



## wwPDB EM Validation Summary Report ⓘ

Dec 30, 2024 – 08:24 AM EST

PDB ID : 8AGV  
EMDB ID : EMD-15425  
Title : Yeast RQC complex in state H  
Authors : Tesina, P.; Buschauer, R.; Beckmann, R.  
Deposited on : 2022-07-20  
Resolution : 2.60 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>.

---

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 : 2022.3.0, CSD as543be (2022)  
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) : 2.40

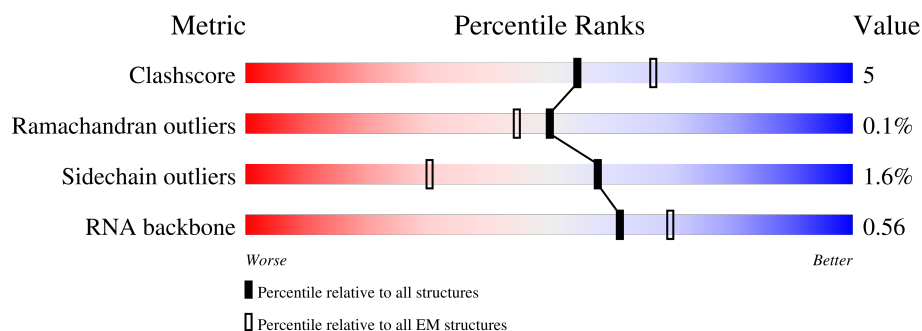
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.60 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.







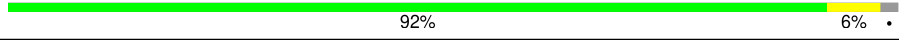
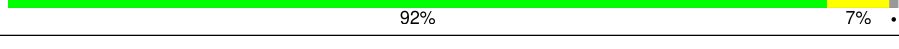
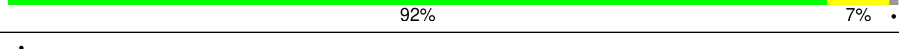
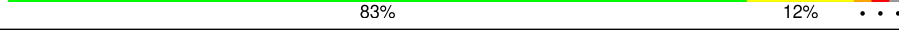
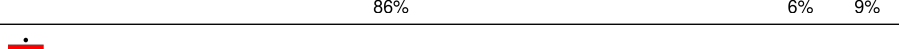
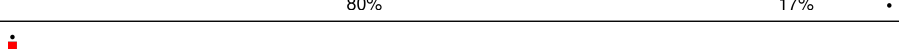
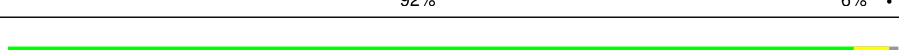
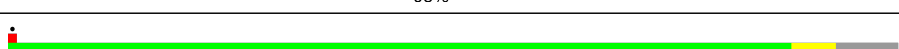
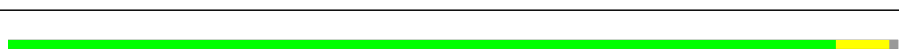
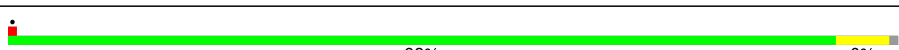
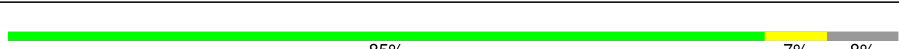

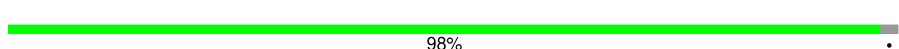

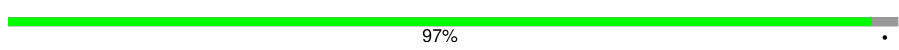
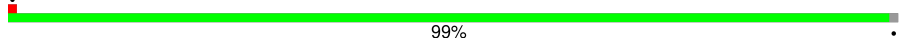
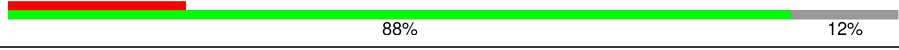
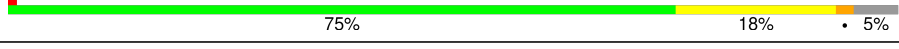



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A	204	
2	B	199	
3	C	184	
4	D	186	
5	E	189	
6	F	172	
7	G	160	

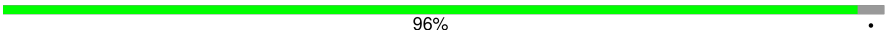

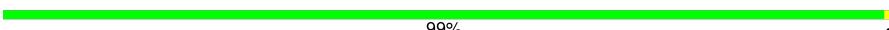
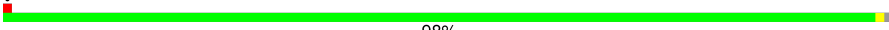






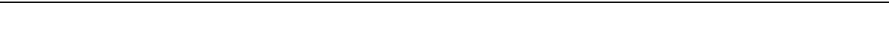

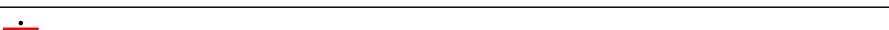
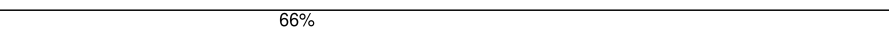
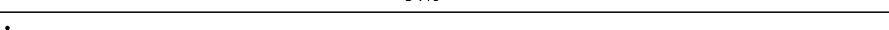

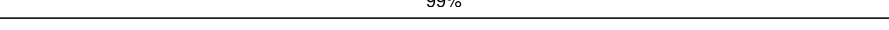




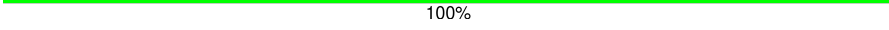
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	H	121	
9	I	137	
10	J	155	
11	K	142	
12	L	127	
13	M	136	
14	N	149	
15	O	59	
16	P	105	
17	Q	113	
18	R	130	
19	S	107	
20	T	121	
21	U	120	
22	V	100	
23	W	88	
24	X	78	
25	Y	51	
26	Z	128	
27	b	106	
28	c	92	
29	d	25	
30	f	3395	
31	h	121	
32	i	158	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	j	254	 96% .
34	k	387	 99% .
35	l	362	 99% .
36	m	297	 98% ..
37	n	176	 94% . 5%
38	o	244	 91% 9%
39	p	256	 89% . 9%
40	q	191	 98% ..
41	r	221	 98% ..
42	s	174	 95% .. .
43	t	199	 96% . .
44	u	138	 97% ..
45	a	1038	 78% . 18%
46	e	1562	 66% 94% . .
47	g	245	 91% 8%
48	w	217	 99%
49	x	76	 67% 30% .
49	y	76	 57% 39% .
50	z	165	 89% . 10%
51	0	312	 31% 7% . 61%
52	1	18	 100%
53	v	157	 88% . 10%

## 2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 151349 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 L15-A.

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

- Molecule 2 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 3 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 4 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 5 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O		0	0
			1258	781	265	212			

- Molecule 6 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 7 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 8 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 9 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	63	Total	C	N	O	S	0	0
			518	333	102	82	1		

- Molecule 11 is a protein called 60S ribosomal protein L25.

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

- Molecule 12 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	125	Total	C	N	O	S	0	0
			984	620	191	173			

- Molecule 13 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	135	Total	C	N	O	S	0	0
			1080	701	199	180			

- Molecule 14 is a protein called 60S ribosomal protein L28.

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

- Molecule 15 is a protein called 60S ribosomal protein L29.

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

- Molecule 16 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 17 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 19 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 23 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L38.

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

- Molecule 25 is a protein called 60S ribosomal protein L39.

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

- Molecule 26 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 27 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 28 is a protein called 60S ribosomal protein L43-A.



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

- Molecule 29 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	22	Total	C	N	O	S	0	0
			207	127	56	23	1		

- Molecule 30 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	3216	Total	C	N	O	P	1	0
			68802	30732	12391	22462	3217		

- Molecule 31 is a RNA chain called 5S rRNA.

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

- Molecule 32 is a RNA chain called 5.8S rRNA.

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

- Molecule 33 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	j	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

- Molecule 34 is a protein called 60S ribosomal protein L3.

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

- Molecule 35 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 37 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	n	167	Total	C	N	O	0	0
			1307	843	234	230		

- Molecule 38 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 41 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 42 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 43 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 45 is a protein called RQC2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	a	848	Total	C	N	O	S	0	0
			6569	4188	1138	1226	17		

- Molecule 46 is a protein called E3 ubiquitin-protein ligase listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	e	1527	Total	C	N	O	S	0	0
			11516	7358	1937	2183	38		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	g	225	Total	C	N	O	S	0	0
			1651	1030	282	332	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	w	216	Total	C	N	O	S	0	0
			1709	1092	298	310	9		

- Molecule 49 is a RNA chain called Ala tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	x	74	Total	C	N	O	P	0	0
			1579	702	278	525	74		
49	y	73	Total	C	N	O	P	0	0
			1556	692	273	518	73		

- Molecule 50 is a protein called 60S ribosomal protein L12-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	z	148	Total	C	N	O	0	0
			728	432	148	148		

- Molecule 51 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	0	121	Total	C	N	O	S	0	0
			961	618	167	173	3		

- Molecule 52 is a protein called CAT-tailed nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	1	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 53 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	142	Total	C	N	O	S	0	0
			1085	676	183	217	9		

- Molecule 54 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	A	1	Total	Mg	0
			1	1	
54	C	1	Total	Mg	0
			1	1	
54	E	1	Total	Mg	0
			1	1	
54	I	1	Total	Mg	0
			1	1	
54	R	1	Total	Mg	0
			1	1	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		AltConf
54	T	1	Total 1	Mg 1	0
54	f	3	Total 3	Mg 3	0
54	h	1	Total 1	Mg 1	0
54	j	2	Total 2	Mg 2	0
54	k	1	Total 1	Mg 1	0

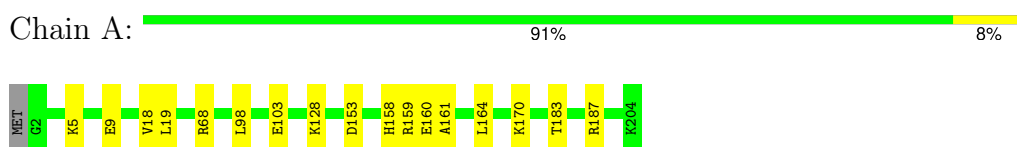
- Molecule 55 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	T	1	Total 1	Zn 1	0
55	W	1	Total 1	Zn 1	0
55	Z	1	Total 1	Zn 1	0
55	b	1	Total 1	Zn 1	0
55	c	1	Total 1	Zn 1	0
55	e	2	Total 2	Zn 2	0

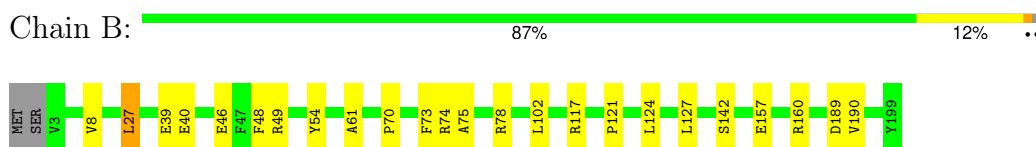
### 3 Residue-property plots [i](#)

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

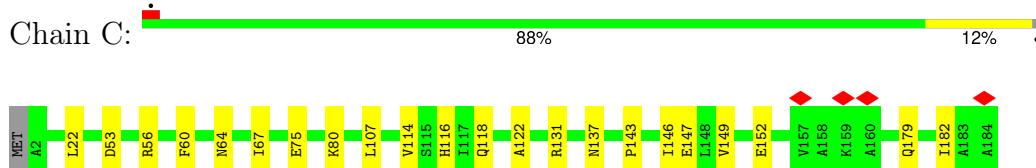
- Molecule 1: 60S ribosomal protein L15-A



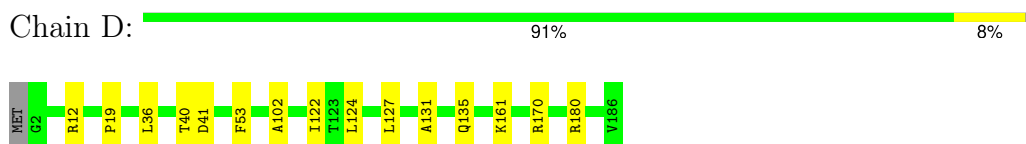
- Molecule 2: 60S ribosomal protein L16-A



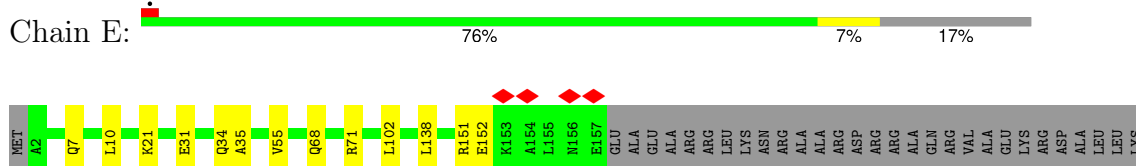
- Molecule 3: 60S ribosomal protein L17-A



- Molecule 4: 60S ribosomal protein L18-A



- Molecule 5: 60S ribosomal protein L19-A



GLU  
ASP  
ALA

- Molecule 6: 60S ribosomal protein L20-A

Chain F:  87% 12%


- Molecule 7: 60S ribosomal protein L21-A

Chain G:  90% 9%

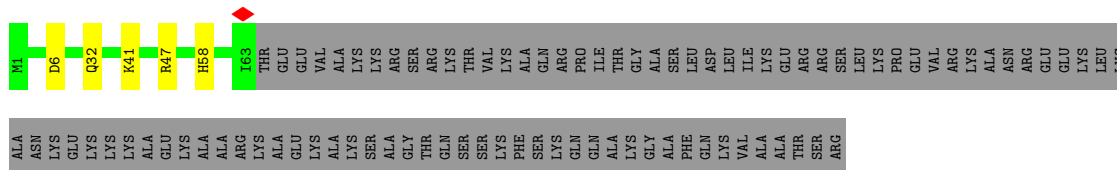
- Molecule 8: 60S ribosomal protein L22-A

Chain H:  74% 9% 17%


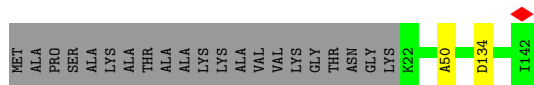
- Molecule 9: 60S ribosomal protein L23-A

Chain I:  90% 9%

- Molecule 10: 60S ribosomal protein L24-A

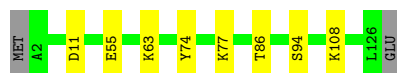
Chain J:  37% 59%

- Molecule 11: 60S ribosomal protein L25

Chain K:  84% 15%

- Molecule 12: 60S ribosomal protein L26-A

Chain L:  92% 6% .



- Molecule 13: 60S ribosomal protein L27-A

Chain M:  92% 7% .




- Molecule 14: 60S ribosomal protein L28

Chain N:  92% 7% .




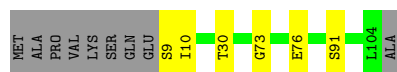
- Molecule 15: 60S ribosomal protein L29

Chain O:  83% 12% . . .




- Molecule 16: 60S ribosomal protein L30

Chain P:  86% 6% 9%



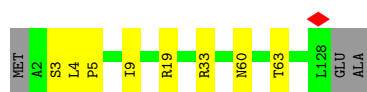
- Molecule 17: 60S ribosomal protein L31-A

Chain Q:  80% 17% .



- Molecule 18: 60S ribosomal protein L32

Chain R:  92% 6% .




- Molecule 19: 60S ribosomal protein L33-A

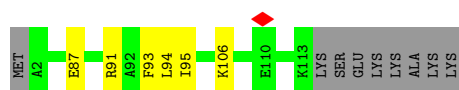


Chain S:  95% . .



- Molecule 20: 60S ribosomal protein L34-A

Chain T:  88% 5% 7%



- Molecule 21: 60S ribosomal protein L35-A

Chain U:  93% 6% .




- Molecule 22: 60S ribosomal protein L36-A

Chain V:  93% 6% .




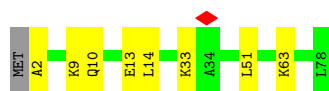
- Molecule 23: 60S ribosomal protein L37-A

Chain W:  85% 7% 8%



- Molecule 24: 60S ribosomal protein L38

Chain X:  88% 10% .

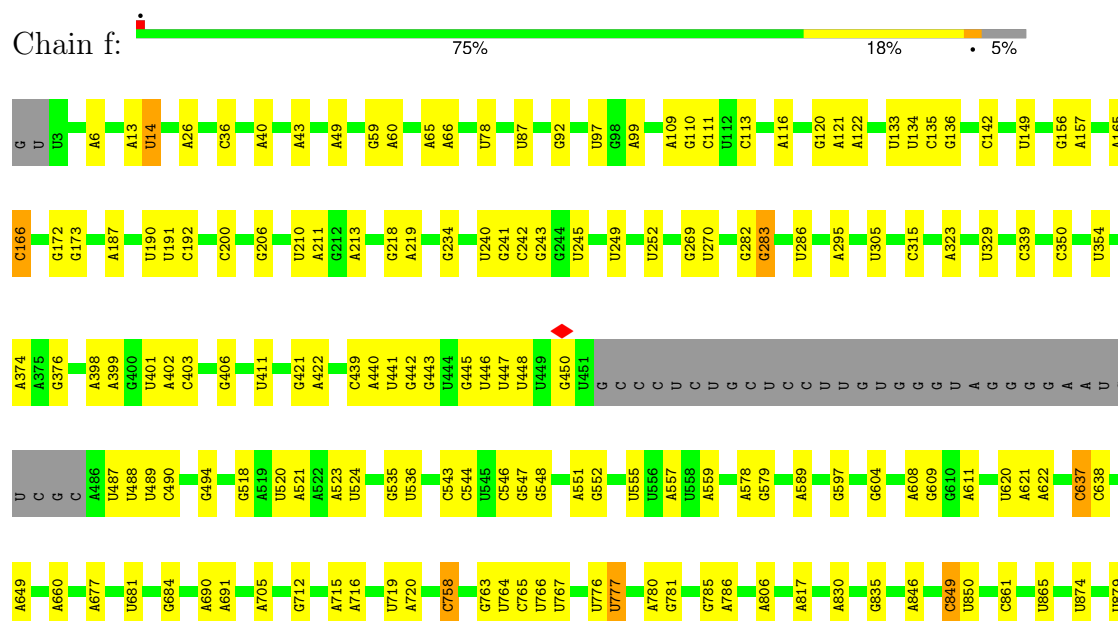


- Molecule 25: 60S ribosomal protein L39

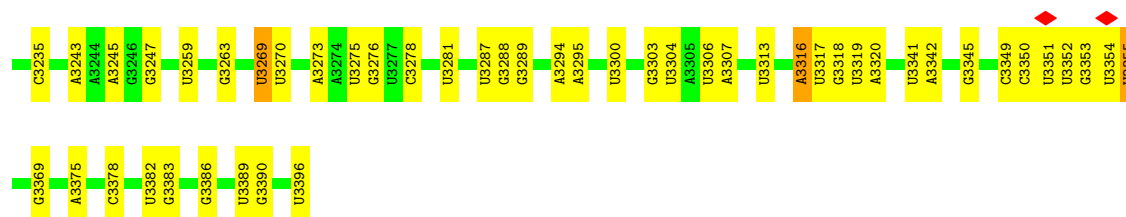
Chain Y:  98% .



- Molecule 26: Ubiquitin-60S ribosomal protein L40



U3078	U3079	C2844	A2845	U2846	C2849	U2860	C2867	G2871	A2872	U2873	C2876	A2887	G2898	C2899	A2911	G2914	U2923	U2935	A2936	A2941	C2942	G2947	A2971	C2983	G2990	A3180	C3181	A3186	A3187	U3196	U3207	G3208	A3209	U3214	C3217	A3218	G3219	C3228	G3229				
A2689	G2690	A2691	A2694	U2695	A2696	A2704	G2714	U2719	C2726	U2727	U2728	U2729	A2740	U2752	G2753	C2754	C2755	C2764	C2772	C2773	G2777	G2778	U2783	C2788	G2796	G2800	A2801	A2802	U2803	C2810	G2814	U2817	U2818	C2821	G2834	U2835	C2836	U2842					
C2531	U2537	U2538	C2539	A2540	U2541	U2542	U2543	U2544	A2547	C2548	U2549	U2550	U2551	C2552	U2553	A2554	C2555	A2561	C2568	A2569	U2570	U2571	C2572	C2573	U2581	C2585	A2593	C2594	G2606	C2607	G2614	U2617	C2622	C2638	G2648	G2651	U2652	A2656	A2674	G2677	A2678		
G2403	A2404	C2405	U2411	U2416	A2419	G2437	C2444	U2445	U2446	A2447	G2450	A2461	C2462	G2463	U2464	A2468	G2469	U2470	U2471	U2472	C2473	G2474	C2479	A2480	A2484	U2485	A2486	U2487	A2488	A2494	C2495	U2497	U2498	U2499	A2500	U2501	U2502	G2503	U2505	U2514	A2515	G2522	C2526
A2224	U2225	A2228	C2235	G2249	U2254	U2254	A2254	A2254	C2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	A2254	
G	C	U	U	C	U	A	U	U	C	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U		
U	A	G	G	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C			
C1762	U1763	U1764	U1765	G1766	G1770	G1775	G1780	A1797	A1814	U1815	A1816	U1819	U1820	U1821	A1835	A1839	U1840	A1841	A1842	C1846	C1849	A1850	C1866	A1867	C1872	G1878	A1879	U1880	A1881	A1893	G1906	C1907	C1943	C1951	G1952	G1953	G1954	U1955	A	G	U		
U1568	U1569	U1572	U1573	C1574	A1575	G1576	G1577	A1580	C1581	C1582	A1583	A1589	G1590	C1597	G1604	A1605	U1607	C1608	U1620	U1629	C1639	A1642	A1643	C1644	U1645	C1657	A1683	U1688	U1716	U1717	U1724	C1725	U1732	G1736	A1741	A1750	G1751	A1760	C1761				
U1351	A1352	G1353	G1354	A1355	U1356	G1357	A1386	G1392	A1399	G1400	A1419	U1425	G1434	C1437	A1446	U1447	A1448	A1449	G1450	A1481	A1482	G1483	G1487	G1488	C1496	C1502	C1508	G1525	G1536	A1539	U1554	U1555	C1556	U1557	G1560	U1561	C1562	A1566	U1567				
U1218	C1219	G1222	A1225	U1226	C1227	U1235	G1236	G1237	C1238	C1239	A1240	G1242	G1243	A1244	A1245	A1251	A1252	U1253	C1254	U1258	A1263	G1264	U1265	U1269	C1272	C1277	A1278	C1279	G1282	G1285	A1286	A1287	G1295	G1307	A1308	U1309	G1313	A1330	U1348	G1349	A1350		
A1036	U1041	A1047	A1048	C1049	G1063	A1064	A1065	G1072	U1081	U1082	G1087	A1093	U1094	U1095	U1096	G1097	A1098	A1103	G1104	G1115	G1116	G1117	G1131	U1144	A1153	A1159	C1160	G1177	A1180	U1181	A1190	U1191	C1192	A1193	C1196	A1197	C1201	A1202	U1208	U1217			
C890	A896	G907	G908	A914	A915	A916	A917	A920	A921	U922	G923	G924	A925	G937	C944	U954	C959	U960	C969	U981	C982	U985	U986	G991	G994	U995	G1001	A1002	G1010	U1015	C1016	C1017	G1018	G1021	G1024	A1025	U1026	A1027	U1028				



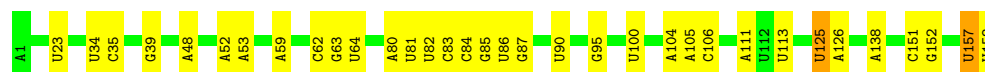
• Molecule 31: 5S rRNA

Chain h: 86% 14%



• Molecule 32: 5.8S rRNA

Chain i: 78% 20%



• Molecule 33: 60S ribosomal protein L2-A

Chain j: 96%



• Molecule 34: 60S ribosomal protein L3

Chain k: 99%



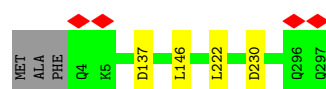
• Molecule 35: 60S ribosomal protein L4-A

Chain l: 99%



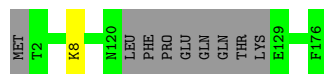
• Molecule 36: 60S ribosomal protein L5

Chain m: 98%



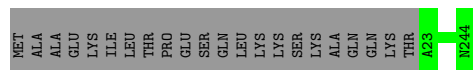
- Molecule 37: 60S ribosomal protein L6-B

Chain n:  94% • 5%




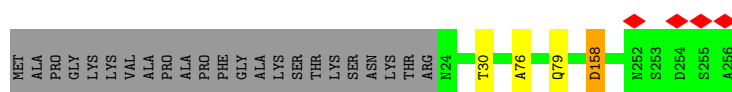
- Molecule 38: 60S ribosomal protein L7-A

Chain o:  91% 9%



- Molecule 39: 60S ribosomal protein L8-A

Chain p:  89% • 9%



- Molecule 40: 60S ribosomal protein L9-A

Chain q:  98% ..



- Molecule 41: 60S ribosomal protein L10

Chain r:  98% ..



- Molecule 42: 60S ribosomal protein L11-A

Chain s:  95% ..



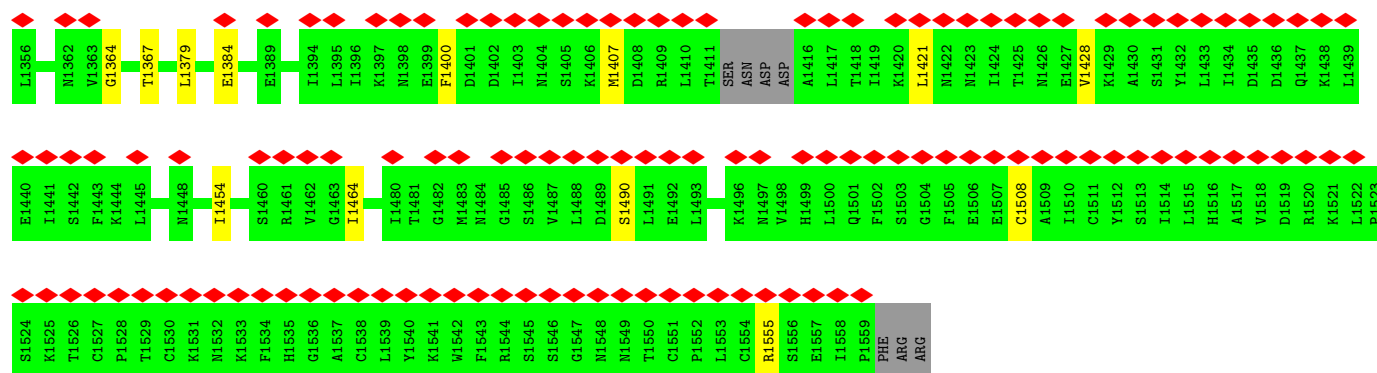
- Molecule 43: 60S ribosomal protein L13-A

Chain t:  96% ..

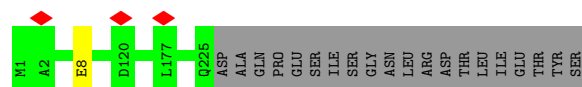




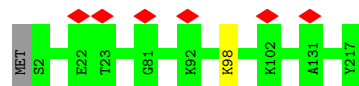
Q1293	L1294	K1295	E1296	A1297	Q1298	L1299	I1300	N1301	R1302	M1303	F1306	D1309	D1312	L1313	R1314	D1315	T1316	E1317	F1318	W1319	K1320	Q1321	V1322	D1323	T1324	K1325	E1326	I1327	S1328	E1329	Y1330	N1331	I1332	V1333	G1334	N1335	N1336	F1337	S1338	P1339	Y1340	K1341	E1342	D1343	I1344	F1345	E1346	E1347	C1348	K1349	K1350	L1351	L1352	C1353	H1354	T1355								
SER	ALA	SER	ASP	ASN	ASP	VAL	N1235	S1236	K1237	F1238	K1239	L1240	F1241	Q1242	K1243	L1244	L1245	Q1246	K1247	V1248	T1249	D1250	E1251	P1253	K1254	E1255	Y1256	L1257	E1258	Y1259	E1260	N1261	K1262	N1263	S1264	Y1268	L1269	W1270	Y1271	H1273	L1276	F1279	K1280	S1283	Y1284	N1285	M1286	R1287	Q1288	I1289	F1290	I1291	E1292											
T1108	L1109	S1110	Q1111	GLY	VAL	SER	L1174	F1175	E1176	GLY	GLU	ILE	SER	E1122	Y1123	G1124	D1125	E1126	I1127	Q1128	E1129	N1130	L1131	I1132	E1133	L1134	M1135	F1136	L1137	N1138	F1139	N1140	Q1141	E1142	R1143	N1144	M1145	Q1146	V1147	S1148	T1149	L1150	F1151	Y1152	Q1153	K1154	L1155	Y1156	K1157	V1158	I1159	S1160	S1161	M1162	GLN	LYS	GLN	THR	GLY	SER	ASP	VAL	ASP	GLY
E1168	S1169	Q1170	Y1171	K1172	R1173	L1174	F1175	E1176	V1177	GLU	ILE	L1178	L1179	M1180	D1181	K1182	D1183	I1184	G1185	S1186	M1187	I1188	N1189	Q1190	S1191	L1192	L1193	L1194	T1195	L1196	L1197	L1198	G1199	S1200	L1201	V1202	V1203	K1204	T1205	Q1206	Q1207	D1208	I1209	I1210	I1211	E1212	E1214	L1215	L1216	I1217	GLN	LYS	GLN	THR	GLY	SER	ASP	VAL	ASP	GLY				
E128	D629	F630	M631	K632	N633	Y634	K635	F636	D637	D638	S639	G640	E641	I642	F643	K644	G645	N646	M647	K648	F649	L650	N651	Q652	R653	T654	I655	T656	T657	L658	Y659	R660	L661	A662	A663	A664	N665	G666	Q667	V668	E669	Q670	I671	C672	C673	V674	L675	S676	K677	L678	D679	E680	T681	F682	F683	S684	L685	L686	L687					
N569	S570	K571	F572	F573	K574	M575	N576	T577	D578	A579	I580	T581	S582	L583	E584	D585	F586	F587	I588	V589	A590	L591	S592	F593	N594	L595	P596	K597	T598	I599	I600	L601	A602	A662	A663	A664	N665	G666	Q667	V668	E669	Q670	I671	C672	C673	V674	L675	S676	K677	L678	D679	E680	T681	F682	F683	S684	L685	L686	L687					
L688	N689	T690	D691	F692	L693	S694	C695	A696	L697	Y698	E699	V700	S701	E702	D703	T704	N705	E706	K707	L708	F709	L710	L711	S712	L713	Q714	L715	A716	K717	G718	Y659	N719	S720	E721	I722	A723	N724	K725	L726	A727	Q728	S729	I730	L731	C732	C733	A734	L735	S736	V737	F738	S739	P740	G741	A742	K743	I804	L745	Y746	V747				
T748	H749	A750	V751	E752	L753	I754	N755	G756	T757	N758	D759	T760	S761	Q762	I763	F764	F765	F766	A767	N768	A769	I770	E771	V772	H773	A774	R775	Y776	M777	F778	T839	A779	I780	D781	I782	R783	S784	S785	L786	T787	S788	S789	L790	S791	T792	N793	T794	H795	L796	L797	L798	T799	D800	I801	K802	P803	I804	N805	L806	K807				
N808	M809	Q810	K811	L812	L813	R814	Y815	A816	L817	F818	L819	D820	A821	L822	L823	D824	A825	L826	P827	E828	R829	V830	N831	N832	H833	I834	V835	A836	F837	I838	T839	V840	N841	S842	R843	L844	V845	T846	Y848	N849	C850	L851	S852	E853	E854	P855	N856	L858	Y859	Y860	D861	F862	G863	H864	T865	F866	F867							
K868	H869	G870	K871	V872	N873	L874	N875	F876	S877	D878	I879	V880	G881	N882	V883	I884	Q885	P886	A887	N888	G889	S890	D891	A892	H893	L894	T895	F896	D897	I898	A899	E900	S901	N902	S903	V904	Y905	F906	F907	Y908	Y909	S910	R911	V912	L913	Y914	K915	V916	L917	L918	N919	S920	I921	D922	T923	V924	S925	S926	T927					
T928	L929	N930	G931	L932	L933	A934	S935	V936	E937	S938	F939	V940	T941	K942	T943	V944	D945	D946	Q947	K948	S949	T950	D951	K952	D953	Y954	L955	L956	C957	A958	I959	L960	L961	L962	N963	F964	N965	R966	S967	N968	S969	K970	D971	E972	L973	T974	K975	L976	R977	T978	L979	L980	A981	S982	Q983	L984	I985	G986	I987					
R988	E989	V990	E991	L992	V993	D994	Q995	E996	F997	K998	S999	L1000	A1001	L1002	L1003	N1004	L1005	L1006	L1007	D1008	I1009	P1010	Q1011	A1012	D1013	K1014	Q1015	F1016	V1017	P1018	I1019	A1020	P1021	Q1022	R1023	L1024	N1025	M1026	I1027	F1028	R1029	S1030	I1031	L1032	K1033	W1034	L1035	D1036	S1037	D1038	L1039	A1040	I1041	D1042	P1043	S1044	S1046	T1047						
V1048	R1049	L1050	L1051	L1052	L1053	D1054	F1055	F1056	T1057	K1058	L1059	M1060	R1061	F1062	E1063	G1064	V1065	R1066	D1067	G1069	I1070	T1071	A1072	F1073	E1074	L1075	S1076	E1077	R1078	L1079	L1080	A1081	D1082	S1083	L1084	S1085	M1086	C1087	Q1088	T1089	D1090	D1091	L1092	L1093	Y1094	L1095	L1096	E1097	L1098	R1099	S1100	S1101	C1102	L1103	N1104	Y1106	E1107							
T1108	L1109	S1110	Q1111	GLY	VAL	SER	L1174	F1175	E1176	GLY	GLU	ILE	SER	E1122	Y1123	G1124	D1125	E1126	I1127	Q1128	E1129	N1130	L1131	I1132	E1133	L1134	M1135	F1136	L1137	N1138	F1139	N1140	Q1141	E1142	R1143	N1144	M1145	Q1146	V1147	S1148	T1149	L1150	F1151	Y1152	Q1153	K1154	L1155	Y1156	K1157	V1158	I1159	S1160	S1161	M1162	GLN	LYS	GLN	THR	GLY	SER	ASP	VAL	ASP	GLY
E1168	S1169	Q1170	Y1171	K1172	R1173	L1174	F1175	E1176	V1177	GLU	ILE	L1178	L1179	M1180	D1181	K1182	D1183	I1184	G1185	S1186	M1187	I1188	N1189	Q1190	S1191	L1192	L1193	L1194	T1195	L1196	L1197	L1198	G1199	S1200	L1201	V1202	V1203	K1204	T1205	Q1206	Q1207	D1208	I1209	I1210	I1211	E1212	E1214	L1215	L1216	I1217	GLN	LYS	GLN	THR	GLY	SER	ASP	VAL	ASP	GLY				



- Molecule 47: Eukaryotic translation initiation factor 6



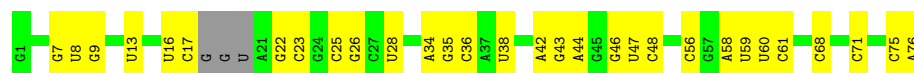
- Molecule 48: 60S ribosomal protein L1-A



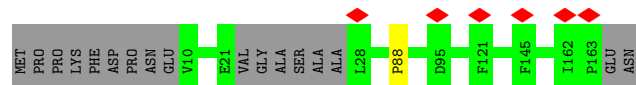
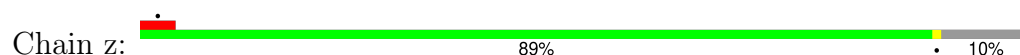
- Molecule 49: Ala tRNA



- Molecule 49: Ala tRNA

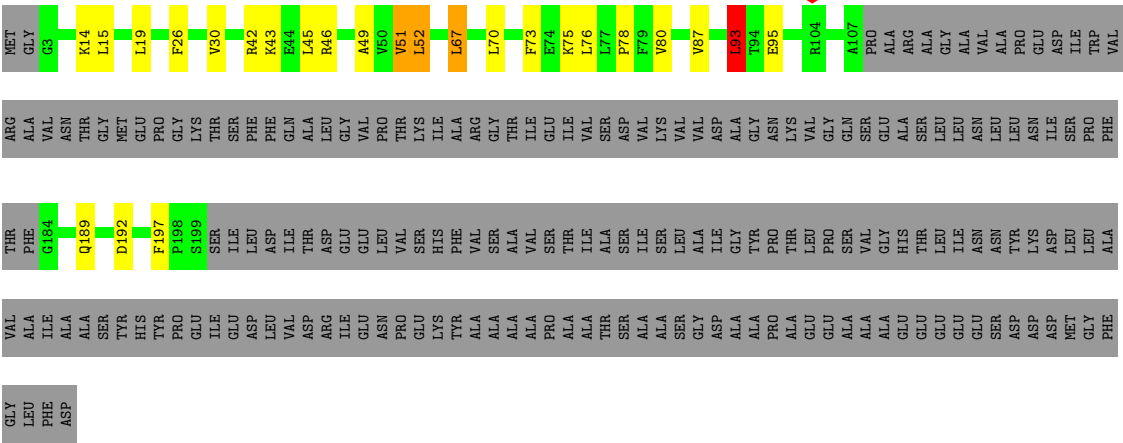


- Molecule 50: 60S ribosomal protein L12-B

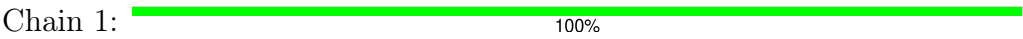


- Molecule 51: 60S acidic ribosomal protein P0



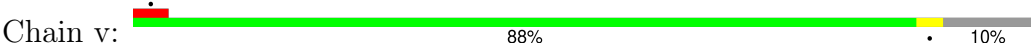


- Molecule 52: CAT-tailed nascent peptide



There are no outlier residues recorded for this chain.

- Molecule 53: Eukaryotic translation initiation factor 5A-1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54175	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	46	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.799	Depositor
Minimum map value	-0.723	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.132	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	476.55002, 476.55002, 476.55002	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5CT, ZN, MG

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	0.39	0/1757	0.70	1/2354 (0.0%)
2	B	0.39	0/1585	0.64	1/2128 (0.0%)
3	C	0.36	0/1439	0.71	2/1938 (0.1%)
4	D	0.34	0/1465	0.67	1/1965 (0.1%)
5	E	0.37	0/1275	0.67	1/1702 (0.1%)
6	F	0.38	0/1473	0.65	0/1980
7	G	0.36	0/1296	0.62	0/1739
8	H	0.37	0/812	0.73	3/1099 (0.3%)
9	I	0.35	0/1018	0.64	0/1369
10	J	0.36	0/530	0.63	0/703
11	K	0.41	0/979	0.69	1/1321 (0.1%)
12	L	0.35	0/995	0.68	1/1329 (0.1%)
13	M	0.36	0/1106	0.61	0/1485
14	N	0.40	0/1200	0.62	0/1607
15	O	0.32	0/473	0.72	2/629 (0.3%)
16	P	0.35	0/745	0.68	0/1001
17	Q	0.39	0/890	0.77	2/1196 (0.2%)
18	R	0.32	0/1034	0.59	0/1385
19	S	0.38	0/868	0.61	0/1168
20	T	0.35	0/890	0.67	0/1189
21	U	0.34	0/978	0.65	1/1301 (0.1%)
22	V	0.34	0/772	0.66	0/1026
23	W	0.38	0/660	0.69	0/875
24	X	0.33	0/618	0.78	1/826 (0.1%)
25	Y	0.33	0/443	0.65	0/588
26	Z	0.33	0/416	0.70	0/553
27	b	0.36	0/836	0.66	0/1104
28	c	0.36	0/701	0.66	0/934
29	d	0.26	0/208	0.84	0/267
30	f	0.61	1/77011 (0.0%)	1.03	297/120065 (0.2%)
31	h	0.53	0/2883	0.98	8/4491 (0.2%)
32	i	0.60	0/3746	0.96	7/5832 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	j	0.39	0/1908	0.68	0/2564
34	k	0.36	0/3146	0.64	1/4228 (0.0%)
35	l	0.36	0/2800	0.64	2/3790 (0.1%)
36	m	0.34	0/2400	0.67	4/3239 (0.1%)
37	n	0.36	0/1329	0.67	0/1794
38	o	0.37	0/1821	0.61	0/2451
39	p	0.34	0/1836	0.62	2/2481 (0.1%)
40	q	0.37	0/1529	0.68	2/2060 (0.1%)
41	r	0.33	0/1801	0.64	0/2416
42	s	0.33	0/1367	0.70	3/1834 (0.2%)
43	t	0.36	0/1568	0.68	1/2106 (0.0%)
44	u	0.34	0/1068	0.66	1/1438 (0.1%)
45	a	0.30	0/6679	0.49	0/9012
46	e	0.38	0/11715	0.55	2/15908 (0.0%)
47	g	0.32	0/1672	0.63	0/2281
48	w	0.33	0/1736	0.65	0/2332
49	x	0.21	0/1761	0.64	0/2742
49	y	0.23	0/1735	0.65	0/2701
50	z	0.37	0/726	0.60	0/1006
51	0	0.33	0/976	0.55	0/1313
53	v	0.32	0/1084	0.63	1/1456 (0.1%)
All	All	0.50	1/161759 (0.0%)	0.87	348/236301 (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
15	O	0	1
21	U	0	1
34	k	0	1
35	l	0	2
39	p	0	3
40	q	0	1
44	u	0	1
47	g	0	1
All	All	0	11

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	f	2416	U	O3'-P	-5.92	1.54	1.61

The worst 5 of 348 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	f	3217	C	N1-C2-O2	12.13	126.18	118.90
30	f	3217	C	C2-N1-C1'	11.32	131.25	118.80
30	f	3217	C	N3-C2-O2	-9.75	115.08	121.90
11	K	134	ASP	CB-CG-OD1	9.69	127.02	118.30
30	f	922	U	C2-N1-C1'	9.30	128.86	117.70

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	O	20	GLY	Peptide
21	U	83	LYS	Peptide
34	k	141	GLY	Peptide
35	l	13	GLY	Peptide
35	l	318	LEU	Peptide

## 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	1720	0	1779	10	0
2	B	1555	0	1659	13	0
3	C	1416	0	1433	11	0
4	D	1441	0	1543	8	0
5	E	1258	0	1342	6	0
6	F	1437	0	1475	15	0
7	G	1272	0	1312	9	0
8	H	796	0	812	4	0
9	I	1003	0	1048	7	0
10	J	518	0	542	3	0
11	K	964	0	1025	1	0
12	L	984	0	1075	4	0
13	M	1080	0	1122	5	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	N	1169	0	1211	7	0
15	O	462	0	491	6	0
16	P	737	0	792	3	0
17	Q	876	0	912	9	0
18	R	1013	0	1077	5	0
19	S	850	0	880	2	0
20	T	880	0	942	3	0
21	U	969	0	1078	3	0
22	V	766	0	844	4	0
23	W	645	0	645	3	0
24	X	612	0	682	3	0
25	Y	436	0	475	0	0
26	Z	410	0	442	0	0
27	b	824	0	888	0	0
28	c	694	0	734	0	0
29	d	207	0	250	0	0
30	f	68802	0	34573	0	0
31	h	2579	0	1304	0	0
32	i	3353	0	1695	0	0
33	j	1874	0	1943	0	0
34	k	3075	0	3142	0	0
35	l	2748	0	2859	0	0
36	m	2351	0	2294	0	0
37	n	1307	0	1377	0	0
38	o	1784	0	1862	0	0
39	p	1804	0	1877	0	0
40	q	1508	0	1572	0	0
41	r	1764	0	1804	0	0
42	s	1346	0	1370	0	0
43	t	1543	0	1608	0	0
44	u	1053	0	1149	0	0
45	a	6569	0	6460	0	0
46	e	11516	0	10776	0	0
47	g	1651	0	1613	0	0
48	w	1709	0	1799	0	0
49	x	1579	0	799	0	0
49	y	1556	0	789	0	0
50	z	728	0	337	0	0
51	0	961	0	979	11	0
52	1	90	0	21	0	0
53	v	1085	0	1086	0	0
54	A	1	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	C	1	0	0	0	0
54	E	1	0	0	0	0
54	I	1	0	0	0	0
54	R	1	0	0	0	0
54	T	1	0	0	0	0
54	f	3	0	0	0	0
54	h	1	0	0	0	0
54	j	2	0	0	0	0
54	k	1	0	0	0	0
55	T	1	0	0	0	0
55	W	1	0	0	0	0
55	Z	1	0	0	0	0
55	b	1	0	0	0	0
55	c	1	0	0	0	0
55	e	2	0	0	0	0
All	All	151349	0	113598	146	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 5.

The worst 5 of 146 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)
15:O:16:ALA:O	15:O:20:GLY:HA3	1.69	0.90
15:O:16:ALA:O	15:O:20:GLY:CA	2.36	0.73
23:W:21:ARG:HE	23:W:39:TYR:HB2	1.58	0.69
51:O:26:PHE:HB2	51:O:87:VAL:HB	1.73	0.68
2:B:46[A]:GLU:HB3	2:B:49[A]:ARG:HG3	1.75	0.68

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
2	B	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
3	C	181/184 (98%)	172 (95%)	9 (5%)	0	100	100
4	D	183/186 (98%)	176 (96%)	7 (4%)	0	100	100
5	E	154/189 (82%)	151 (98%)	3 (2%)	0	100	100
6	F	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
7	G	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
8	H	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
9	I	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
10	J	61/155 (39%)	61 (100%)	0	0	100	100
11	K	119/142 (84%)	118 (99%)	1 (1%)	0	100	100
12	L	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
13	M	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
14	N	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
15	O	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	7	14
16	P	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
17	Q	107/113 (95%)	98 (92%)	9 (8%)	0	100	100
18	R	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
19	S	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
20	T	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
21	U	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
22	V	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
23	W	79/88 (90%)	75 (95%)	4 (5%)	0	100	100
24	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
25	Y	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
26	Z	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
27	b	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
28	c	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
29	d	20/25 (80%)	19 (95%)	1 (5%)	0	100	100
33	j	244/254 (96%)	226 (93%)	18 (7%)	0	100	100
34	k	384/387 (99%)	363 (94%)	21 (6%)	0	100	100
35	l	359/362 (99%)	329 (92%)	29 (8%)	1 (0%)	37	59

Continued on next page...



*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	m	292/297 (98%)	277 (95%)	15 (5%)	0	100	100
37	n	163/176 (93%)	154 (94%)	9 (6%)	0	100	100
38	o	220/244 (90%)	207 (94%)	13 (6%)	0	100	100
39	p	231/256 (90%)	220 (95%)	11 (5%)	0	100	100
40	q	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	25	47
41	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
42	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	22	43
43	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	25	47
44	u	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
45	a	842/1038 (81%)	830 (99%)	12 (1%)	0	100	100
46	e	1519/1562 (97%)	1495 (98%)	22 (1%)	2 (0%)	48	71
47	g	223/245 (91%)	215 (96%)	8 (4%)	0	100	100
48	w	214/217 (99%)	211 (99%)	3 (1%)	0	100	100
50	z	144/165 (87%)	135 (94%)	8 (6%)	1 (1%)	19	38
51	0	117/312 (38%)	116 (99%)	0	1 (1%)	14	31
53	v	139/157 (88%)	139 (100%)	0	0	100	100
All	All	9314/10279 (91%)	8956 (96%)	349 (4%)	9 (0%)	50	71

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
50	z	88	PRO
46	e	437	LYS
46	e	855	PRO
35	l	4	PRO
40	q	107	ASP

### 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	175/176 (99%)	175 (100%)	0	100	100
2	B	160/162 (99%)	160 (100%)	0	100	100
3	C	138/146 (94%)	138 (100%)	0	100	100
4	D	150/151 (99%)	149 (99%)	1 (1%)	81	93
5	E	129/154 (84%)	129 (100%)	0	100	100
6	F	155/156 (99%)	155 (100%)	0	100	100
7	G	135/137 (98%)	134 (99%)	1 (1%)	81	93
8	H	87/107 (81%)	87 (100%)	0	100	100
9	I	104/105 (99%)	104 (100%)	0	100	100
10	J	54/129 (42%)	54 (100%)	0	100	100
11	K	104/118 (88%)	104 (100%)	0	100	100
12	L	108/110 (98%)	108 (100%)	0	100	100
13	M	112/116 (97%)	112 (100%)	0	100	100
14	N	117/119 (98%)	117 (100%)	0	100	100
15	O	46/47 (98%)	45 (98%)	1 (2%)	47	72
16	P	81/88 (92%)	81 (100%)	0	100	100
17	Q	92/97 (95%)	92 (100%)	0	100	100
18	R	107/111 (96%)	107 (100%)	0	100	100
19	S	90/91 (99%)	90 (100%)	0	100	100
20	T	95/103 (92%)	94 (99%)	1 (1%)	70	86
21	U	104/105 (99%)	104 (100%)	0	100	100
22	V	80/82 (98%)	80 (100%)	0	100	100
23	W	67/71 (94%)	67 (100%)	0	100	100
24	X	68/69 (99%)	66 (97%)	2 (3%)	37	64
25	Y	45/46 (98%)	45 (100%)	0	100	100
26	Z	45/116 (39%)	45 (100%)	0	100	100
27	b	87/91 (96%)	87 (100%)	0	100	100
28	c	71/72 (99%)	71 (100%)	0	100	100
29	d	20/23 (87%)	20 (100%)	0	100	100
33	j	189/196 (96%)	188 (100%)	1 (0%)	86	95
34	k	321/323 (99%)	319 (99%)	2 (1%)	84	94
35	l	288/289 (100%)	288 (100%)	0	100	100

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	m	241/245 (98%)	241 (100%)	0	100	100
37	n	139/155 (90%)	138 (99%)	1 (1%)	81	93
38	o	186/205 (91%)	186 (100%)	0	100	100
39	p	187/208 (90%)	187 (100%)	0	100	100
40	q	168/171 (98%)	168 (100%)	0	100	100
41	r	185/187 (99%)	183 (99%)	2 (1%)	70	86
42	s	145/150 (97%)	145 (100%)	0	100	100
43	t	154/159 (97%)	154 (100%)	0	100	100
44	u	107/109 (98%)	107 (100%)	0	100	100
45	a	676/949 (71%)	638 (94%)	38 (6%)	17	38
46	e	1152/1451 (79%)	1092 (95%)	60 (5%)	19	41
47	g	180/211 (85%)	180 (100%)	0	100	100
48	w	197/198 (100%)	196 (100%)	1 (0%)	86	95
51	0	104/254 (41%)	95 (91%)	9 (9%)	8	17
53	v	119/132 (90%)	117 (98%)	2 (2%)	56	78
All	All	7564/8690 (87%)	7442 (98%)	122 (2%)	58	79

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	e	271	LEU
48	w	98	LYS
46	e	780	ILE
46	e	1555	ARG
51	0	95	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
46	e	251	ASN
46	e	1141	GLN
47	g	9	ASN
46	e	902	ASN
46	e	1288	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	f	3211/3395 (94%)	591 (18%)	0
31	h	120/121 (99%)	12 (10%)	0
32	i	157/158 (99%)	32 (20%)	0
49	x	72/76 (94%)	23 (31%)	0
49	y	71/76 (93%)	30 (42%)	0
All	All	3631/3826 (94%)	688 (18%)	0

5 of 688 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	f	6	A
30	f	13	A
30	f	14	U
30	f	26	A
30	f	40	A

There are no RNA pucker outliers to report.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
53	5CT	v	51	53	13,14,15	0.78	0	8,15,17	1.29	1 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
53	5CT	v	51	53	-	9/13/14/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	v	51	5CT	C4-C3-C2	-2.20	108.84	113.47

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
53	v	51	5CT	NZ-C1-C2-C3
53	v	51	5CT	O1-C2-C3-C4
53	v	51	5CT	C2-C3-C4-N1
53	v	51	5CT	C-CA-CB-CG
53	v	51	5CT	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 20 are 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](#)

There are no chain breaks in this entry.

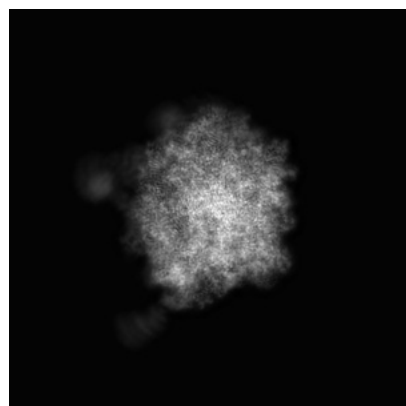
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15425. These allow visual inspection of the internal detail of the map and identification of artifacts.

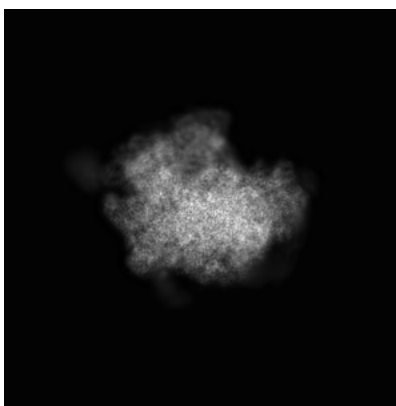
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

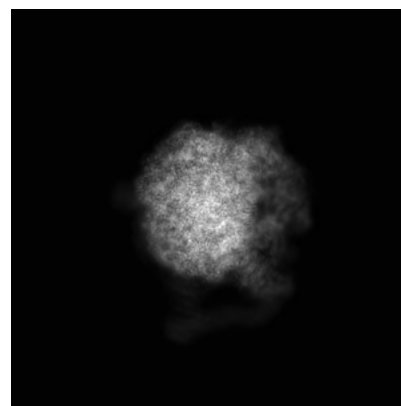
#### 6.1.1 Primary map



X

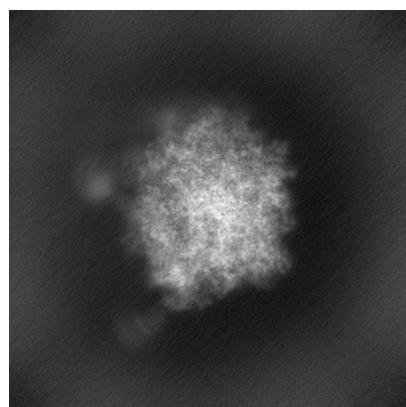


Y

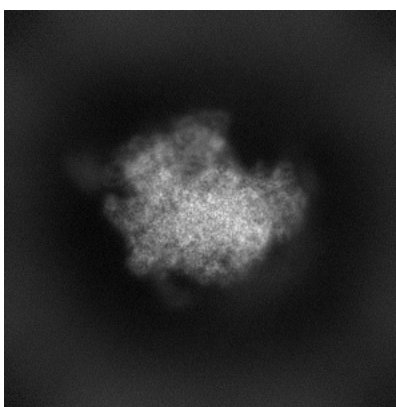


Z

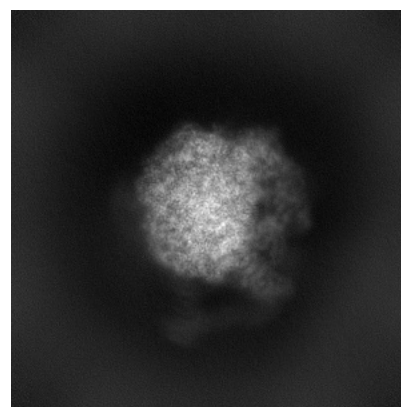
#### 6.1.2 Raw map



X



Y

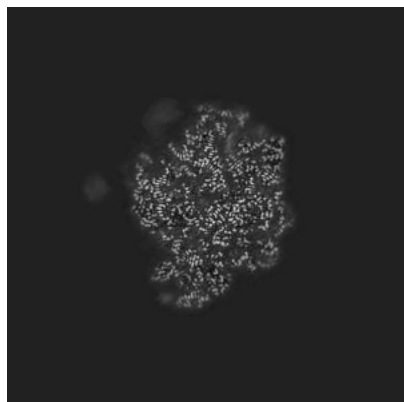


Z

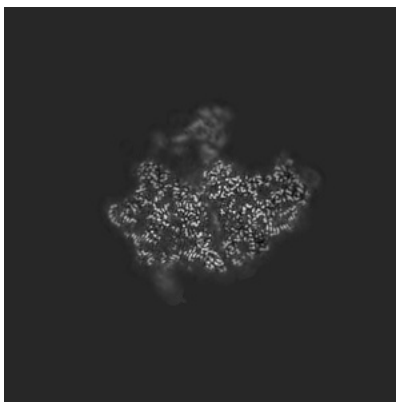
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

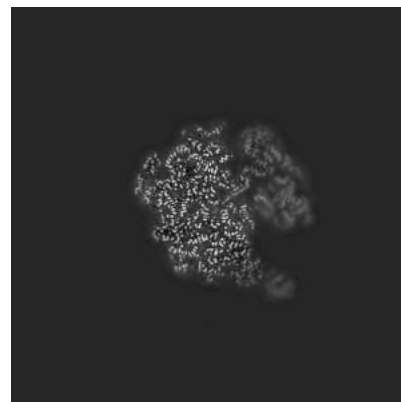
### 6.2.1 Primary map



X Index: 225

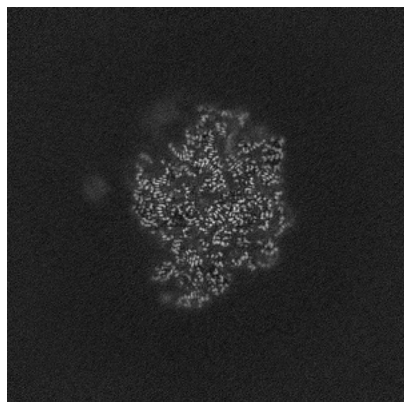


Y Index: 225

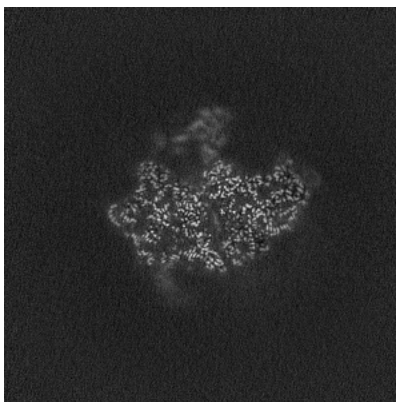


Z Index: 225

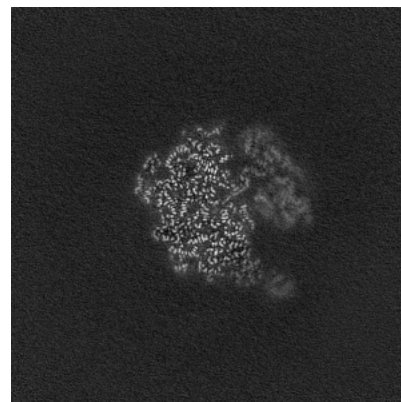
### 6.2.2 Raw map



X Index: 225



Y Index: 225



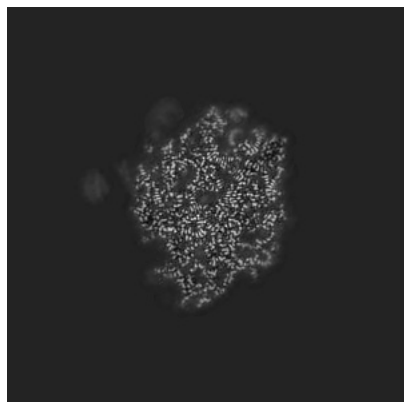
Z Index: 225

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

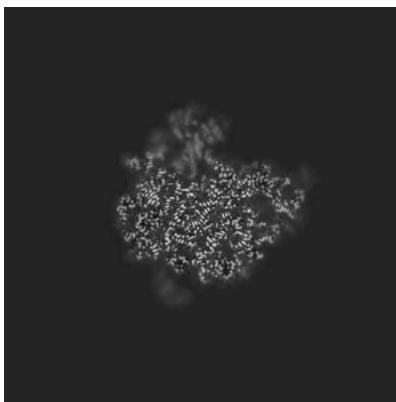


## 6.3 Largest variance slices [i](#)

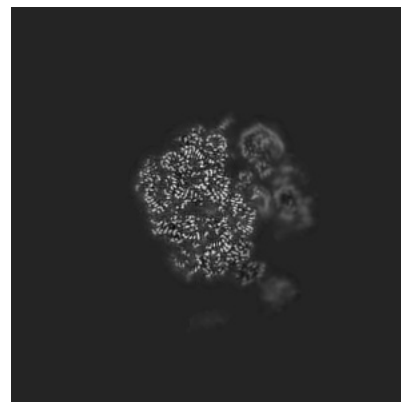
### 6.3.1 Primary map



X Index: 219

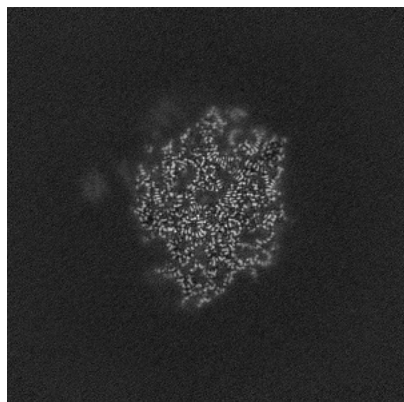


Y Index: 242

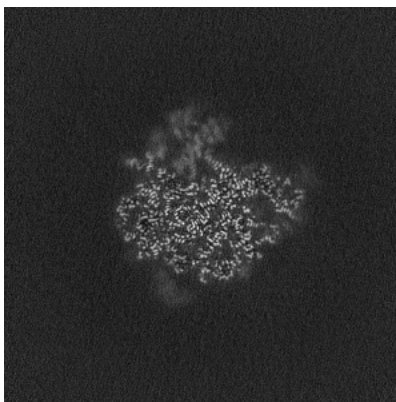


Z Index: 231

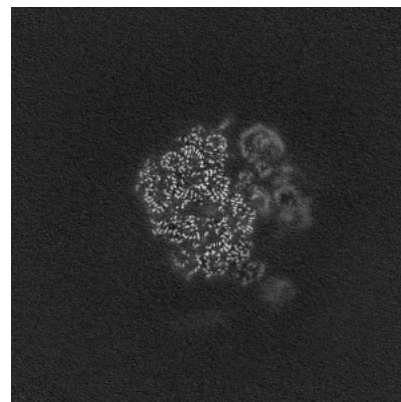
### 6.3.2 Raw map



X Index: 219



Y Index: 241

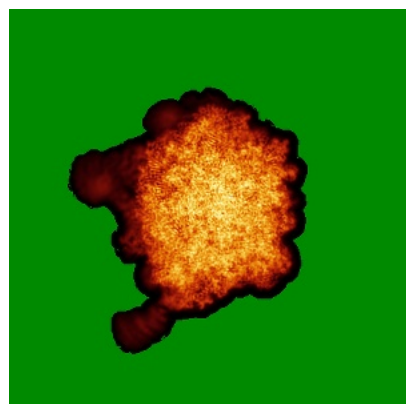


Z Index: 231

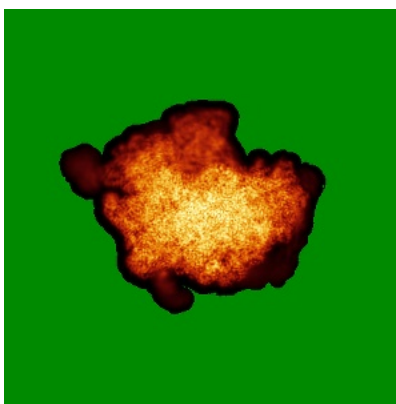
The images above show the largest variance slices of the map in three orthogonal directions.

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

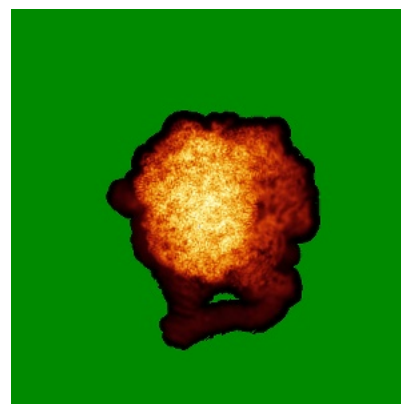
### 6.4.1 Primary map



X

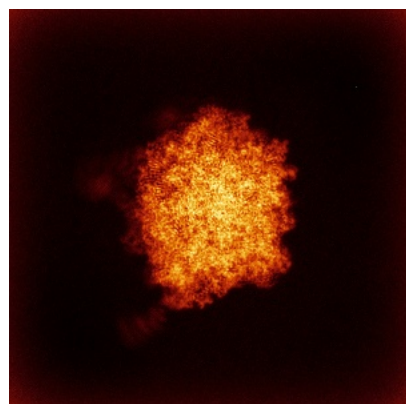


Y

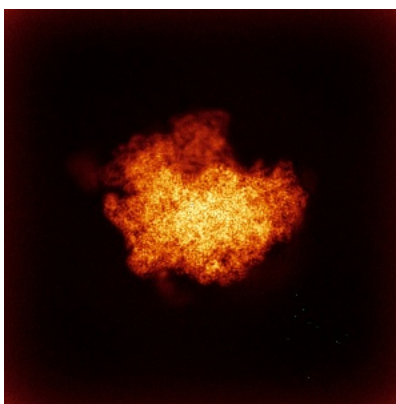


Z

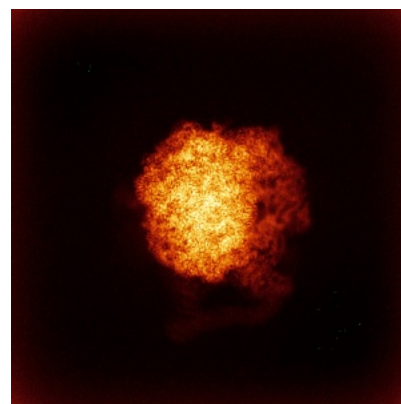
### 6.4.2 Raw map



X



Y

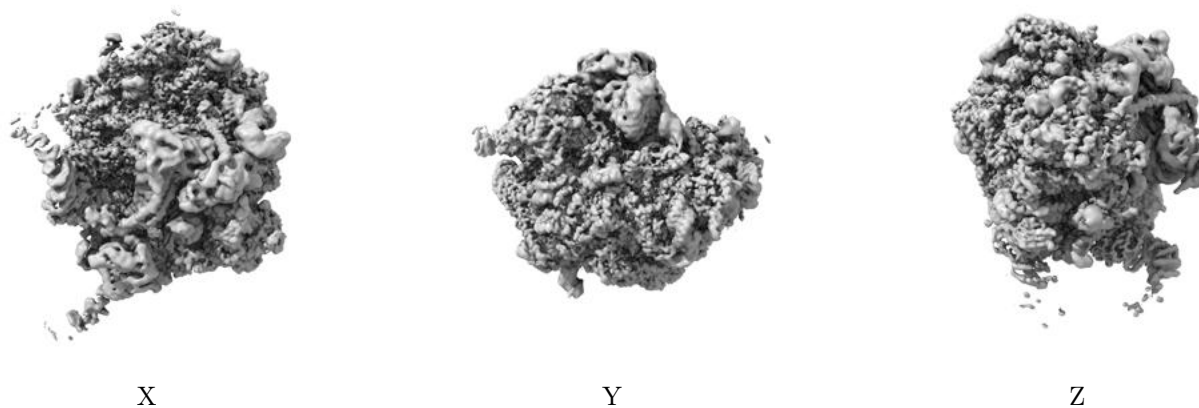


Z

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

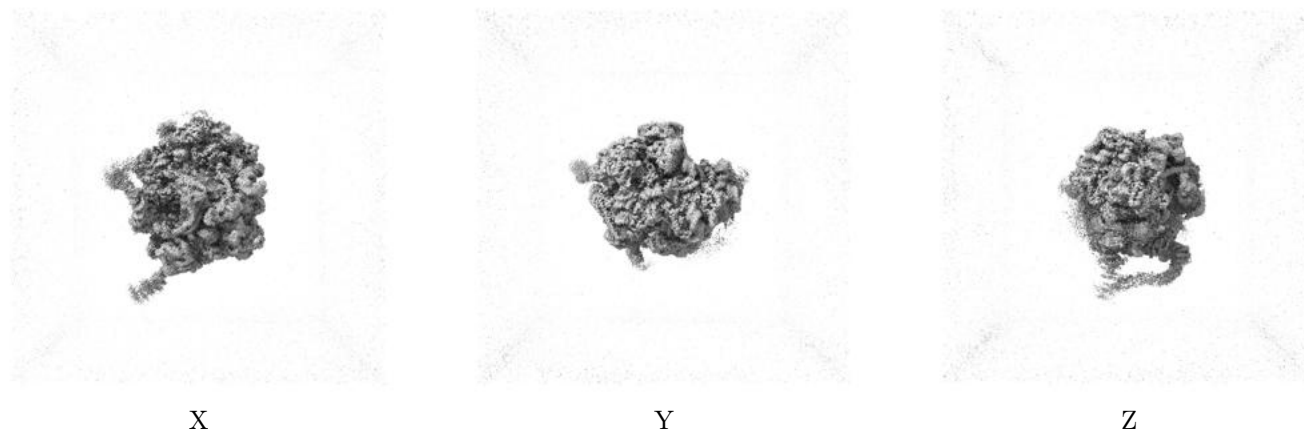
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

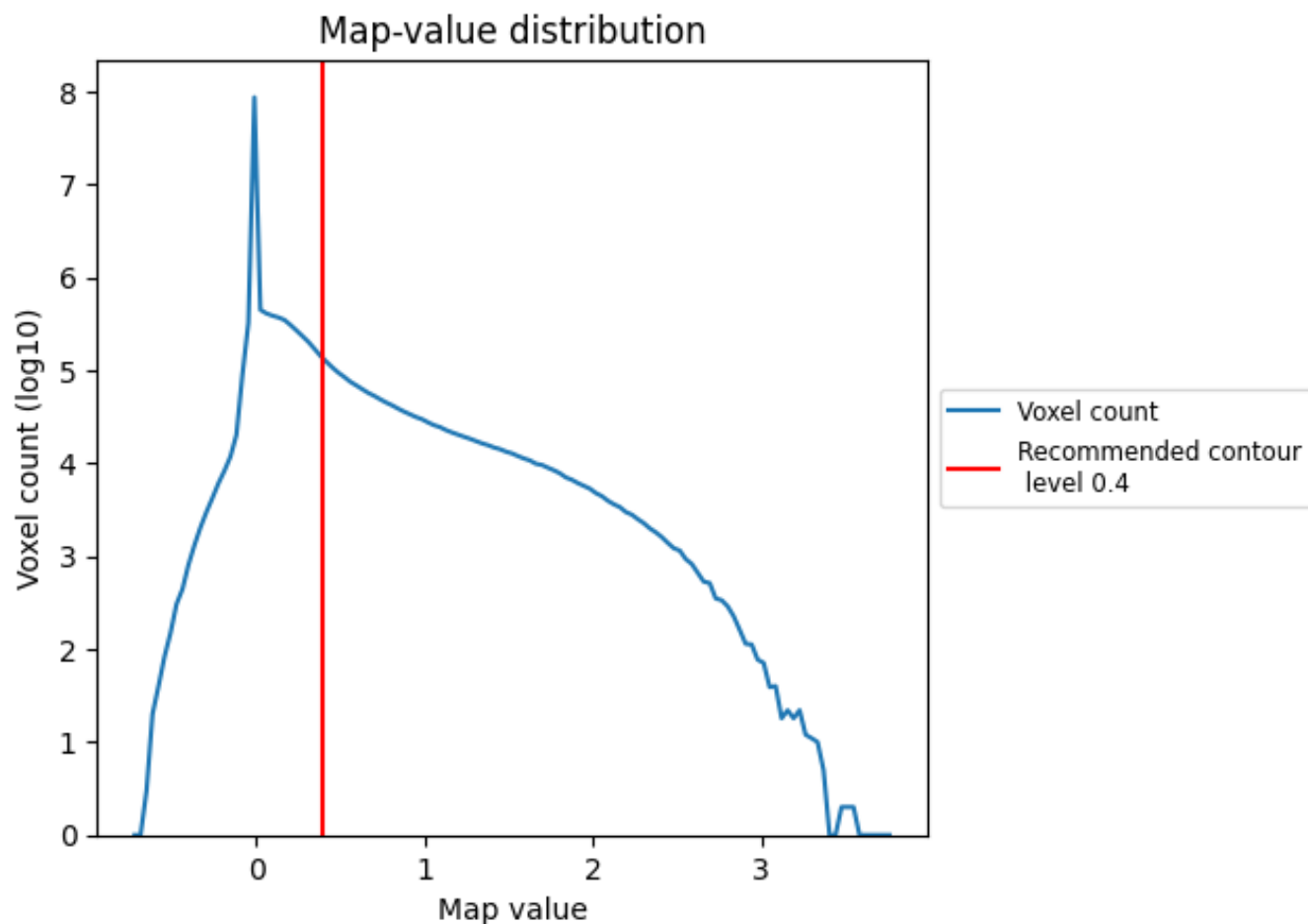
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

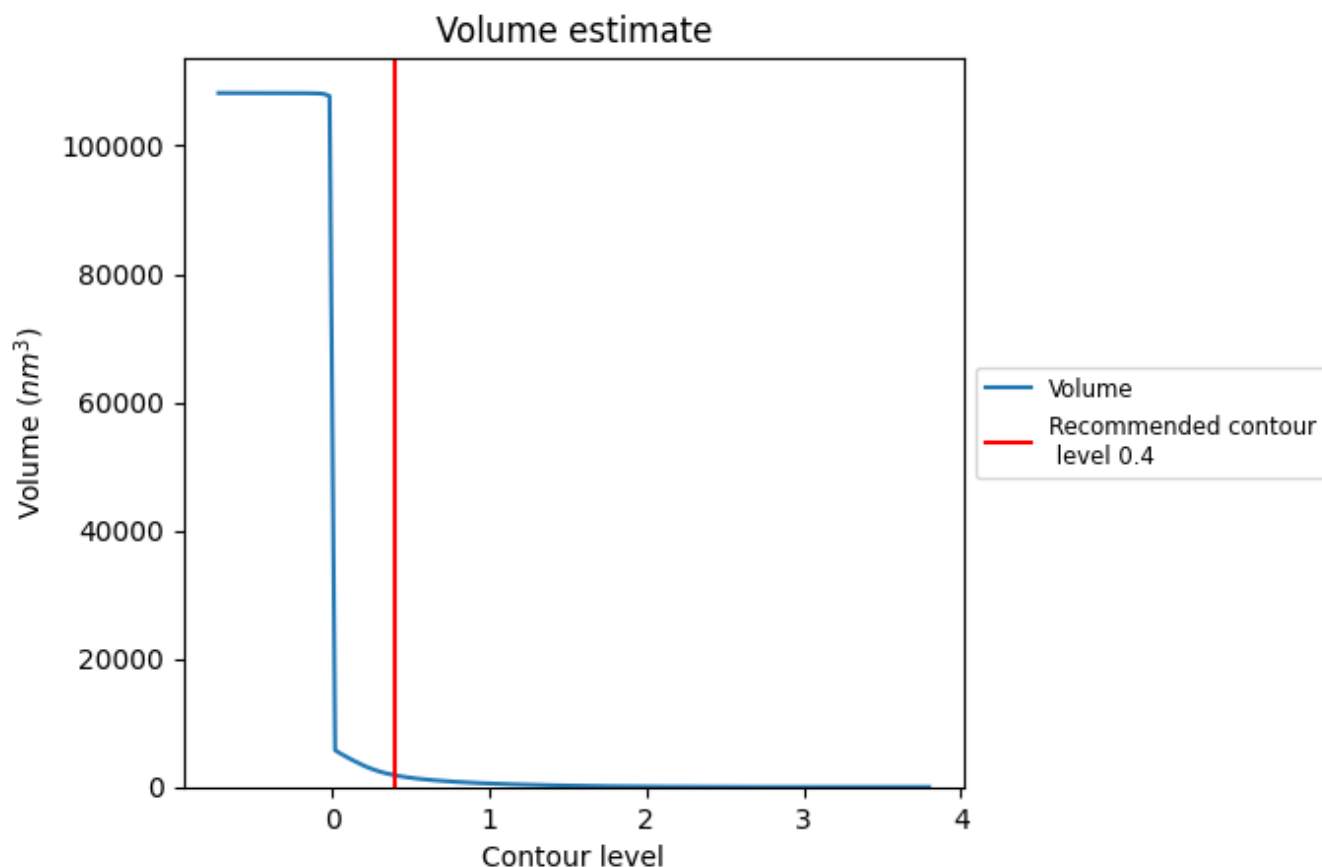
This section contains the results of statistical analysis of the map.

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



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

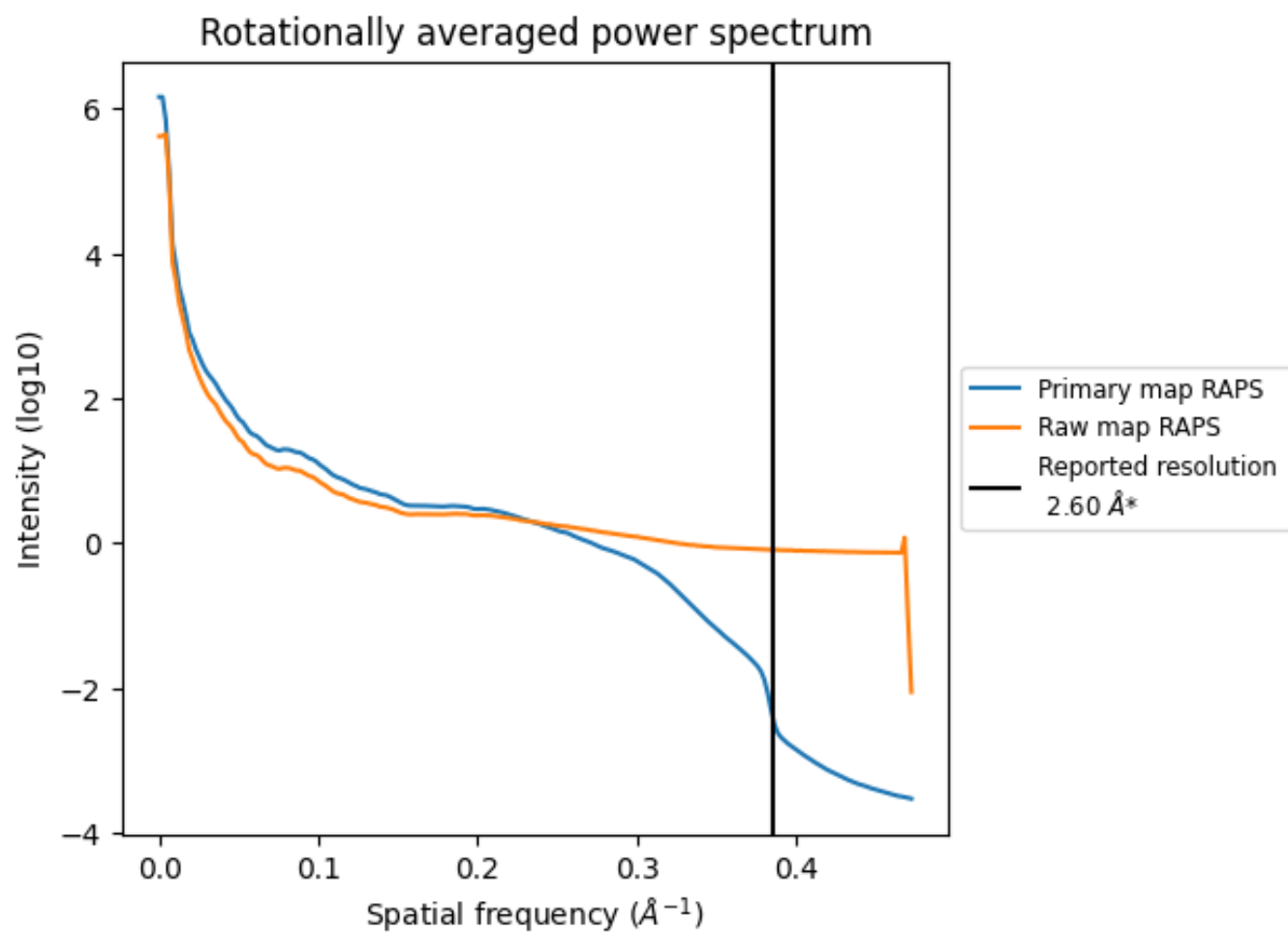
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1819  $\text{nm}^3$ ; this corresponds to an approximate mass of 1643 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 ⓘ

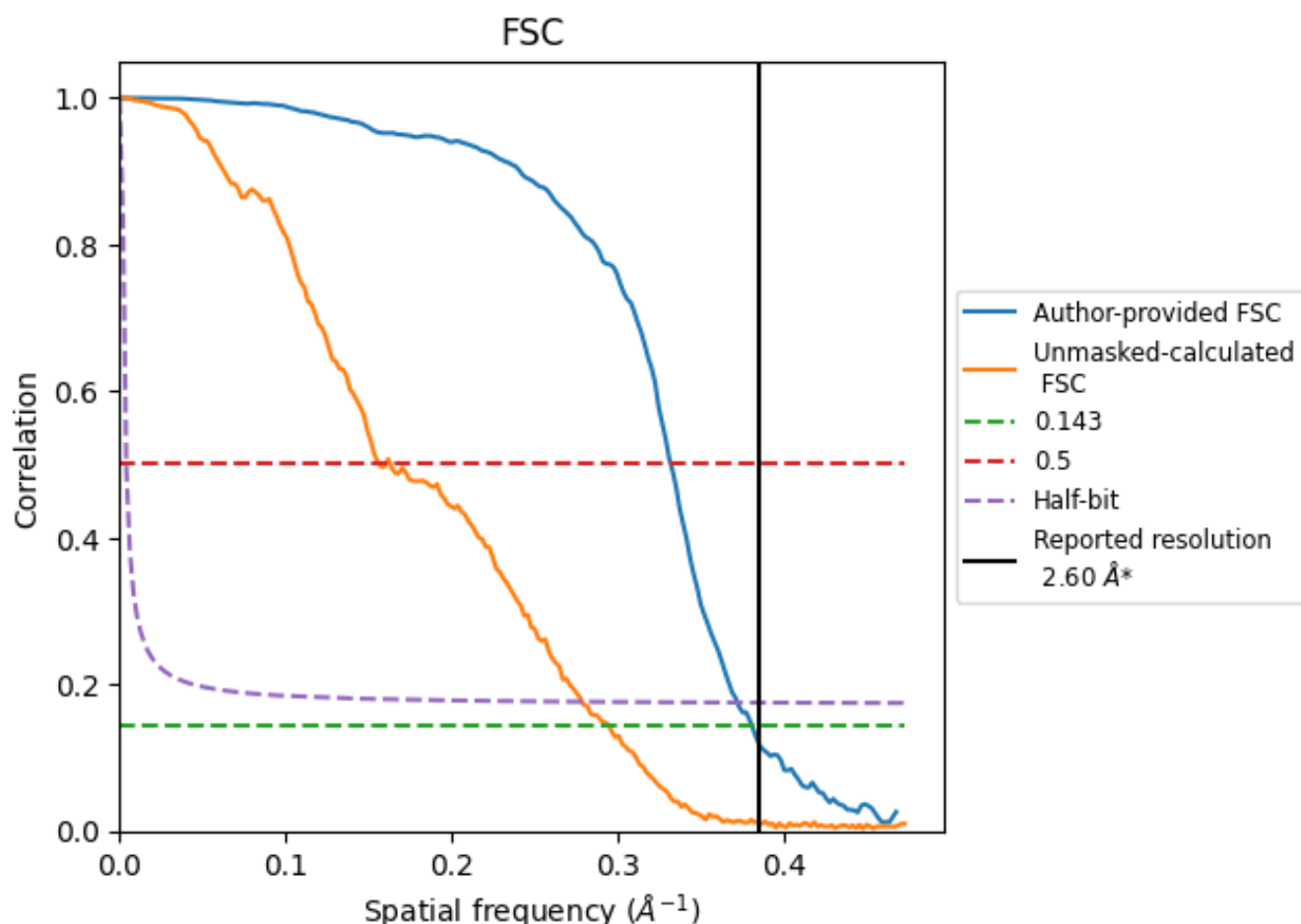


\*Reported resolution corresponds to spatial frequency of  $0.385 \text{ \AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.385 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.63	3.02	2.69
Unmasked-calculated*	3.40	6.40	3.59

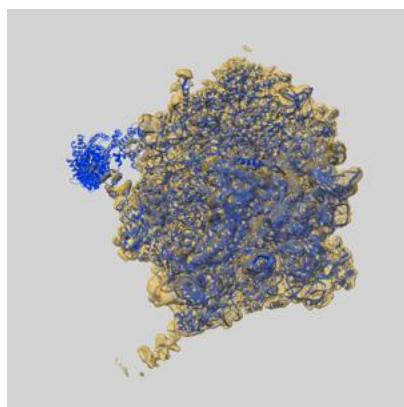
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.40 differs from the reported value 2.6 by more than 10 %



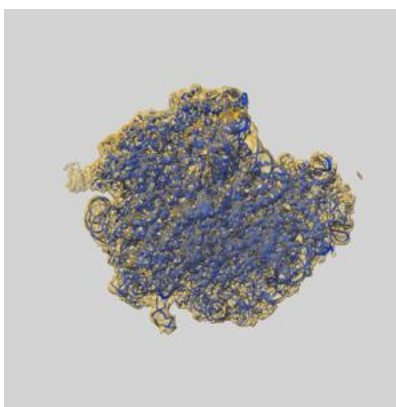
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15425 and PDB model 8AGV. Per-residue inclusion information can be found in section [3](#) on page [14](#).

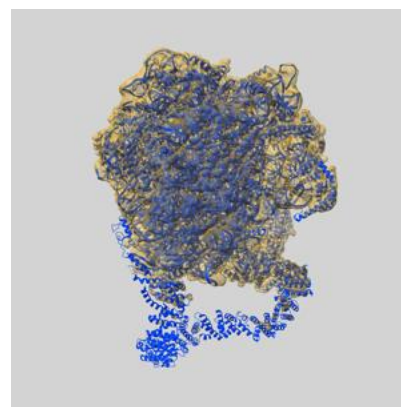
### 9.1 Map-model overlay [i](#)



X



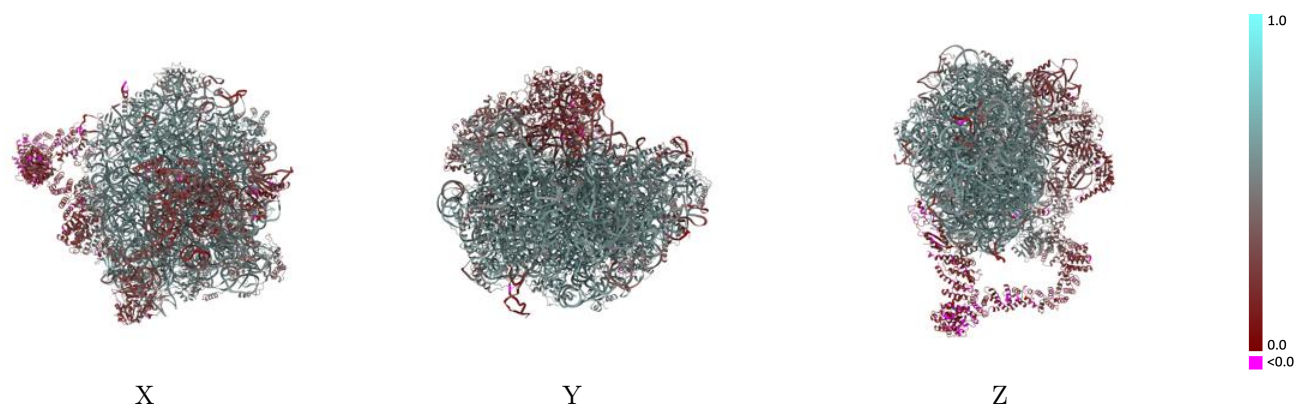
Y



Z

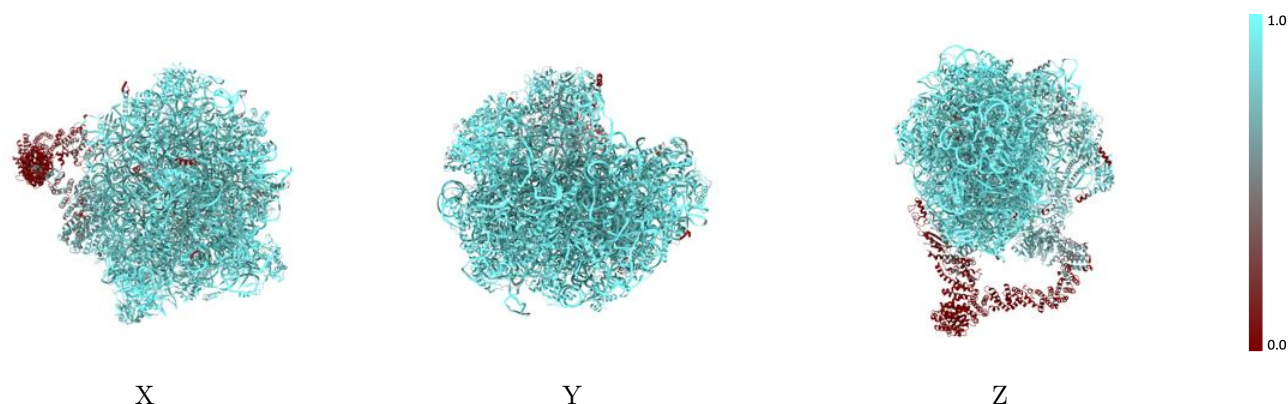
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



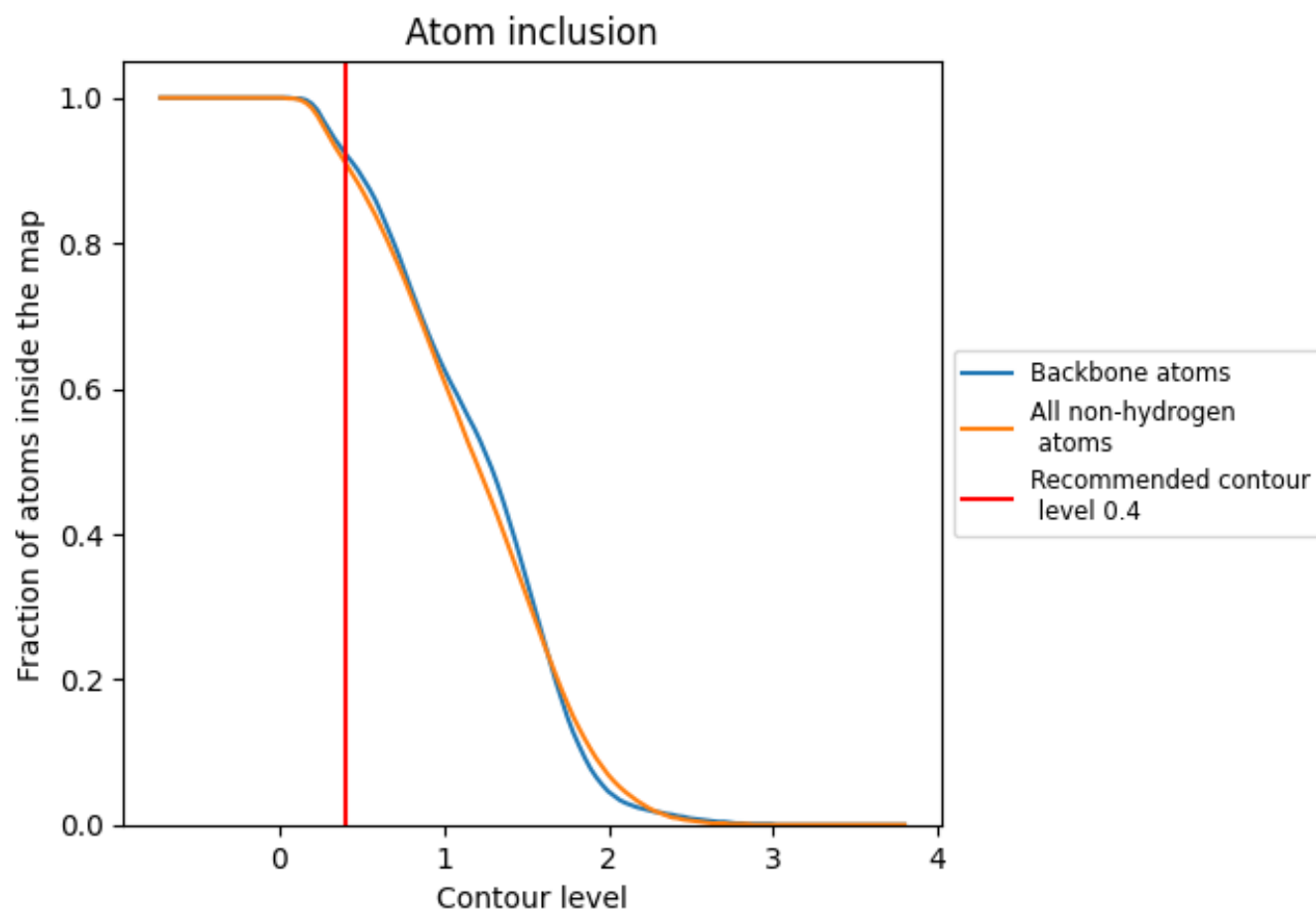
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 91% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9110	 0.5030
0	 0.8290	 0.2900
1	 1.0000	 0.4570
A	 0.9930	 0.6050
B	 0.9760	 0.5790
C	 0.9670	 0.5860
D	 0.9790	 0.5790
E	 0.9420	 0.5390
F	 0.9770	 0.5730
G	 0.9690	 0.5580
H	 0.9310	 0.4750
I	 0.9640	 0.5630
J	 0.9600	 0.5600
K	 0.9660	 0.5650
L	 0.9730	 0.5580
M	 0.9550	 0.5190
N	 0.9800	 0.5870
O	 0.9560	 0.5330
P	 0.9420	 0.5100
Q	 0.9250	 0.5480
R	 0.9810	 0.5950
S	 0.9900	 0.6120
T	 0.9660	 0.5690
U	 0.9670	 0.5480
V	 0.9570	 0.5200
W	 1.0000	 0.6200
X	 0.9200	 0.4970
Y	 0.9950	 0.5950
Z	 0.9670	 0.5650
a	 0.8080	 0.2780
b	 0.9640	 0.5640
c	 0.9720	 0.5620
d	 0.7130	 0.3910
e	 0.2590	 0.1800
f	 0.9910	 0.5650



*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
g	 0.7570	 0.4630
h	 0.9990	 0.5600
i	 0.9950	 0.5920
j	 0.9860	 0.5960
k	 0.9790	 0.5810
l	 0.9760	 0.5680
m	 0.9350	 0.4780
n	 0.9450	 0.5190
o	 0.9690	 0.5640
p	 0.9410	 0.5120
q	 0.9590	 0.5410
r	 0.9530	 0.5300
s	 0.9250	 0.4200
t	 0.9670	 0.5540
u	 0.9680	 0.5400
v	 0.8470	 0.3530
w	 0.7890	 0.2020
x	 0.9770	 0.2800
y	 0.9760	 0.2610
z	 0.9130	 0.2760