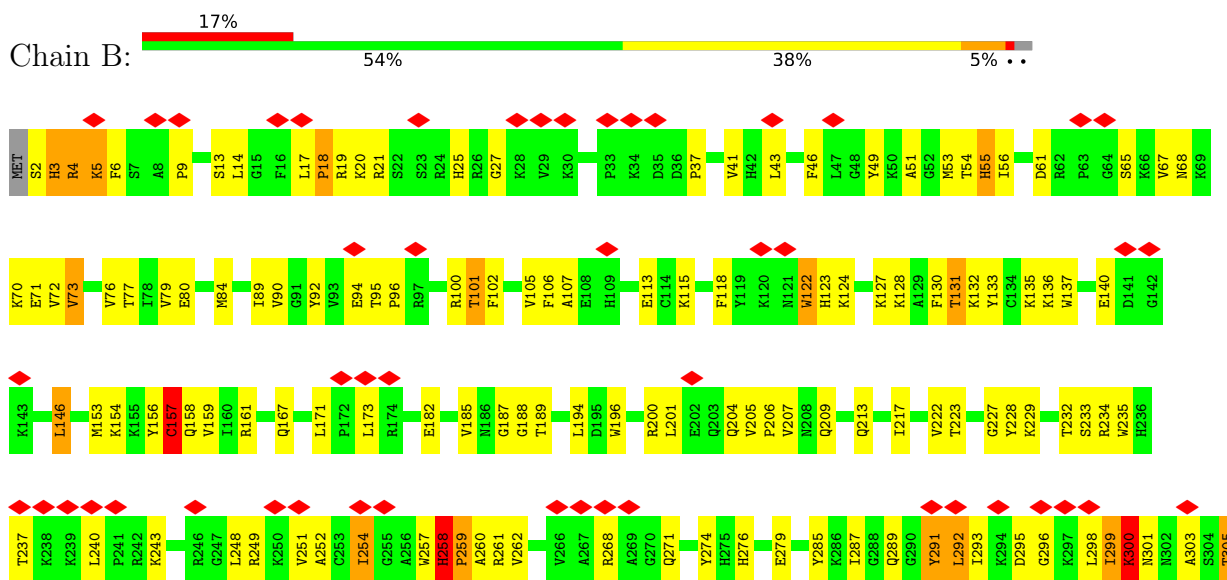
3 Residue-property plots

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.

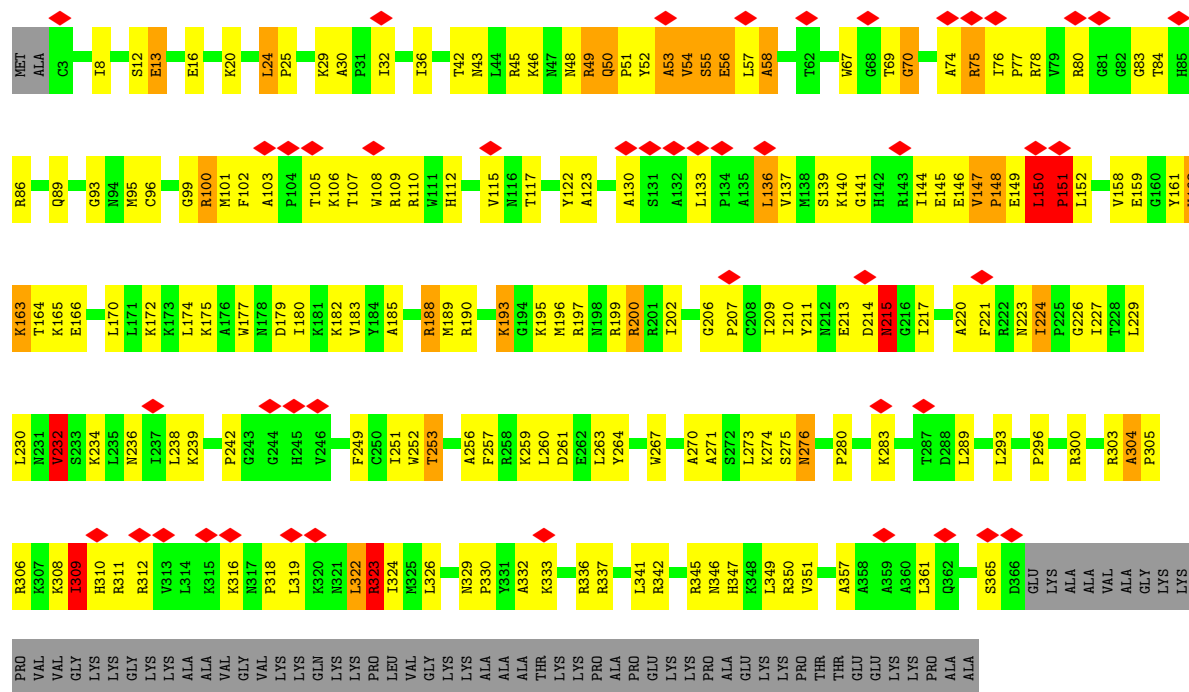
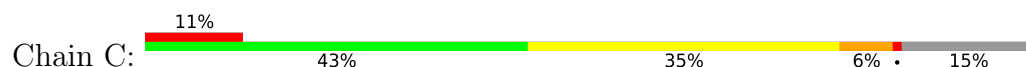
• Molecule 1: 60S RIBOSOMAL PROTEIN UL2



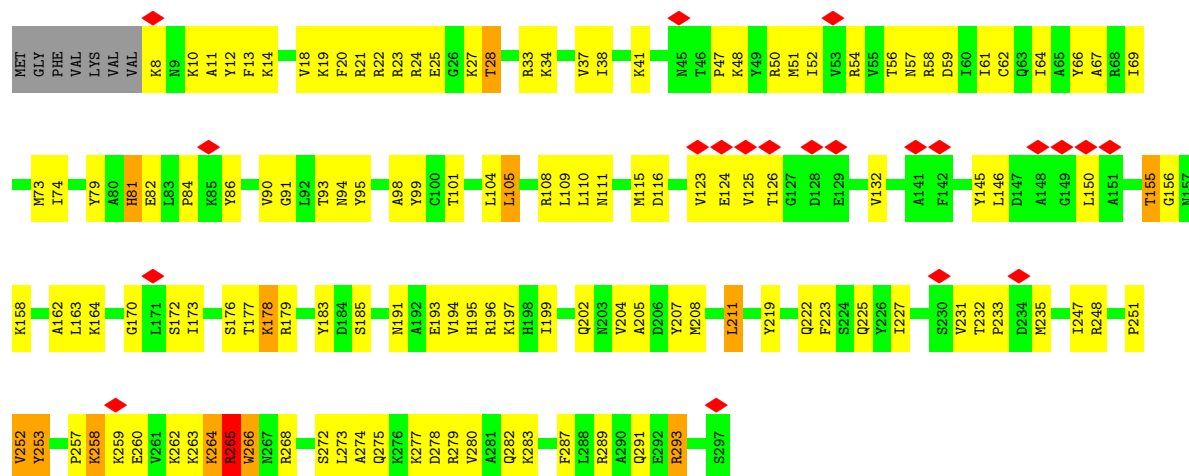
• Molecule 2: 60S RIBOSOMAL PROTEIN UL3



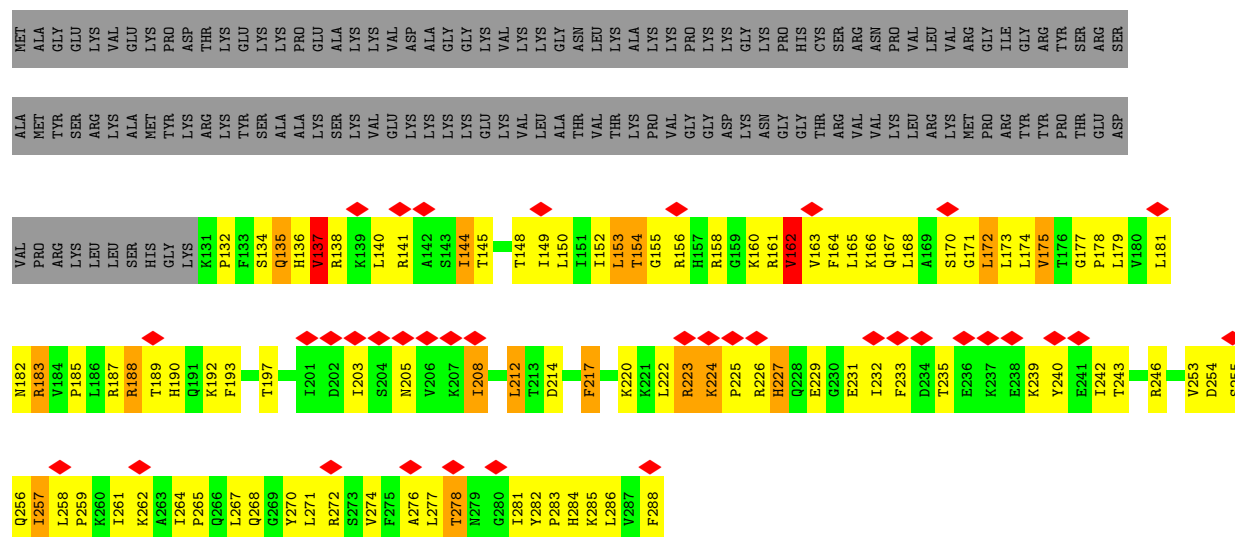
- Molecule 3: 60S RIBOSOMAL PROTEIN UL4



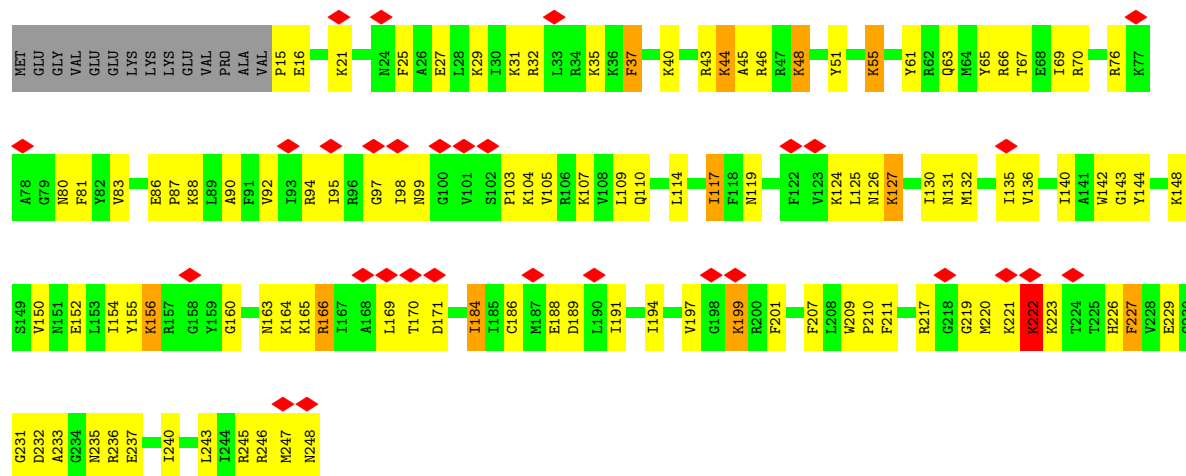
- Molecule 4: 60S RIBOSOMAL PROTEIN UL18



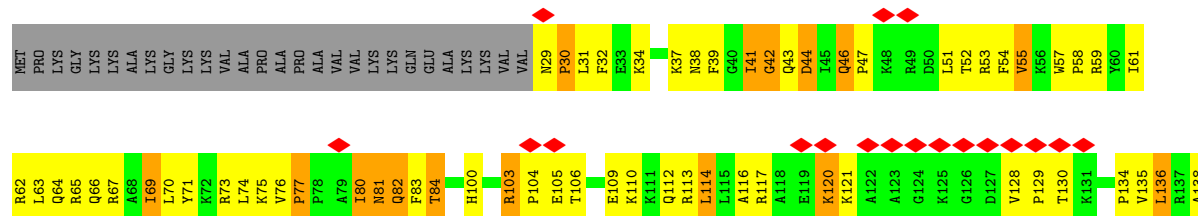
Chain E: 13% 21% 28% 6% 45%

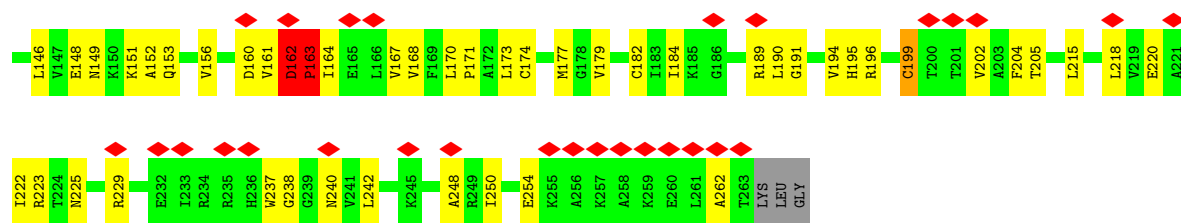


Chain F: 12% 50% 39% 6%

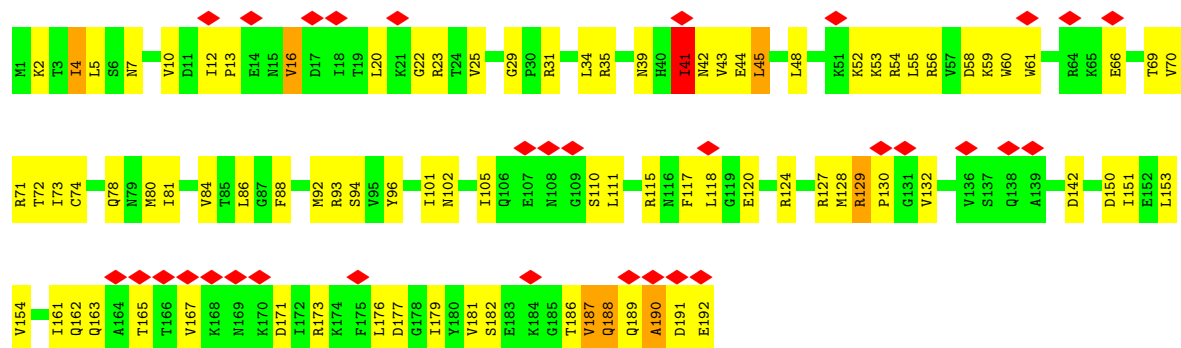


Chain G:

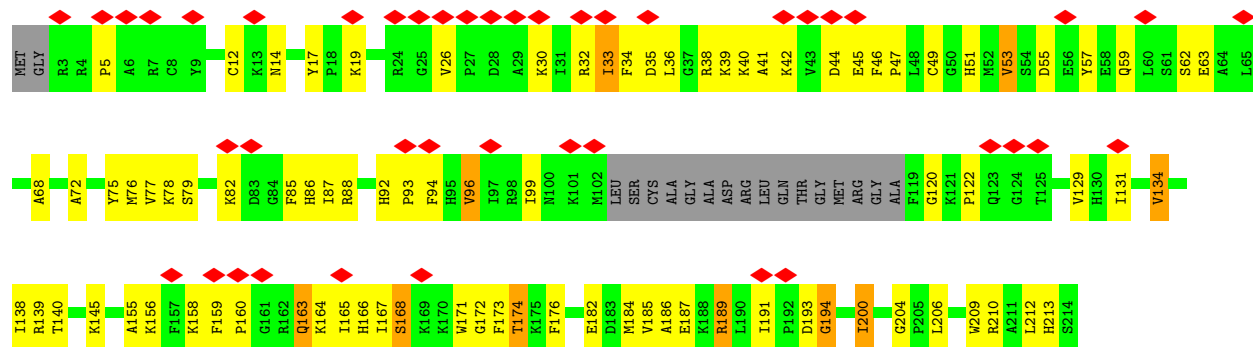




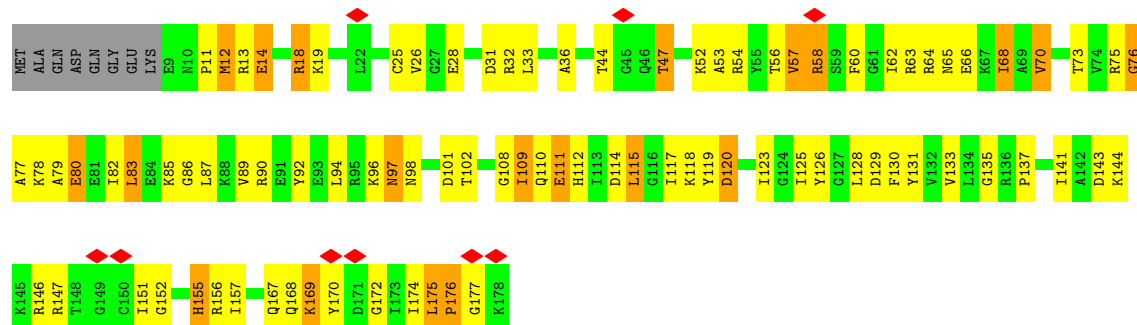
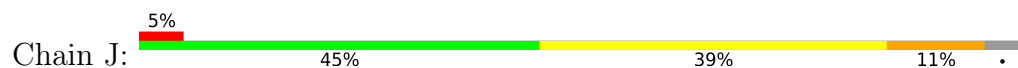
• Molecule 8: 60S RIBOSOMAL PROTEIN UL6



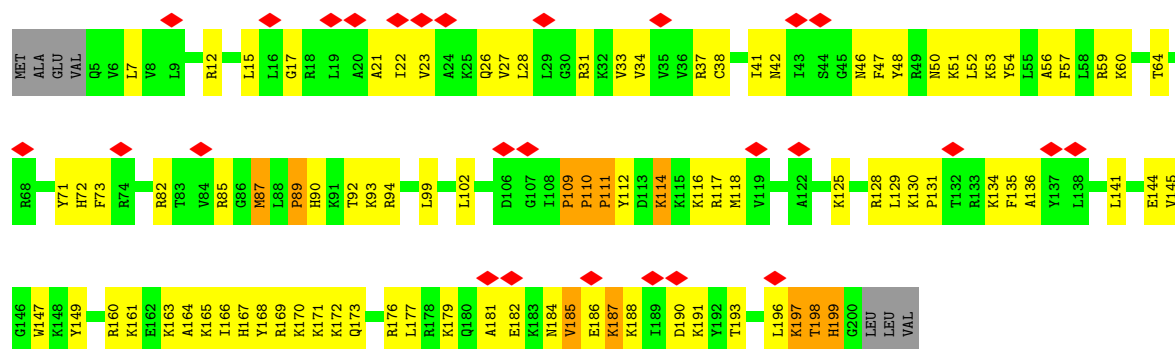
• Molecule 9: 60S RIBOSOMAL PROTEIN UL16



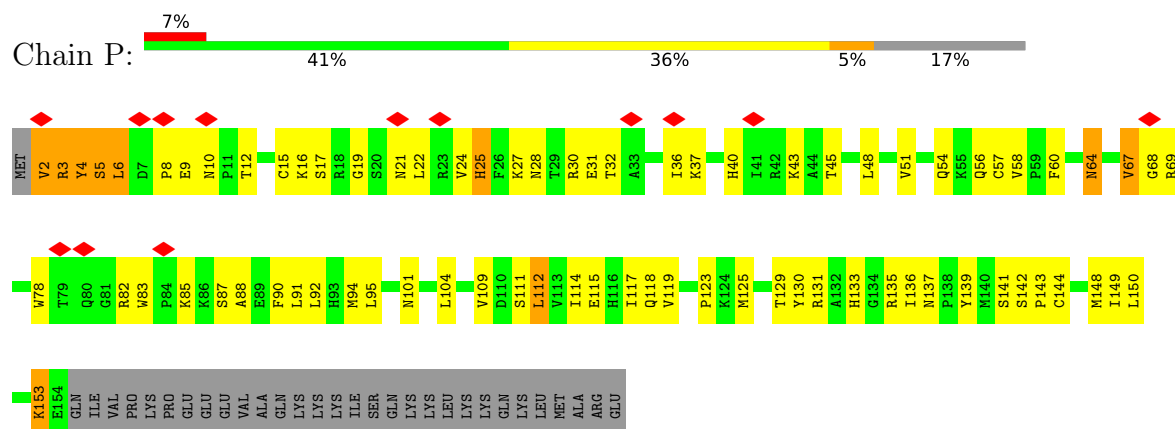
• Molecule 10: 60S RIBOSOMAL PROTEIN UL5



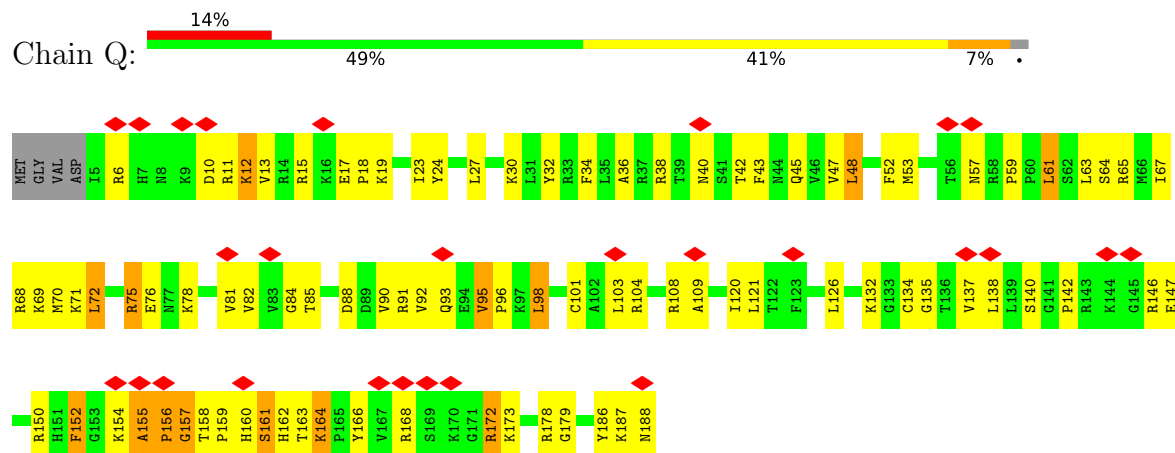




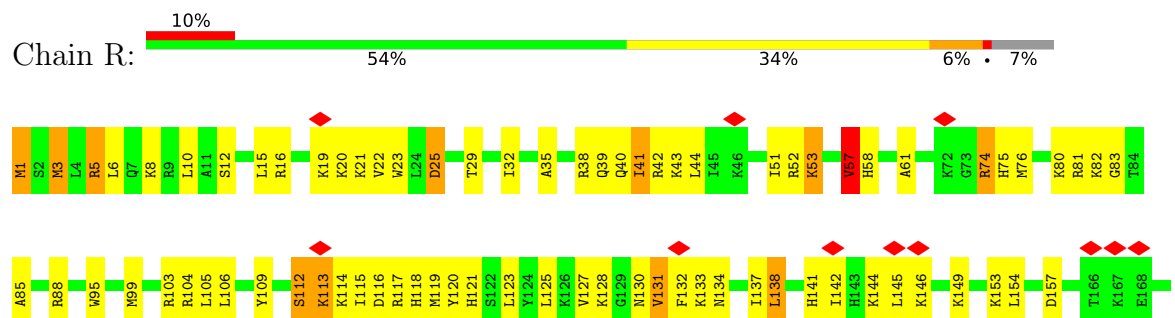
• Molecule 15: 60S RIBOSOMAL PROTEIN UL22

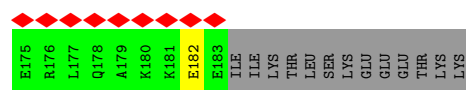


• Molecule 16: 60S RIBOSOMAL PROTEIN EL18

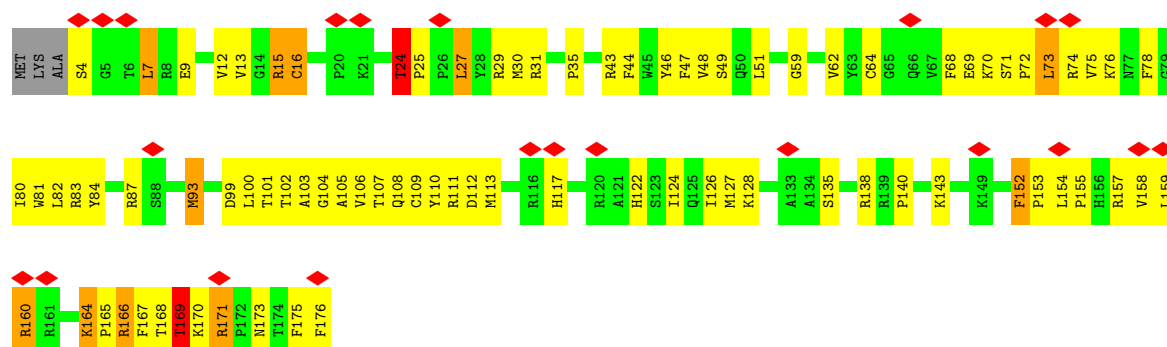


• Molecule 17: 60S RIBOSOMAL PROTEIN UL19

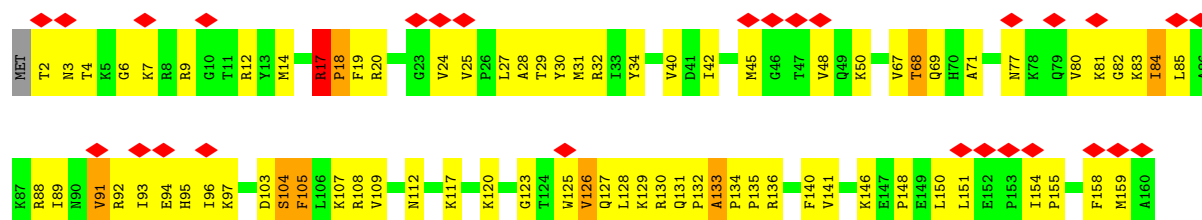




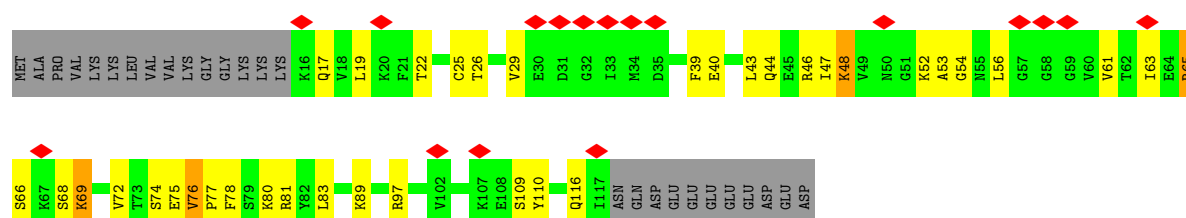
• Molecule 18: 60S RIBOSOMAL PROTEIN EL20



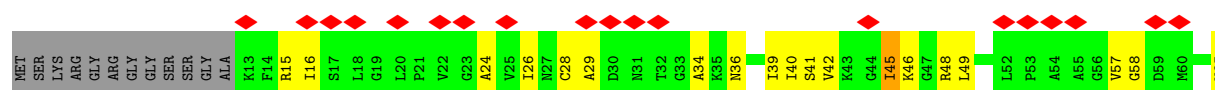
• Molecule 19: 60S RIBOSOMAL PROTEIN EL21



• Molecule 20: 60S RIBOSOMAL PROTEIN EL22



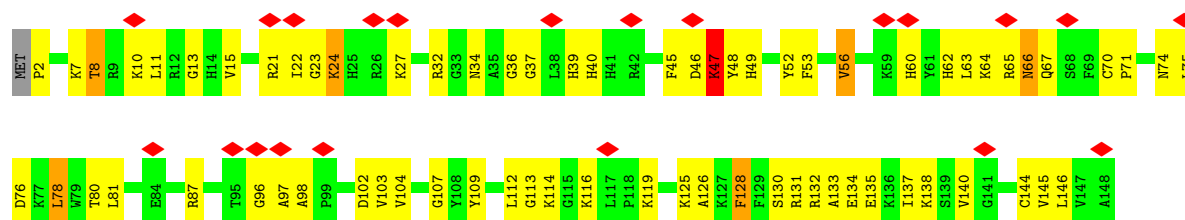
• Molecule 21: 60S RIBOSOMAL PROTEIN UL14



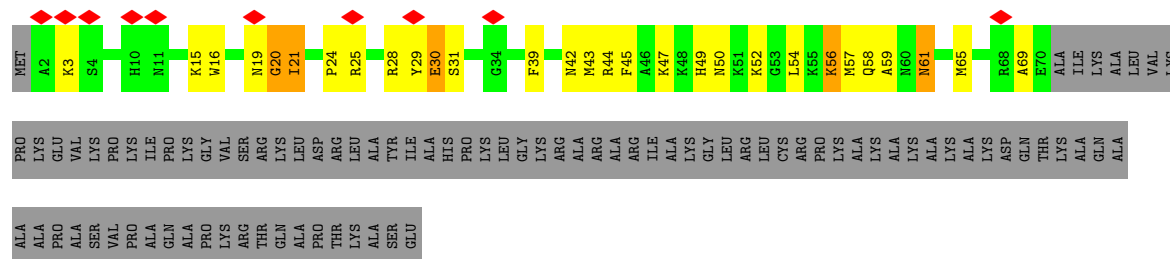




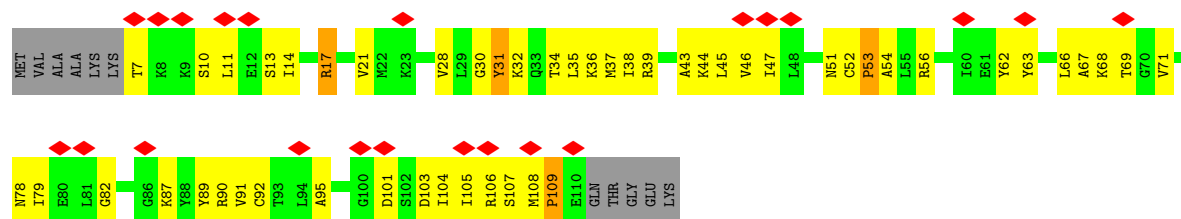
• Molecule 26: 60S RIBOSOMAL PROTEIN UL15



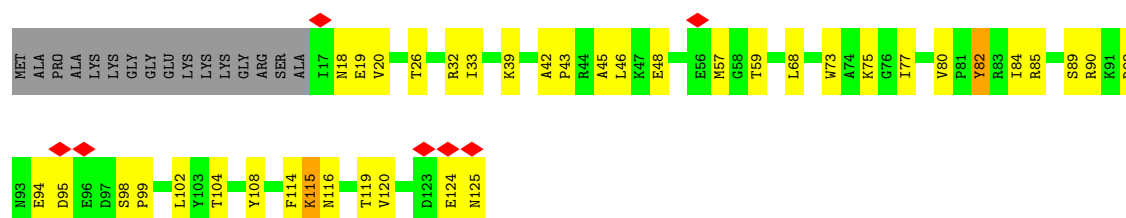
• Molecule 27: 60S RIBOSOMAL PROTEIN EL29



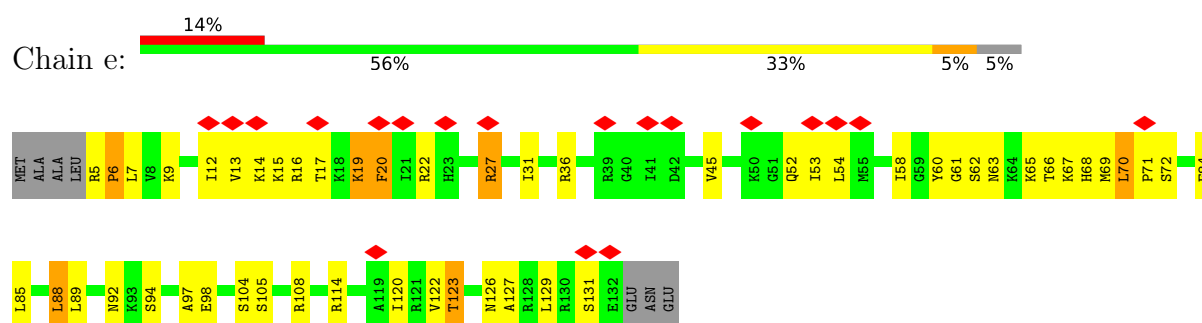
• Molecule 28: 60S RIBOSOMAL PROTEIN EL30



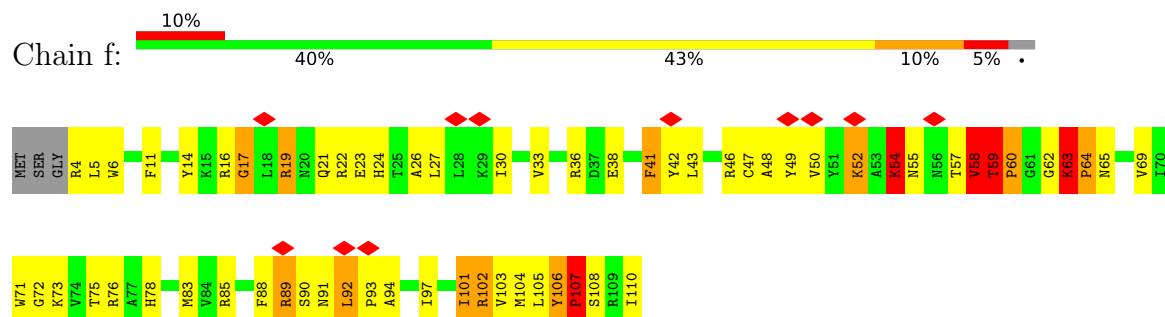
• Molecule 29: 60S RIBOSOMAL PROTEIN EL31



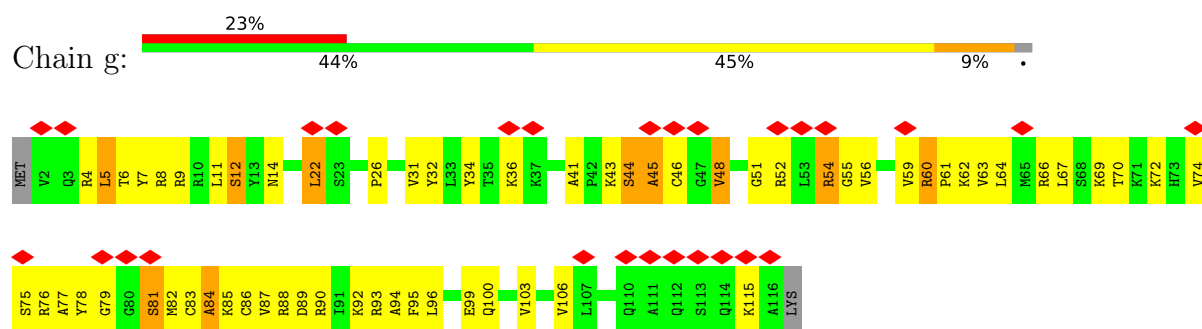
• Molecule 30: 60S RIBOSOMAL PROTEIN EL32



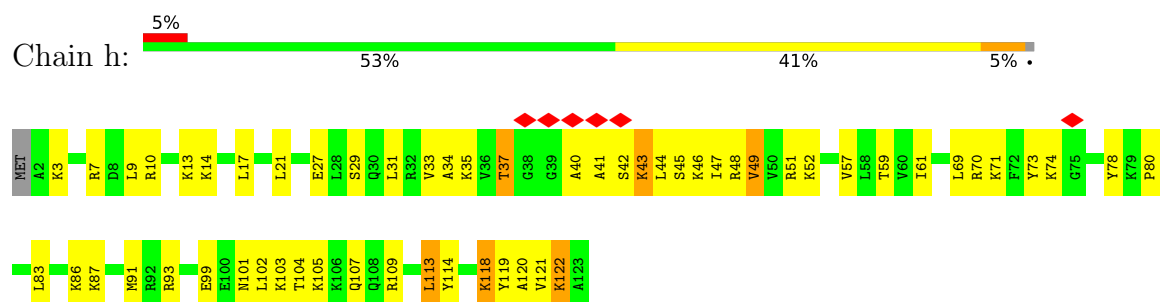
• Molecule 31: 60S RIBOSOMAL PROTEIN EL33



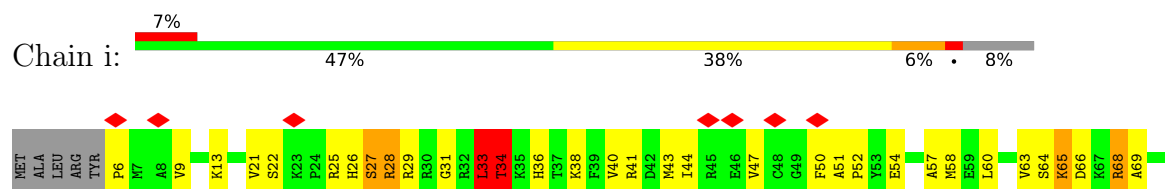
• Molecule 32: 60S RIBOSOMAL PROTEIN EL34



• Molecule 33: 60S RIBOSOMAL PROTEIN UL29

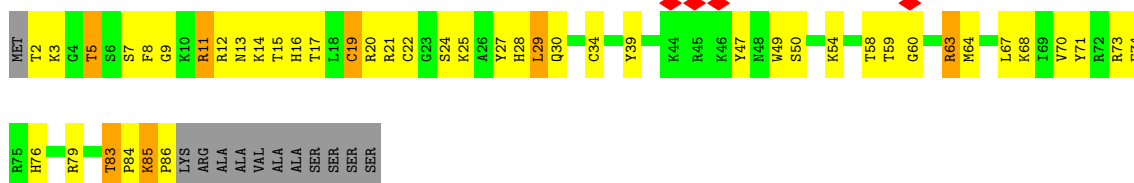


• Molecule 34: 60S RIBOSOMAL PROTEIN EL36





• Molecule 35: 60S RIBOSOMAL PROTEIN EL37



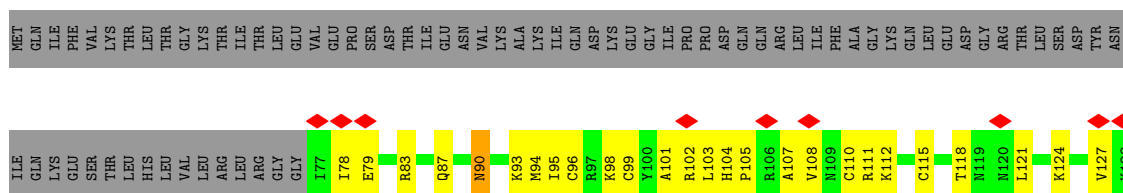
• Molecule 36: 60S RIBOSOMAL PROTEIN EL38



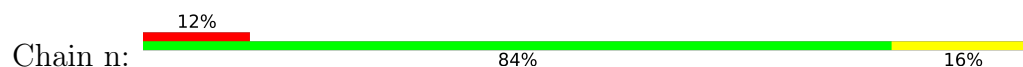
• Molecule 37: 60S RIBOSOMAL PROTEIN EL39



• Molecule 38: 60S RIBOSOMAL PROTEIN EL40

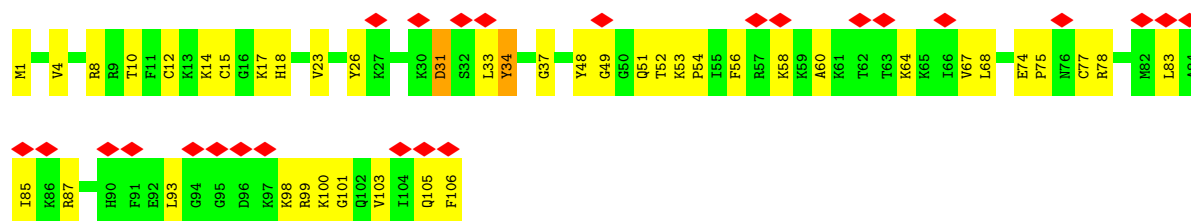


• Molecule 39: 60S RIBOSOMAL PROTEIN EL41

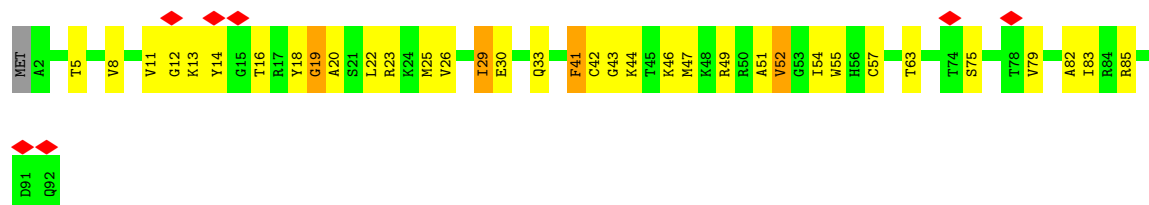


• Molecule 40: 60S RIBOSOMAL PROTEIN EL44

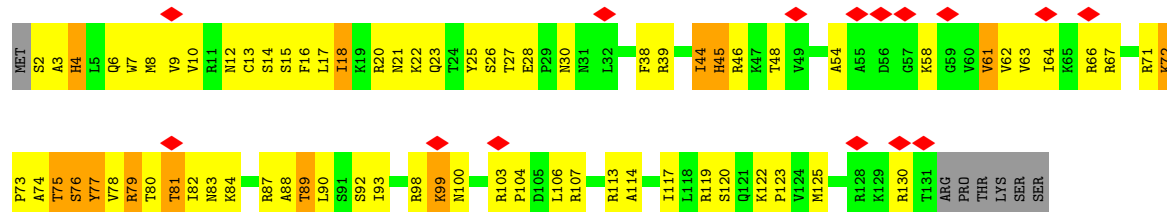
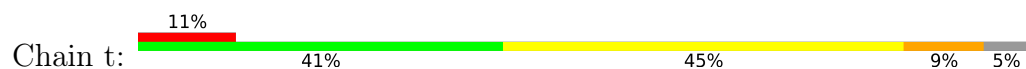




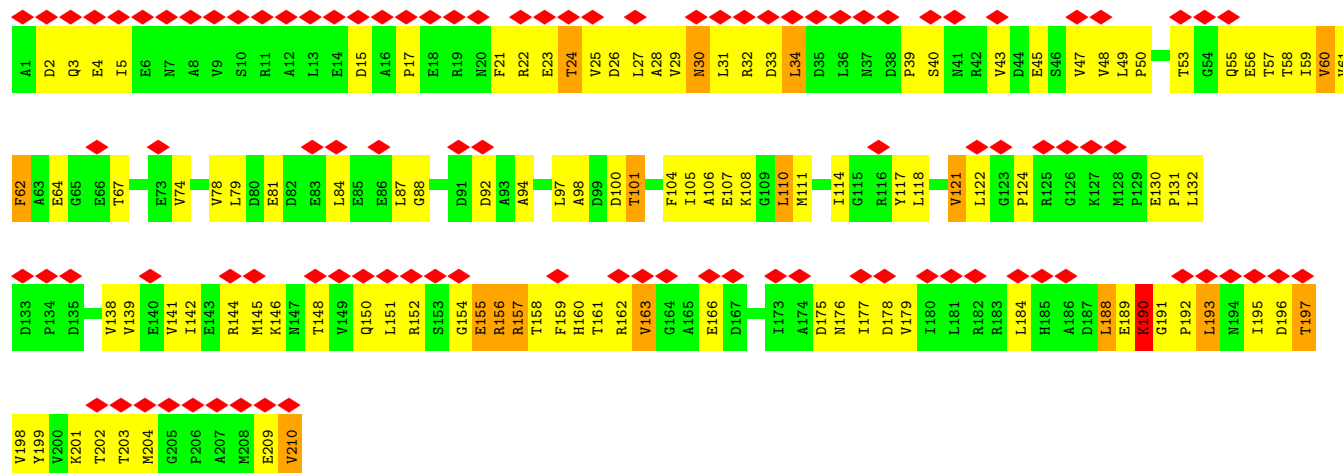
• Molecule 41: 60S RIBOSOMAL PROTEIN EL43



• Molecule 42: 60S RIBOSOMAL PROTEIN EL28



• Molecule 43: 60S RIBOSOMAL PROTEIN UL1



• Molecule 44: 28S Ribosomal RNA



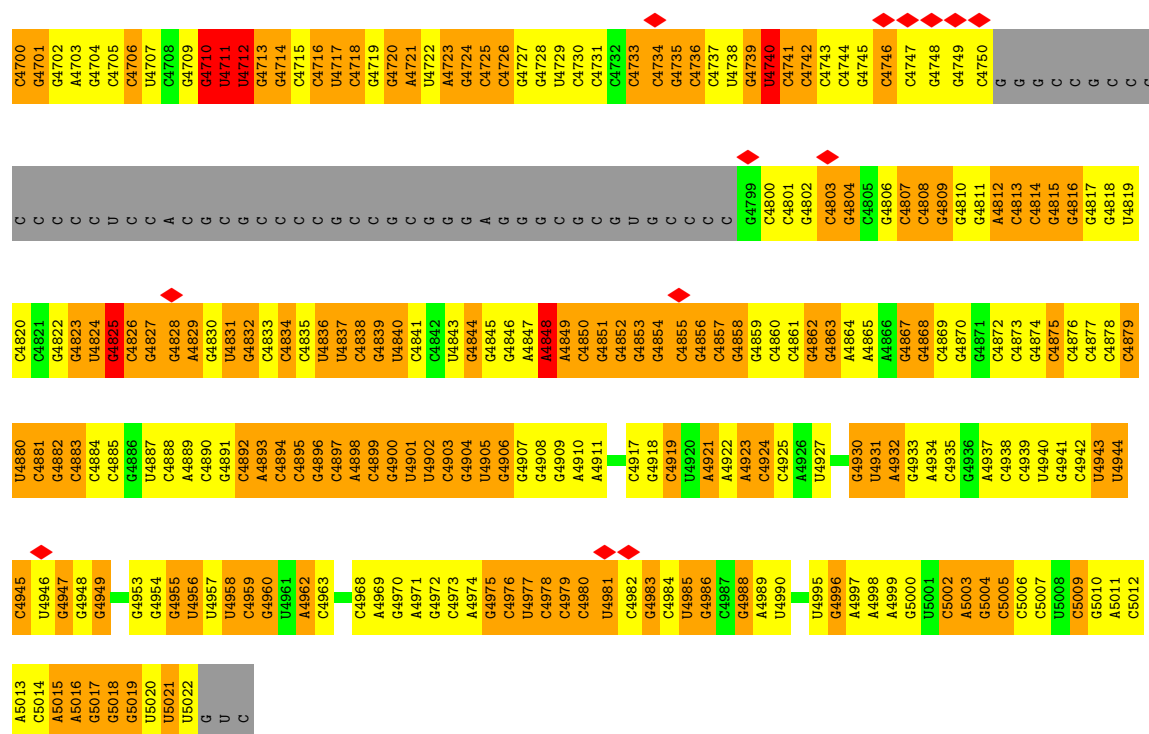




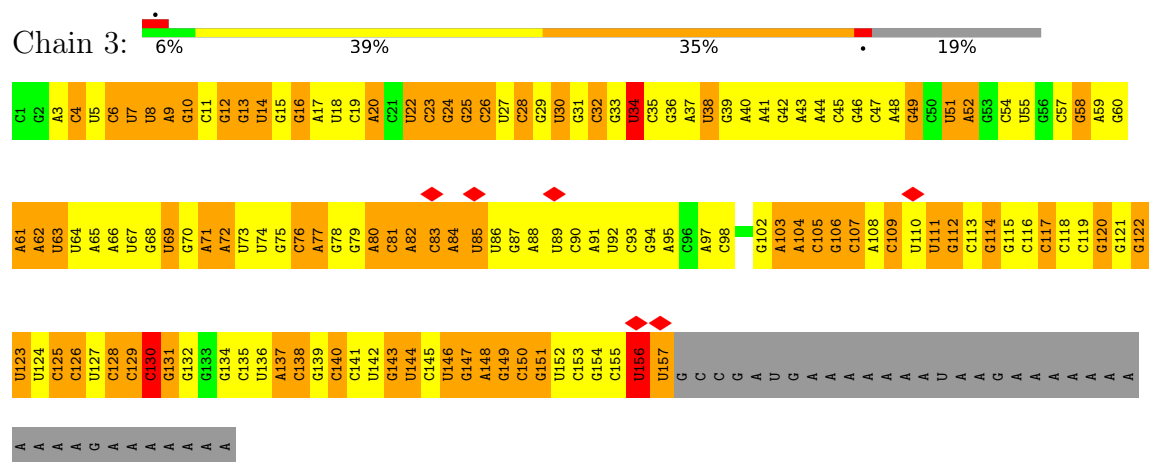
U2746	U2685	C2562	U2502	A2378	G2316	A2255	C2015	C1893
C2747	C2686	G2563	C2503	G2379	G2319	G2256	U2016	G1894
G2748	A2564	A2564	C2504	A2380	G2320	U2257	G2017	U1895
C2749	G2687	C2565	A2504	A2381	G2321	C2258	A2018	C1896
G2689	C2566	C2505	A2506	G2382	U2322	G2259	G2019	G1897
C2750	G2687	A2506	U2507	G2383	C2323	G2260	A2020	C1898
C2690	A2568	U2507	C2508	G2384	G2324	A2261	G2021	G1899
C2691	C2630	C2508	C2509	U2385	A2325	G2262	U2022	G1900
G2692	C2631	U2509	C2510	U2386	G2326	G2263	G2023	A1901
C2693	C2632	C2570	C2511	C2387	A2326	C2264	G2024	C1902
G2694	U2633	C2571	G2512	C2388	U2327	C2265	A2025	G1903
G2695	U2634	C2572	G2513	A2389	G2328	G2266	U2026	C1904
C2696	G2635	G2573	A2514	U2390	C2267	C2267	G2027	U1905
C2697	A2636	C2574	C2514	G2391	C2268	G2268	G2028	C1906
G2698	A2637	A2575	C2515	U2392	U2269	U2269	G2029	A1907
G2699	U2638	G2576	C2516	U2393	C2270	G2270	C2030	U1908
U2700	G2639	A2577	G2517	A2394	C2271	C2271	C2031	C1909
C2701	G2640	A2578	C2518	A2395	G2272	C2272	U2032	A1910
C2702	G2641	C2579	G2519	C2396	G2273	C2273	C2033	G1911
G2703	U2642	C2580	A2520	A2397	U2274	U2274	G2034	A1912
A2704	U2643	C2581	U2521	G2398	G2275	C2275	A2035	C1913
U2705	G2644	G2582	G2522	A2400	A2276	A2276	G2036	G1914
C2706	G2645	C2583	G2523	G2401	G2277	C2277	C2037	C1915
U2707	C2646	G2584	G2524	U2402	C2278	C2278	U2038	C1916
C2708	G2647	G2586	C2525	U2403	C2279	C2279	G2039	A1917
G2709	A2648	A2587	C2526	U2404	U2280	U2280	C2040	G1918
C2710	G2649	A2588	G2527	A2405	U2281	U2281	G2041	C1919
U2711	G2650	C2589	A2528	A2406	A2282	A2282	G2042	A1920
G2712	A2651	C2590	G2529	C2407	A2283	C2283	G2043	G1921
C2715	G2652	C2591	G2530	U2408	U2284	C2284	C2044	A1922
C2716	A2653	C2592	A2531	U2409	G2285	G2285	C2045	G1923
U2717	G2654	C2593	U2532	G2410	C2286	C2286	C2046	U1924
U2718	A2655	G2594	G2533	U2411	U2287	U2287	A2047	G1925
G2719	G2656	C2595	G2534	G2412	U2288	U2288	U2048	C1926
C2720	G2657	G2596	G2535	U2413	A2289	A2289	A2049	U1927
A2721	G2658	G2597	G2536	G2414	A2290	C2290	C2050	U1928
C2722	G2659	A2598	C2537	C2415	A2291	G2291	C2051	G1929
A2723	G2660	G2599	C2538	A2416	C2292	C2292	C2052	G1930
G2724	C2661	A2600	G2539	G2417	C2293	C2293	G2053	U1931
C2725	G2662	U2601	C2540	U2418	A2294	C2294	C2054	U1932
G2726	U2663	G2602	G2541	C2419	C2295	C2295	C2055	G1933
C2727	U2664	U2603	G2542	G2420	G2296	G2296	C2056	A1934
A2728	G2665	C2604	A2543	U2421	C2297	C2297	G2057	U1935
G2729	C2666	U2605	U2544	C2422	U2298	U2298	C1997	A1936
U2730	U2667	C2606	G2544	C2423	C2301	C2301	C2000	G1939
C2731	G2668	U2607	C2545	U2424	G2302	G2302	C2001	A1940
A2732	U2669	U2608	G2546	G2425	G2303	G2303	G2002	G1941
G2733	C2671	U2610	U2547	A2426	U2304	U2304	A2003	A1942
A2734	G2672	C2611	C2548	G2427	U2305	U2305	A2004	G1943
G2735	U2673	U2612	C2549	A2428	G2306	G2306	U2005	C1944
C2736	G2674	U2613	A2550	G2429	C2307	C2307	A2006	A1945
U2737	U2614	U2615	G2551	A2430	A2308	A2308	C2007	G
U2738	G2675	G2616	U2552	U2431	G2309	G2309	A2008	A
G2739	U2676	U2617	G2553	G2432	G2310	G2310	U2009	C
U2740	A2677	C2617	C2554	A2433	G2311	G2311	A2010	C
G2741	U2678	G2618	G2555	G2434	C2312	C2312	A2011	A
A2742	C2681	A2619	G2556	G2435	A2252	A2252	G2012	C
U2743	G2682	G2620	G2557	U2436	C2253	C2253	G2013	G
U2744	U2684	G2621	A2558	C2437	G2254	G2254	U2014	U
C2745			C2559				C2014	G
			C2560					
			C2561					







• Molecule 45: 5.8S Ribosomal RNA



• Molecule 46: 5S Ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	109596	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUPS	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	12.036	Depositor
Minimum map value	-3.841	Depositor
Average map value	0.203	Depositor
Map value standard deviation	0.880	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	467.99997, 467.99997, 467.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.56, 1.56, 1.56	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	A	0.68	1/1926 (0.1%)	1.09	3/2583 (0.1%)
2	B	0.72	2/3258 (0.1%)	1.12	10/4361 (0.2%)
3	C	0.76	1/2943 (0.0%)	1.16	16/3953 (0.4%)
4	D	0.78	6/2406 (0.2%)	1.12	12/3221 (0.4%)
5	E	0.82	1/1311 (0.1%)	1.17	8/1763 (0.5%)
6	F	0.68	0/1985	1.12	10/2644 (0.4%)
7	G	0.75	1/1914 (0.1%)	1.20	14/2578 (0.5%)
8	H	0.64	0/1554	1.10	4/2089 (0.2%)
9	I	0.68	0/1642	1.15	13/2194 (0.6%)
10	J	0.79	0/1385	1.18	9/1852 (0.5%)
11	L	0.82	6/1647 (0.4%)	1.18	14/2205 (0.6%)
12	M	0.79	1/1162 (0.1%)	1.12	1/1556 (0.1%)
13	N	0.69	0/1753	1.07	10/2348 (0.4%)
14	O	0.72	2/1639 (0.1%)	1.15	11/2193 (0.5%)
15	P	0.67	1/1260 (0.1%)	1.09	2/1691 (0.1%)
16	Q	0.71	0/1517	1.15	8/2026 (0.4%)
17	R	0.67	1/1542 (0.1%)	1.08	6/2037 (0.3%)
18	S	0.71	0/1478	1.19	14/1985 (0.7%)
19	T	0.74	0/1325	1.21	14/1770 (0.8%)
20	U	0.74	1/841 (0.1%)	1.16	8/1128 (0.7%)
21	V	0.69	1/977 (0.1%)	1.03	0/1312
22	W	0.64	1/542 (0.2%)	0.98	2/722 (0.3%)
23	X	0.65	0/992	1.12	3/1334 (0.2%)
24	Y	0.74	1/1082 (0.1%)	1.18	5/1441 (0.3%)
25	Z	0.74	0/1137	1.25	5/1517 (0.3%)
26	a	0.72	0/1190	1.11	4/1591 (0.3%)
27	b	0.72	1/570 (0.2%)	1.10	1/752 (0.1%)
28	c	0.71	1/813 (0.1%)	1.05	3/1091 (0.3%)
29	d	0.70	0/919	1.06	2/1238 (0.2%)
30	e	0.71	1/1071 (0.1%)	1.12	5/1428 (0.4%)
31	f	0.75	1/884 (0.1%)	1.22	10/1185 (0.8%)
32	g	0.74	1/917 (0.1%)	1.15	4/1222 (0.3%)
33	h	0.64	0/1022	1.03	1/1351 (0.1%)
34	i	0.70	1/793 (0.1%)	1.18	6/1048 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.77	1/704 (0.1%)	1.16	4/931 (0.4%)
36	k	0.72	0/574	1.18	4/761 (0.5%)
37	l	0.65	0/453	1.04	2/599 (0.3%)
38	m	0.68	0/434	1.22	3/575 (0.5%)
39	n	0.62	0/240	0.86	0/305
40	o	0.70	0/884	1.14	4/1166 (0.3%)
41	p	0.64	0/717	0.97	1/953 (0.1%)
42	t	0.78	1/1058 (0.1%)	1.22	8/1416 (0.6%)
43	u	0.69	0/1638	1.12	6/2222 (0.3%)
44	2	0.34	12/86672 (0.0%)	0.66	30/135198 (0.0%)
45	3	0.30	0/3723	0.63	2/5800 (0.0%)
46	4	0.31	0/2836	0.67	1/4421 (0.0%)
All	All	0.51	47/147330 (0.0%)	0.85	303/217756 (0.1%)

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
44	2	0	34
45	3	0	2
All	All	0	36

The worst 5 of 47 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	1701	C	O5'-C5'	16.69	1.67	1.42
44	2	1701	C	C5'-C4'	14.73	1.73	1.51
44	2	1673	C	C3'-O3'	13.64	1.63	1.43
44	2	1673	C	O3'-P	11.35	1.78	1.61
44	2	1673	C	O5'-C5'	10.39	1.58	1.42

The worst 5 of 303 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1701	C	C2'-C3'-O3'	-18.40	86.10	113.70
44	2	1701	C	C4'-C3'-O3'	16.27	137.41	113.00
44	2	1701	C	O4'-C4'-C3'	-15.18	88.82	104.00
2	B	325	GLU	N-CA-C	12.18	124.63	111.36
44	2	1673	C	C4'-C3'-O3'	10.52	125.19	109.40

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
44	2	1	C	Sidechain
44	2	115	C	Sidechain
44	2	121	A	Sidechain
44	2	149	U	Sidechain
44	2	2	G	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	1888	0	1983	144	0
2	B	3190	0	3327	169	0
3	C	2889	0	3064	307	0
4	D	2361	0	2385	159	0
5	E	1286	0	1398	180	0
6	F	1949	0	2093	133	0
7	G	1881	0	2018	143	0
8	H	1535	0	1611	95	0
9	I	1604	0	1652	61	0
10	J	1362	0	1399	92	0
11	L	1617	0	1725	140	0
12	M	1139	0	1204	123	0
13	N	1708	0	1761	105	0
14	O	1607	0	1745	121	0
15	P	1234	0	1263	89	0
16	Q	1493	0	1612	127	0
17	R	1526	0	1682	80	0
18	S	1438	0	1472	86	0
19	T	1297	0	1366	125	0
20	U	827	0	852	22	0
21	V	963	0	1026	44	0
22	W	529	0	541	27	0
23	X	975	0	1053	68	0
24	Y	1065	0	1145	103	0
25	Z	1114	0	1194	89	0
26	a	1161	0	1213	92	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	b	560	0	590	45	0
28	c	802	0	845	65	0
29	d	904	0	947	29	0
30	e	1053	0	1144	50	0
31	f	865	0	904	104	0
32	g	907	0	1002	105	0
33	h	1014	0	1148	55	0
34	i	783	0	862	77	0
35	j	690	0	719	61	0
36	k	568	0	637	40	0
37	l	443	0	483	19	0
38	m	428	0	466	25	0
39	n	239	0	289	3	0
40	o	870	0	943	51	0
41	p	707	0	760	39	0
42	t	1043	0	1120	137	0
43	u	1621	0	1555	258	0
44	2	77488	0	39153	7886	0
45	3	3334	0	1693	326	0
46	4	2538	0	1286	274	0
All	All	136495	0	98330	10756	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 46.

The worst 5 of 10756 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)
31:f:106:TYR:CD2	31:f:107:PRO:HD2	1.42	1.55
43:u:156:ARG:HG2	44:2:4023:U:C2	0.98	1.48
44:2:1673:C:O3'	44:2:1673:C:C3'	1.63	1.46
43:u:156:ARG:NE	44:2:3935:A:C2	1.72	1.44
34:i:100:ALA:CB	43:u:197:THR:OG1	1.69	1.39

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	A	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	10	44
2	B	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	2	20
3	C	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	2	18
4	D	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	7	36
5	E	156/288 (54%)	141 (90%)	8 (5%)	7 (4%)	2	17
6	F	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	7	36
7	G	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	2	19
8	H	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	7	38
9	I	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	7	38
10	J	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	11
11	L	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	1	14
12	M	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	9	40
13	N	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	8	40
14	O	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	8	40
15	P	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	6	31
16	Q	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	3	21
17	R	181/196 (92%)	174 (96%)	4 (2%)	3 (2%)	7	36
18	S	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	3	20
19	T	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	6	32
20	U	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
21	V	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	7	38
22	W	62/157 (40%)	61 (98%)	1 (2%)	0	100	100
23	X	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
24	Y	126/145 (87%)	119 (94%)	4 (3%)	3 (2%)	4	27
25	Z	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	3	23

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	a	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	3	21
27	b	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	1	13
28	c	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	6	31
29	d	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	14	51
30	e	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	4	27
31	f	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	2	16
32	g	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	3	20
33	h	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	4	26
34	i	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	1	13
35	j	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	4	27
36	k	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	8	40
37	l	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	5	30
38	m	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	6	31
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	6	32
41	p	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	3	21
42	t	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	1	15
43	u	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	9	40
All	All	6479/7422 (87%)	6102 (94%)	200 (3%)	177 (3%)	6	25

5 of 177 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	LYS
1	A	196	TRP
2	B	4	ARG
2	B	5	LYS
2	B	157	CYS

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	A	189/199 (95%)	182 (96%)	7 (4%)	30	51
2	B	344/349 (99%)	322 (94%)	22 (6%)	16	37
3	C	302/348 (87%)	283 (94%)	19 (6%)	16	37
4	D	244/250 (98%)	237 (97%)	7 (3%)	37	58
5	E	143/252 (57%)	133 (93%)	10 (7%)	14	35
6	F	203/215 (94%)	195 (96%)	8 (4%)	28	49
7	G	199/223 (89%)	190 (96%)	9 (4%)	24	46
8	H	171/171 (100%)	165 (96%)	6 (4%)	32	53
9	I	170/181 (94%)	161 (95%)	9 (5%)	20	41
10	J	143/149 (96%)	137 (96%)	6 (4%)	26	48
11	L	167/177 (94%)	157 (94%)	10 (6%)	17	39
12	M	118/161 (73%)	113 (96%)	5 (4%)	26	48
13	N	172/172 (100%)	167 (97%)	5 (3%)	37	58
14	O	168/174 (97%)	165 (98%)	3 (2%)	51	68
15	P	133/163 (82%)	126 (95%)	7 (5%)	20	41
16	Q	162/165 (98%)	157 (97%)	5 (3%)	35	56
17	R	161/175 (92%)	151 (94%)	10 (6%)	16	38
18	S	155/157 (99%)	149 (96%)	6 (4%)	28	49
19	T	139/140 (99%)	135 (97%)	4 (3%)	37	58
20	U	91/115 (79%)	91 (100%)	0	100	100
21	V	100/107 (94%)	100 (100%)	0	100	100
22	W	55/126 (44%)	52 (94%)	3 (6%)	19	41
23	X	107/133 (80%)	105 (98%)	2 (2%)	50	67
24	Y	119/135 (88%)	114 (96%)	5 (4%)	26	48
25	Z	118/118 (100%)	114 (97%)	4 (3%)	32	54
26	a	120/121 (99%)	115 (96%)	5 (4%)	26	48
27	b	58/126 (46%)	57 (98%)	1 (2%)	53	69
28	c	88/97 (91%)	87 (99%)	1 (1%)	65	76
29	d	100/110 (91%)	97 (97%)	3 (3%)	36	57
30	e	115/121 (95%)	111 (96%)	4 (4%)	32	53
31	f	87/89 (98%)	77 (88%)	10 (12%)	5	18

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	g	98/100 (98%)	89 (91%)	9 (9%)	8	27
33	h	109/110 (99%)	105 (96%)	4 (4%)	30	51
34	i	82/89 (92%)	76 (93%)	6 (7%)	13	34
35	j	71/80 (89%)	69 (97%)	2 (3%)	38	60
36	k	64/65 (98%)	64 (100%)	0	100	100
37	l	47/48 (98%)	46 (98%)	1 (2%)	47	65
38	m	48/116 (41%)	45 (94%)	3 (6%)	16	37
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	94/94 (100%)	90 (96%)	4 (4%)	26	47
41	p	74/75 (99%)	72 (97%)	2 (3%)	39	61
42	t	113/121 (93%)	108 (96%)	5 (4%)	25	47
43	u	177/177 (100%)	161 (91%)	16 (9%)	9	27
All	All	5642/6318 (89%)	5394 (96%)	248 (4%)	27	47

5 of 248 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	M	45	VAL
40	o	83	LEU
17	R	41	ILE
38	m	115	CYS
43	u	53	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 147 such sidechains are listed below:

Mol	Chain	Res	Type
26	a	74	ASN
42	t	23	GLN
28	c	15	ASN
33	h	101	ASN
10	J	168	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	2	3605/5025 (71%)	2056 (57%)	325 (9%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	3	156/194 (80%)	81 (51%)	6 (3%)
46	4	118/119 (99%)	69 (58%)	9 (7%)
All	All	3879/5338 (72%)	2206 (56%)	340 (8%)

5 of 2206 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	2	2	G
44	2	3	C
44	2	5	A
44	2	6	C
44	2	8	U

5 of 340 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	2	3873	G
44	2	4659	U
44	2	4033	G
44	2	4338	A
44	2	4740	U

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

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

5.5 Carbohydrates [i](#)

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 ⓘ

There are no chain breaks in this entry.

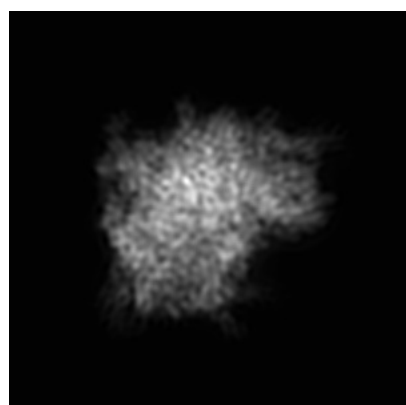
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2810. These allow visual inspection of the internal detail of the map and identification of artifacts.

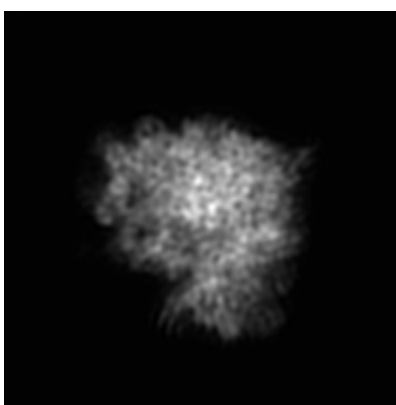
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

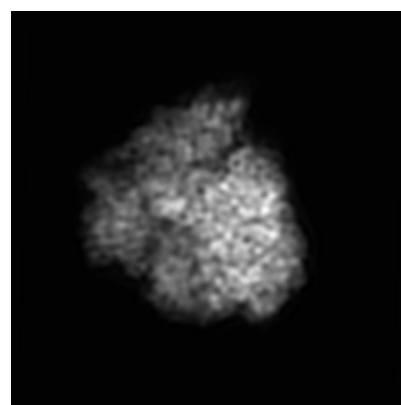
6.1.1 Primary map



X



Y

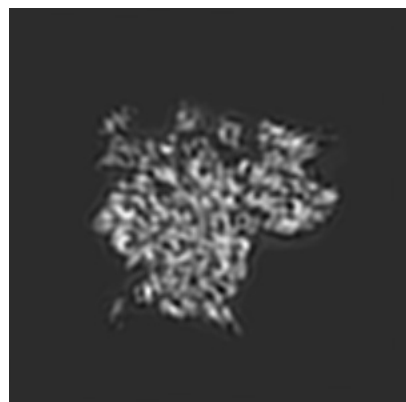


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 150



Y Index: 150



Z Index: 150

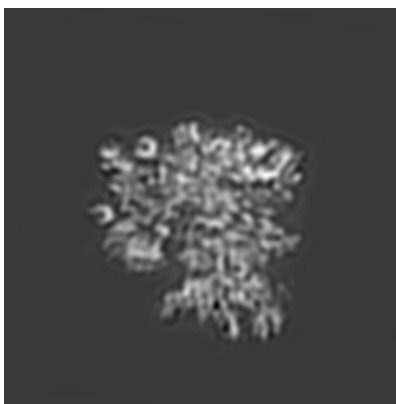
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 173



Y Index: 149

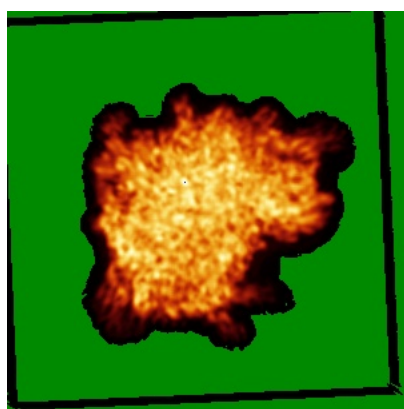


Z Index: 154

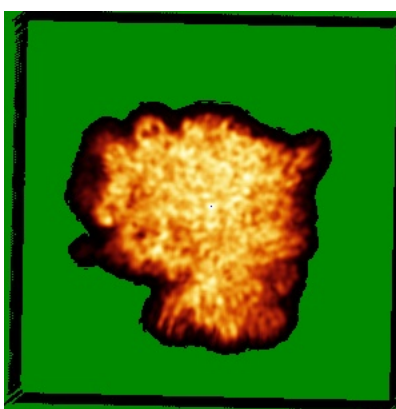
The images above show the largest variance slices of the map in three orthogonal directions.

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

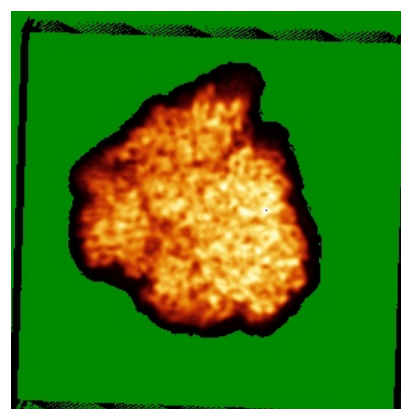
6.4.1 Primary map



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

This section was not generated.

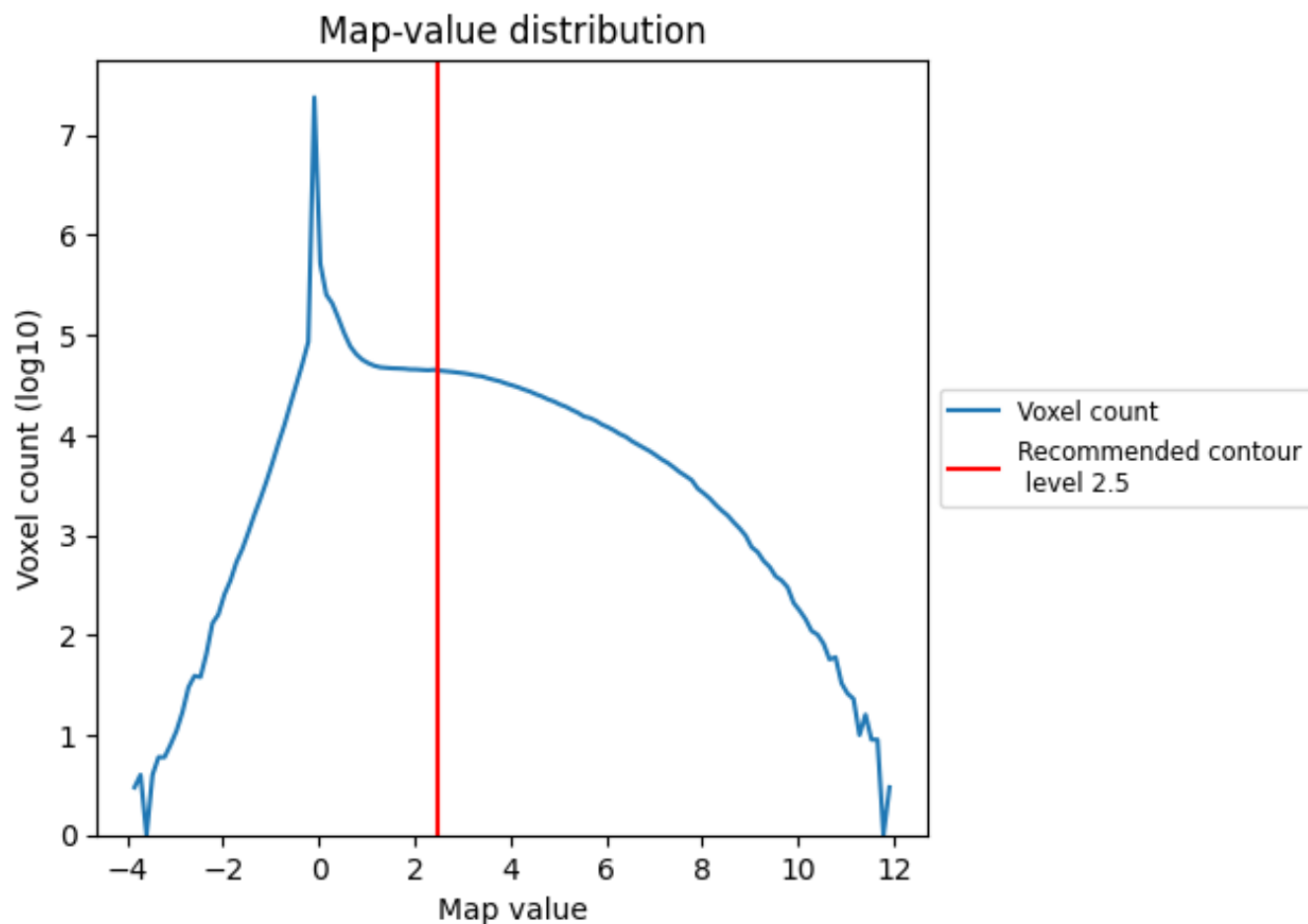
6.6 Mask visualisation

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

7 Map analysis [i](#)

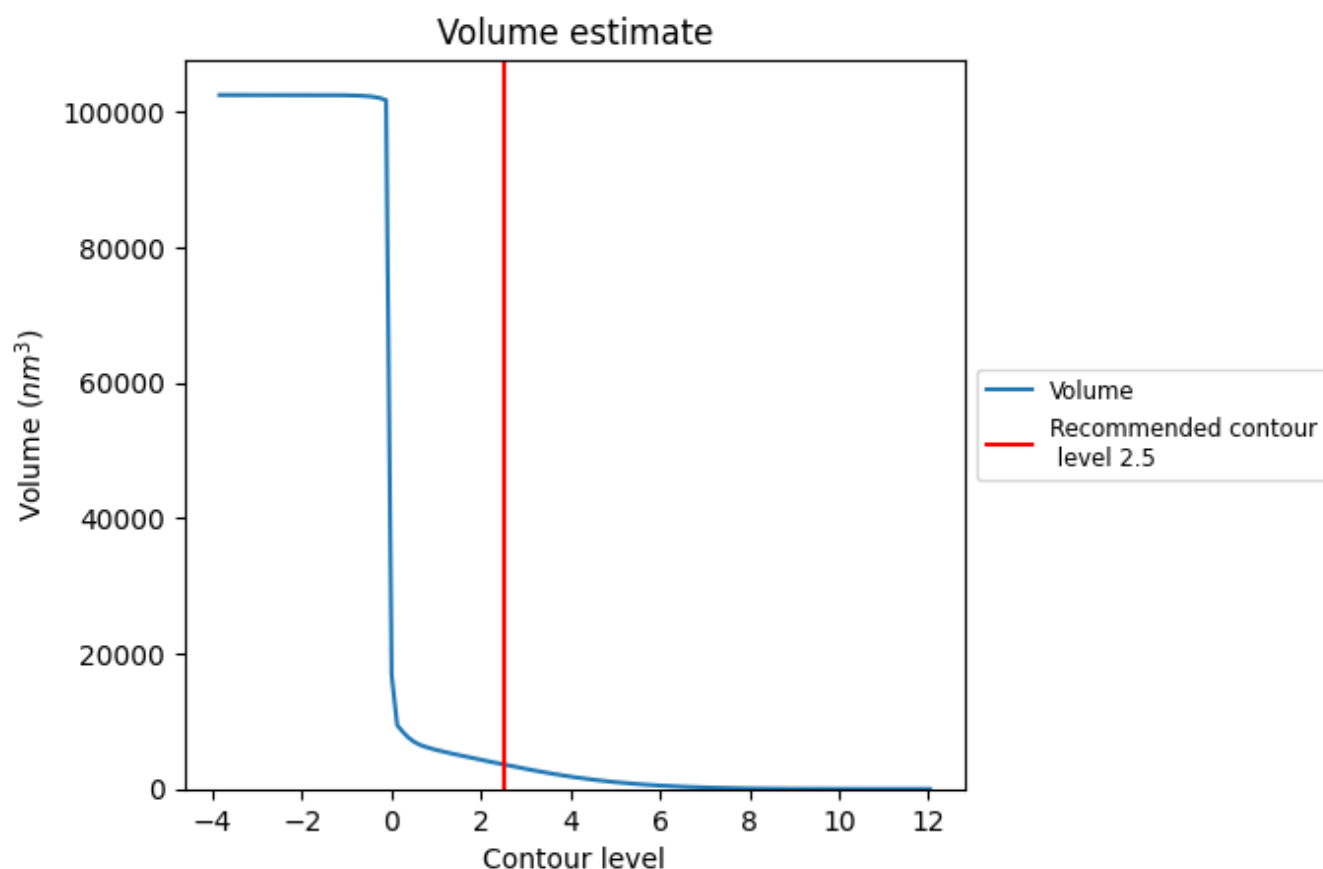
This section contains the results of statistical analysis of the map.

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.

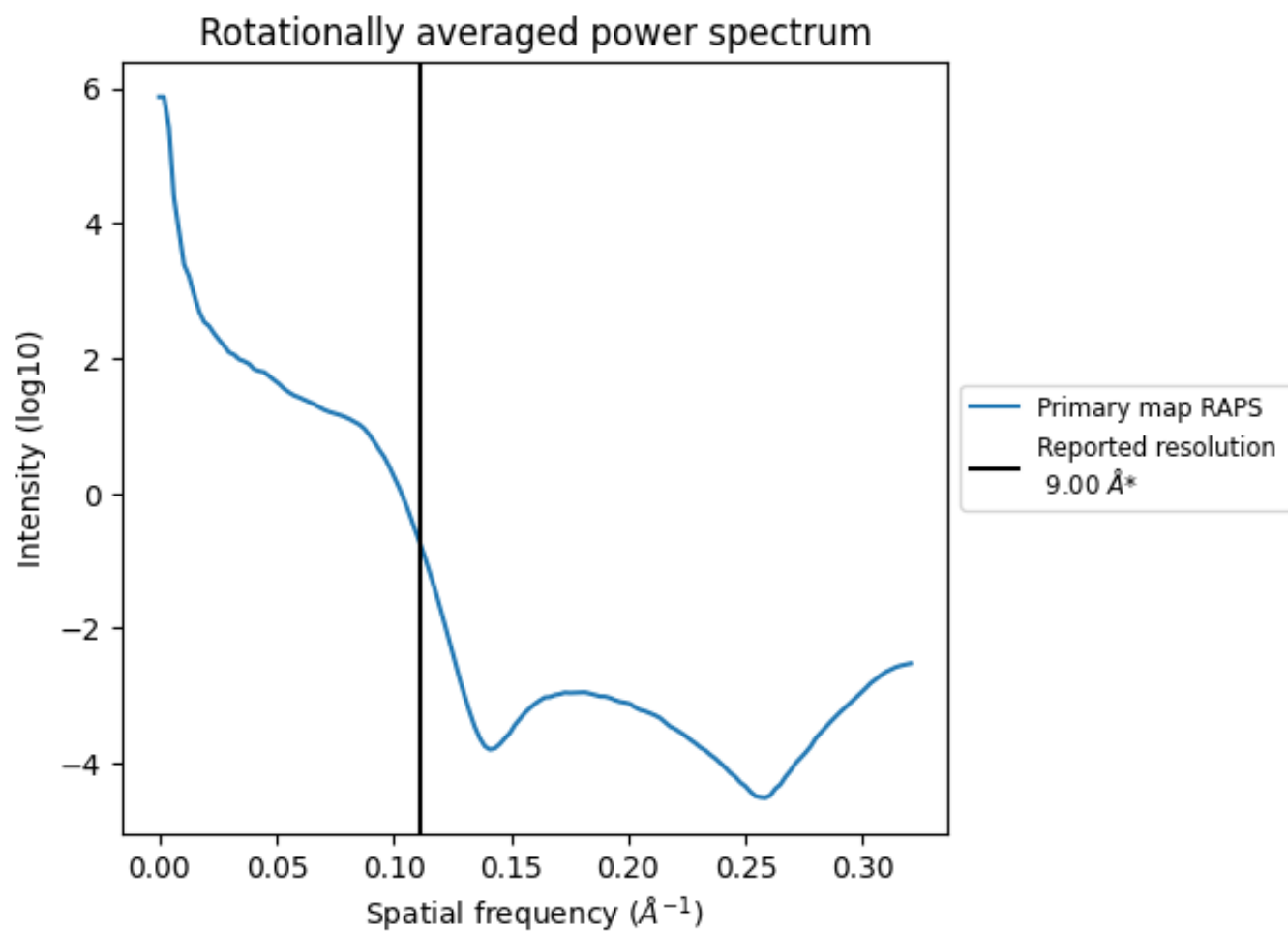
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3628 nm^3 ; this corresponds to an approximate mass of 3277 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 0.111 Å⁻¹

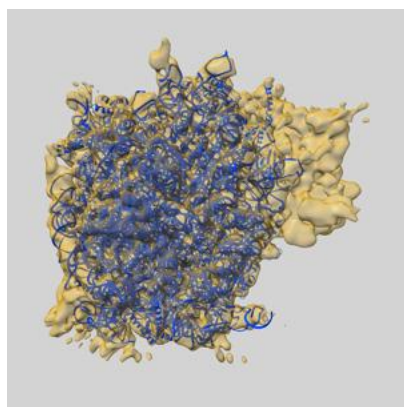
8 Fourier-Shell correlation

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

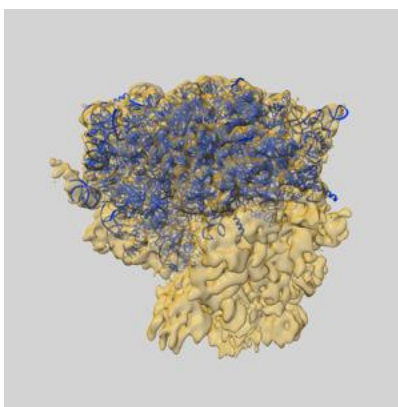
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2810 and PDB model 4D5Y. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

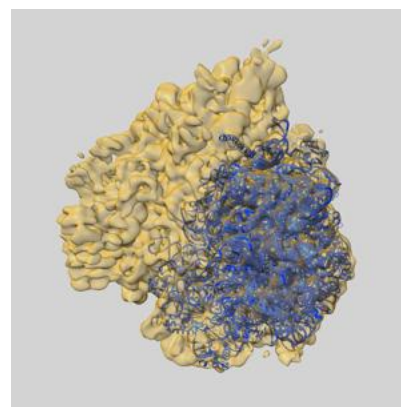
9.1 Map-model overlay [i](#)



X



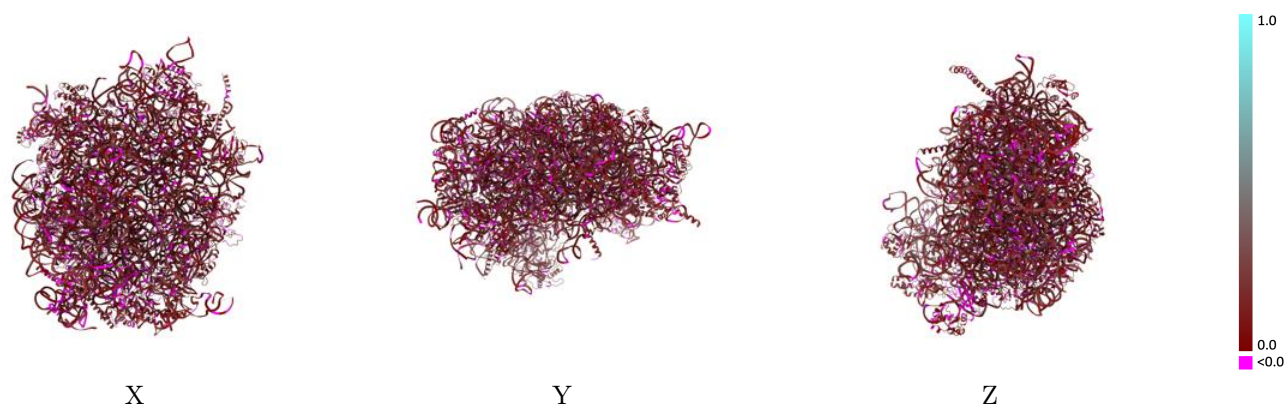
Y



Z

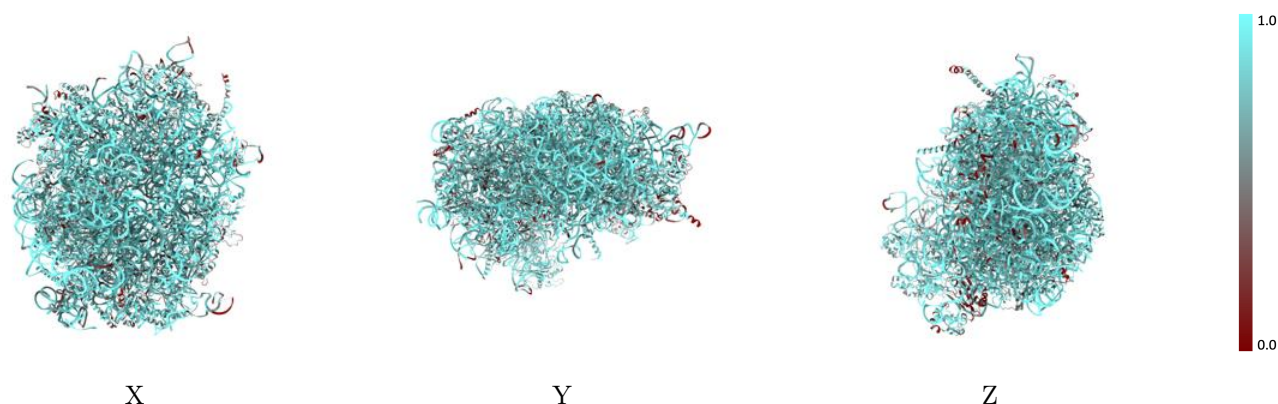
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



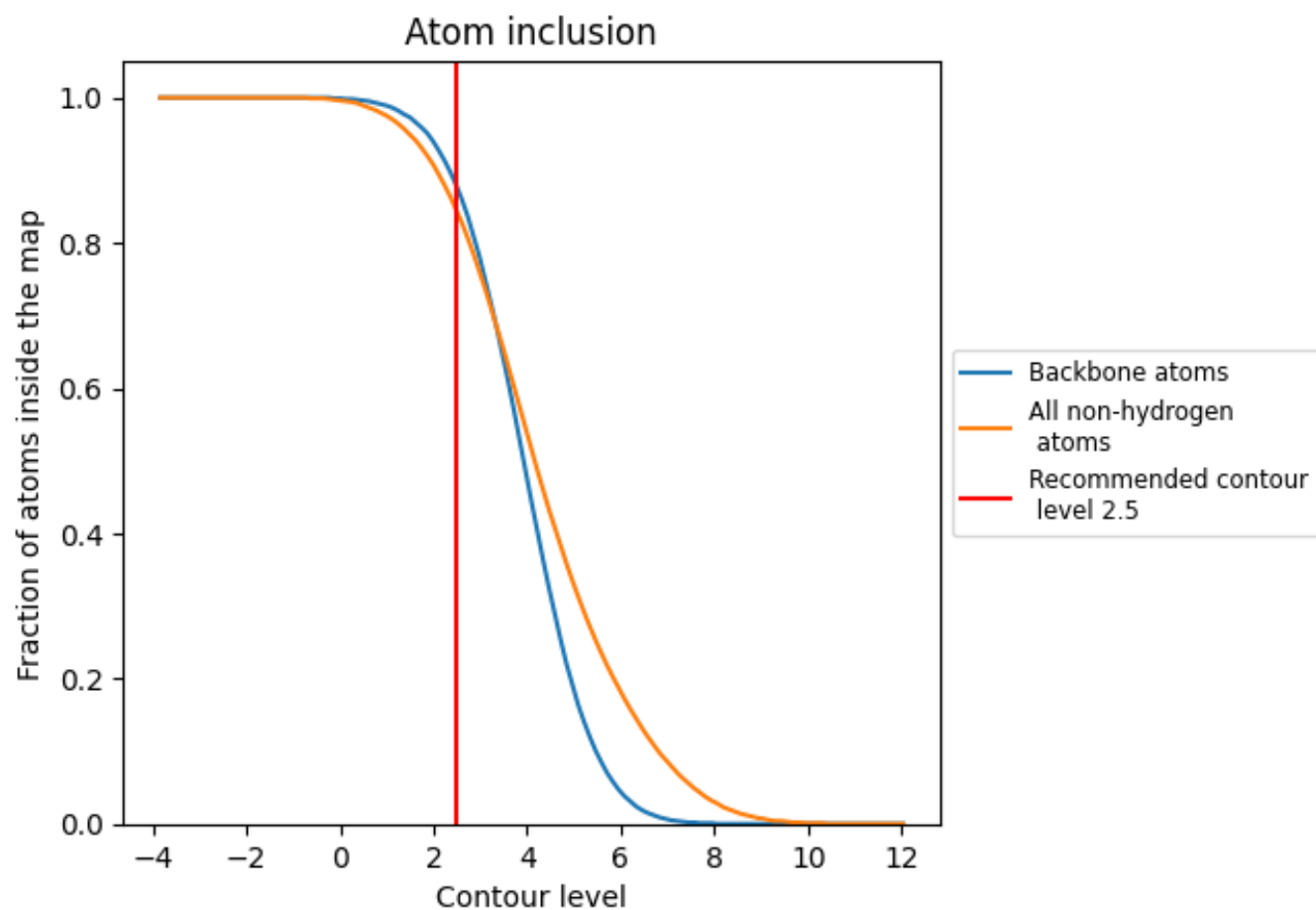
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8430	 0.1160
2	 0.9150	 0.1330
3	 0.9260	 0.1360
4	 0.9710	 0.1440
A	 0.6420	 0.0660
B	 0.6990	 0.0730
C	 0.7630	 0.0770
D	 0.8170	 0.1040
E	 0.6630	 0.0560
F	 0.7330	 0.0970
G	 0.7000	 0.1150
H	 0.6920	 0.1120
I	 0.6320	 0.0940
J	 0.8340	 0.1070
L	 0.7360	 0.0930
M	 0.7890	 0.1210
N	 0.7350	 0.0510
O	 0.7310	 0.0970
P	 0.8130	 0.0830
Q	 0.7230	 0.0850
R	 0.7470	 0.1130
S	 0.7390	 0.0890
T	 0.7090	 0.0750
U	 0.7330	 0.1180
V	 0.5930	 0.0880
W	 0.8240	 0.1080
X	 0.7020	 0.0850
Y	 0.8290	 0.0980
Z	 0.6760	 0.0910
a	 0.7630	 0.0680
b	 0.7450	 0.0890
c	 0.6790	 0.1080
d	 0.8310	 0.1090
e	 0.7430	 0.0770
f	 0.7320	 0.0640



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
g	 0.6340	 0.0470
h	 0.8150	 0.1260
i	 0.7550	 0.1180
j	 0.8480	 0.0780
k	 0.7180	 0.1220
l	 0.7770	 0.0870
m	 0.6790	 0.0800
n	 0.7200	 0.0910
o	 0.5900	 0.0690
p	 0.7380	 0.1070
t	 0.7950	 0.0900
u	 0.4640	 0.0430