



wwPDB EM Validation Summary Report ⓘ

Jul 14, 2024 – 06:32 am BST

PDB ID : 8AGW
EMDB ID : EMD-15426
Title : Yeast RQC complex in state D
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

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.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

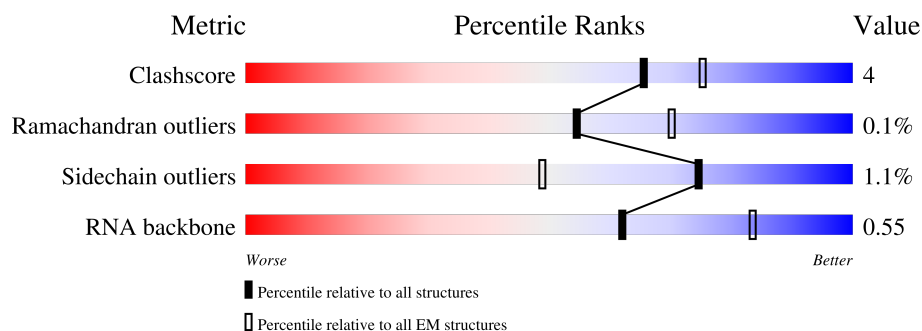
1 Overall quality at a glance

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.







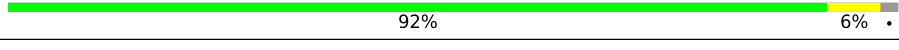
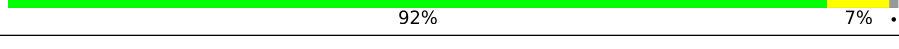
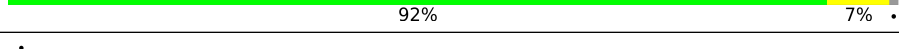
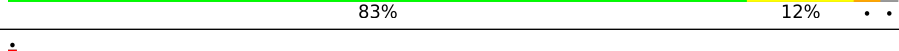
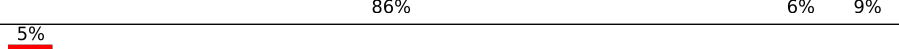
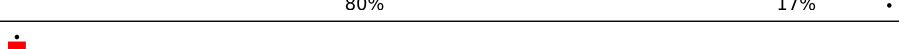
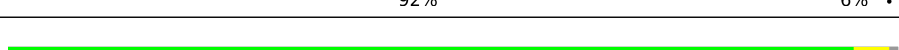
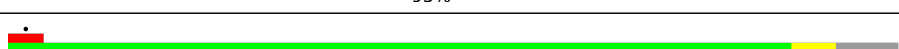
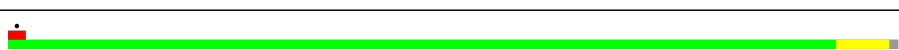
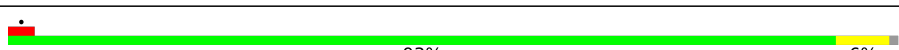
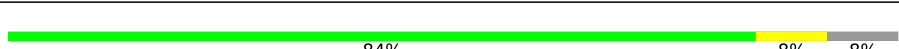

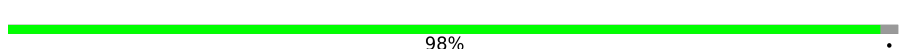

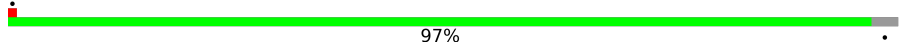
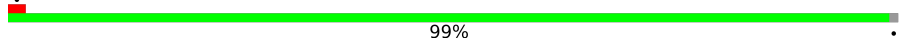
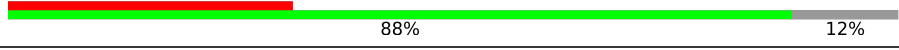
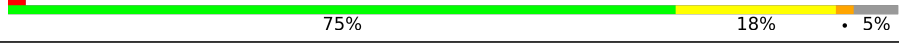



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	204	
2	B	199	
3	C	184	
4	D	186	
5	E	189	
6	F	172	
7	G	160	

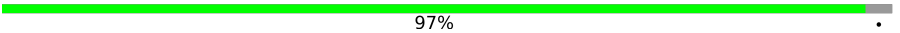
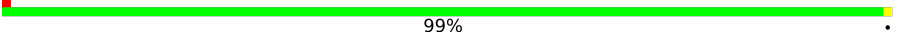
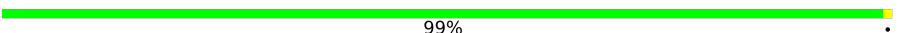
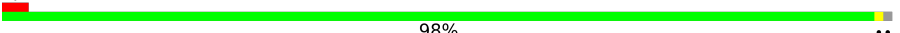
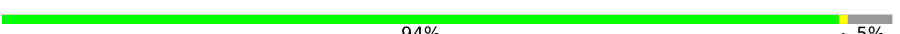









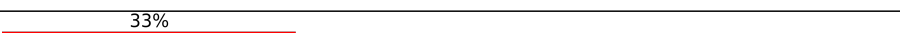
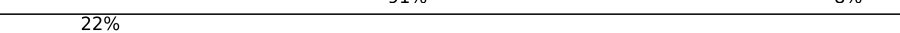




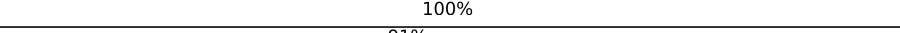
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Mol	Chain	Length	Quality of chain
8	H	121	
9	I	137	
10	J	155	
11	K	142	
12	L	127	
13	M	136	
14	N	149	
15	O	59	
16	P	105	
17	Q	113	
18	R	130	
19	S	107	
20	T	121	
21	U	120	
22	V	100	
23	W	88	
24	X	78	
25	Y	51	
26	Z	128	
27	b	106	
28	c	92	
29	d	25	
30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

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Mol	Chain	Length	Quality of chain
33	j	254	 97% .
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	 52% 81% 18%
46	e	1562	 82% 94% . .
47	g	245	 33% 91% 8%
48	x	76	 22% 63% 34% .
48	y	76	 9% 62% 34% .
49	z	165	 28% 88% . 10%
50	0	312	 31% 7% . 61%
51	1	17	 6% 100%
52	w	217	 91% 99%

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 150269 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	S	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		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
			6573	4191	1139	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
			11512	7356	1937	2181	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 RNA chain called Ala tRNA.

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

- Molecule 49 is a protein called 60S ribosomal protein L12-A.

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

- Molecule 50 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	0	121	Total	C	N	O	S	0	0
			961	618	167	173	3		

- Molecule 51 is a protein called CAT-tailed nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	1	17	Total	C	N	O	0	0
			85	51	17	17		

- Molecule 52 is a protein called 60S ribosomal protein L1-A.

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

- Molecule 53 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
53	A	1	Total	Mg	0
			1	1	
53	C	1	Total	Mg	0
			1	1	
53	E	1	Total	Mg	0
			1	1	
53	I	1	Total	Mg	0
			1	1	
53	R	1	Total	Mg	0
			1	1	
53	T	1	Total	Mg	0
			1	1	
53	f	3	Total	Mg	0
			3	3	
53	h	1	Total	Mg	0
			1	1	
53	j	2	Total	Mg	0
			2	2	

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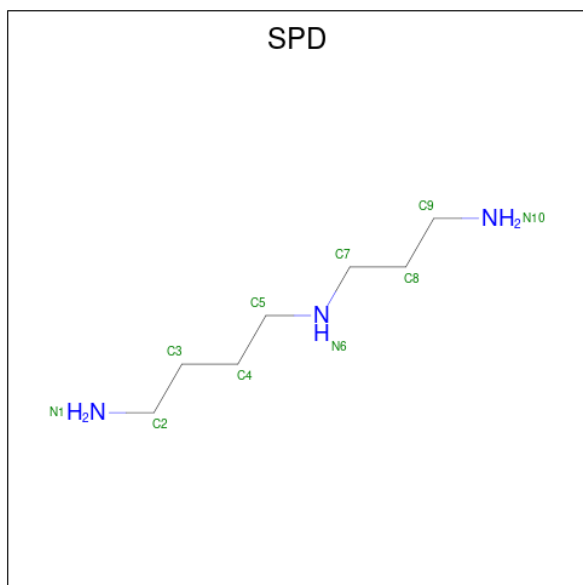
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Mol	Chain	Residues	Atoms		AltConf
53	k	1	Total	Mg	0
			1	1	

- Molecule 54 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 55 is SPERMIDINE (three-letter code: SPD) (formula: C₇H₁₉N₃).



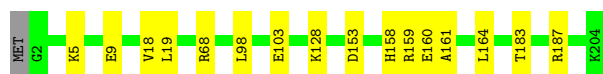
Mol	Chain	Residues	Atoms			AltConf
55	f	1	Total	C	N	0
			10	7	3	

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

Chain A: 




- Molecule 2: 60S ribosomal protein L16-A

Chain B: 




- Molecule 3: 60S ribosomal protein L17-A

Chain C: 



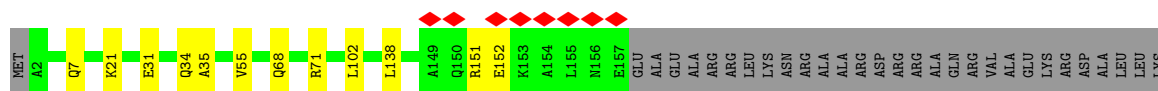
- Molecule 4: 60S ribosomal protein L18-A

Chain D: 



- Molecule 5: 60S ribosomal protein L19-A

Chain E: 



- 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:  5% 80% 17% .



- Molecule 18: 60S ribosomal protein L32

Chain R:  92% 6% .



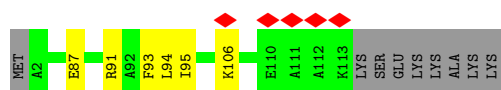
- Molecule 19: 60S ribosomal protein L33-A

Chain S: 95%



- Molecule 20: 60S ribosomal protein L34-A

Chain T: 88%



- Molecule 21: 60S ribosomal protein L35-A

Chain U: 93%



- Molecule 22: 60S ribosomal protein L36-A

Chain V: 93%



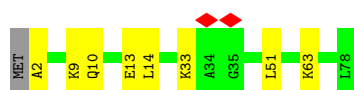
- Molecule 23: 60S ribosomal protein L37-A

Chain W: 84%



- Molecule 24: 60S ribosomal protein L38

Chain X: 88%



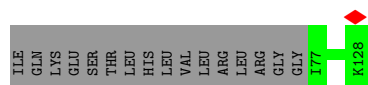
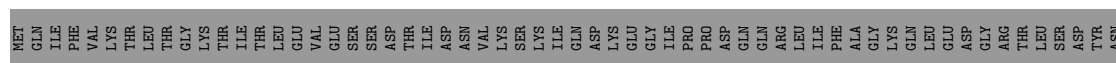
- Molecule 25: 60S ribosomal protein L39

Chain Y:  98%



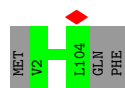
- Molecule 26: Ubiquitin-60S ribosomal protein L40

Chain Z:  41% 59%



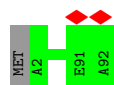
- Molecule 27: 60S ribosomal protein L42-A

Chain b:  97%




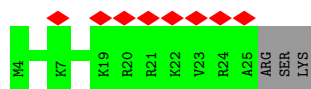
- Molecule 28: 60S ribosomal protein L43-A

Chain c:  99%



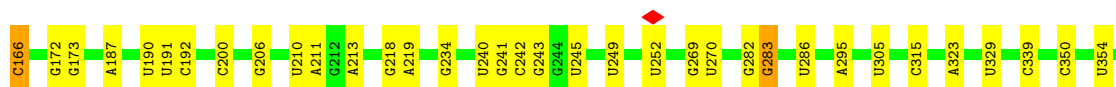
- Molecule 29: 60S ribosomal protein L41-A

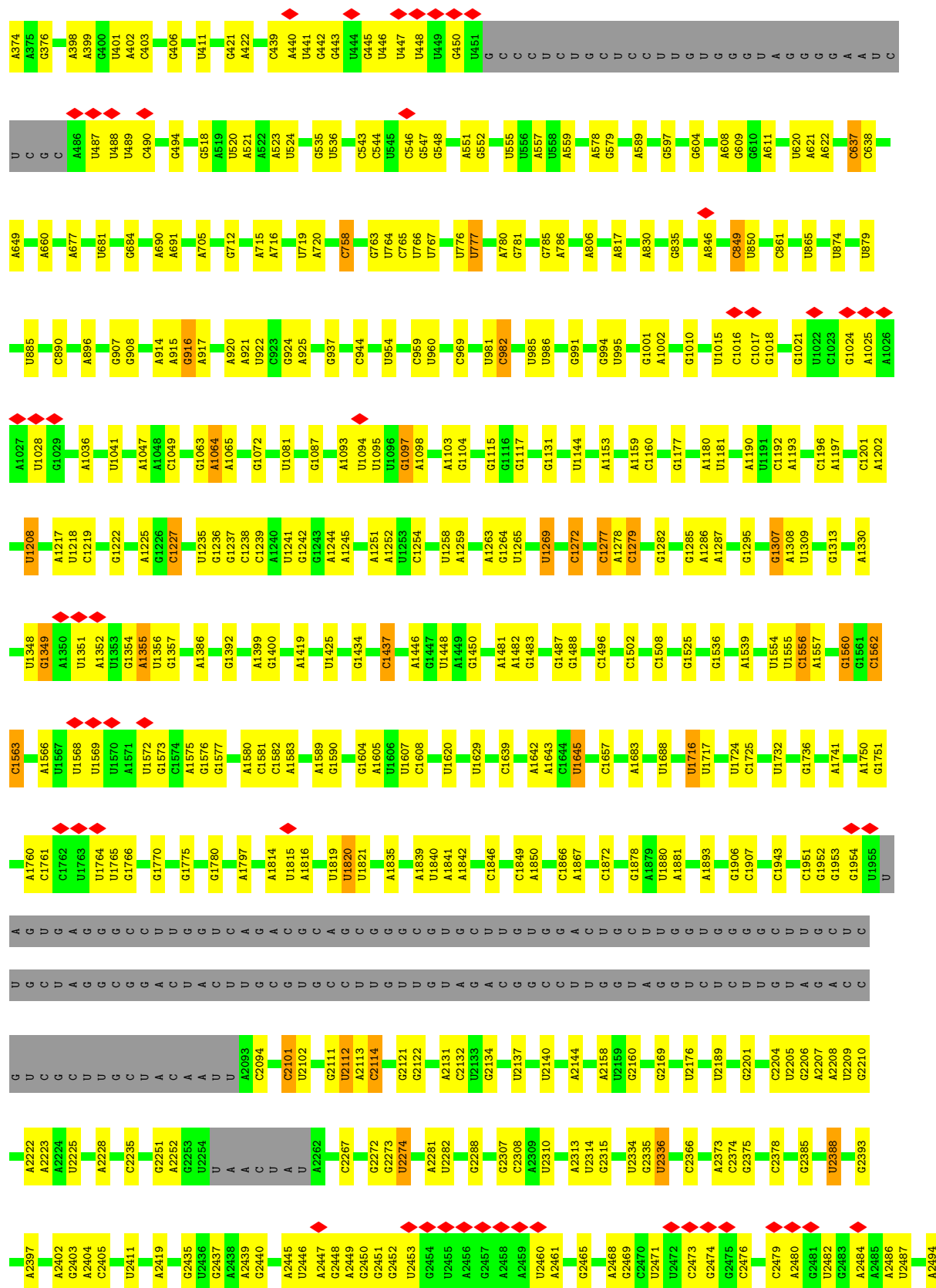
Chain d:  32% 88% 12%

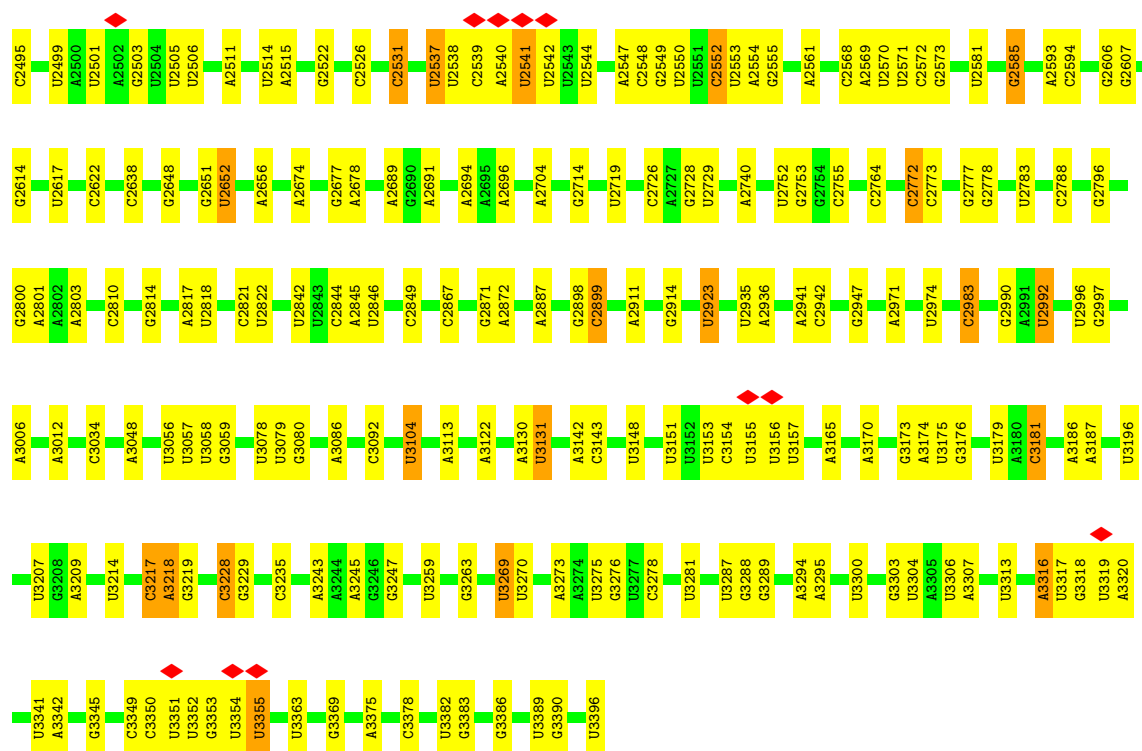


- Molecule 30: 25S rRNA

Chain f:  75% 18% 5%

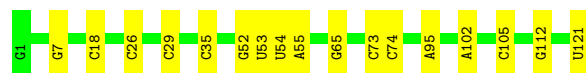






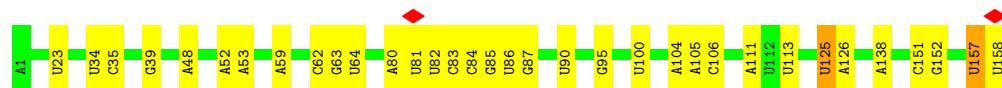
• Molecule 31: 5S rRNA

Chain h: 86% 14%



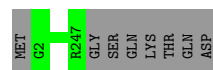
• Molecule 32: 5.8S rRNA

Chain i: 78% 20%



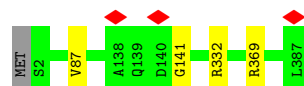
• Molecule 33: 60S ribosomal protein L2-A

Chain j: 97%



• Molecule 34: 60S ribosomal protein L3

Chain k: 99%



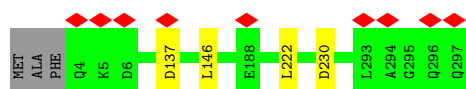
- Molecule 35: 60S ribosomal protein L4-A

Chain l:  99%



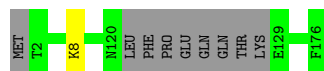
- Molecule 36: 60S ribosomal protein L5

Chain m:  98%

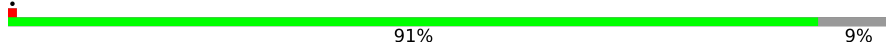


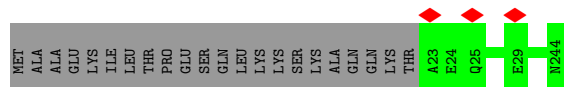
- Molecule 37: 60S ribosomal protein L6-B

Chain n:  94%

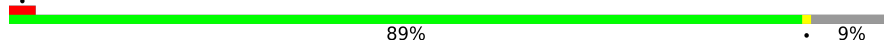


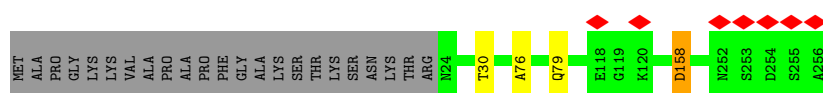
- Molecule 38: 60S ribosomal protein L7-A

Chain o:  91%



- Molecule 39: 60S ribosomal protein L8-A

Chain p:  89%



- Molecule 40: 60S ribosomal protein L9-A

Chain q:  98%

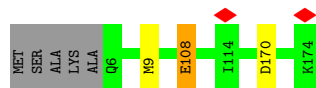


- Molecule 41: 60S ribosomal protein L10

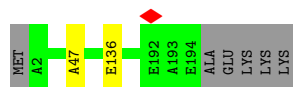
Chain r:  98%



- Molecule 42: 60S ribosomal protein L11-A



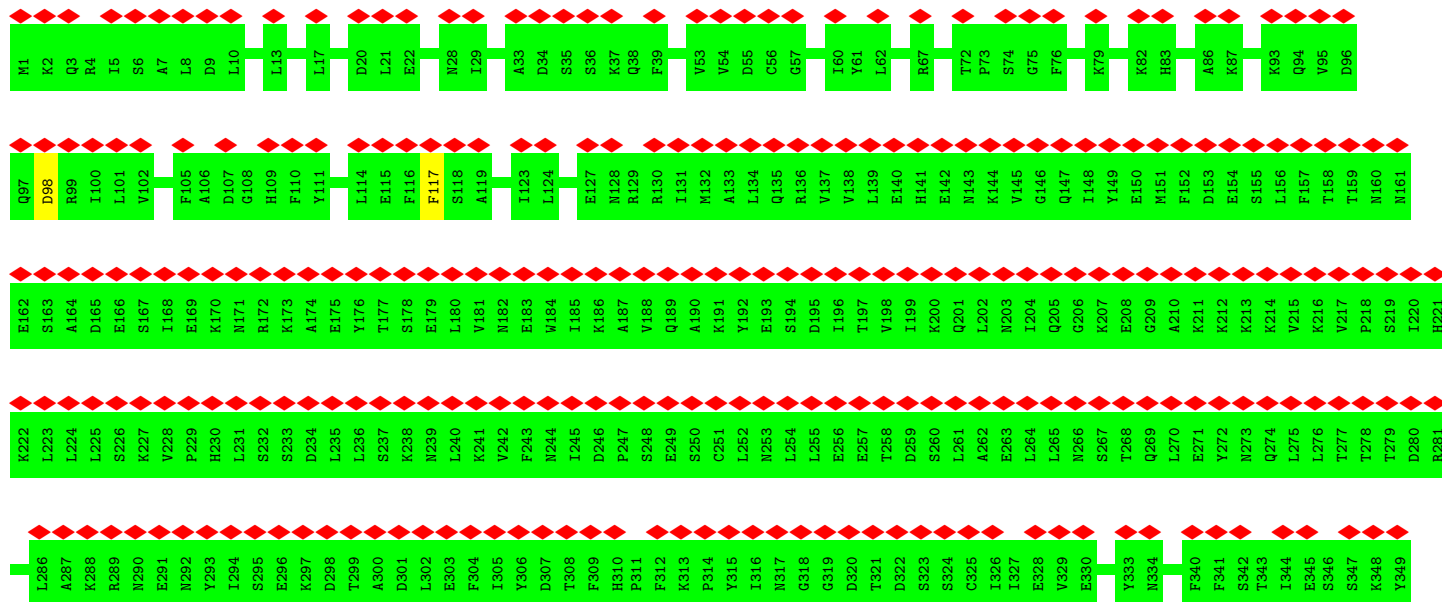
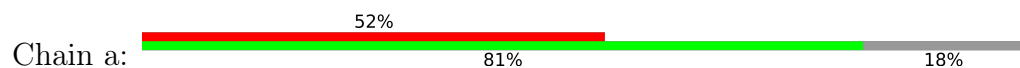
- Molecule 43: 60S ribosomal protein L13-A



- Molecule 44: 60S ribosomal protein L14-A



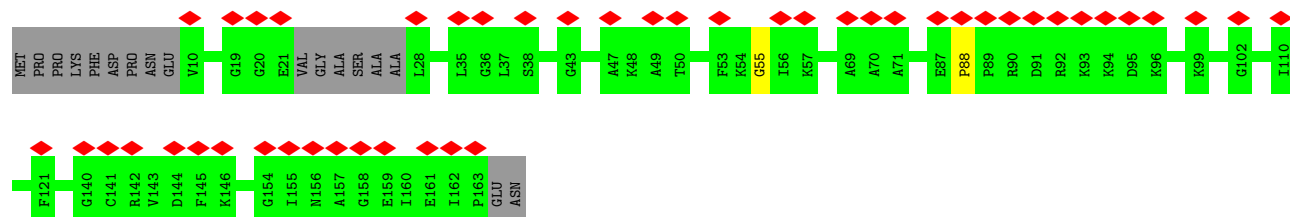
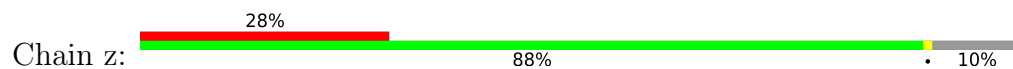
- Molecule 45: RQC2 isoform 1



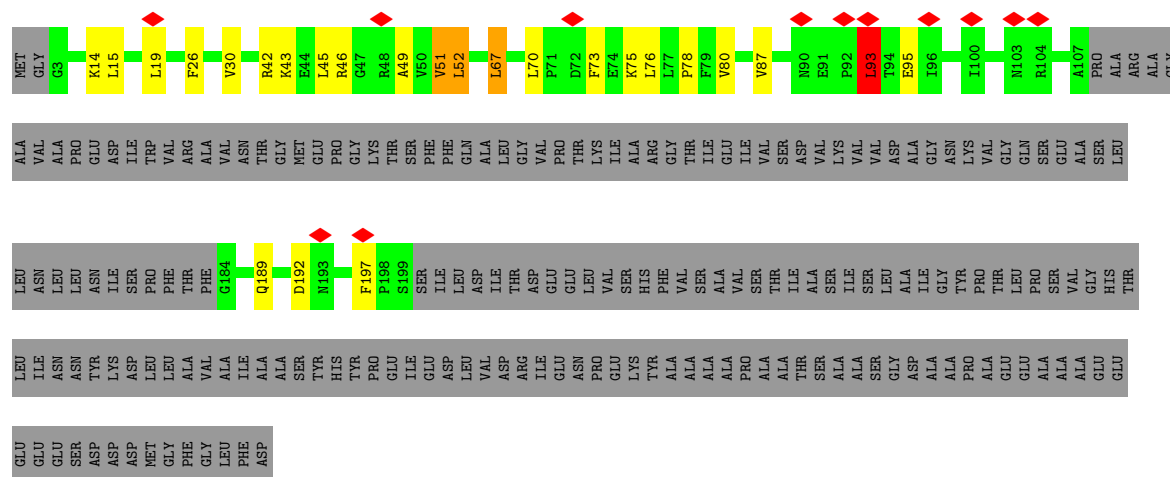
Q1141	A1081	P1021	L961	S901	V841	D781	E721	S661	L601	I541	K481	V421
E1142	D1082	Q1022	L962	N902	S842	Y782	I722	A662	A602	G542	N482	K422
R1143	S1083	R1023	M963	S903	E843	R783	A723	V663	T603	K543	L483	K423
M1144	L1084	L1024	F964	Y904	L844	S784	N724	A664	M504	F544	F484	M424
M1145	S1085	M1025	N965	Y905	V845	S785	K725	N665	E905	I545	A485	V425
Q1146	M1086	M1026	R966	F906	T846	L786	L726	G666	E906	I546	A486	E426
V1147	C1087	I1027	S967	F907	D847	V787	A727	Q667	L607	E547	L487	S427
S1148	Q1088	F1028	N968	Y908	Y848	S788	Q728	V668	D608	I548	V488	E428
T1149	I1089	S969	S969	Y909	N849	S789	Q729	E669	N609	P549	T489	I429
L1150	D1090	S1030	K970	S910	C950	L790	I730	Q670	D610	T550	S490	F430
F1151	D1091	I1031	D971	R911	L851	S791	L731	F771	I611	L551	P491	N431
Y1152	T1092	L1032	E972	Y912	S852	T792	Q732	C672	Y612	V552	N492	S432
Q1153	L1093	K1033	I973	L913	E853	M793	H733	A673	Q613	Q553	N493	L433
K1154	Y1094	W1034	T974	Y914	E854	T794	A734	V674	Q614	E554	E494	S434
L1155	L1095	L1035	K975	X915	P855	H795	Q735	L675	L615	S555	S495	C435
Y1156	L1096	D1036	L976	Y916	N856	L796	V736	S676	M616	T556	A496	G436
K1157	E1097	S1037	R977	L917	D857	L797	Y737	K677	K617	Y557	I497	K437
V1158	L1098	D1038	T978	L918	L858	L798	F738	L678	S618	Q558	S498	S438
I1159	R1099	L1039	L979	N919	V859	T799	S739	D679	D619	N559	R499	L439
S1160	S1100	A1040	L980	S920	V860	D800	P740	E680	S620	F560	L500	S440
S1161	S1101	Y1041	A981	I921	D861	D801	G741	N681	L621	A561	F501	E441
M1162	C1102	E1042	S982	D922	F862	K802	A742	T682	E622	D502	D502	Y442
E1163	L1103	P1043	Q983	T923	G863	P603	K743	F683	L623	I563	F503	T443
L1164	N1104	S1044	L984	V924	H864	I804	E744	S684	E624	M564	F504	K444
K1165	L1105	F1045	I985	S925	T865	N805	K745	T685	L625	A565	V505	L445
K1166	Y1106	S1046	G986	S926	F866	L806	V746	L686	Y626	Q566	Q506	N446
L1167	E1107	T1047	I987	T927	P867	K807	V747	L687	I627	Y567	L507	Q447
E1168	T1108	V1048	R988	T928	K868	N808	T748	N688	E628	S568	I508	T448
S1169	L1109	R1049	E989	L929	H869	M609	H749	N689	D629	N569	E509	L449
Q1170	S1110	L1050	V990	N930	G870	Q810	A750	T690	F630	S570	T510	S450
Y1171	Q1111	L1051	E991	G931	K871	K811	V751	D891	M631	K571	D511	G451
K1172	GLY	L1052	L992	L932	V872	L812	E752	F692	K632	F572	P512	V452
A1173	SER	L1053	V993	L933	N873	I813	L753	L693	M633	F573	S513	F453
I1174	LYS	D1054	D994	A934	L874	R814	I754	S694	Y634	K574	N514	P454
F1175	ASN	F1055	Q995	S935	N875	Y815	N755	C895	K635	M575	V515	P455
E1176	GLY	F1056	E996	V936	F876	A816	G756	A696	F636	N576	F516	D456
V1177	GLU	T1057	F997	E937	S877	L817	C757	L697	D637	T577	N517	K457
V1178	ILE	K1058	K998	S938	D878	F818	N758	Y698	D638	D578	K518	V458
L1179	SER	L1059	S999	F939	I879	L819	D759	E699	S639	A579	Y519	E459
M1180	E1122	M1060	L1000	V940	V880	D820	T760	V700	G640	I580	D520	R460
D1181	Y1123	R1061	A1001	T941	G881	A821	S761	S701	E941	T581	G521	E461
K1182	G1124	F1062	L1002	K942	N882	L822	Q762	E702	I642	S582	V522	I462
D1183	D1125	E1063	L1003	T943	V883	L823	I763	D703	F643	L583	Y523	E463
I1184	E1126	G1064	N1004	V944	T884	D824	F764	T704	K644	E584	D524	D464
K1185	I1127	V1065	N1005	R945	Q885	A825	F765	N705	G645	D585	A525	Y465
S1186	Q1128	L1066	L1006	D946	P886	L826	V766	E706	N646	F586	A526	F466
N1187	E1129	D1067	L1007	Q947	A887	P827	A767	K707	M647	F587	N527	T467
I1188	N1130	M1068	D1008	K948	N888	E828	N768	L708	K648	I588	Y528	S468
M1189	L1131	G1069	I1009	S949	G889	R629	A769	F709	F649	V589	F529	D469
Q1190	I1132	P1070	P1010	T950	G990	V830	I770	K710	L650	A590	L530	E470
S1191	E1133	T1071	Q1011	D951	D891	N831	E771	L711	M651	L591	D531	D471
R1192	L1134	A1072	A1012	K952	A892	N832	V772	S712	Q652	S592	S532	I472
L1193	M1135	F1073	D1013	D953	N893	H833	F773	L713	R653	F593	D533	R473
L1194	F1136	E1074	K1014	Y954	L894	T834	A774	Q714	T654	N594	M534	K474
T1195	L1137	L1075	Q1015	L955	T895	V835	R775	L715	I655	L595	I535	I475
T1196	N1138	S1076	F1016	L956	F896	A836	V776	A716	T656	P596	F536	K476
L1197	F1139	E1077	V1017	C957	D897	F837	M777	K717	T657	K597	L537	V477
L1198	N1140	R1078	P1018	A958	T898	T838	P778	G718	L658	T598	L538	S478
G1199		L1079	I1019	P959	A899	T639	A779	N719	Y659	I599	G539	F479
S1200		A1020		L960	E900	V840	I780	S720	R660	I600	K540	E480



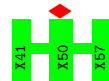
- Molecule 49: 60S ribosomal protein L12-A



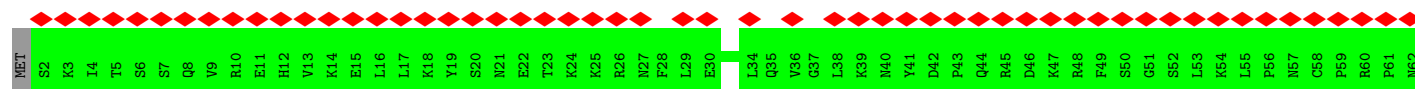
- Molecule 50: 60S acidic ribosomal protein P0



- Molecule 51: CAT-tailed nascent peptide



- Molecule 52: 60S ribosomal protein L1-A



I183	I184	M185	S186	M188	F189	F190	V191	S192	L193	L194	K195	K196	W197	Q198	Q199	G202	S203	L204	V205	V206	F214	R215	L216	Y217	L123	L124	G125	P126	L128	S129	K130	A131	G132	K133	F134	P135	T136	P137	S138	S139	H140	N141	D142	D143	L144	Y145	G146	K147	V148	T149	D150	V151	R152	S153	T154	L155	K156	F157	Q158	L159	K160	K161	V162	L163	G164	L165	A166	V167	A168	V169	G170	M171	V172	E173	M174	E175	E176	D177	V178	L179	V180	N181	K182	M63	S64	I65	C66	I67	F68	G69	D70	A71	F72	D73	V74	D75	R76	A77	K78	S79	C80	G81	V82	D83	A84	M85	S86	V87	D88	D89	L90	K91	K92	L93	N94	K95	N96	K97	K98	L99	I100	K101	K102	L103	S104	K105	K106	V107	N108	A109	F110	I111	A112	S113	E114	V115	L116	I117	K118	Q119	V120	P121	R122
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58513	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	3.793	Depositor
Minimum map value	-0.656	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.131	Depositor
Recommended contour level	0.55	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: ZN, MG, SPD

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	0.72	2/1938 (0.1%)
4	D	0.34	0/1465	0.67	1/1965 (0.1%)
5	E	0.37	0/1275	0.68	0/1702
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	0.35	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	0.67	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	0.39	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	0.67	0/934
29	d	0.26	0/208	0.84	0/267
30	f	0.61	0/77011	1.01	272/120065 (0.2%)
31	h	0.53	0/2883	0.98	8/4491 (0.2%)
32	i	0.61	0/3746	0.96	7/5832 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	j	0.37	0/1908	0.67	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	0.31	0/6683	0.57	3/9016 (0.0%)
46	e	0.39	0/11711	0.55	2/15903 (0.0%)
47	g	0.32	0/1672	0.63	0/2281
48	x	0.20	0/1761	0.65	0/2742
48	y	0.23	0/1735	0.65	0/2701
49	z	0.37	0/726	0.60	0/1006
50	0	0.33	0/976	0.55	0/1313
52	w	0.33	0/1736	0.65	0/2332
All	All	0.50	0/160675	0.86	324/234844 (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
46	e	0	1
47	g	0	1
All	All	0	12

There are no bond length outliers.

The worst 5 of 324 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	f	3217	C	N1-C2-O2	12.05	126.13	118.90
30	f	3217	C	C2-N1-C1'	11.35	131.29	118.80
30	f	3217	C	N3-C2-O2	-9.71	115.10	121.90
11	K	134	ASP	CB-CG-OD1	9.66	126.99	118.30
30	f	922	U	C2-N1-C1'	9.31	128.87	117.70

There are no chirality outliers.

5 of 12 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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1720	0	1779	9	0
2	B	1555	0	1659	13	0
3	C	1416	0	1433	11	0
4	D	1441	0	1543	7	0
5	E	1258	0	1342	6	0
6	F	1437	0	1475	14	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
14	N	1169	0	1211	7	0
15	O	462	0	491	5	0
16	P	737	0	792	3	0
17	Q	876	0	912	9	0
18	R	1013	0	1077	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	842	4	0
23	W	645	0	645	4	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	6573	0	6471	0	0
46	e	11512	0	10772	0	0
47	g	1651	0	1613	0	0
48	x	1579	0	800	0	0
48	y	1556	0	788	0	0
49	z	728	0	337	0	0
50	0	961	0	979	11	0
51	1	85	0	21	0	0
52	w	1709	0	1797	0	0
53	A	1	0	0	0	0
53	C	1	0	0	0	0
53	E	1	0	0	0	0
53	I	1	0	0	0	0
53	R	1	0	0	0	0
53	T	1	0	0	0	0
53	f	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	h	1	0	0	0	0
53	j	2	0	0	0	0
53	k	1	0	0	0	0
54	T	1	0	0	0	0
54	W	1	0	0	0	0
54	Z	1	0	0	0	0
54	b	1	0	0	0	0
54	c	1	0	0	0	0
54	e	2	0	0	0	0
55	f	10	0	19	0	0
All	All	150269	0	112534	143	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 143 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
50:O:26:PHE:HB2	50:O:87:VAL:HB	1.73	0.69
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	8	16
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%)	41	64
36	m	292/297 (98%)	277 (95%)	15 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	n	163/176 (93%)	155 (95%)	8 (5%)	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%)	29	52
41	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
42	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	25	47
43	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	29	52
44	u	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
45	a	842/1038 (81%)	827 (98%)	15 (2%)	0	100	100
46	e	1519/1562 (97%)	1497 (99%)	20 (1%)	2 (0%)	51	75
47	g	223/245 (91%)	215 (96%)	8 (4%)	0	100	100
49	z	144/165 (87%)	135 (94%)	7 (5%)	2 (1%)	11	22
50	0	117/312 (38%)	116 (99%)	0	1 (1%)	17	35
52	w	214/217 (99%)	211 (99%)	3 (1%)	0	100	100
All	All	9175/10122 (91%)	8817 (96%)	348 (4%)	10 (0%)	54	75

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
49	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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	138/146 (94%)	138 (100%)	0	100	100
4	D	150/151 (99%)	149 (99%)	1 (1%)	84	94
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%)	84	94
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%)	52	76
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%)	73	88
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%)	42	68
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%)	189 (100%)	0	100	100
34	k	320/323 (99%)	318 (99%)	2 (1%)	86	95
35	l	288/289 (100%)	288 (100%)	0	100	100
36	m	241/245 (98%)	241 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	n	139/155 (90%)	138 (99%)	1 (1%)	84	94
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%)	73	88
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	677/949 (71%)	676 (100%)	1 (0%)	93	98
46	e	1151/1451 (79%)	1093 (95%)	58 (5%)	24	47
47	g	180/211 (85%)	180 (100%)	0	100	100
50	0	104/254 (41%)	95 (91%)	9 (9%)	10	20
52	w	197/198 (100%)	196 (100%)	1 (0%)	88	96
All	All	7444/8558 (87%)	7364 (99%)	80 (1%)	74	88

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	e	1341	LYS
50	0	51	VAL
46	e	1367	THR
46	e	1428	VAL
50	0	80	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
46	e	1499	HIS
50	0	36	GLN
47	g	9	ASN
46	e	902	ASN
46	e	1477	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	f	3211/3395 (94%)	600 (18%)	0
31	h	120/121 (99%)	12 (10%)	0
32	i	157/158 (99%)	32 (20%)	0
48	x	72/76 (94%)	26 (36%)	0
48	y	71/76 (93%)	26 (36%)	0
All	All	3631/3826 (94%)	696 (19%)	0

5 of 696 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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 20 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
55	SPD	f	3401	-	9,9,9	0.32	0	8,8,8	0.86	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	SPD	f	3401	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	f	3401	SPD	C3-C4-C5-N6
55	f	3401	SPD	N6-C7-C8-C9
55	f	3401	SPD	C2-C3-C4-C5
55	f	3401	SPD	C8-C7-N6-C5
55	f	3401	SPD	C4-C5-N6-C7

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.

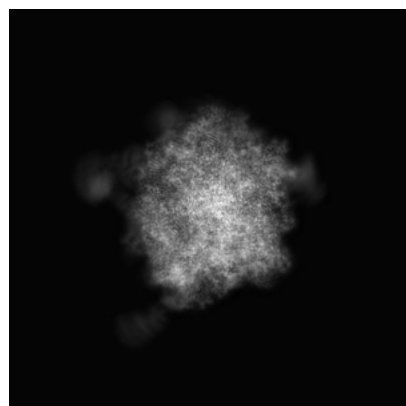
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15426. These allow visual inspection of the internal detail of the map and identification of artifacts.

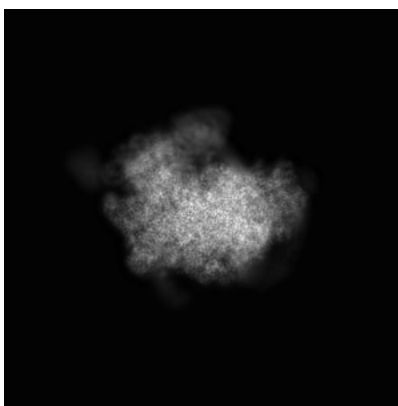
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

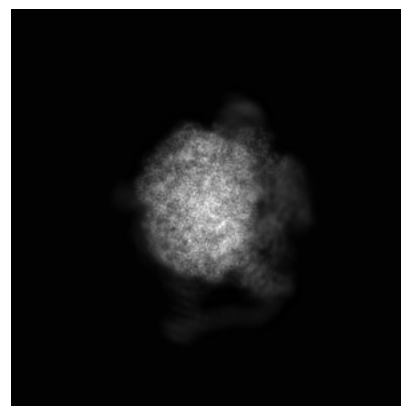
6.1.1 Primary map



X

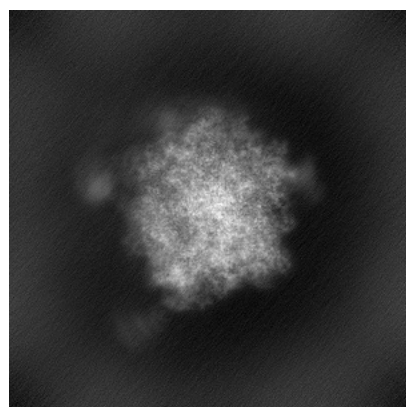


Y

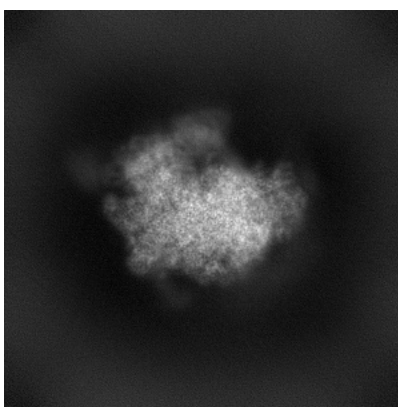


Z

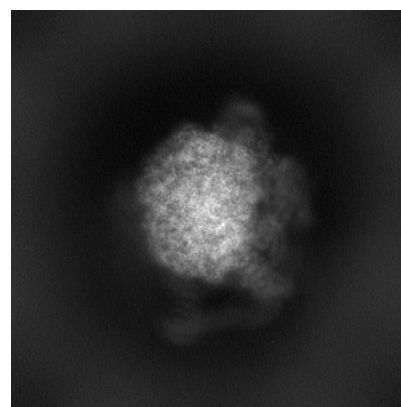
6.1.2 Raw map



X



Y

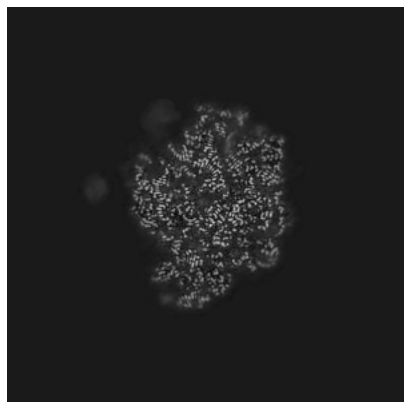


Z

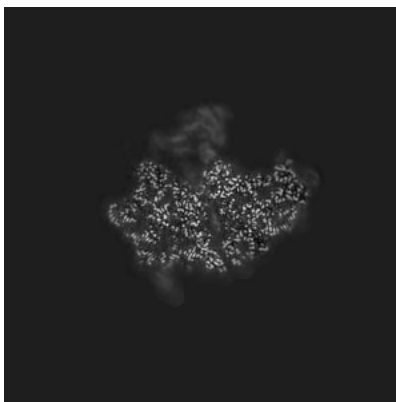
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

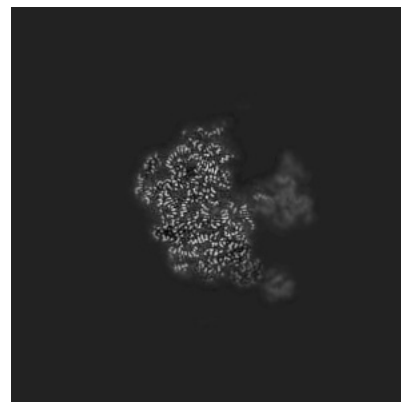
6.2.1 Primary map



X Index: 225

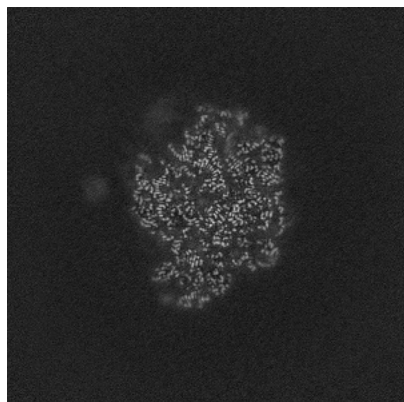


Y Index: 225

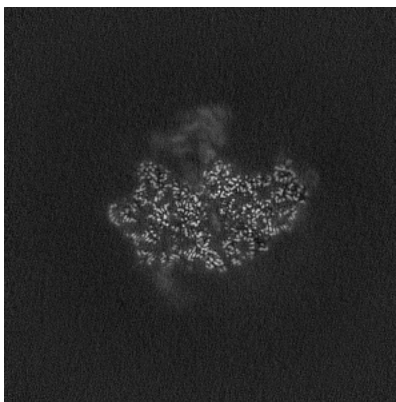


Z Index: 225

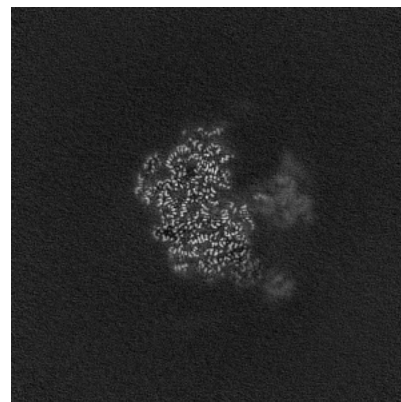
6.2.2 Raw map



X Index: 225



Y Index: 225

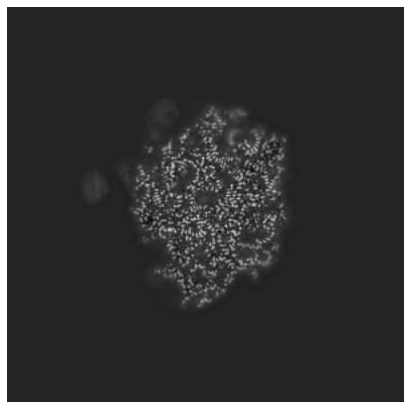


Z Index: 225

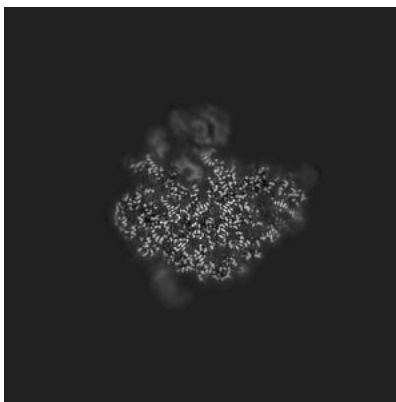
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

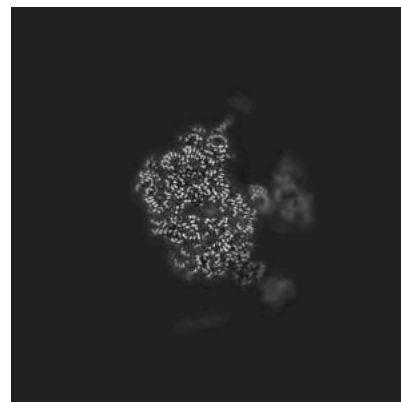
6.3.1 Primary map



X Index: 219

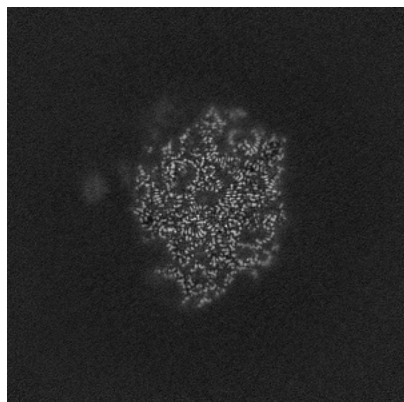


Y Index: 237

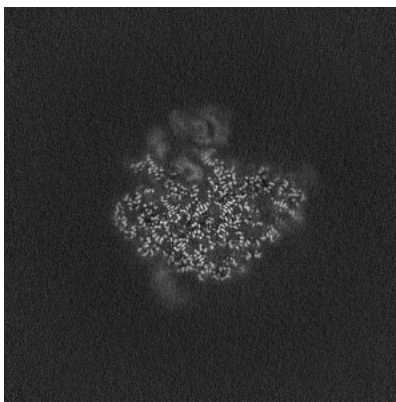


Z Index: 230

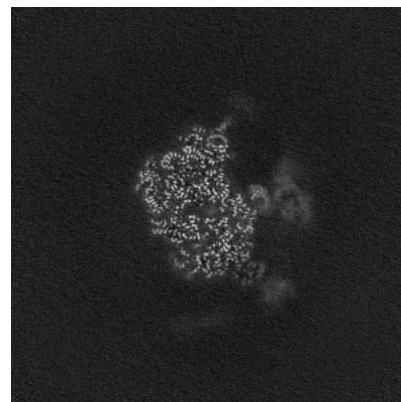
6.3.2 Raw map



X Index: 219



Y Index: 237

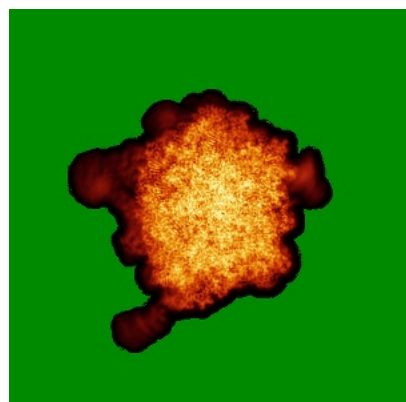


Z Index: 230

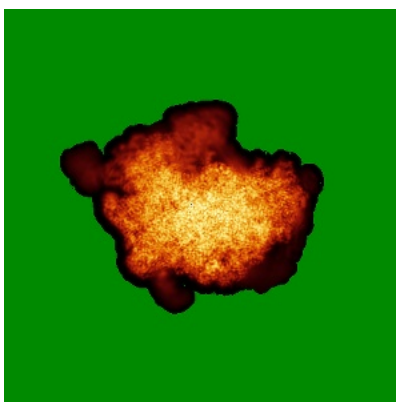
The images above show the largest variance slices of the map in three orthogonal directions.

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

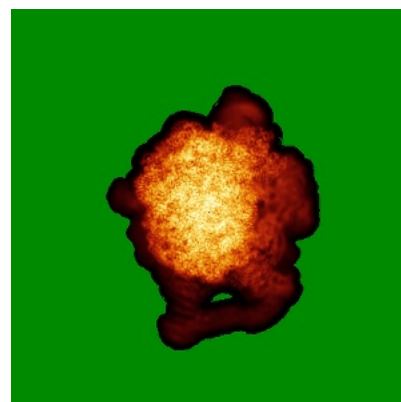
6.4.1 Primary map



X

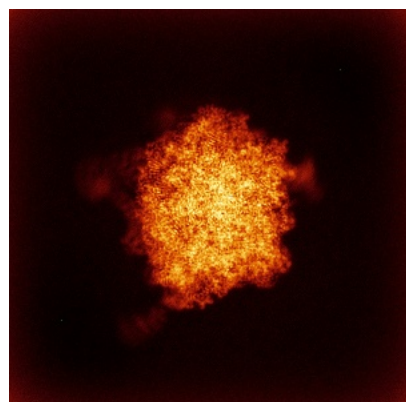


Y

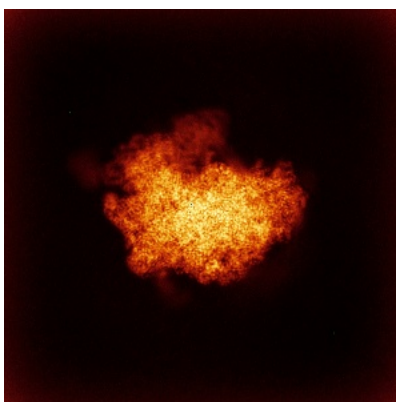


Z

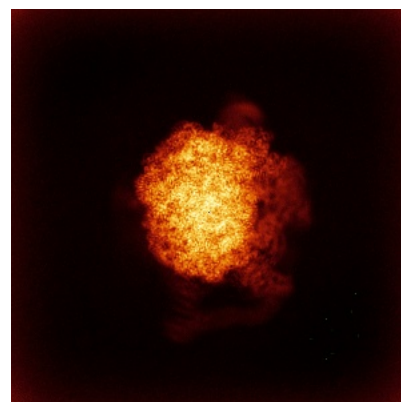
6.4.2 Raw map



X



Y

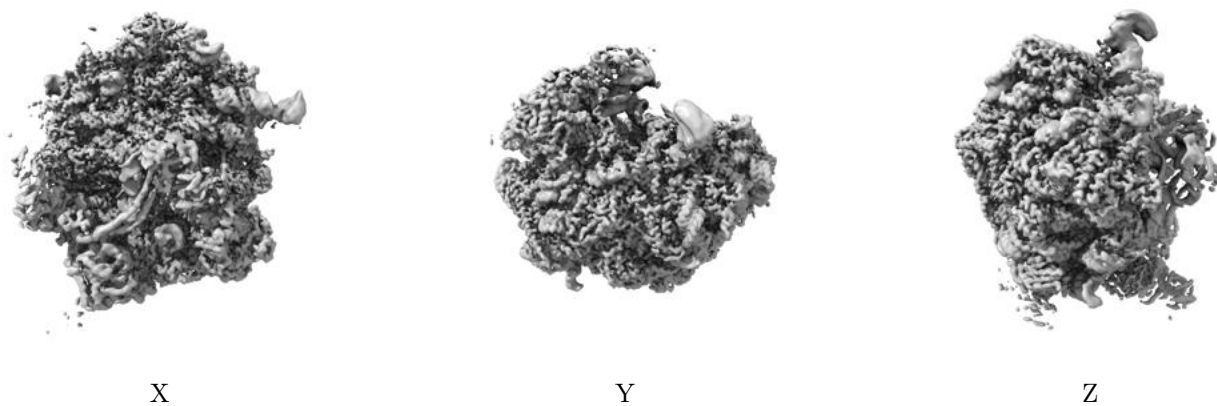


Z

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.

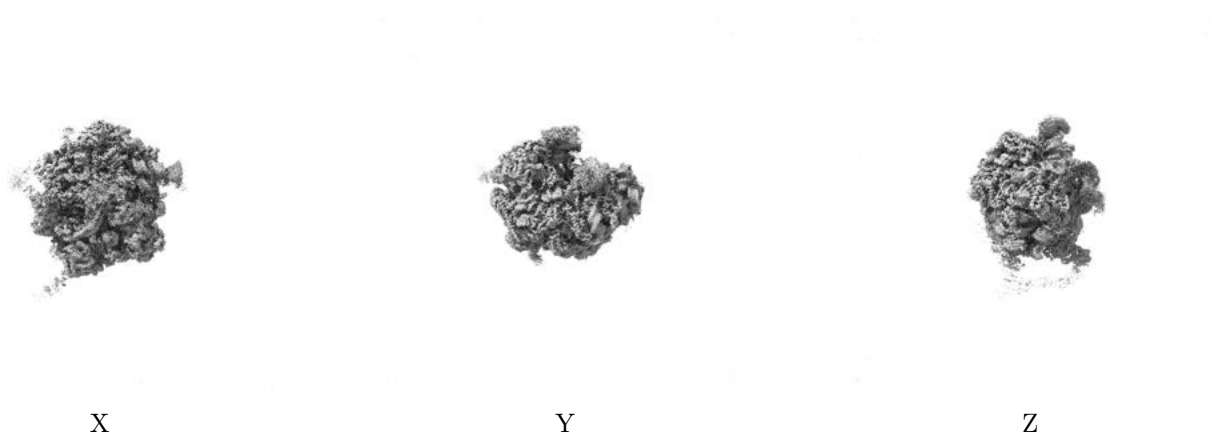
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.55. 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.

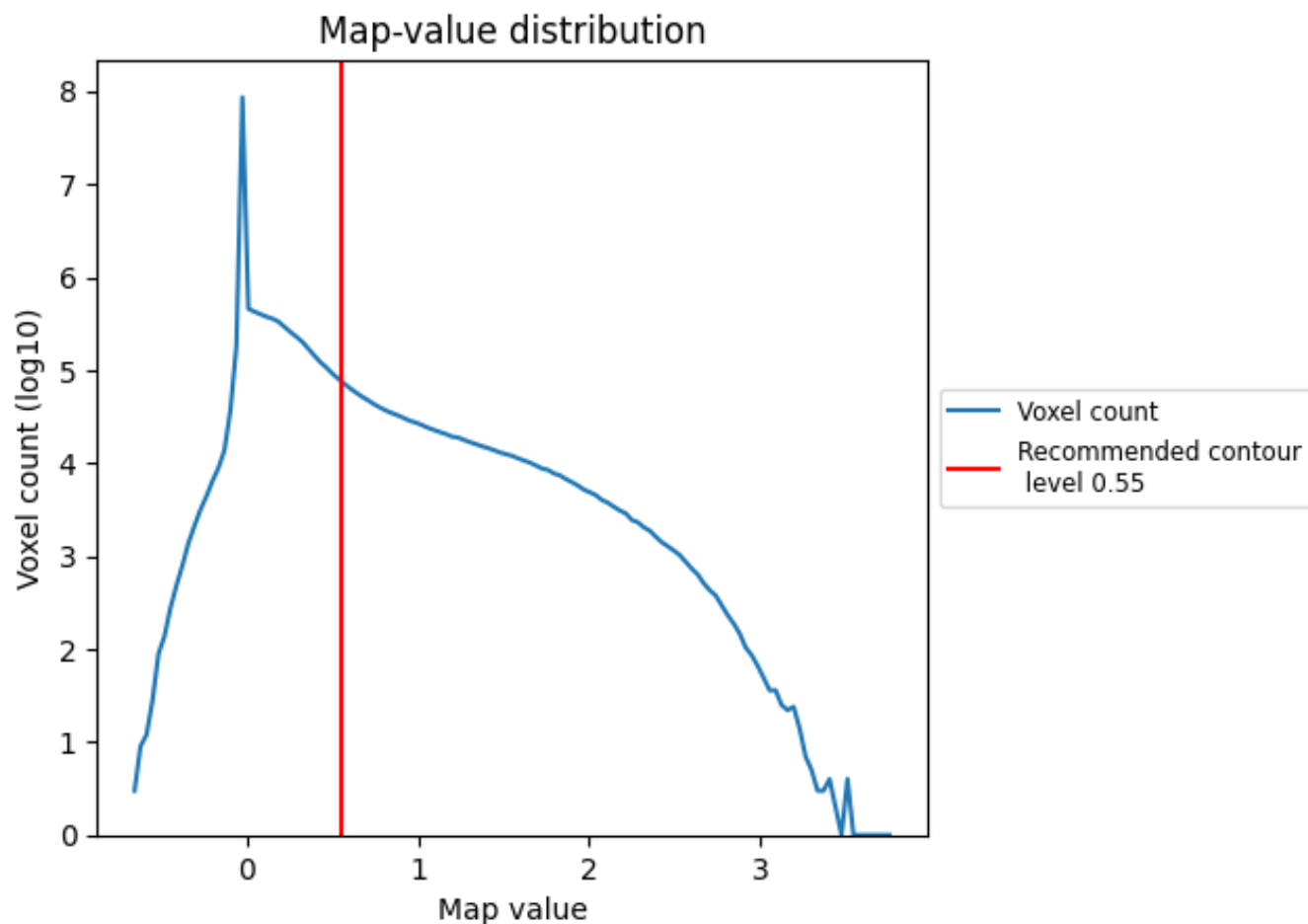
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

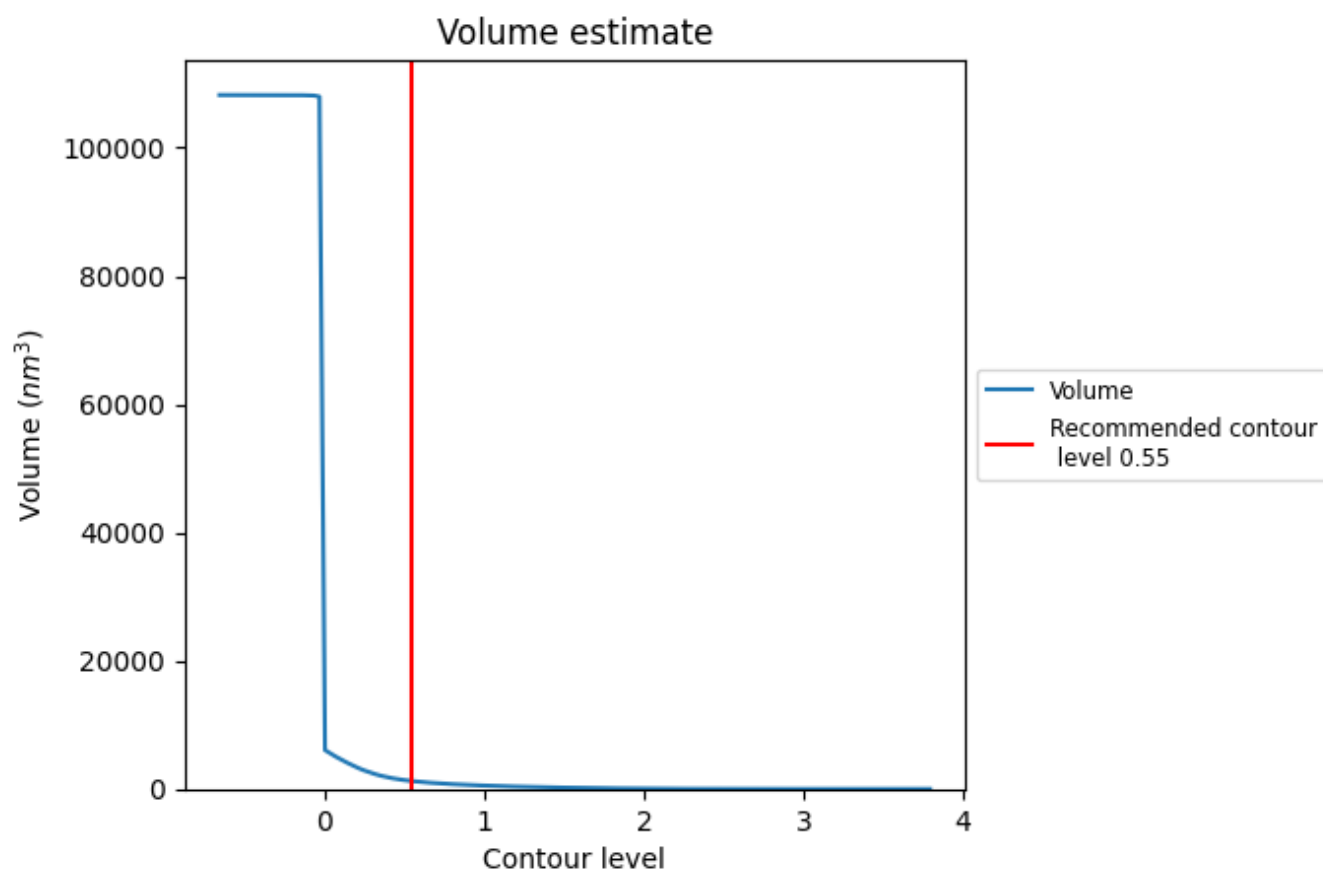
This section contains the results of statistical analysis of the map.

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.

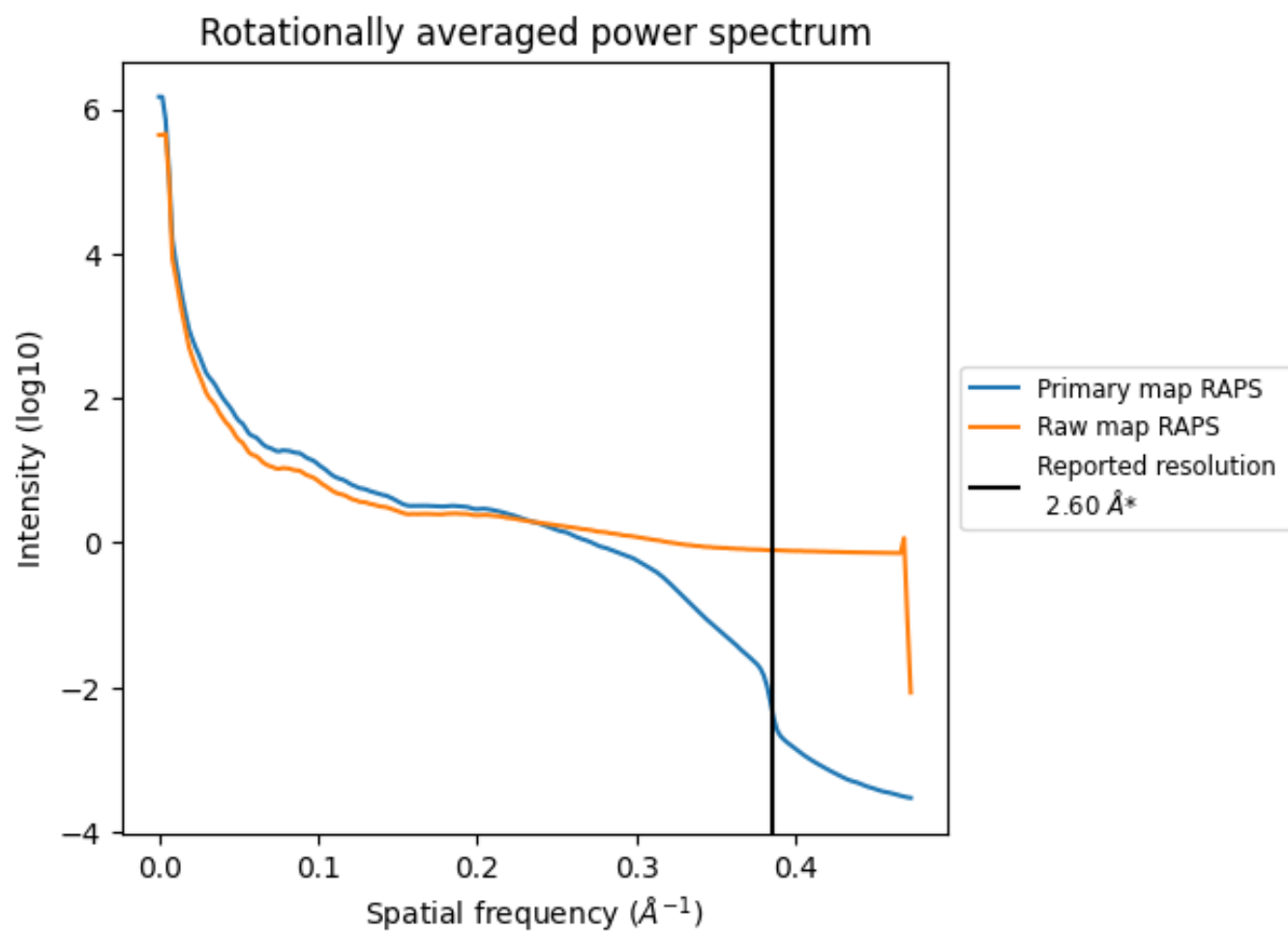
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1231 nm^3 ; this corresponds to an approximate mass of 1112 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 ⓘ

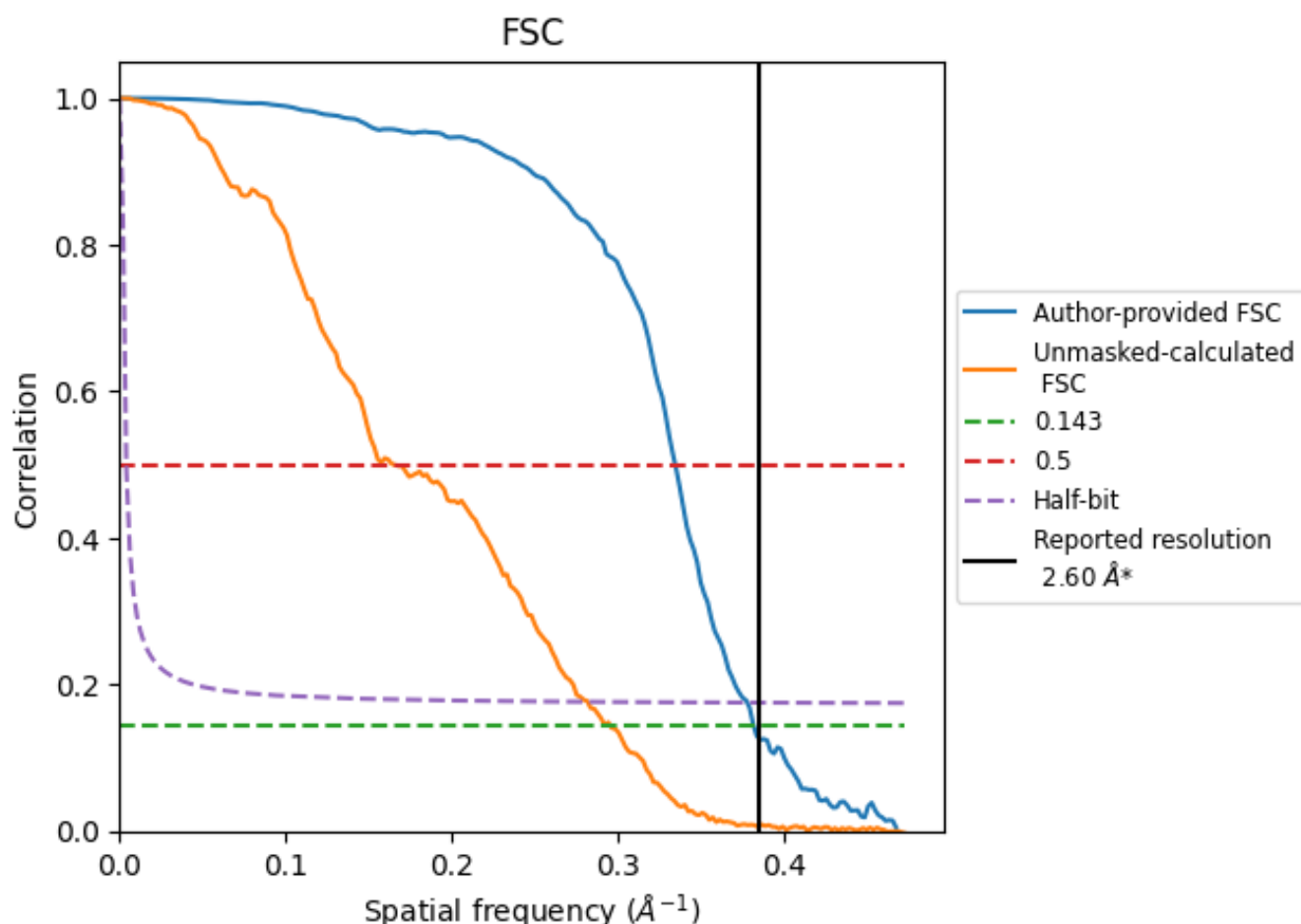


*Reported resolution corresponds to spatial frequency of 0.385 \AA^{-1}

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⁻¹

8.2 Resolution estimates [i](#)

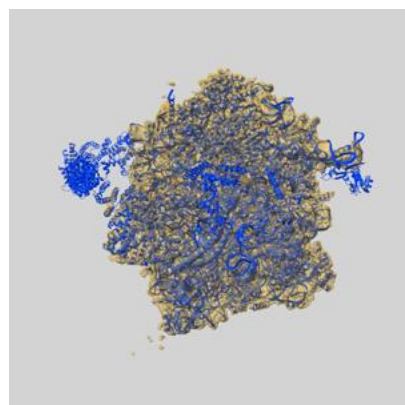
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.62	2.99	2.65
Unmasked-calculated*	3.39	6.07	3.55

*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 3.39 differs from the reported value 2.6 by more than 10 %

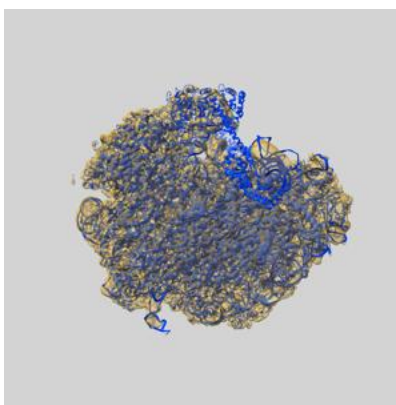
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15426 and PDB model 8AGW. Per-residue inclusion information can be found in section [3](#) on page [14](#).

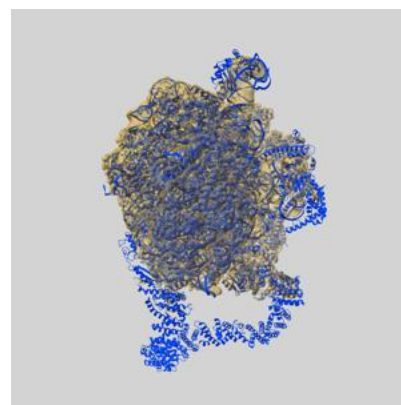
9.1 Map-model overlay [i](#)



X



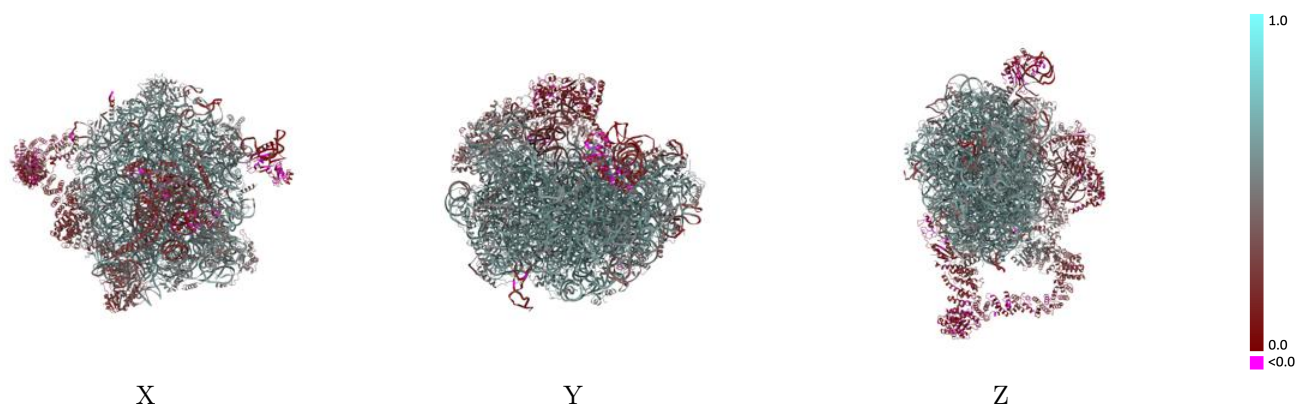
Y



Z

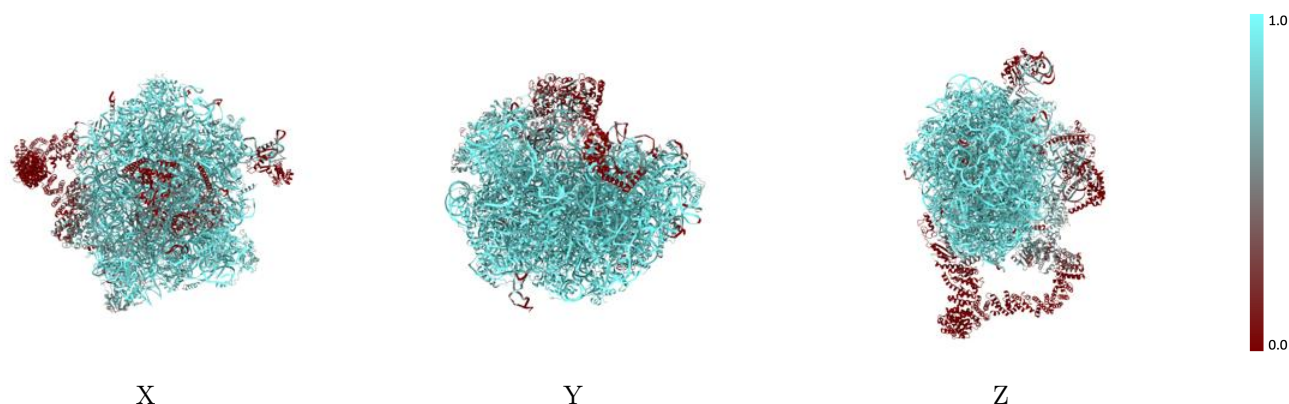
The images above show the 3D surface view of the map at the recommended contour level 0.55 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



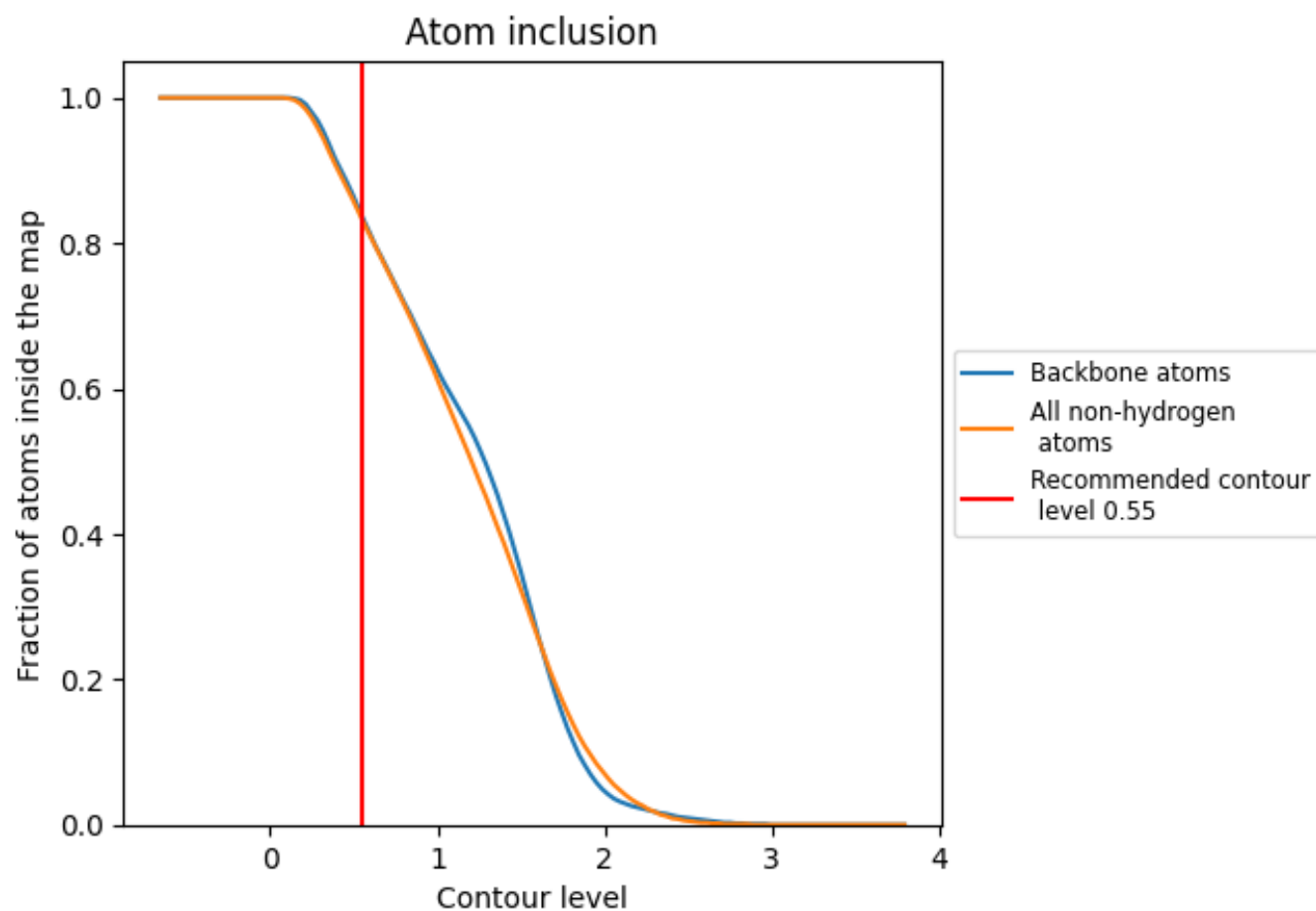
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.55).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 83% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8320	 0.5020
0	 0.6230	 0.2810
1	 0.9060	 0.4570
A	 0.9790	 0.6090
B	 0.9510	 0.5820
C	 0.9320	 0.5860
D	 0.9490	 0.5800
E	 0.8870	 0.5450
F	 0.9340	 0.5750
G	 0.9110	 0.5620
H	 0.8130	 0.4670
I	 0.9220	 0.5690
J	 0.9220	 0.5700
K	 0.9200	 0.5680
L	 0.9350	 0.5660
M	 0.8800	 0.5230
N	 0.9480	 0.5880
O	 0.9090	 0.5330
P	 0.8540	 0.5240
Q	 0.8820	 0.5500
R	 0.9510	 0.5960
S	 0.9670	 0.6090
T	 0.9210	 0.5680
U	 0.9180	 0.5520
V	 0.9030	 0.5180
W	 0.9950	 0.6250
X	 0.8130	 0.4940
Y	 0.9710	 0.5990
Z	 0.9290	 0.5650
a	 0.2800	 0.1930
b	 0.9090	 0.5700
c	 0.9160	 0.5660
d	 0.5000	 0.3930
e	 0.1380	 0.1850
f	 0.9680	 0.5670



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Chain	Atom inclusion	Q-score
g	 0.4690	 0.4560
h	 0.9930	 0.5710
i	 0.9830	 0.5960
j	 0.9590	 0.6030
k	 0.9460	 0.5800
l	 0.9370	 0.5730
m	 0.8560	 0.4820
n	 0.8820	 0.5280
o	 0.9390	 0.5660
p	 0.8780	 0.5160
q	 0.9110	 0.5430
r	 0.9040	 0.5460
s	 0.8140	 0.4390
t	 0.9210	 0.5600
u	 0.9270	 0.5460
w	 0.0770	 0.0750
x	 0.5600	 0.2560
y	 0.7970	 0.2340
z	 0.6130	 0.3040