



## wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 08:26 am GMT

PDB ID : 6R87  
EMDB ID : EMD-4753  
Title : Yeast Vms1 (Q295L)-60S ribosomal subunit complex (pre-state without Arb1)  
Authors : Su, T.; Izawa, T.; Cheng, J.; Yamashita, Y.; Berninghausen, O.; Inada, T.;  
Neupert, W.; Beckmann, R.  
Deposited on : 2019-03-31  
Resolution : 3.40 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev113  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

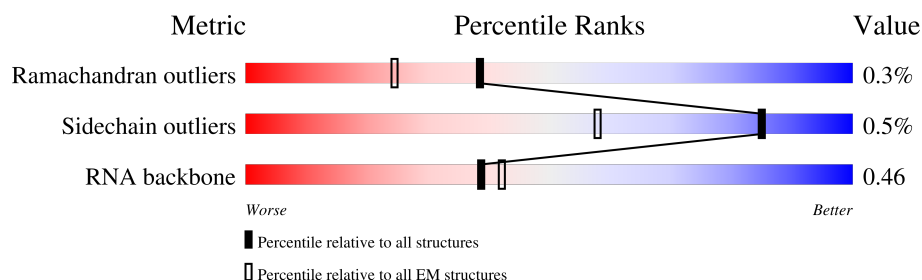
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.40 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.



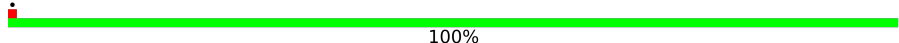
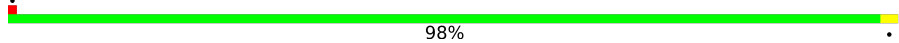
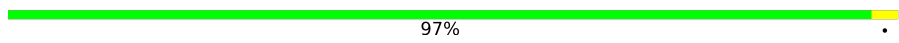
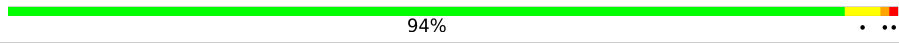
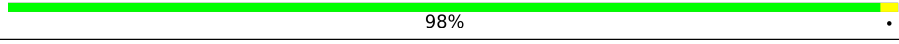
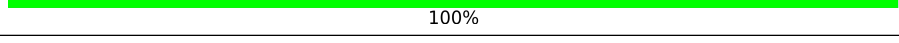
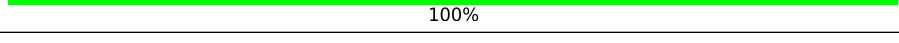
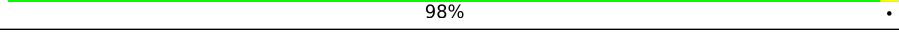
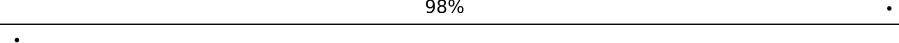
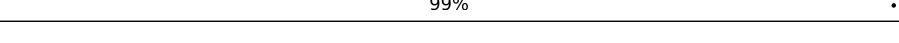
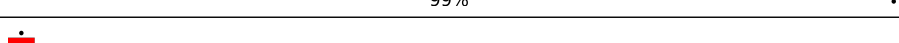
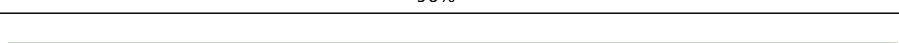



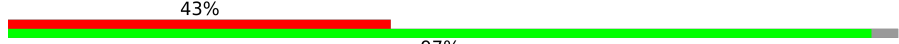

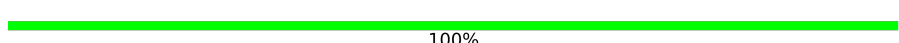

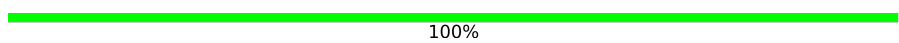

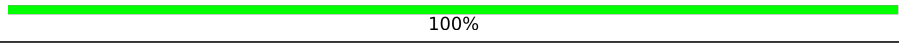
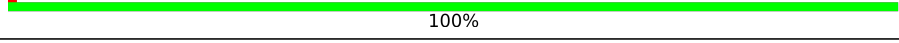


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	R	475	
2	X	224	
3	i	112	
4	J	222	
5	j	119	
6	K	233	
7	k	99	
8	7	191	

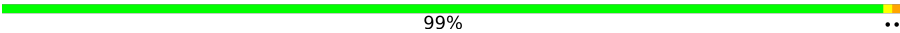
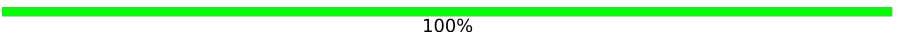
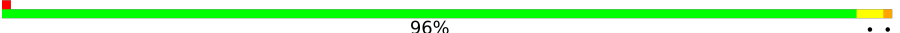
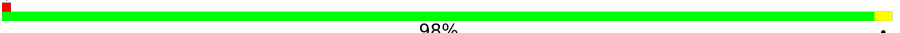
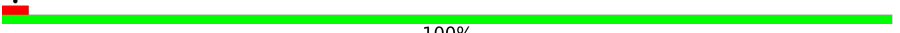
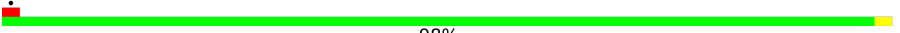




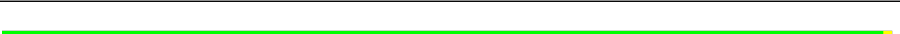


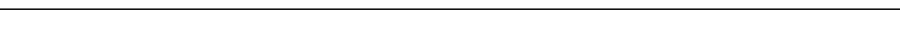

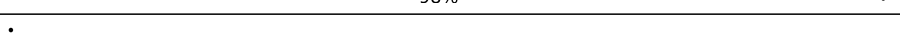
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Mol	Chain	Length	Quality of chain
9	l	87	 100%
10	M	169	 98%
11	m	77	 97%
12	N	193	 94%
13	n	50	 98%
14	O	136	 100%
15	o	52	 100%
16	p	203	 98%
17	Q	197	 98%
18	5	183	 99%
19	S	185	 99%
20	s	220	 96%
21	T	152	 99%
22	U	172	 99%
23	V	159	 100%
24	W	100	 100%
25	P	155	 43% 97%
26	r	197	 11% 61% 39%
27	x	136	 100%
28	3	121	 70% 27%
29	Y	62	 100%
30	4	158	 63% 32% 5%
31	Z	121	 100%
32	a	126	 100%
33	B	76	 70% 29%

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Mol	Chain	Length	Quality of chain
34	b	135	 99% ..
35	C	105	 100%
36	c	148	 96% ..
37	D	91	 98% .
38	d	58	 100%
39	E	252	 98% .
40	e	97	 100%
41	F	386	 98% .
42	f	109	 100%
43	G	361	 99% .
44	g	127	 99% .
45	H	296	 99% .
46	h	106	 100%
47	I	175	 89% 11%
48	L	204	 54% 98% .
49	1	3316	 60% 32% 8%

## 2 Entry composition [i](#)

There are 50 unique types of molecules in this entry. The entry contains 135255 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 Protein VMS1,Vms1,Protein VMS1,Vms1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	R	355	Total	C	N	O	S	Se	0	0
			2777	1772	494	498	12	1		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	224	Total	C	N	O	S	0	0
			1633	1019	279	328	7		

- Molecule 3 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 4 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 5 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 6 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 7 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L11-B.

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

- Molecule 11 is a protein called 60S ribosomal protein L38.

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

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 13 is a protein called 60S ribosomal protein L39.

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

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 15 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	5	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	s	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 21 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	152	Total	C	N	O	0	0
			1228	763	260	205		

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	P	150	Total	C	N	O	0	0
			737	437	150	150		

- Molecule 26 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	r	121	Total	C	N	O	S	0	0
			967	621	170	173	3		

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	x	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 28 is a RNA chain called 5S rRNA.



Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 29 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 30 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 31 is a protein called 60S ribosomal protein L25.

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

- Molecule 32 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 33 is a RNA chain called tRNA-Ala.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B	76	Total	C	N	O	P	0	0
			1622	721	285	540	76		

- Molecule 34 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 35 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L28.

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

- Molecule 37 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L29.

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

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L30.

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

- Molecule 41 is a protein called 60S ribosomal protein L3.

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

- Molecule 42 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 43 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L32.

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

- Molecule 45 is a protein called 60S ribosomal protein L5.

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

- Molecule 46 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L1-A.

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

- Molecule 49 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	3316	Total	C	N	O	P	0	0
			70924	31675	12770	23163	3316		

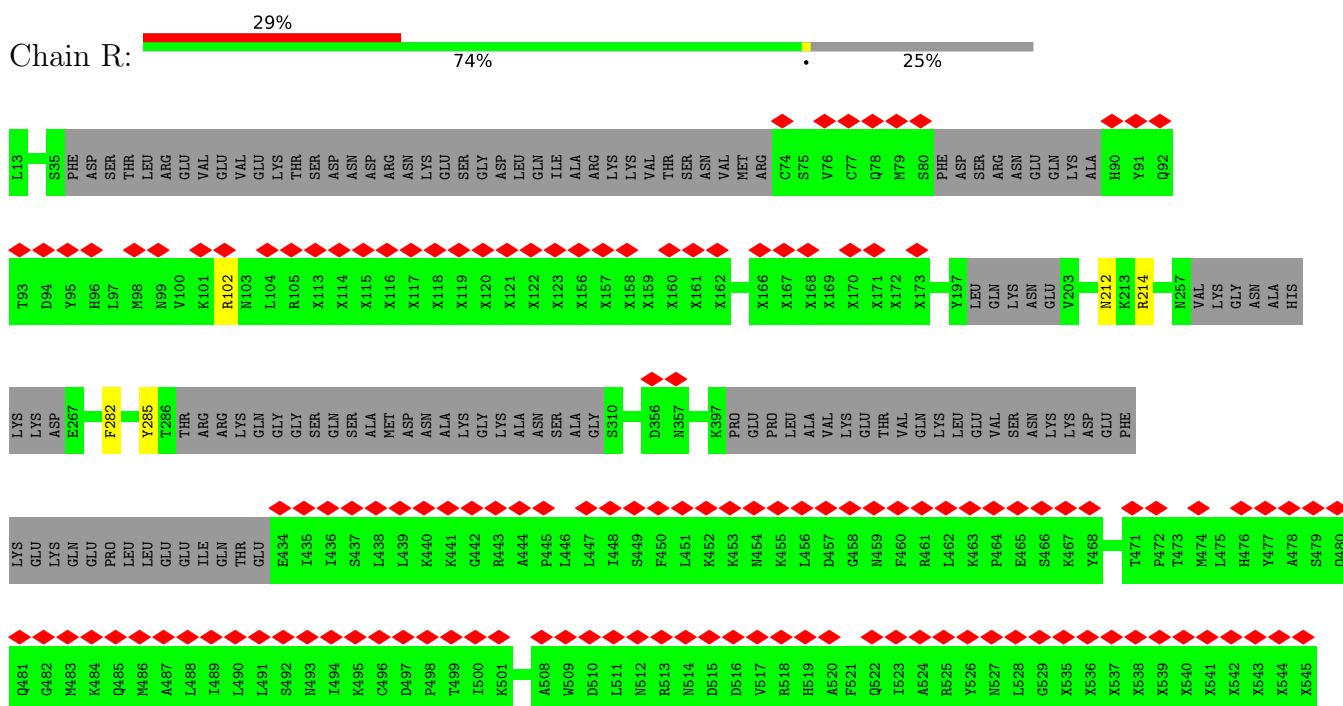
- Molecule 50 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
50	R	1	Total	Zn	0
			1	1	

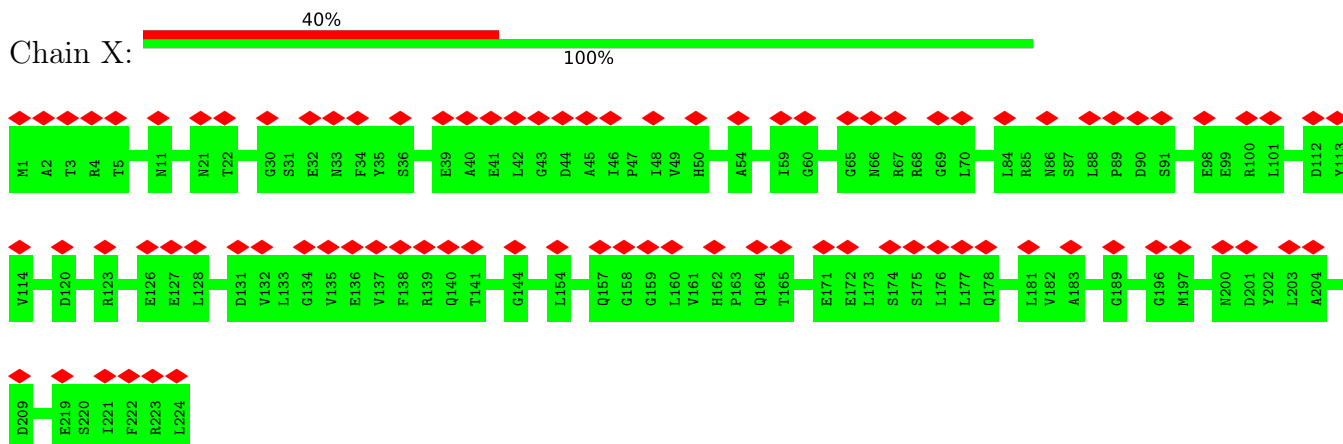
### 3 Residue-property plots

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: Protein VMS1,Vms1,Protein VMS1,Vms1



- Molecule 2: Eukaryotic translation initiation factor 6



- Molecule 3: 60S ribosomal protein L34-A

Chain i:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: 60S ribosomal protein L7-A

Chain J:  99%



- Molecule 5: 60S ribosomal protein L35-A

Chain j:  97%



- Molecule 6: 60S ribosomal protein L8-A

Chain K:  97%



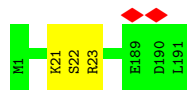
- Molecule 7: 60S ribosomal protein L36-A

Chain k:  99%



- Molecule 8: 60S ribosomal protein L9-A

Chain 7:  98%



- Molecule 9: 60S ribosomal protein L37-A

Chain l:  100%



- Molecule 10: 60S ribosomal protein L11-B

Chain M:  98%



- Molecule 11: 60S ribosomal protein L38

Chain m:  97%



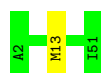
- Molecule 12: 60S ribosomal protein L13-A

Chain N:  94%



- Molecule 13: 60S ribosomal protein L39

Chain n:  98%



- Molecule 14: 60S ribosomal protein L14-A

Chain O:  100%



- Molecule 15: Ubiquitin-60S ribosomal protein L40

Chain o:  100%

There are no outlier residues recorded for this chain.

- Molecule 16: 60S ribosomal protein L15-A

Chain p:  98%



- Molecule 17: 60S ribosomal protein L16-A

Chain Q:  98%



- Molecule 18: 60S ribosomal protein L17-A

Chain 5: 99%



- Molecule 19: 60S ribosomal protein L18-A

Chain S: 99%



- Molecule 20: 60S ribosomal protein L10

Chain s: 96%



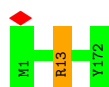
- Molecule 21: 60S ribosomal protein L19-A

Chain T: 99%



- Molecule 22: 60S ribosomal protein L20-A

Chain U: 99%



- Molecule 23: 60S ribosomal protein L21-A

Chain V: 100%

There are no outlier residues recorded for this chain.

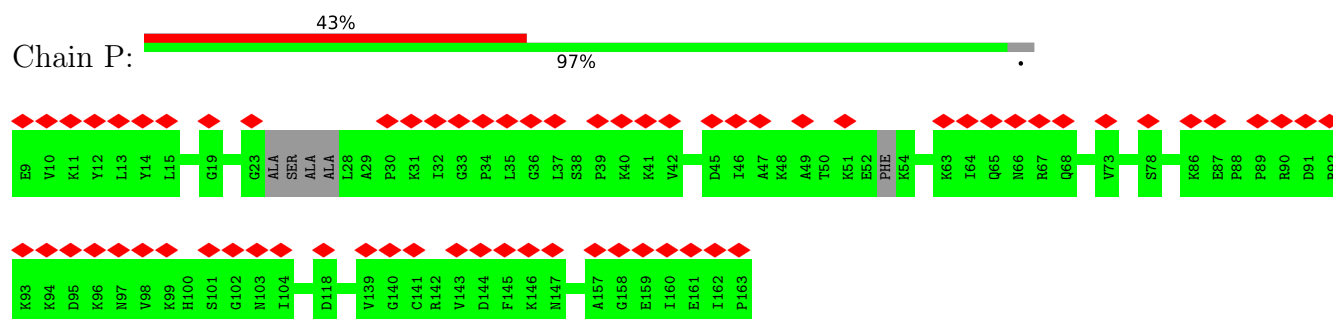
- Molecule 24: 60S ribosomal protein L22-A

Chain W: 100%

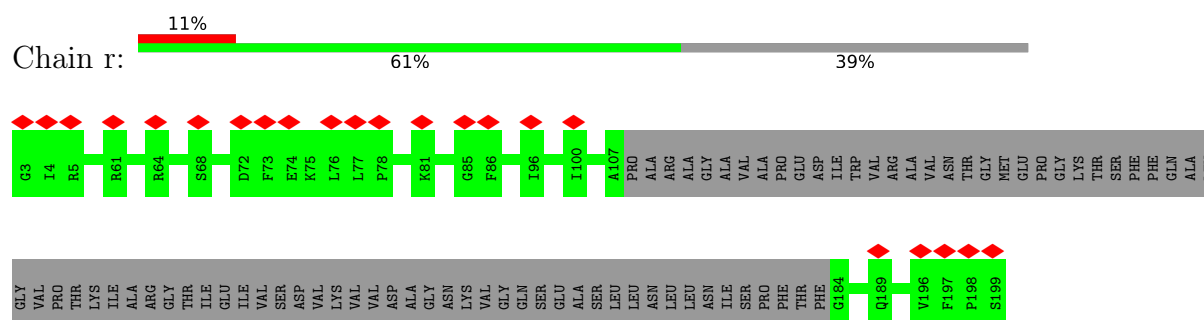
There are no outlier residues recorded for this chain.



- Molecule 25: 60S ribosomal protein L12-A



- Molecule 26: 60S acidic ribosomal protein P0

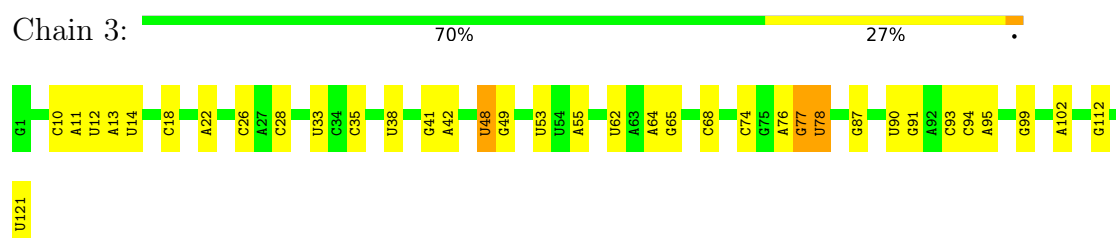


- Molecule 27: 60S ribosomal protein L23-A



There are no outlier residues recorded for this chain.

- Molecule 28: 5S rRNA

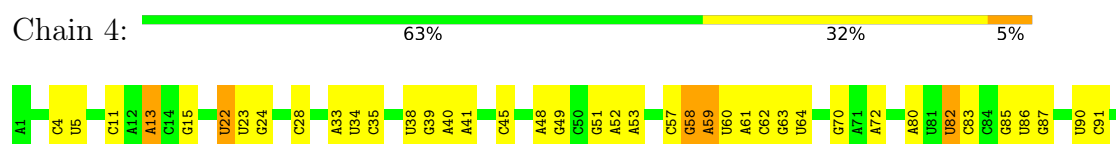


- Molecule 29: 60S ribosomal protein L24-A



There are no outlier residues recorded for this chain.

- Molecule 30: 5.8S rRNA





- Molecule 31: 60S ribosomal protein L25

Chain Z: 100%

There are no outlier residues recorded for this chain.

- Molecule 32: 60S ribosomal protein L26-A

Chain a: 100%



- Molecule 33: tRNA-Ala

Chain B: 70% 29%



- Molecule 34: 60S ribosomal protein L27-A

Chain b: 99%



- Molecule 35: 60S ribosomal protein L42-A

Chain C: 100%

There are no outlier residues recorded for this chain.

- Molecule 36: 60S ribosomal protein L28

Chain c: 96%



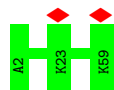
- Molecule 37: 60S ribosomal protein L43-A

Chain D: 98%



- Molecule 38: 60S ribosomal protein L29

Chain d: 100%



- Molecule 39: 60S ribosomal protein L2-A

Chain E: 98%



- Molecule 40: 60S ribosomal protein L30

Chain e: 100%



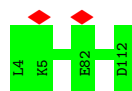
- Molecule 41: 60S ribosomal protein L3

Chain F: 98%



- Molecule 42: 60S ribosomal protein L31-A

Chain f: 100%



- Molecule 43: 60S ribosomal protein L4-A

Chain G: 99%



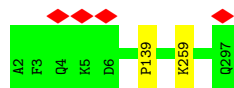
- Molecule 44: 60S ribosomal protein L32

Chain g:  99%



- Molecule 45: 60S ribosomal protein L5

Chain H:  99%




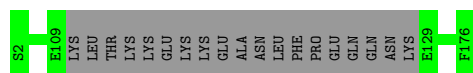
- Molecule 46: 60S ribosomal protein L33-A

Chain h:  100%

There are no outlier residues recorded for this chain.

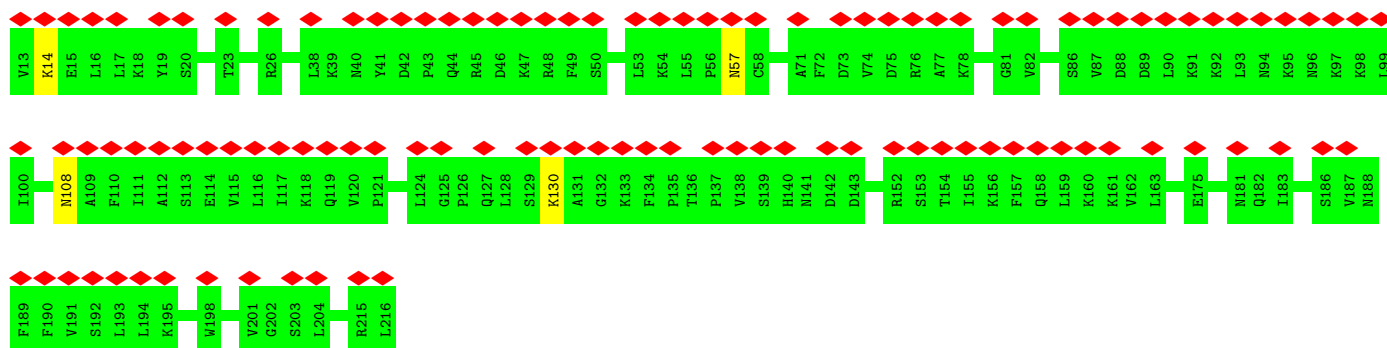
- Molecule 47: 60S ribosomal protein L6-A

Chain I:  89%



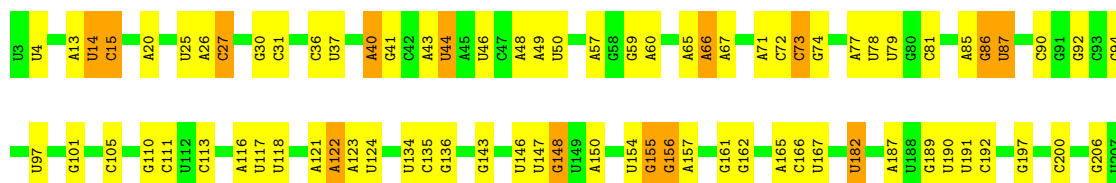
- Molecule 48: 60S ribosomal protein L1-A

Chain L:  54%



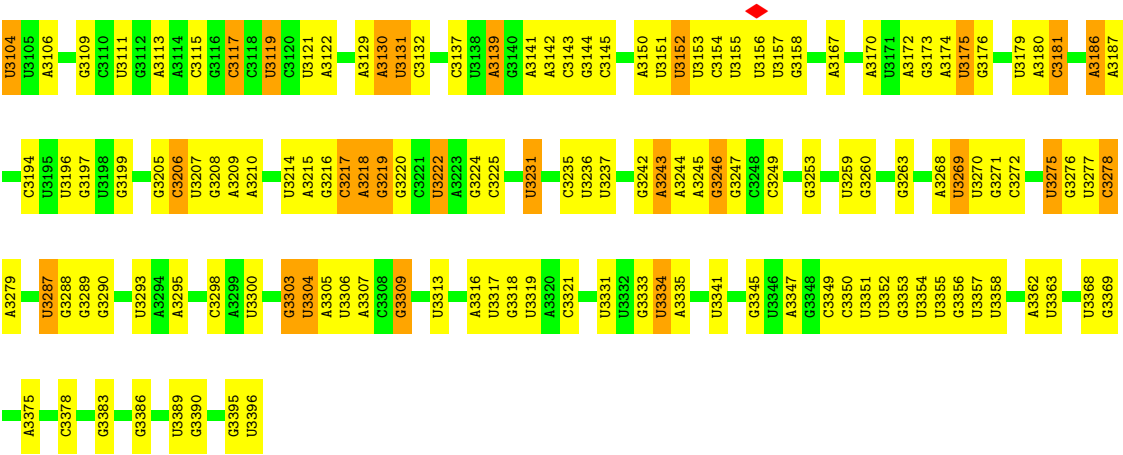
- Molecule 49: 25S rRNA

Chain 1:  60%





C2889	U2996	G2800	U2688	C2567	U2482	A2401	U2310	A2208	C2118	G2017	G1939	U1855	U1746
C2894	G2997	A2801	A2689	C2568	G2482	A2402	A2313	A2209	G2121	C2018	C1943	C1856	A1749
G2895	C2894	A2802	G2690	A2569	A2484	A2403	G2403	G2210	G2122	U2019	U1951	A1857	A1750
A2896	A2804	A2803	G2691	A2485	A2405	G2406	G2315	G2211	G2123	A2020	G1953	A1858	G1751
C2897	C2809	A2694	U2694	U2570	C2407	C2408	U2319	U2225	A2126	G2021	G1954	G1861	A1752
C2898	C2810	A2703	U2703	C2572	U2487	U2408	U2334	A2232	U2127	G2022	G1955	A1864	C1766
C2899	G2814	A2704	U2704	U2581	U2411	U2409	U2335	A2233	U2128	C2023	U1954	A1865	C1760
A2911	G2815	A2705	U2705	U2582	U2412	U2410	G2336	C2235	U2129	G2024	U1955	A1866	C1761
G2912	G2816	G2706	U2706	C2583	A2413	A2411	U2337	C2236	A2130	G2025	U1956	A1867	C1762
C2913	A2817	C2707	U2707	G2585	G2414	G2412	C2338	C2237	A2131	A1960	U1957	U1871	U1763
U2923	U2818	C2711	U2711	C2586	C2415	C2413	C2339	A2242	U2132	G1961	G1958	C1872	U1764
U2924	A2819	U2712	U2712	A2589	U2416	U2414	U2340	A2243	U2133	A1962	U1959	U1873	U1765
C2925	U2822	U2713	U2713	C2590	U2417	A2415	A2341	A2244	U2134	G1963	U1960	A1874	G1766
C2928	U2823	G2714	U2714	G2591	G2418	A2416	U2342	A2245	U2135	C1964	A1961	G1875	
C2929	U2824	A2715	U2715	U2592	A2419	A2417	C2343	G2249	A2136		A1962	U1879	G1770
A2930	G2826	U2716	U2716	U2593	C2422	U2418	U2344	G2250	U2137	G1969	A1963	A1880	
U2935	U2827	U2719	U2719	G2606	U2423	C2422	A2345	G2251	U2138		A1972	A1881	G1780
U2936	G2828	G2720	U2720	G2607	A2424	U2423	C2346	U2252	A2139	A1973	A1882	C1788	
A2936	U2829	A2721	U2721	G2614	G2425	U2424	U2347	A2253	U2140	U1974	A1883	C1793	
C2941	G2834	U2722	U2722	U2615	U2426	U2425	A2348	C2254	U2141	G1975	U1885	G1794	
C2942	U2835	U2725	U2725	U2616	C2431	C2431	A2352	U2255	U2142	G1976	U1886	U1795	
C2943	C2836	C2726	U2726	G2618	U2434	U2433	G2355	U2256	A2143	G1977	U1887	G1796	
A3048	U2842	A2727	U2727	G2619	G2435	G2434	G2356	A2257	A2144	U1978	U1888	A1797	
A3049	G2843	G2728	U2728	G2620	G2436	C2444	C2359	C2258	C2151	G1979	U1889	U1890	
G3053	U2844	U2729	U2729	G2621	U2437	C2445	A2362	C2259	U2154	G1981	U1893	G1808	
A2946	A2845	C2737	U2737	C2622	G2440	G2441	C2367	U2260	U2155	U1986	G1898	A1813	
U3054	U2846	U2738	U2738	C2623	A2441	A2442	C2368	U2261	A2156	U1990	G1899	U1814	
U3055	A2847	C2742	U2742	A2625	G2442	A2443	C2369	U2262	U2157	G1991	G1899	U1815	
G3058	G2848	U2749	U2749	A2626	C2443	C2444	C2370	A2270	U2160	G1992	A1901	U1816	
C3059	U2849	G2752	U2752	A2635	G2444	G2445	G2371	A2271	G2163	U1993	G1902	U1817	
C3060	C2857	G2753	U2753	A2636	G2445	G2446	G2372	A2272	G2169	U1994	U1903	U1818	
G3066	U2860	G2754	U2754	A2637	U2446	G2447	A2373	A2273	U2170	G1995	G1904	U1819	
G3069	U2861	C2755	U2755	C2638	U2447	G2448	G2374	A2274	G2171	U1996	G1905	U1820	
A3077	U2866	C2756	U2756	C2639	U2448	G2449	G2375	A2275	G2174	C1997	G1906	C1822	
U3078	C2867	A2762	U2762	C2644	U2453	G2454	G2376	A2276	U2175	U1997	A1908	C1832	
U3079	U2871	C2772	U2772	A2647	U2454	G2455	G2377	A2277	U2176	G1998	A1913	A1835	
C3082	A2872	C2773	U2773	U2652	U2459	U2460	C2378	U2282	U2177	C1999	G1914	A1839	
A3086	U2873	G2774	U2774	U2653	U2461	U2462	G2385	U2283	G2178	U2000	U1920	U1840	
C3089	A2874	G2775	U2775	U2654	U2462	G2463	A2386	C2284	A2179	A2086	G1926	C1844	
U3090	U2875	U2776	U2776	A2657	U2467	G2468	U2388	U2285	G2185	G2002	G1927	G1845	
C3091	G2878	U2777	U2777	C2666	U2468	G2469	C2389	U2286	U2186	G2003	G1928	G1846	
C3092	C2879	U2778	U2778	U2667	U2469	G2470	A2390	U2287	U2187	U2004	G1929	C1847	
C3093	U2880	C2788	U2788	A2674	U2470	G2471	G2393	U2288	G2193	G2005	A1930	A1847	
A3094	U2881	G2789	U2789	C2675	U2471	U2472	G2394	U2289	G2194	G2006	U1931	G1848	
C3095	U2882	U2790	U2790	U2676	U2472	G2473	G2395	A2290	U2197	G2007	A1932	C1849	
U3096	C2883	G2791	U2791	C2677	U2473	G2474	G2396	A2291	A2107	G2008	A1933	A1850	
C3097	U2884	U2792	U2792	A2678	U2474	G2475	A2397	C2306	G2199	U2010	G1934	G1851	
A2990	C2885	C2793	U2793	U2679	U2475	G2476	A2398	G2307	G2200	G2011	U1938	C1854	
A2991	U2886	C2794	U2794	U2681	U2476	G2477	A2399	C2308	A2111	G2012			
U2992	A2887	U2795	U2795	U2682	U2477	G2478	A2400	C2309	A2112	G2013			
	U2888	G2796	U2796	U2683	U2478	G2479	G2400		A2113	G2014			
		C2797	U2797	U2684	U2479	G2480			A2114	G2015			
		U2798	U2798	U2685	U2480	G2481			G2115	G2016			
		C2799	U2799	U2686	U2481	G2482			A2116				
		U2800	U2800	U2687	U2482	G2483			G2117				
		G2801	U2801	U2688	U2483	G2484			U2205				
		A2802	G2802	U2689	U2484	G2485							
		G2803	U2803	U2690	U2485	G2486							
		A2804	G2804	U2691	U2486	U2487							
		C2809	U2809	U2692	U2487	U2488							
		C2810	U2810	U2693	U2488	U2489							
		G2814	U2814	U2694	U2489	U2490							
		A2815	G2815	U2695	U2490	U2491							
		G2816	U2816	U2696	U2491	U2492							
		A2817	U2817	U2697	U2492	U2493							
		U2818	U2818	U2698	U2493	U2494							
		A2819	U2819	U2699	U2494	U2495							
		U2822	U2822	U2700	U2495	U2496							
		G2826	U2826	U2701	U2496	U2497							
		U2827	U2827	U2702	U2497	U2498							
		G2828	U2828	U2703	U2498	U2499							
		U2829	U2829	U2704	U2499	U2500							
		A2834	U2834	U2705	U2500	U2501							
		G2835	U2835	U2706	U2501	U2502							
		C2836	U2836	U2707	U2502	U2503							
		U2842	U2842	U2708	U2503	U2504							
		G2843	U2843	U2709	U2504	U2505							
		U2844	U2844	U2710	U2505	U2506							
		A2845	U2845	U2711	U2506	U2507							
		U2846	U2846	U2712	U2507	U2508							
		G2847	U2847	U2713	U2508	U2509							
		C2848	U2848	U2714	U2509	U2510							
		U2849	U2849	U2715	U2510	U2511							
		G2857	U2857	U2716	U2511	U2512							
		U2860	U2860	U2717	U2512	U2513							
		U2861	U2861	U2718	U2513	U2514							
		U2866	U2866	U2719	U2514	U2515							
		C2867	U2867	U2720	U2515	U2516							
		G2871	U2871	U2721	U2516	U2517							
		A2872	U2872	U2722	U2517	U2518							
		U2873	U2873	U2723	U2518	U2519							
		G2874	U2874	U2724	U2519	U2520							
		U2875	U2875	U2725	U2520	U2521							
		G2878	U2878	U2726	U2521	U2522							
		C2879	U2879	U2727	U2522	U2523							
		U2880	U2880	U2728	U2523	U2524							
		G2883	U2883	U2729	U2524	U2525							
		C2884	U2884	U2730	U2525	U2526							
		U2885	U2885	U2731	U2526	U2527							
		G2886	U2886	U2732	U2527	U2528							
		A2887	U2887	U2733	U2528	U2529							
		U2888	U2888	U2734	U2529	U2530							
		G2889	U2889	U2735	U2530	U2531							
		C2890	U2890	U2736	U2531	U2532							
		A2891	U2891	U2737	U2532	U2533							
		U2892	U2892	U2738	U2533	U2534							
		G2893	U2893	U2739	U2534	U2535							
		C2894	U2894	U2740	U2535	U2536							
		U2895	U2895	U2741	U2536	U2537							
		G2896	U2896	U2742	U2537	U2538							
		A2897	U2897	U2743	U2538	U2539							
		U2898	U2898	U2744	U2539	U2540							
		G2899	U2899	U2745	U2540	U2541							
		C2900	U2900	U2									



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52740	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	2.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.477	Depositor
Minimum map value	-0.263	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.025	Depositor
Map size ( $\text{\AA}$ )	429.264, 429.264, 429.264	wwPDB
Map dimensions	396, 396, 396	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.084, 1.084, 1.084	Depositor



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	R	0.34	0/2624	0.52	0/3522
2	X	0.29	0/1653	0.53	0/2255
3	i	0.77	0/890	0.72	0/1189
4	J	0.63	0/1821	0.65	0/2451
5	j	0.52	0/978	0.69	0/1301
6	K	0.55	0/1836	0.68	0/2481
7	k	0.48	0/778	0.71	0/1034
8	7	0.63	0/1539	0.65	0/2073
9	l	0.80	0/696	0.76	0/923
10	M	0.41	0/1374	0.64	0/1842
11	m	0.51	0/618	0.64	0/826
12	N	0.57	0/1568	0.69	2/2106 (0.1%)
13	n	0.79	0/443	0.80	1/588 (0.2%)
14	O	0.57	0/1068	0.65	0/1438
15	o	0.59	0/423	0.69	0/562
16	p	0.81	0/1757	0.76	1/2354 (0.0%)
17	Q	0.75	0/1585	0.71	3/2128 (0.1%)
18	5	0.74	0/1443	0.74	0/1944
19	S	0.55	0/1465	0.69	1/1965 (0.1%)
20	s	0.60	0/1807	0.74	2/2425 (0.1%)
21	T	0.69	0/1245	0.75	1/1661 (0.1%)
22	U	0.71	0/1481	0.69	0/1990
23	V	0.64	0/1300	0.66	0/1743
24	W	0.56	0/812	0.61	0/1099
25	P	0.25	0/734	0.54	0/1015
26	r	0.30	0/982	0.59	0/1320
27	x	0.66	0/1018	0.68	0/1369
28	3	1.13	0/2883	1.24	18/4491 (0.4%)
29	Y	0.62	0/525	0.66	0/696
30	4	1.40	4/3746 (0.1%)	1.26	23/5832 (0.4%)
31	Z	0.67	0/979	0.69	0/1321
32	a	0.53	0/1004	0.64	0/1341

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	B	0.84	1/1810 (0.1%)	1.21	7/2821 (0.2%)
34	b	0.61	0/1118	0.63	0/1497
35	C	0.57	0/860	0.71	0/1136
36	c	0.63	0/1204	0.71	0/1612
37	D	0.80	1/701 (0.1%)	0.76	0/934
38	d	0.49	0/473	0.63	0/629
39	E	0.76	1/1948 (0.1%)	0.72	1/2617 (0.0%)
40	e	0.61	0/751	0.68	0/1008
41	F	0.80	2/3146 (0.1%)	0.73	0/4228
42	f	0.73	0/890	0.70	0/1196
43	G	0.62	0/2800	0.70	0/3790
44	g	0.60	0/1041	0.66	0/1394
45	H	0.48	1/2425 (0.0%)	0.61	0/3271
46	h	0.75	0/868	0.68	0/1168
47	I	0.51	0/1260	0.60	0/1694
48	L	0.29	0/1634	0.59	0/2195
49	1	1.38	127/79382 (0.2%)	1.37	995/123763 (0.8%)
All	All	1.13	137/145386 (0.1%)	1.16	1055/214238 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	J	0	2
5	j	0	2
6	K	0	5
7	k	0	1
8	7	0	1
10	M	0	1
11	m	0	1
12	N	0	4
16	p	0	1
20	s	0	5
34	b	0	2
36	c	0	2
41	F	0	1
43	G	0	4
45	H	0	1
All	All	0	33

The worst 5 of 137 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	B	3	G	O3'-P	28.76	1.95	1.61
41	F	237	LYS	C-N	-10.70	1.09	1.34
49	1	920	A	N9-C4	-7.43	1.33	1.37
49	1	1589	A	N9-C4	-7.34	1.33	1.37
49	1	2149	A	N9-C4	-7.15	1.33	1.37

The worst 5 of 1055 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	B	3	G	P-O3'-C3'	-15.53	101.06	119.70
49	1	2080	C	N3-C2-O2	-14.72	111.60	121.90
49	1	2080	C	N1-C2-O2	14.16	127.39	118.90
49	1	2873	U	C2-N1-C1'	12.00	132.10	117.70
49	1	922	U	C2-N1-C1'	11.85	131.92	117.70

There are no chirality outliers.

5 of 33 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	J	157	ASN	Peptide
4	J	232	ARG	Peptide
6	K	36	ILE	Peptide
5	j	90	ARG	Peptide
5	j	91	ALA	Peptide

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	299/475 (63%)	288 (96%)	11 (4%)	0	100	100
2	X	222/224 (99%)	211 (95%)	11 (5%)	0	100	100
3	i	110/112 (98%)	101 (92%)	9 (8%)	0	100	100
4	J	220/222 (99%)	202 (92%)	17 (8%)	1 (0%)	25	54
5	j	117/119 (98%)	105 (90%)	9 (8%)	3 (3%)	4	22
6	K	231/233 (99%)	212 (92%)	18 (8%)	1 (0%)	30	60
7	k	97/99 (98%)	87 (90%)	10 (10%)	0	100	100
8	7	189/191 (99%)	177 (94%)	11 (6%)	1 (0%)	25	54
9	l	85/87 (98%)	73 (86%)	12 (14%)	0	100	100
10	M	167/169 (99%)	148 (89%)	17 (10%)	2 (1%)	11	35
11	m	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
12	N	191/193 (99%)	174 (91%)	11 (6%)	6 (3%)	3	18
13	n	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
14	O	134/136 (98%)	122 (91%)	12 (9%)	0	100	100
15	o	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
16	p	201/203 (99%)	179 (89%)	21 (10%)	1 (0%)	25	54
17	Q	195/197 (99%)	187 (96%)	8 (4%)	0	100	100
18	5	181/183 (99%)	167 (92%)	14 (8%)	0	100	100
19	S	183/185 (99%)	171 (93%)	12 (7%)	0	100	100
20	s	218/220 (99%)	193 (88%)	25 (12%)	0	100	100
21	T	150/152 (99%)	139 (93%)	10 (7%)	1 (1%)	19	47
22	U	170/172 (99%)	152 (89%)	17 (10%)	1 (1%)	22	50
23	V	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
24	W	98/100 (98%)	88 (90%)	10 (10%)	0	100	100
25	P	144/155 (93%)	121 (84%)	23 (16%)	0	100	100
26	r	117/197 (59%)	109 (93%)	8 (7%)	0	100	100
27	x	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
29	Y	60/62 (97%)	60 (100%)	0	0	100	100
31	Z	119/121 (98%)	110 (92%)	9 (8%)	0	100	100
32	a	124/126 (98%)	115 (93%)	9 (7%)	0	100	100
34	b	133/135 (98%)	121 (91%)	11 (8%)	1 (1%)	16	44
35	C	103/105 (98%)	89 (86%)	14 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	c	146/148 (99%)	126 (86%)	17 (12%)	3 (2%)	5	24
37	D	89/91 (98%)	80 (90%)	9 (10%)	0	100	100
38	d	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
39	E	250/252 (99%)	226 (90%)	24 (10%)	0	100	100
40	e	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
41	F	384/386 (100%)	348 (91%)	35 (9%)	1 (0%)	37	66
42	f	107/109 (98%)	98 (92%)	9 (8%)	0	100	100
43	G	359/361 (99%)	314 (88%)	44 (12%)	1 (0%)	37	66
44	g	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
45	H	294/296 (99%)	273 (93%)	21 (7%)	0	100	100
46	h	104/106 (98%)	96 (92%)	8 (8%)	0	100	100
47	I	152/175 (87%)	144 (95%)	8 (5%)	0	100	100
48	L	202/204 (99%)	167 (83%)	35 (17%)	0	100	100
All	All	7085/7457 (95%)	6476 (91%)	586 (8%)	23 (0%)	38	66

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
36	c	47	LYS
43	G	339	LEU
4	J	158	LYS
5	j	85	THR
5	j	91	ALA

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	287/392 (73%)	282 (98%)	5 (2%)	56	74
2	X	177/192 (92%)	177 (100%)	0	100	100
3	i	95/95 (100%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	J	186/186 (100%)	186 (100%)	0	100	100
5	j	104/104 (100%)	104 (100%)	0	100	100
6	K	187/191 (98%)	187 (100%)	0	100	100
7	k	81/81 (100%)	81 (100%)	0	100	100
8	7	171/171 (100%)	170 (99%)	1 (1%)	84	90
9	l	70/70 (100%)	70 (100%)	0	100	100
10	M	147/147 (100%)	146 (99%)	1 (1%)	81	88
11	m	68/68 (100%)	67 (98%)	1 (2%)	60	76
12	N	154/154 (100%)	151 (98%)	3 (2%)	52	71
13	n	45/45 (100%)	45 (100%)	0	100	100
14	O	107/107 (100%)	107 (100%)	0	100	100
15	o	47/47 (100%)	47 (100%)	0	100	100
16	p	175/175 (100%)	174 (99%)	1 (1%)	84	90
17	Q	160/160 (100%)	160 (100%)	0	100	100
18	5	140/145 (97%)	138 (99%)	2 (1%)	62	77
19	S	150/150 (100%)	150 (100%)	0	100	100
20	s	184/186 (99%)	183 (100%)	1 (0%)	86	91
21	T	126/126 (100%)	126 (100%)	0	100	100
22	U	156/156 (100%)	155 (99%)	1 (1%)	84	90
23	V	136/136 (100%)	136 (100%)	0	100	100
24	W	87/87 (100%)	87 (100%)	0	100	100
26	r	105/166 (63%)	105 (100%)	0	100	100
27	x	104/104 (100%)	104 (100%)	0	100	100
29	Y	54/54 (100%)	54 (100%)	0	100	100
31	Z	104/105 (99%)	104 (100%)	0	100	100
32	a	109/109 (100%)	109 (100%)	0	100	100
34	b	115/115 (100%)	115 (100%)	0	100	100
35	C	90/90 (100%)	90 (100%)	0	100	100
36	c	118/118 (100%)	116 (98%)	2 (2%)	56	74
37	D	71/71 (100%)	70 (99%)	1 (1%)	62	77
38	d	46/46 (100%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	E	193/194 (100%)	190 (98%)	3 (2%)	58	75
40	e	81/81 (100%)	81 (100%)	0	100	100
41	F	319/322 (99%)	317 (99%)	2 (1%)	84	90
42	f	92/96 (96%)	92 (100%)	0	100	100
43	G	288/288 (100%)	288 (100%)	0	100	100
44	g	109/109 (100%)	108 (99%)	1 (1%)	75	86
45	H	244/244 (100%)	244 (100%)	0	100	100
46	h	90/90 (100%)	90 (100%)	0	100	100
47	I	134/152 (88%)	134 (100%)	0	100	100
48	L	185/185 (100%)	181 (98%)	4 (2%)	47	68
All	All	5891/6110 (96%)	5862 (100%)	29 (0%)	85	91

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	s	6	ARG
48	L	108	ASN
36	c	78	LEU
44	g	27	ARG
36	c	56	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
38	d	12	GLN
43	G	110	ASN
39	E	79	ASN
42	f	57	GLN
44	g	13	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	3	120/121 (99%)	29 (24%)	1 (0%)
30	4	157/158 (99%)	45 (28%)	6 (3%)
33	B	75/76 (98%)	20 (26%)	5 (6%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	1	3313/3316 (99%)	975 (29%)	181 (5%)
All	All	3665/3671 (99%)	1069 (29%)	193 (5%)

5 of 1069 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	3	10	C
28	3	11	A
28	3	12	U
28	3	13	A
28	3	14	U

5 of 193 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	1	2101	C
49	1	2509	U
49	1	2144	A
49	1	2283	G
49	1	2635	A

## 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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	R	4
49	1	4
33	B	1
45	H	1
41	F	1

The worst 5 of 11 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	173:UNK	C	188:SER	N	35.01
1	1	2087:C	O3'	2093:A	P	28.51
1	R	105:ARG	C	113:UNK	N	19.16
1	R	529:GLY	C	535:UNK	N	16.65
1	R	123:UNK	C	156:UNK	N	13.22

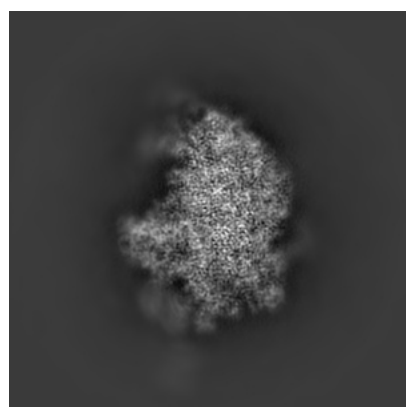
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4753. These allow visual inspection of the internal detail of the map and identification of artifacts.

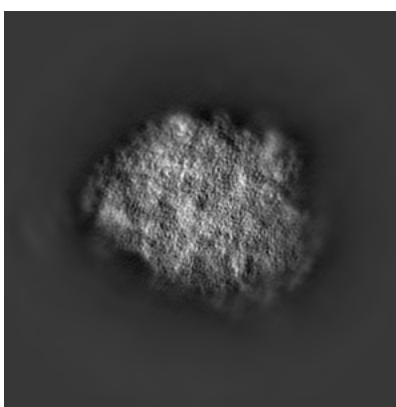
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

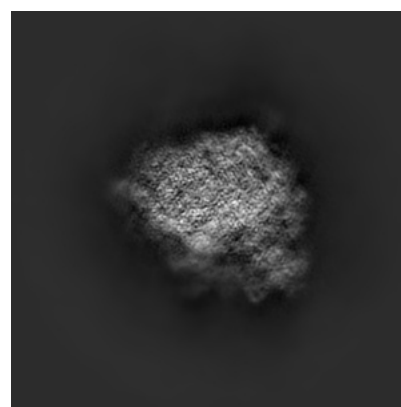
#### 6.1.1 Primary map



X



Y

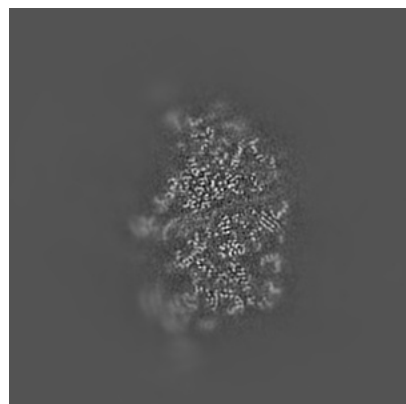


Z

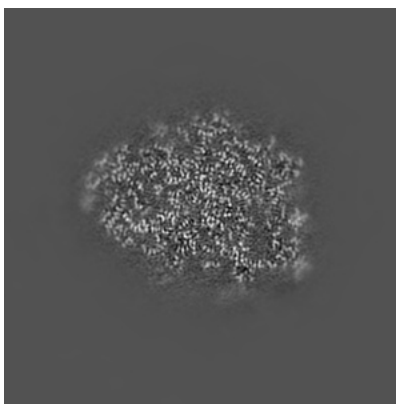
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

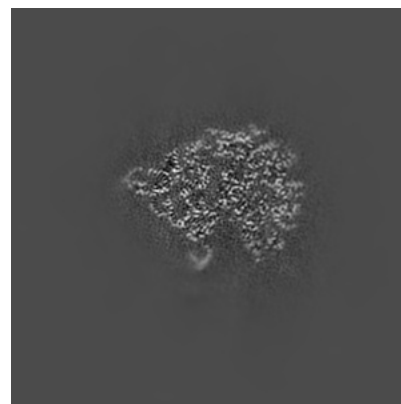
#### 6.2.1 Primary map



X Index: 198



Y Index: 198

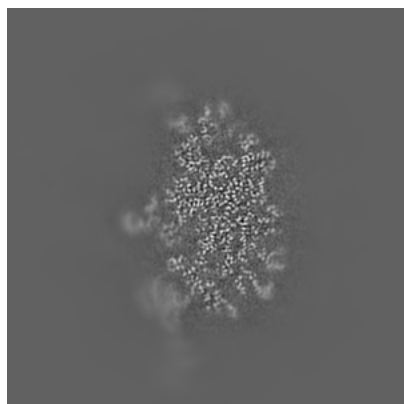


Z Index: 198

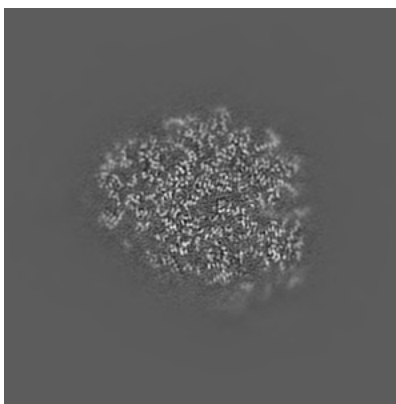
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

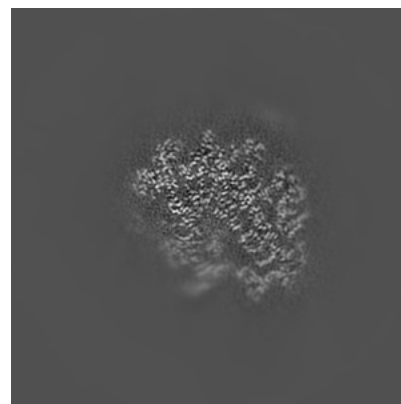
### 6.3.1 Primary map



X Index: 187



Y Index: 207

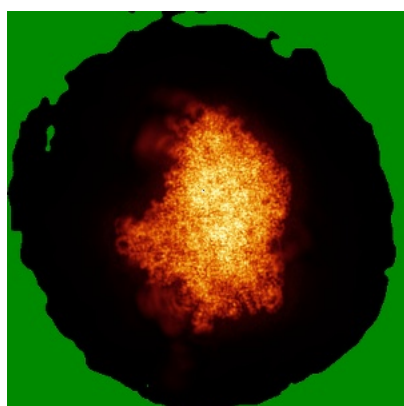


Z Index: 182

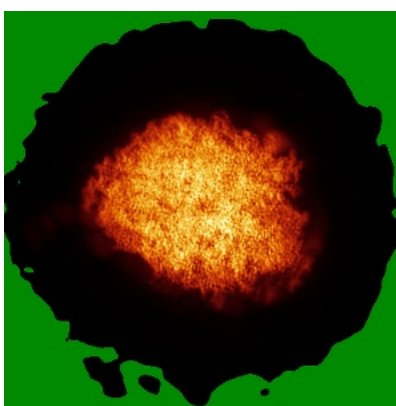
The images above show the largest variance slices of the map in three orthogonal directions.

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

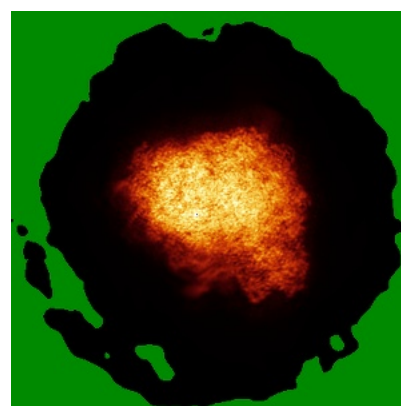
### 6.4.1 Primary map



X



Y



Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

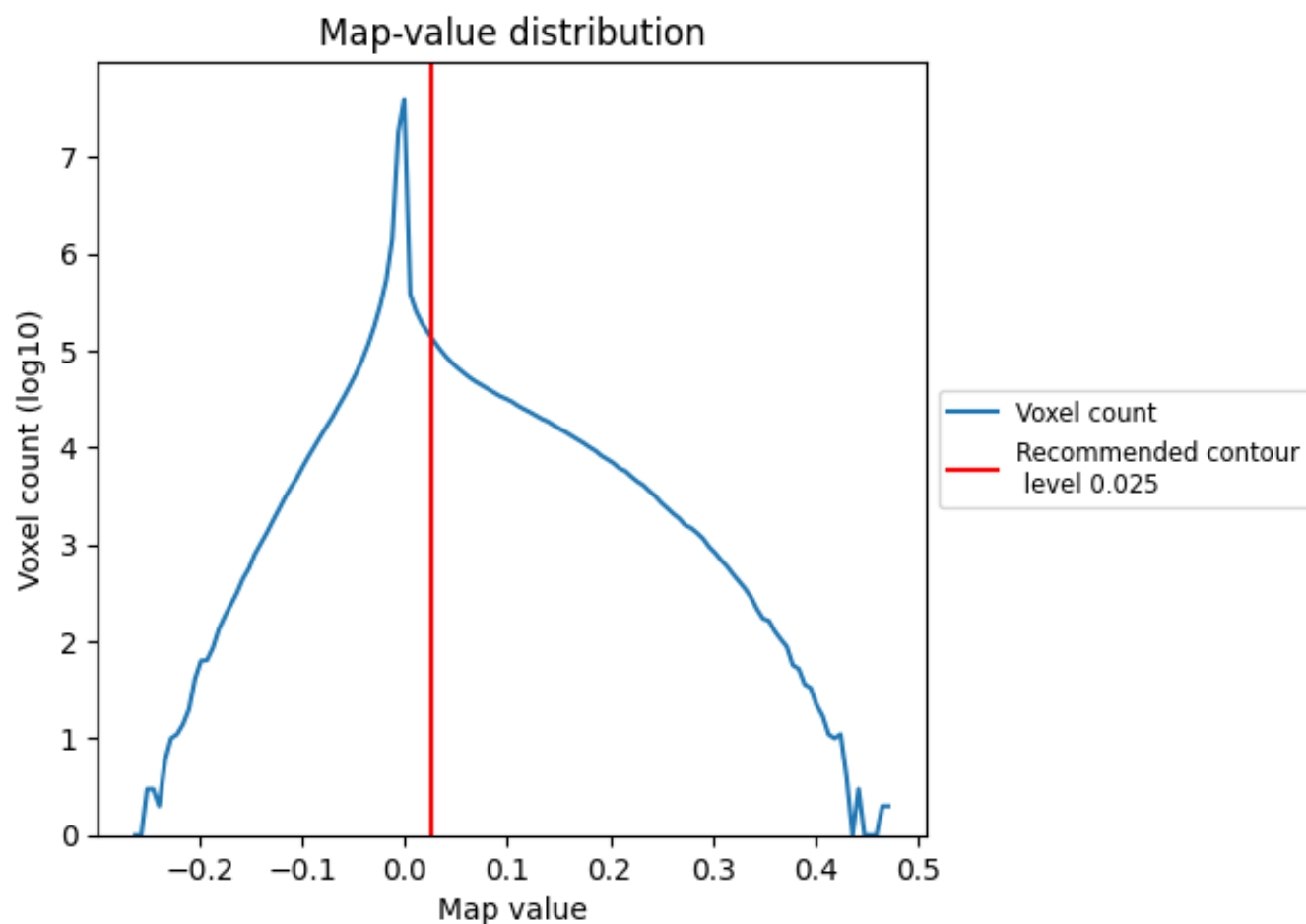
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

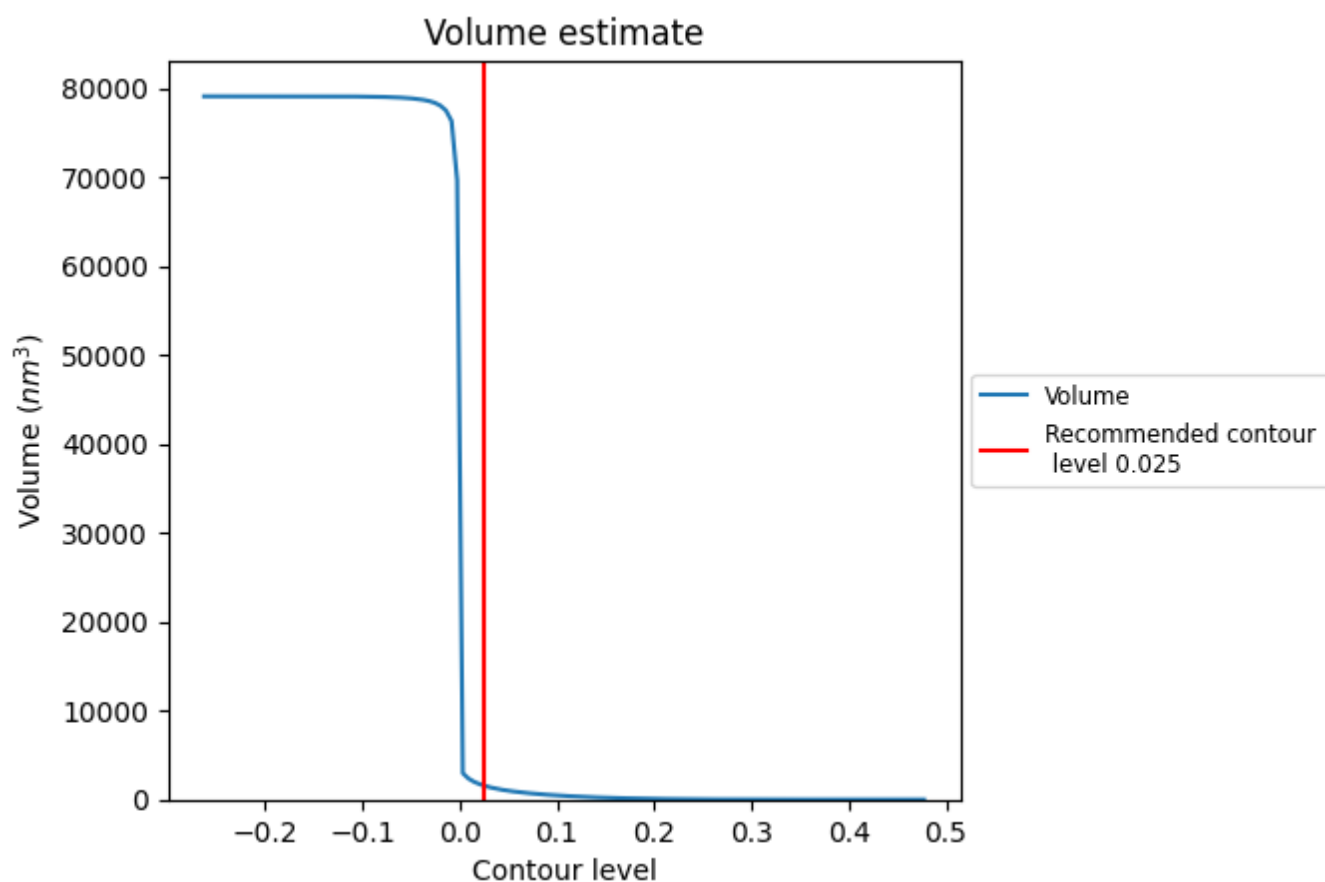
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

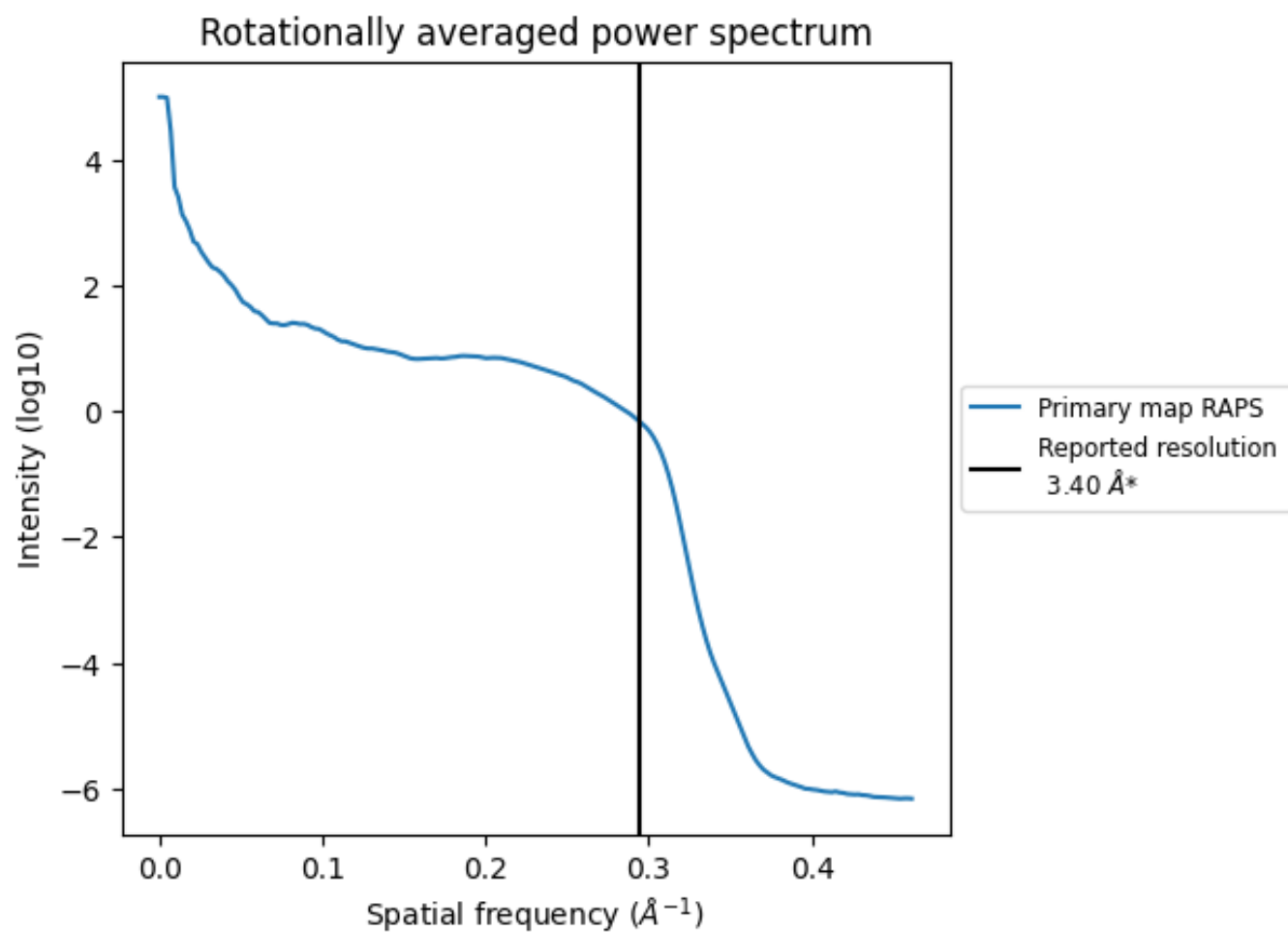
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1576 nm<sup>3</sup>; this corresponds to an approximate mass of 1423 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 0.294 Å<sup>-1</sup>

## 8 Fourier-Shell correlation

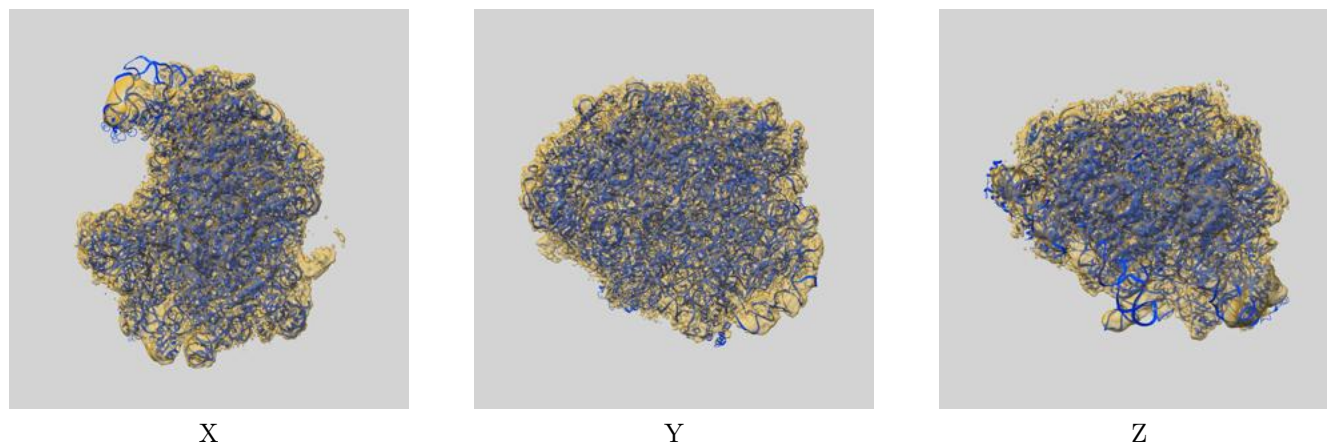
This section was not generated. No FSC curve or half-maps provided.



## 9 Map-model fit [i](#)

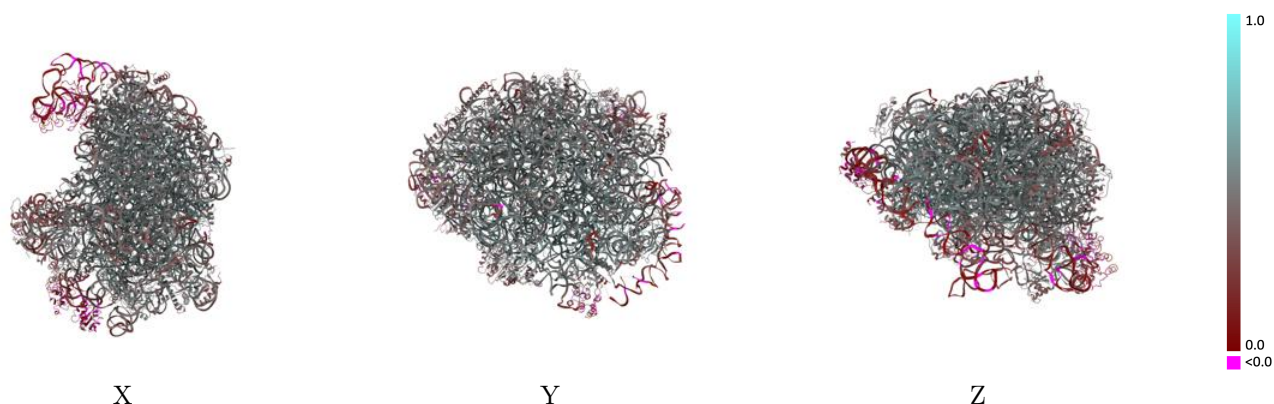
This section contains information regarding the fit between EMDB map EMD-4753 and PDB model 6R87. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

### 9.1 Map-model overlay [i](#)



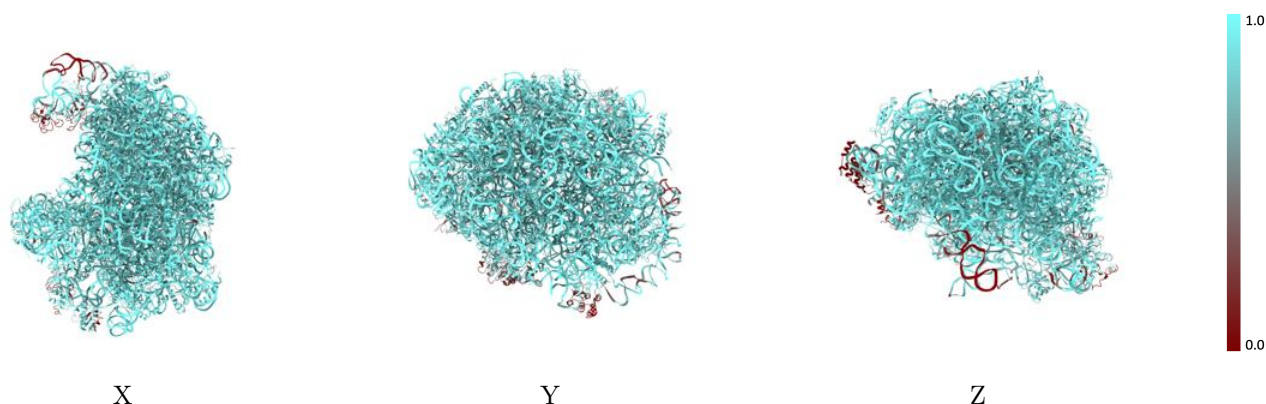
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



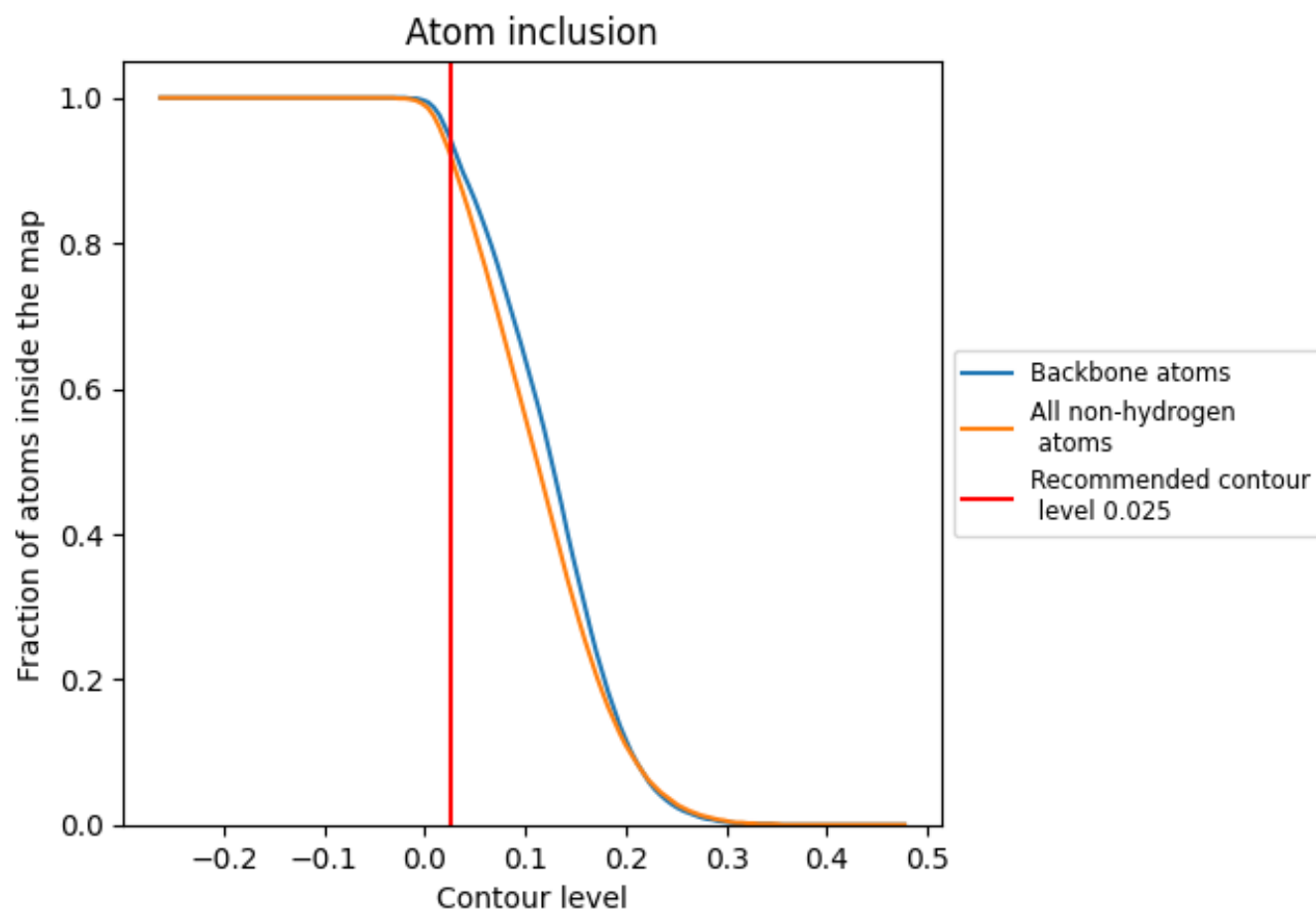
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9240	 0.4550
1	 0.9610	 0.4660
3	 0.9910	 0.4600
4	 0.9860	 0.5000
5	 0.9290	 0.5000
7	 0.9270	 0.4830
B	 0.9330	 0.2550
C	 0.8960	 0.4630
D	 0.9420	 0.5070
E	 0.9360	 0.5290
F	 0.9500	 0.5170
G	 0.9230	 0.4860
H	 0.8850	 0.3900
I	 0.9130	 0.4590
J	 0.9130	 0.4730
K	 0.9160	 0.4480
L	 0.4100	 0.0660
M	 0.8790	 0.3840
N	 0.9220	 0.4730
O	 0.9180	 0.4690
P	 0.5470	 0.1000
Q	 0.9450	 0.5180
R	 0.5930	 0.2820
S	 0.9200	 0.4850
T	 0.9390	 0.5050
U	 0.9210	 0.5010
V	 0.9060	 0.4850
W	 0.9140	 0.4440
X	 0.4590	 0.3440
Y	 0.9340	 0.4980
Z	 0.9490	 0.5090
a	 0.9390	 0.4800
b	 0.9220	 0.4760
c	 0.9260	 0.4890
d	 0.8940	 0.4440



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Chain	Atom inclusion	Q-score
e	 0.9120	 0.4580
f	 0.9140	 0.5080
g	 0.9430	 0.5120
h	 0.9440	 0.5220
i	 0.9510	 0.5190
j	 0.9190	 0.4690
k	 0.8980	 0.4480
l	 0.9500	 0.5380
m	 0.8560	 0.4360
n	 0.9520	 0.5290
o	 0.9450	 0.4990
p	 0.9460	 0.5300
r	 0.7330	 0.0850
s	 0.8890	 0.4550
x	 0.9340	 0.5120