



## wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 09:35 PM UTC

PDB ID : 9T4R / pdb\_00009t4r  
EMDB ID : EMD-55526  
Title : Staphylococcus aureus 70S initiation complex with a natural mRNA  
Authors : Bahena Ceron, R.; Klaholz, B.; Marzi, S.  
Deposited on : 2025-10-30  
Resolution : 2.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

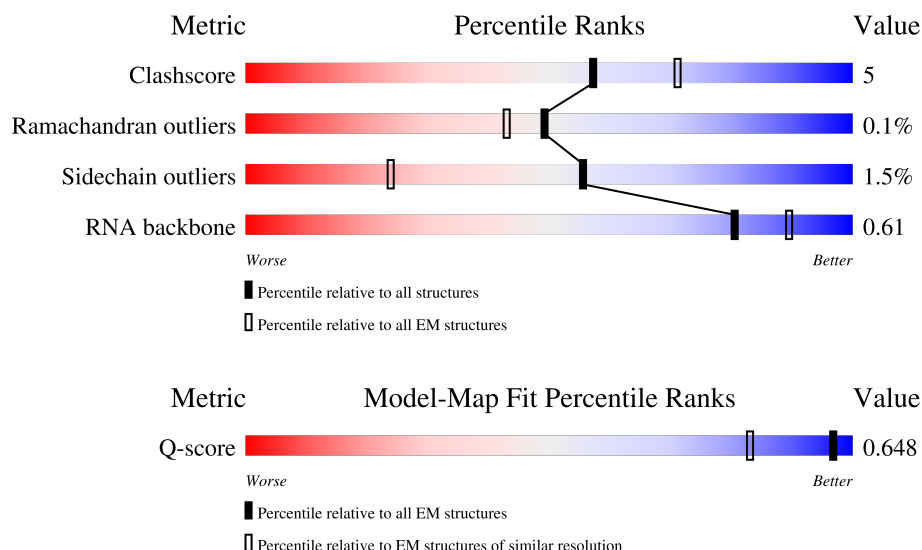
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




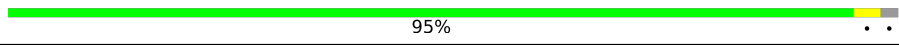

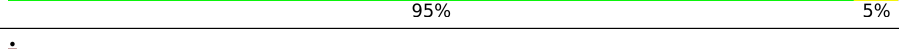
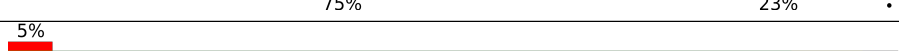

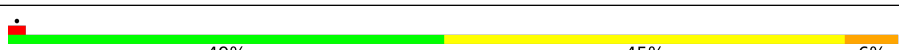
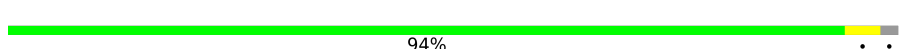

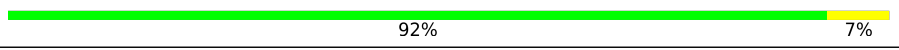

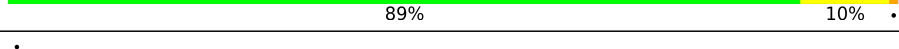
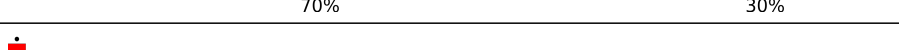

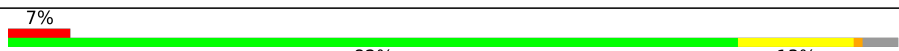

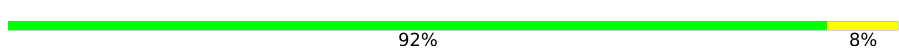

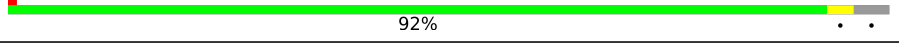

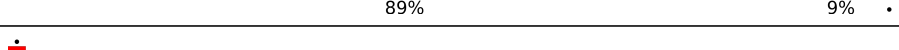




Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4254 ( 1.80 - 2.80 )

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	0	49	<div> <div>12%</div> <div>84%</div> <div>16%</div> </div>
2	X	17	<div> <div>24%</div> <div>59%</div> <div>18%</div> </div>
3	1	45	<div> <div>89%</div> <div>9%</div> </div>




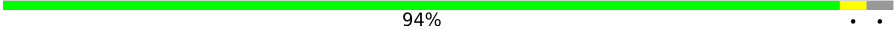

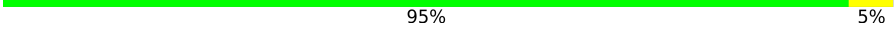




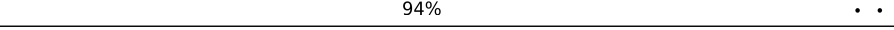


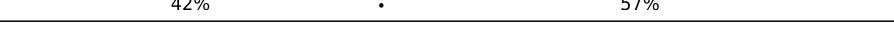



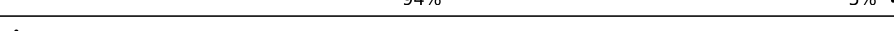



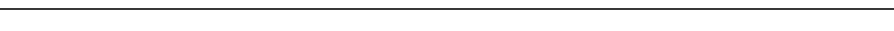


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Mol	Chain	Length	Quality of chain
4	Z	76	
5	2	66	
6	a	2917	
7	3	37	
8	b	115	
9	4	83	
10	c	277	
11	A	1548	
12	d	220	
13	B	255	
14	e	207	
15	C	217	
16	f	179	
17	D	200	
18	g	176	
19	E	166	
20	j	102	
21	F	98	
22	k	146	
23	G	155	
24	l	144	
25	H	132	
26	m	122	
27	I	131	
28	n	119	

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Mol	Chain	Length	Quality of chain
29	J	145	 92% 8%
30	o	116	 88% 6% 6%
31	K	129	 84% 6% 9%
32	p	118	 94% . .
33	L	137	 91% 8% .
34	q	102	 95% 5%
35	M	121	 85% 12% .
36	r	117	 90% 6% .
37	N	61	 87% 11% .
38	s	91	 92% 5% .
39	O	89	 94% . .
40	t	90	 84% 14% .
41	P	91	 86% 8% . .
42	u	217	 42% . 57%
43	Q	87	 79% 14% .. 5%
44	v	94	 82% . 14%
45	R	80	 74% 9% 18%
46	w	62	 94% 5% .
47	S	92	 77% 13% . 9%
48	x	69	 84% 10% 6%
49	T	83	 96% ...
50	y	59	 92% . 5%
51	U	122	 92% 8%
52	z	57	 86% 9% 5%

## 2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 213800 atoms, of which 70874 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 Large ribosomal subunit protein bL33B.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	49	Total	C	H	N	O	S	0	0
			775	243	369	82	76	5		

- Molecule 2 is a RNA chain called aur mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	17	Total	C	N	O	P	0	0
			375	167	76	115	17		

- Molecule 3 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	1	44	Total	C	H	N	O	S	0	0
			751	228	378	90	54	1		

- Molecule 4 is a RNA chain called Methionine tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	Z	76	Total	C	H	N	O	P	0	0
			2448	723	825	294	530	76		

- Molecule 5 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	2	65	Total	C	H	N	O	S	0	0
			1066	330	536	115	83	2		

- Molecule 6 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	a	2912	Total	C	H	N	O	P	0	0
			93441	27872	31011	11414	20232	2912		

- Molecule 7 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	3	37	Total	C	H	N	O	S	0	0
			605	186	309	60	45	5		

- Molecule 8 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	b	115	Total	C	H	N	O	P	0	0
			3309	1094	861	435	804	115		

- Molecule 9 is a protein called Large ribosomal subunit protein bL31B.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	4	80	Total	C	H	N	O	S	0	0
			1207	417	555	109	123	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	?	-	ARG	deletion	UNP Q2FWD8

- Molecule 10 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	c	273	Total	C	H	N	O	S	0	0
			4023	1297	1938	413	370	5		

- Molecule 11 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	A	1548	Total	C	N	O	P		0	0
			33149	14800	6040	10761	1548			

- Molecule 12 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	d	215	Total	C	H	N	O	S	0	0
			3092	1018	1464	299	306	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	B	225	Total	C	H	N	O	S	0	0
			3465	1153	1655	316	334	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	206	ILE	ALA	conflict	UNP Q2FZ25
B	207	ALA	ILE	conflict	UNP Q2FZ25

- Molecule 14 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	e	206	Total	C	H	N	O	S	0	0
			2997	986	1424	288	297	2		

- Molecule 15 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	C	203	Total	C	H	N	O	S	0	0
			3063	1007	1463	301	290	2		

- Molecule 16 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	f	179	Total	C	H	N	O	S	0	0
			2730	902	1310	245	265	8		

- Molecule 17 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	D	199	Total	C	N	O	S		0	0
			1615	1018	302	293	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	25	ASP	GLU	conflict	UNP A7X3F0
D	26	VAL	LEU	conflict	UNP A7X3F0

- Molecule 18 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	g	175	Total	C	H	N	O	S	0	0
			2601	850	1233	250	265	3		

- Molecule 19 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	E	157	Total	C	H	N	O	S	0	0
			2248	735	1080	214	217	2		

- Molecule 20 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	j	98	Total	C	H	N	O	S	0	0
			1517	494	734	143	145	1		

- Molecule 21 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	F	95	Total	C	H	N	O	S	0	0
			1484	498	695	138	150	3		

- Molecule 22 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	k	146	Total	C	H	N	O	S	0	0
			2100	680	1002	215	202	1		

- Molecule 23 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	G	153	Total	C	H	N	O	S	0	0
			2332	759	1111	236	222	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	VAL	deletion	UNP P48940

- Molecule 24 is a protein called Large ribosomal subunit protein uL16.



Mol	Chain	Residues	Atoms						AltConf	Trace
24	l	138	Total	C	H	N	O	S	0	0
			2140	706	1039	208	183	4		

- Molecule 25 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	H	131	Total	C	H	N	O	S	0	0
			1988	652	957	183	192	4		

- Molecule 26 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	m	119	Total	C	H	N	O	S	0	0
			1813	575	874	181	182	1		

- Molecule 27 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	I	127	Total	C	H	N	O	S	0	0
			1915	623	907	201	183	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	?	-	LYS	deletion	UNP Q2FW39

- Molecule 28 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	n	118	Total	C	H	N	O	S	0	0
			1751	564	844	173	169	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	62	ILE	ASP	conflict	UNP Q2FW22
n	63	ALA	ILE	conflict	UNP Q2FW22

- Molecule 29 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	J	145	Total	C	H	N	O	S	0	0
			2157	717	1007	211	219	3		

- Molecule 30 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	o	109	Total	C	H	N	O		0	0
			1718	552	841	176	149			

- Molecule 31 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	K	117	Total	C	H	N	O	S	0	0
			1644	537	777	163	164	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	126	LYS	ARG	conflict	UNP Q2FW31

- Molecule 32 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	p	115	Total	C	H	N	O	S	0	0
			1828	588	892	188	156	4		

- Molecule 33 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	L	135	Total	C	H	N	O	S	0	0
			2066	658	1004	218	184	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	56	ARG	LYS	conflict	UNP P0A0H0
L	101	ARG	LYS	conflict	UNP P0A0H0

- Molecule 34 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	q	102	Total	C	H	N	O	S	0	0
			1535	506	737	142	149	1		

- Molecule 35 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	M	118	Total	C	H	N	O	S	0	0
			1811	575	875	186	174	1		

- Molecule 36 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	r	112	Total	C	H	N	O	S	0	0
			1675	537	813	164	158	3		

- Molecule 37 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	N	60	Total	C	H	N	O	S	0	0
			972	317	471	100	79	5		

- Molecule 38 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	s	89	Total	C	H	N	O	S	0	0
			1400	457	675	130	134	4		

- Molecule 39 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	O	88	Total	C	H	N	O	S	0	0
			1421	454	684	153	129	1		

- Molecule 40 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	t	90	Total	C	H	N	O	S	0	0
			1354	434	665	129	125	1		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	?	-	PRO	deletion	UNP A7X5E7
t	?	-	THR	deletion	UNP A7X5E7
t	?	-	GLN	deletion	UNP A7X5E7
t	?	-	LEU	deletion	UNP A7X5E7
t	53	ALA	PRO	conflict	UNP A7X5E7
t	54	GLN	GLU	conflict	UNP A7X5E7
t	?	-	GLY	deletion	UNP A7X5E7
t	?	-	ILE	deletion	UNP A7X5E7
t	56	ILE	LEU	conflict	UNP A7X5E7

- Molecule 41 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	P	87	Total	C	H	N	O	S	0	0
			1310	433	622	127	127	1		

- Molecule 42 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	u	93	Total	C	H	N	O	S	0	0
			1419	466	689	130	133	1		

- Molecule 43 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	Q	83	Total	C	H	N	O	S	0	0
			1325	432	641	123	128	1		

- Molecule 44 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	v	81	Total	C	H	N	O		0	0
			1183	383	562	121	117			

- Molecule 45 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	R	66	Total	C	H	N	O	S	0	0
			1060	347	517	101	92	3		

- Molecule 46 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	w	61	Total	C	H	N	O	S	0	0
			946	298	465	104	78	1		

- Molecule 47 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	S	84	Total	C	H	N	O	S	0	0
			1281	435	604	123	117	2		

- Molecule 48 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	x	65	Total	C	H	N	O		0	0
			1040	330	504	101	105			

- Molecule 49 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	T	82	Total	C	H	N	O	S	0	0
			1205	375	587	121	120	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	82	SER	ASN	conflict	UNP Q2FXY6

- Molecule 50 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	y	56	Total	C	H	N	O		0	0
			856	271	420	82	83			

- Molecule 51 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	U	122	Total	C	H	N	O	S	0	0
			1783	572	864	174	169	4		

- Molecule 52 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	z	54	Total	C	H	N	O	S	0	0
			811	259	384	87	76	5		

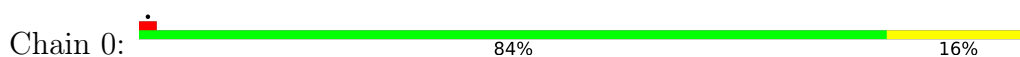
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	?	-	ARG	deletion	UNP Q2FZF1

### 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.

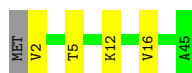
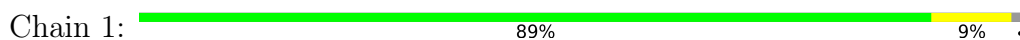
- Molecule 1: Large ribosomal subunit protein bL33B



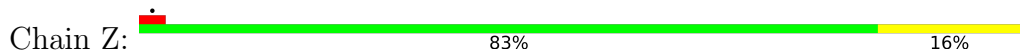
- Molecule 2: aur mRNA



- Molecule 3: Large ribosomal subunit protein bL34




- Molecule 4: Methionine tRNA

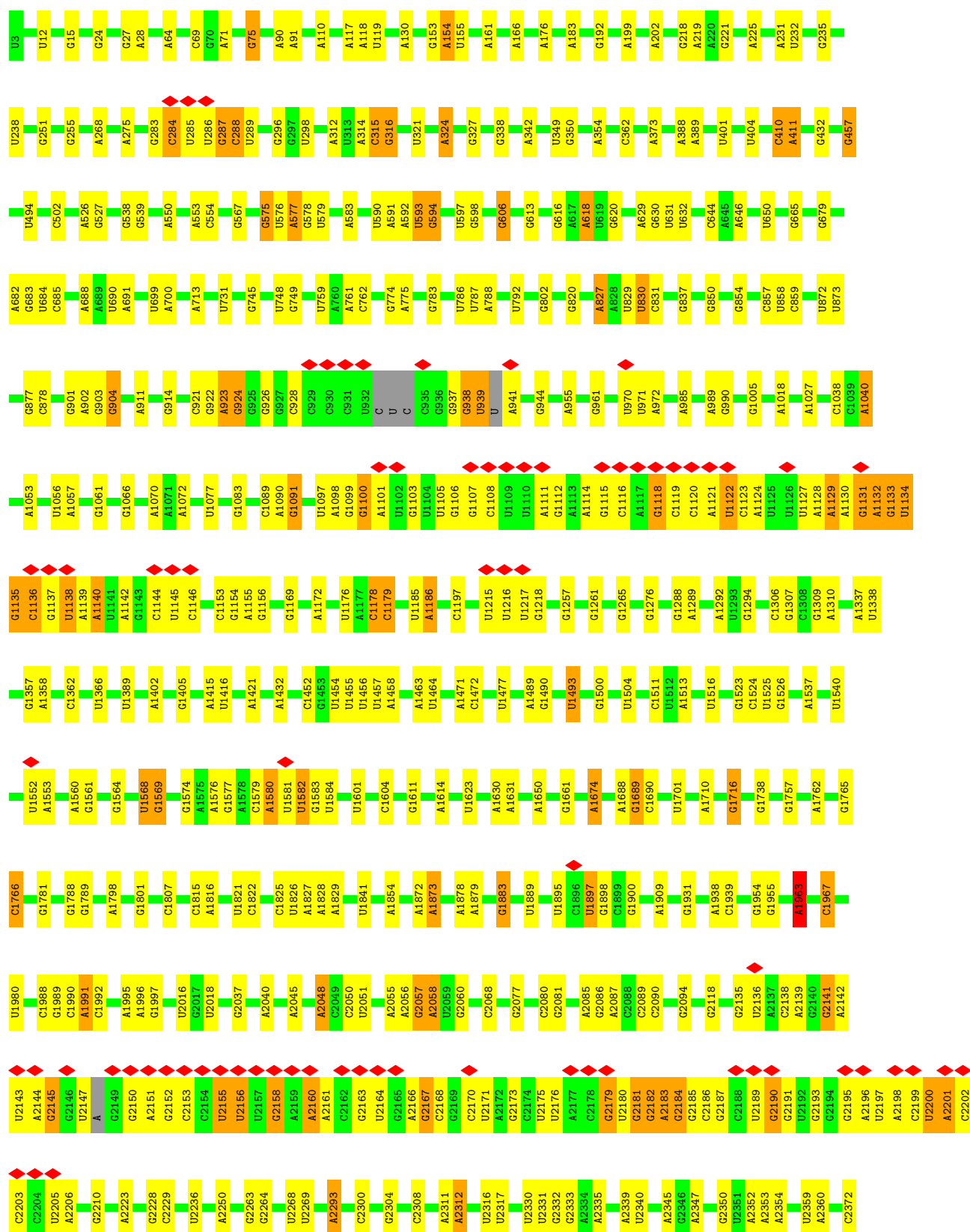


- Molecule 5: Large ribosomal subunit protein bL35

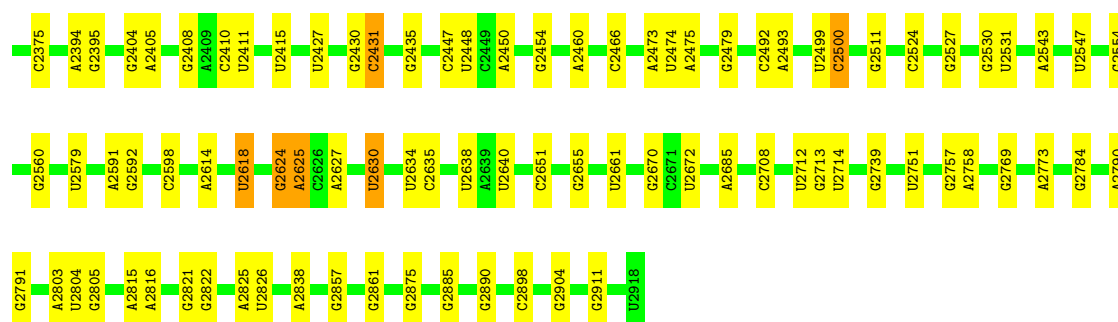


- Molecule 6: 23S rRNA

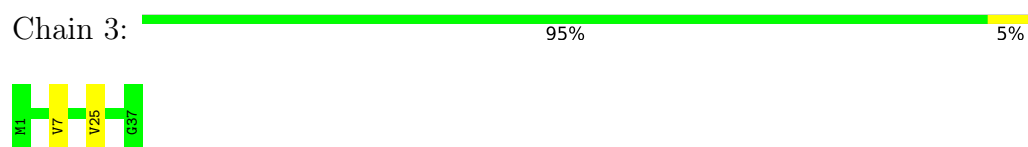
Chain a: 



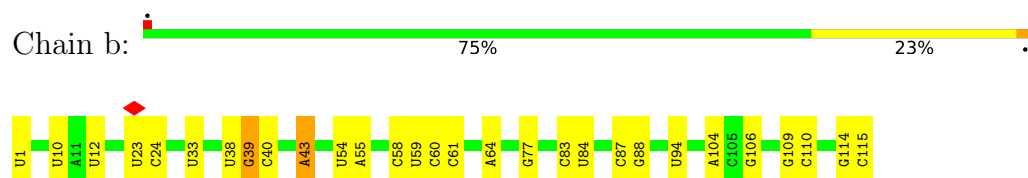




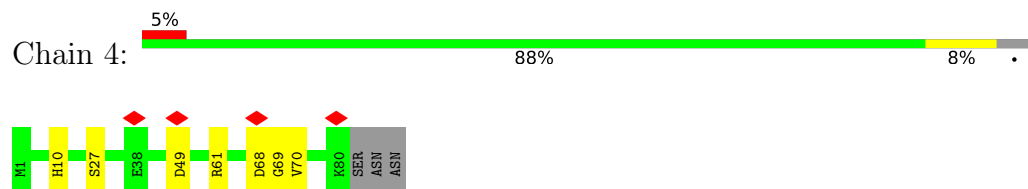
• Molecule 7: Large ribosomal subunit protein bL36



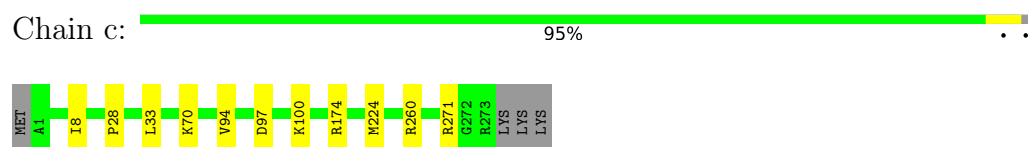
• Molecule 8: 5S rRNA



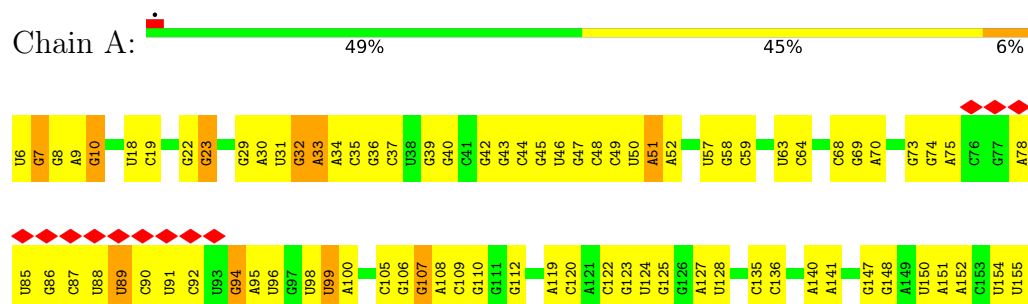
• Molecule 9: Large ribosomal subunit protein bL31B



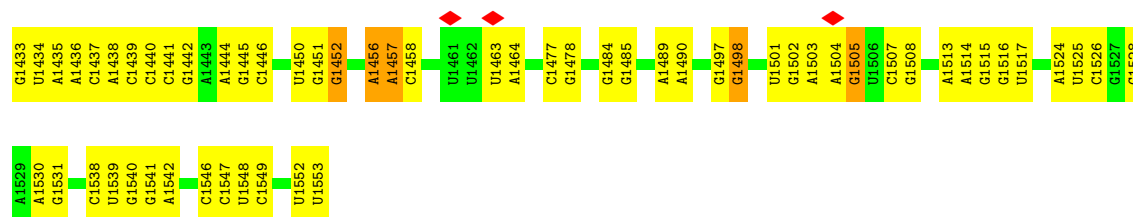
• Molecule 10: Large ribosomal subunit protein uL2



• Molecule 11: 16S rRNA



G1341	A1342	A1343	G1344	G1347	G1348	G1269	G1270	A1181	G1185	G1187	G1188	A1189	C1354	A1284	A1285	G1286	C1287	G1288	G1289	A1290	A1291	C1292	A1367	C1368	A1370	A1373	C1376	A1377	A1378	C1379	G1380	A1385	G1386	A1387	C1388	G1389	G1390	G1391	C1392	C1393	U1401	G1402	C1407	A1408	C1412	C1413	G1415	A1420	C1421	C1422	A1423	U1431	U1432
U1097	G1105	U1106	C1107	G1110	C1111	G1112	A1113	C1114	G1130	C1131	U1132	U1133	A1134	G1135	U1136	U1137	G1138	C1139	C1140	U1212	G1213	A1214	U1215	C1220	U1221	U1222	A1223	U1227	U1228	U1229	A1235	C1236	A1237	C1238	C1244	U1245	A1246	C1247	A1248	A1255	A1256	U1257	A1260	A1261	A1262	G1263	G1264	G1265	C1266	A1267	G1268		
U1018	C1019	G1022	A1023	G1024	A1025	G1030	C1031	C1032	U1033	U1034	C1035	C1036	C1037	C1038	U1039	U1040	G1042	G1043	G1044	G1045	A1046	C1048	A1049	A1050	A1051	G1052	U1053	G1054	A1055	C1056	A1057	U1063	A1066	U1071	G1072	U1073	C1074	G1075	U1076	U1081	C1082	G1083	U1084	G1085	U1089	G1090	A1091	G1092	U1096				
A927	A928	U929	G929	A930	G931	A932	G935	C943	A944	G954	A955	G956	G963	U964	U969	G975	C976	A977	A978	C979	G980	C981	A984	G985	U991	A992	C993	C994	A995	A996	U997	U998	C999	U1000	U1001	G1002	A1003	C1004	A1005	U1006	C1007	C1008	U1009	U1010	U1011	G1012	A1013	C1014	A1015	A1016	C1017		
A824	C825	U828	G829	A830	G831	U835	A836	A837	G838	U839	G847	G848	U849	U850	C852	C853	G854	C855	U866	G867	A873	A874	C877	A878	U879	U880	A881	A885	C886	C891	C892	U893	G899	U900	A901	G902	G903	A904	C905	G915	A916	A917	A918	U920	C921	A922							
A716	U717	G721	G722	A723	A724	U731	A736	A737	U744	U745	U746	G749	U755	A756	A757	C758	U759	G760	G763	C764	U765	G766	G771	C772	A775	A776	G777	G783	G784	A785	U786	C787	A788	G793	G794	A800	U801	A802	A810	G811	C814	A815	C816	A823									
G504	A505	A506	A507	G508	C509	C510	C519	U520	G521	C522	G523	U524	G525	G529	C530	A531	G532	C533	A540	U546	A547	G548	G551	G552	C553	A554	A555	G556	A561	U562	C563	C564	U572	A580	A581	A582	U583	C584	G585	C588	G589	A591	U598	U599	U600	U602							
G605	U606	U613	A622	C623	G624	G625	G635	G636	A637	U641	C642	U645	G646	G647	A649	A656	A657	A658	C659	U660	U661	G666	G669	A670	A671	G672	A673	G679	U680	G681	G682	A683	U685	U686	C687	G691	U692	G693	U694	A703	A704	U705	C709	A710									
A716	U717	G721	G722	A723	A724	U731	A736	A737	U744	U745	U746	G749	U755	A756	A757	C758	U759	G760	G763	C764	U765	G766	G771	C772	A775	A776	G777	G783	G784	A785	U786	C787	A788	G793	G794	A800	U801	A802	A810	G811	C814	A815	C816	A823									
A824	C825	U828	G829	A830	G831	U835	A836	A837	G838	U839	G847	G848	U849	U850	C852	C853	G854	C855	U866	G867	A873	A874	C877	A878	U879	U880	A881	A885	C886	C891	C892	U893	G899	U900	A901	G902	G903	A904	C905	G915	A916	A917	A918	U920	C921	A922							
A927	A928	U929	G929	A930	G931	A932	G935	C943	A944	G954	A955	G956	G963	U964	U969	G975	C976	A977	A978	C979	G980	C981	A984	G985	U991	A992	C993	C994	A995	A996	U997	U998	C999	U1000	U1001	G1002	A1003	C1004	A1005	U1006	C1007	C1008	U1009	U1010	U1011	G1012	A1013	C1014	A1015	A1016	C1017		
U1018	C1019	G1022	A1023	G1024	A1025	G1030	C1031	C1032	U1033	U1034	C1035	C1036	C1037	C1038	U1039	U1040	G1042	G1043	G1044	G1045	A1046	C1048	A1049	A1050	A1051	G1052	U1053	G1054	A1055	C1056	A1057	U1063	A1066	U1071	G1072	U1073	C1074	G1075	U1076	U1081	C1082	G1083	U1084	G1085	U1089	G1090	A1091	G1092	U1096				
U1097	G1105	U1106	C1107	G1110	C1111	G1112	A1113	C1114	G1130	C1131	U1132	U1133	A1134	G1135	U1136	U1137	G1138	C1139	C1140	U1212	G1213	A1214	U1215	C1220	U1221	U1222	A1223	U1227	U1228	U1229	A1235	C1236	A1237	C1238	C1244	U1245	A1246	C1247	A1248	A1255	A1256	U1257	A1260	A1261	A1262	G1263	G1264	G1265	C1266	A1267	G1268		
G1269	G1270	A1271	G1276	G1279	U1282	C1283	A1284	A1285	U1286	G1287	A1288	A1289	A1290	U1291	C1292	C1293	A1294	U1295	U1296	A1297	U1298	A1299	G1300	U1301	U1302	C1306	G1310	U1311	A1312	C1313	G1314	G1315	A1316	U1317	U1318	G1319	C1324	U1325	C1326	C1327	A1328	A1329	C1330	U1331	G1332	G1333	A1334	C1335	U1336	A1337	C1338	A1339	U1340
G1341	G1342	A1343	G1344	G1347	G1348	G1269	G1270	A1181	G1185	G1187	G1188	A1189	C1354	A1284	A1285	G1286	C1287	G1288	G1289	A1290	A1291	C1292	A1367	C1368	A1370	A1373	C1376	A1377	A1378	C1379	G1380	A1385	G1386	A1387	C1388	G1389	G1390	G1391	C1392	C1393	U1401	G1402	C1407	A1408	C1412	C1413	G1415	A1420	C1421	C1422	A1423	U1431	U1432



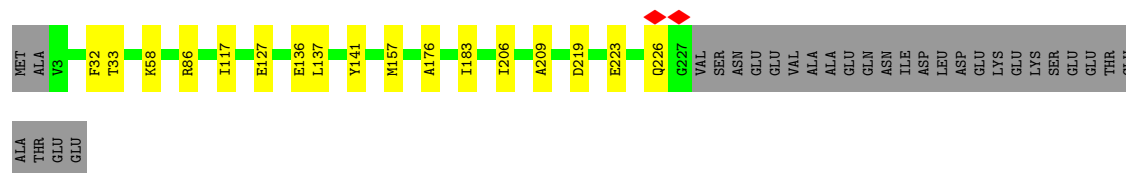
- Molecule 12: Large ribosomal subunit protein uL3

Chain d: 94%



- Molecule 13: Small ribosomal subunit protein uS2

Chain B: 82% 7% 12%



- Molecule 14: Large ribosomal subunit protein uL4

Chain e: 92% 7%



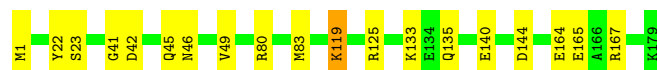
- Molecule 15: Small ribosomal subunit protein uS3

Chain C: 84% 9% 6%



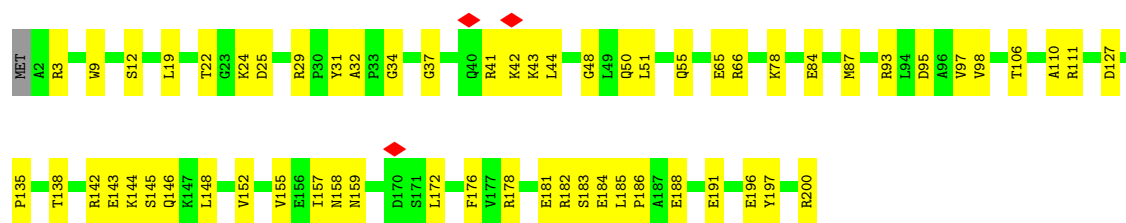
- Molecule 16: Large ribosomal subunit protein uL5

Chain f: 89% 10%

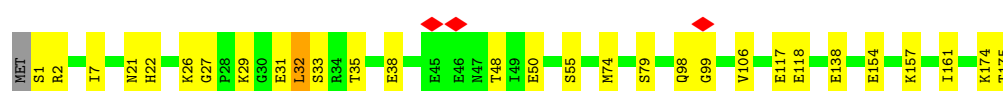
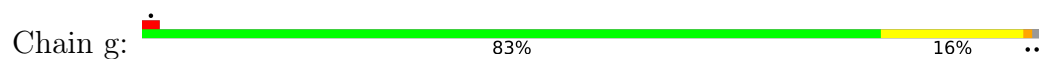


- Molecule 17: Small ribosomal subunit protein uS4

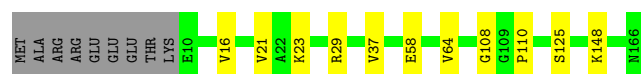
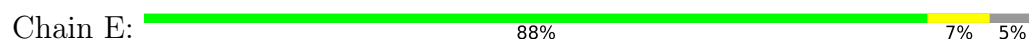
Chain D: 70% 30%



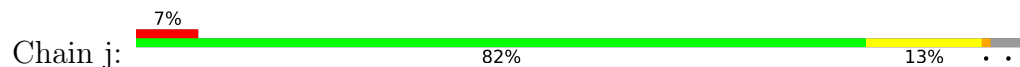
- Molecule 18: Large ribosomal subunit protein uL6



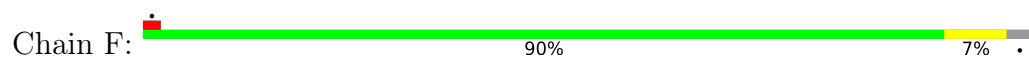
- Molecule 19: Small ribosomal subunit protein uS5



- Molecule 20: Small ribosomal subunit protein uS10



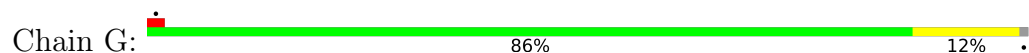
- Molecule 21: Small ribosomal subunit protein bS6

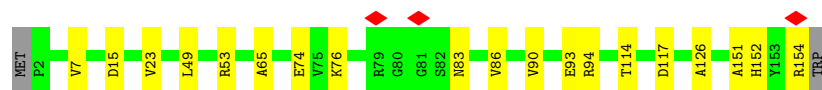


- Molecule 22: Large ribosomal subunit protein uL15

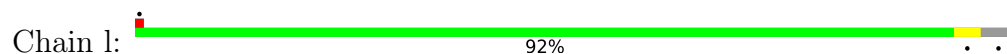


- Molecule 23: Small ribosomal subunit protein uS7

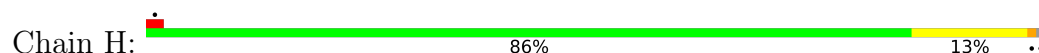




- Molecule 24: Large ribosomal subunit protein uL16



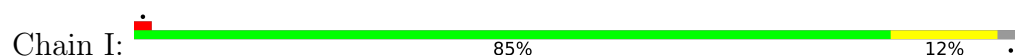
- Molecule 25: Small ribosomal subunit protein uS8



- Molecule 26: Large ribosomal subunit protein bL17



- Molecule 27: Small ribosomal subunit protein uS9




- Molecule 28: Large ribosomal subunit protein uL18

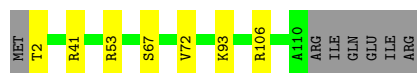


- Molecule 29: Large ribosomal subunit protein uL13




- Molecule 30: Large ribosomal subunit protein bL19

Chain o:  88% 6% 6%



- Molecule 31: Small ribosomal subunit protein uS11

Chain K:  84% 6% 9%




- Molecule 32: Large ribosomal subunit protein bL20

Chain p:  94% . .



- Molecule 33: Small ribosomal subunit protein uS12

Chain L:  91% 8% .



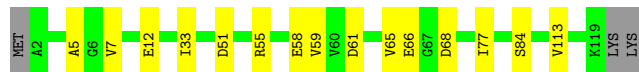
- Molecule 34: Large ribosomal subunit protein bL21

Chain q:  95% 5%




- Molecule 35: Small ribosomal subunit protein uS13

Chain M:  85% 12% .



- Molecule 36: Large ribosomal subunit protein uL22

Chain r:  90% 6% .



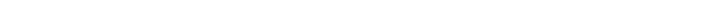
- Molecule 37: Small ribosomal subunit protein uS14B

- Chain s:  92% 5%

Diagram illustrating the structure of the E2F1 transcription factor, showing the DNA-binding domain (MET, E2, T13, S16, D30, V33, E84, F90, ASN) and the transcription factor domain (T13, S16, D30, V33, E84, F90).

- Chain 0:  94% ..

Diagram illustrating the protein structure with domains labeled: MET, A2, K8, K73, R88, and R89.


- Chain t:  84% 14%

- Chain P:  86% 8% ..

MET A2 R6 R14 R32 I33 T43 S44 A45 N46 A47 K88 LYS ALA LYS

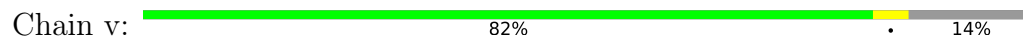
- Chain u:  42% . 57%

[illegible]

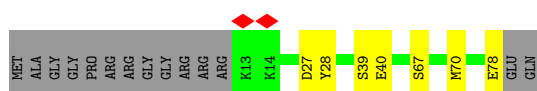
- Chain Q:  79% 14% .. 5%



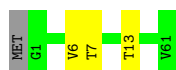
- Molecule 44: Large ribosomal subunit protein bL27



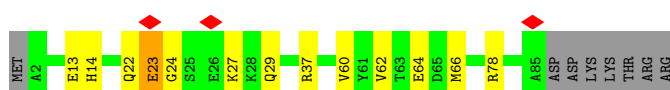
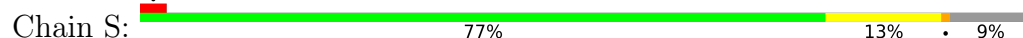
- Molecule 45: Small ribosomal subunit protein bS18



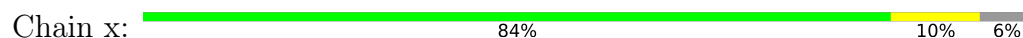
- Molecule 46: Large ribosomal subunit protein bL28



- Molecule 47: Small ribosomal subunit protein uS19



- Molecule 48: Large ribosomal subunit protein uL29



- Molecule 49: Small ribosomal subunit protein bS20



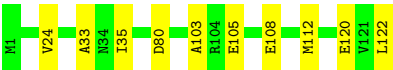
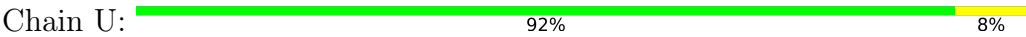
- Molecule 50: Large ribosomal subunit protein uL30



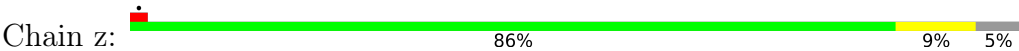




- Molecule 51: Large ribosomal subunit protein uL14



- Molecule 52: Large ribosomal subunit protein bL32



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	316031	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.056	Depositor
Minimum map value	-0.324	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.078	Depositor
Map size (Å)	437.4, 437.4, 437.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.729, 0.729, 0.729	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	0	0.22	0/409	0.28	0/544
2	X	0.19	0/422	0.23	0/658
3	1	0.29	0/377	0.37	0/491
4	Z	0.22	0/1813	0.27	0/2825
5	2	0.27	0/535	0.37	0/701
6	a	0.42	28/69913 (0.0%)	0.37	24/109032 (0.0%)
7	3	0.25	0/299	0.35	0/393
8	b	0.25	0/2736	0.26	0/4261
9	4	0.17	0/669	0.38	0/897
10	c	0.25	0/2120	0.34	0/2847
11	A	0.25	0/37112	0.28	0/57874
12	d	0.26	0/1652	0.39	0/2216
13	B	0.18	0/1837	0.35	0/2465
14	e	0.24	0/1596	0.32	0/2155
15	C	0.18	0/1622	0.30	0/2178
16	f	0.19	0/1438	0.32	0/1928
17	D	0.18	0/1645	0.28	0/2209
18	g	0.18	0/1386	0.34	0/1865
19	E	0.22	0/1182	0.33	0/1595
20	j	0.18	0/795	0.36	0/1071
21	F	0.20	0/800	0.35	0/1073
22	k	0.25	0/1112	0.36	0/1482
23	G	0.17	0/1239	0.34	0/1665
24	l	0.26	0/1125	0.36	0/1509
25	H	0.21	0/1043	0.33	0/1401
26	m	0.26	0/942	0.35	0/1259
27	I	0.19	0/1024	0.35	0/1375
28	n	0.20	0/915	0.31	0/1224
29	J	0.26	0/1172	0.30	0/1578
30	o	0.24	0/889	0.33	0/1189
31	K	0.19	0/882	0.37	0/1190
32	p	0.26	0/947	0.35	0/1254
33	L	0.20	0/1079	0.33	0/1445
34	q	0.25	0/808	0.30	0/1080

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	M	0.19	0/943	0.35	0/1264
36	r	0.25	0/870	0.37	0/1171
37	N	0.21	0/511	0.33	0/678
38	s	0.24	0/733	0.31	0/978
39	O	0.20	0/746	0.34	0/996
40	t	0.24	0/695	0.39	0/926
41	P	0.20	0/699	0.45	0/942
42	u	0.19	0/738	0.28	0/990
43	Q	0.18	0/692	0.32	0/925
44	v	0.26	0/627	0.35	0/831
45	R	0.22	0/552	0.41	0/738
46	w	0.25	0/487	0.33	0/649
47	S	0.19	0/695	0.35	0/933
48	x	0.22	0/537	0.37	0/714
49	T	0.19	0/618	0.36	0/825
50	y	0.24	0/438	0.34	0/590
51	U	0.23	0/926	0.34	0/1243
52	z	0.27	0/434	0.34	0/578
All	All	0.33	28/155476 (0.0%)	0.34	24/232900 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	a	0	1
40	t	0	1
All	All	0	2

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	a	2625	A	P-OP1	-20.82	1.07	1.49
6	a	1967	C	P-OP2	-19.42	1.10	1.49
6	a	2618	U	P-OP1	-18.36	1.12	1.49
6	a	2625	A	P-OP2	-17.71	1.13	1.49
6	a	2630	U	P-OP2	-17.63	1.13	1.49

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	a	1990	C	O3'-P-O5'	20.21	134.31	104.00
6	a	1493	U	OP1-P-O3'	-9.57	79.28	108.00
6	a	1989	G	O3'-P-O5'	9.01	117.51	104.00
6	a	1990	C	C3'-C2'-O2'	8.64	123.67	110.70
6	a	1990	C	OP1-P-O3'	-7.60	85.19	108.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	a	1963	A	Sidechain
40	t	59	THR	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	0	406	369	416	5	0
2	X	375	0	185	10	0
3	1	373	378	420	2	0
4	Z	1623	825	825	5	0
5	2	530	536	601	1	0
6	a	62430	31011	31374	197	0
7	3	296	309	342	1	0
8	b	2448	861	1238	16	0
9	4	652	555	631	5	0
10	c	2085	1938	2195	8	0
11	A	33149	0	16689	645	0
12	d	1628	1464	1670	5	0
13	B	1810	1655	1872	9	0
14	e	1573	1424	1622	9	0
15	C	1600	1463	1662	14	0
16	f	1420	1310	1482	16	0
17	D	1615	0	1642	43	0
18	g	1368	1233	1402	19	0
19	E	1168	1080	1229	8	0
20	j	783	734	825	9	0
21	F	789	695	788	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	k	1098	1002	1142	5	0
23	G	1221	1111	1257	10	0
24	l	1101	1039	1169	5	0
25	H	1031	957	1082	11	0
26	m	939	874	993	8	0
27	I	1008	907	1026	12	0
28	n	907	844	960	4	0
29	J	1150	1007	1145	6	0
30	o	877	841	945	7	0
31	K	867	777	886	7	0
32	p	936	892	1006	4	0
33	L	1062	1004	1130	6	0
34	q	798	737	836	3	0
35	M	936	875	988	11	0
36	r	862	813	920	5	0
37	N	501	471	527	6	0
38	s	725	675	761	3	0
39	O	737	684	769	3	0
40	t	689	665	751	10	0
41	P	688	622	713	6	0
42	u	730	689	781	2	0
43	Q	684	641	722	11	0
44	v	621	562	643	3	0
45	R	543	517	580	5	0
46	w	481	465	526	2	0
47	S	677	604	682	11	0
48	x	536	504	570	4	0
49	T	618	587	667	2	0
50	y	436	420	473	1	0
51	U	919	864	981	8	0
52	z	427	384	436	3	0
All	All	142926	70874	95177	1121	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 1121 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)
6:a:1967:C:OP1	6:a:1967:C:P	1.15	1.54
6:a:2625:A:P	6:a:2625:A:OP2	1.13	1.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:a:2630:U:P	6:a:2630:U:OP2	1.13	1.52
6:a:2618:U:P	6:a:2618:U:OP1	1.12	1.51
6:a:1967:C:P	6:a:1967:C:OP2	1.10	1.48

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	0	47/49 (96%)	46 (98%)	1 (2%)	0	100	100
3	1	42/45 (93%)	42 (100%)	0	0	100	100
5	2	63/66 (96%)	62 (98%)	1 (2%)	0	100	100
7	3	35/37 (95%)	35 (100%)	0	0	100	100
9	4	78/83 (94%)	76 (97%)	2 (3%)	0	100	100
10	c	271/277 (98%)	262 (97%)	9 (3%)	0	100	100
12	d	213/220 (97%)	201 (94%)	12 (6%)	0	100	100
13	B	223/255 (88%)	219 (98%)	4 (2%)	0	100	100
14	e	204/207 (99%)	197 (97%)	7 (3%)	0	100	100
15	C	201/217 (93%)	194 (96%)	7 (4%)	0	100	100
16	f	177/179 (99%)	168 (95%)	9 (5%)	0	100	100
17	D	197/200 (98%)	191 (97%)	6 (3%)	0	100	100
18	g	173/176 (98%)	160 (92%)	13 (8%)	0	100	100
19	E	155/166 (93%)	153 (99%)	2 (1%)	0	100	100
20	j	96/102 (94%)	91 (95%)	5 (5%)	0	100	100
21	F	93/98 (95%)	90 (97%)	3 (3%)	0	100	100
22	k	144/146 (99%)	139 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	G	151/155 (97%)	147 (97%)	4 (3%)	0	100	100
24	l	136/144 (94%)	131 (96%)	5 (4%)	0	100	100
25	H	129/132 (98%)	124 (96%)	5 (4%)	0	100	100
26	m	117/122 (96%)	112 (96%)	5 (4%)	0	100	100
27	I	125/131 (95%)	118 (94%)	7 (6%)	0	100	100
28	n	116/119 (98%)	112 (97%)	4 (3%)	0	100	100
29	J	143/145 (99%)	142 (99%)	1 (1%)	0	100	100
30	o	107/116 (92%)	105 (98%)	2 (2%)	0	100	100
31	K	115/129 (89%)	111 (96%)	3 (3%)	1 (1%)	14	17
32	p	113/118 (96%)	110 (97%)	3 (3%)	0	100	100
33	L	133/137 (97%)	127 (96%)	6 (4%)	0	100	100
34	q	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
35	M	116/121 (96%)	112 (97%)	4 (3%)	0	100	100
36	r	110/117 (94%)	110 (100%)	0	0	100	100
37	N	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
38	s	87/91 (96%)	87 (100%)	0	0	100	100
39	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
40	t	88/90 (98%)	81 (92%)	7 (8%)	0	100	100
41	P	85/91 (93%)	80 (94%)	4 (5%)	1 (1%)	10	12
42	u	91/217 (42%)	89 (98%)	2 (2%)	0	100	100
43	Q	81/87 (93%)	77 (95%)	2 (2%)	2 (2%)	4	3
44	v	79/94 (84%)	74 (94%)	5 (6%)	0	100	100
45	R	64/80 (80%)	64 (100%)	0	0	100	100
46	w	59/62 (95%)	57 (97%)	2 (3%)	0	100	100
47	S	82/92 (89%)	79 (96%)	3 (4%)	0	100	100
48	x	63/69 (91%)	62 (98%)	1 (2%)	0	100	100
49	T	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
50	y	54/59 (92%)	52 (96%)	2 (4%)	0	100	100
51	U	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
52	z	52/57 (91%)	50 (96%)	2 (4%)	0	100	100
All	All	5352/5755 (93%)	5174 (97%)	174 (3%)	4 (0%)	49	60



All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	K	119	ASN
41	P	45	ALA
43	Q	26	VAL
43	Q	82	GLU

### 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	0	47/47 (100%)	47 (100%)	0	100	100
3	1	39/40 (98%)	38 (97%)	1 (3%)	40	59
5	2	56/57 (98%)	56 (100%)	0	100	100
7	3	35/35 (100%)	35 (100%)	0	100	100
9	4	71/74 (96%)	70 (99%)	1 (1%)	59	76
10	c	220/224 (98%)	219 (100%)	1 (0%)	81	90
12	d	173/177 (98%)	172 (99%)	1 (1%)	78	89
13	B	195/221 (88%)	193 (99%)	2 (1%)	68	82
14	e	168/169 (99%)	164 (98%)	4 (2%)	43	62
15	C	164/175 (94%)	160 (98%)	4 (2%)	43	62
16	f	158/158 (100%)	155 (98%)	3 (2%)	50	69
17	D	174/175 (99%)	167 (96%)	7 (4%)	28	42
18	g	153/154 (99%)	151 (99%)	2 (1%)	61	77
19	E	123/131 (94%)	122 (99%)	1 (1%)	73	86
20	j	88/91 (97%)	84 (96%)	4 (4%)	24	37
21	F	83/86 (96%)	81 (98%)	2 (2%)	43	62
22	k	112/112 (100%)	111 (99%)	1 (1%)	70	84
23	G	129/131 (98%)	126 (98%)	3 (2%)	44	63
24	l	114/119 (96%)	113 (99%)	1 (1%)	70	84
25	H	112/113 (99%)	109 (97%)	3 (3%)	39	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	m	100/102 (98%)	100 (100%)	0	100	100
27	I	105/108 (97%)	104 (99%)	1 (1%)	68	82
28	n	93/94 (99%)	90 (97%)	3 (3%)	34	51
29	J	123/123 (100%)	121 (98%)	2 (2%)	55	73
30	o	95/102 (93%)	95 (100%)	0	100	100
31	K	93/104 (89%)	92 (99%)	1 (1%)	65	81
32	p	95/98 (97%)	95 (100%)	0	100	100
33	L	117/119 (98%)	114 (97%)	3 (3%)	40	59
34	q	86/86 (100%)	85 (99%)	1 (1%)	63	79
35	M	101/104 (97%)	97 (96%)	4 (4%)	28	42
36	r	91/94 (97%)	90 (99%)	1 (1%)	65	81
37	N	52/53 (98%)	52 (100%)	0	100	100
38	s	80/82 (98%)	80 (100%)	0	100	100
39	O	80/81 (99%)	79 (99%)	1 (1%)	61	77
40	t	75/75 (100%)	74 (99%)	1 (1%)	61	77
41	P	74/77 (96%)	73 (99%)	1 (1%)	59	76
42	u	82/190 (43%)	81 (99%)	1 (1%)	63	79
43	Q	78/82 (95%)	74 (95%)	4 (5%)	21	32
44	v	64/75 (85%)	64 (100%)	0	100	100
45	R	59/68 (87%)	59 (100%)	0	100	100
46	w	51/52 (98%)	51 (100%)	0	100	100
47	S	72/80 (90%)	70 (97%)	2 (3%)	38	56
48	x	59/62 (95%)	58 (98%)	1 (2%)	53	72
49	T	68/69 (99%)	67 (98%)	1 (2%)	57	75
50	y	51/53 (96%)	51 (100%)	0	100	100
51	U	100/100 (100%)	100 (100%)	0	100	100
52	z	48/50 (96%)	46 (96%)	2 (4%)	26	40
All	All	4606/4872 (94%)	4535 (98%)	71 (2%)	55	75

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	O	73	LYS

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Mol	Chain	Res	Type
41	P	33	ILE
47	S	14	HIS
18	g	32	LEU
17	D	183	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
30	o	43	GLN
45	R	21	ASN
31	K	77	HIS
35	M	38	ASN
46	w	29	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1547/1548 (99%)	174 (11%)	6 (0%)
2	X	16/17 (94%)	2 (12%)	1 (6%)
4	Z	75/76 (98%)	6 (8%)	0
6	a	2905/2917 (99%)	379 (13%)	0
8	b	114/115 (99%)	12 (10%)	0
All	All	4657/4673 (99%)	573 (12%)	7 (0%)

5 of 573 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	X	11	G
2	X	12	A
4	Z	17(A)	U
4	Z	19	G
4	Z	20	U

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	1033	U
11	A	1034	U
11	A	1407	C
11	A	1036	C

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Mol	Chain	Res	Type
11	A	554	A

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

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

#### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

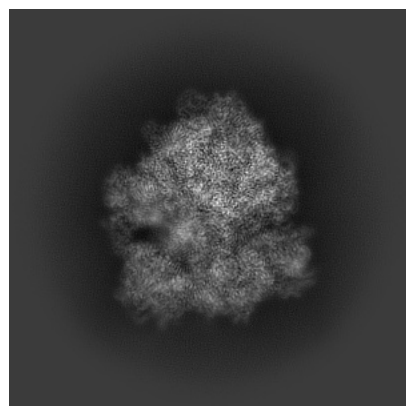
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55526. These allow visual inspection of the internal detail of the map and identification of artifacts.

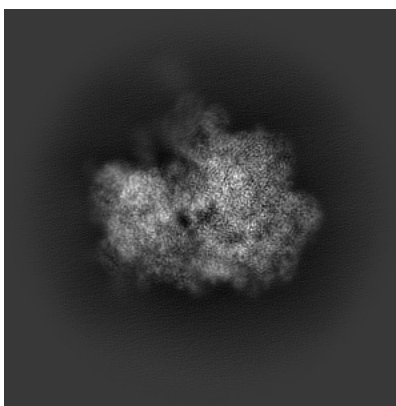
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

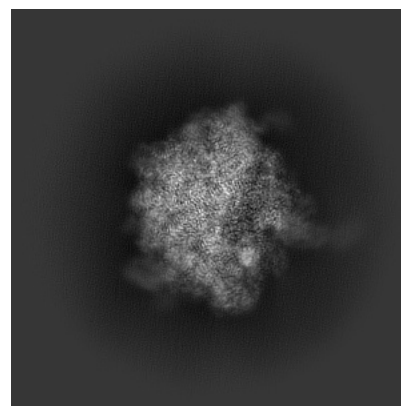
#### 6.1.1 Primary map



X

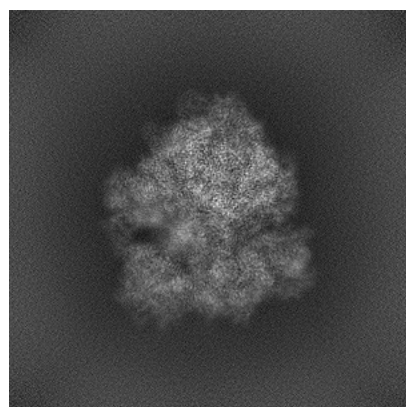


Y

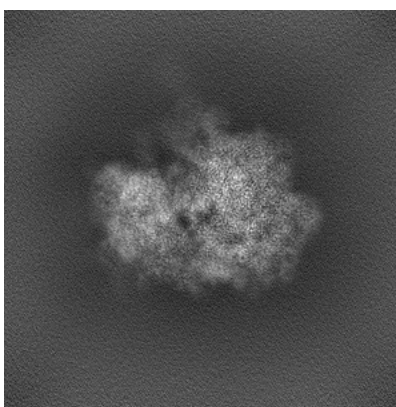


Z

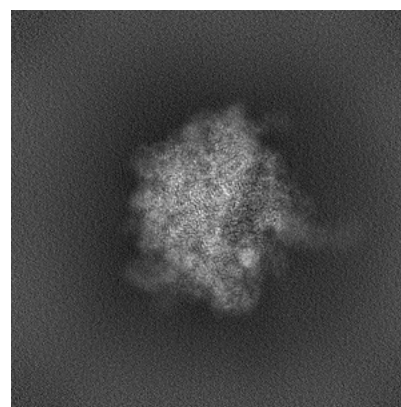
#### 6.1.2 Raw map



X



Y

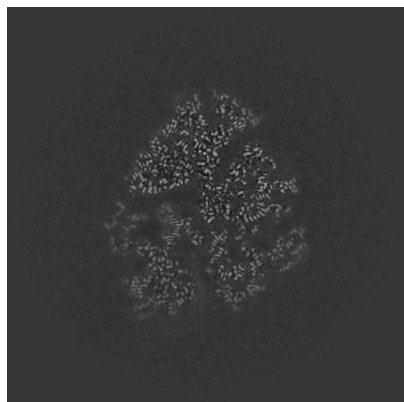


Z

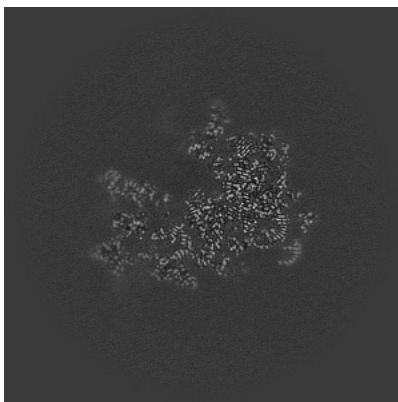
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

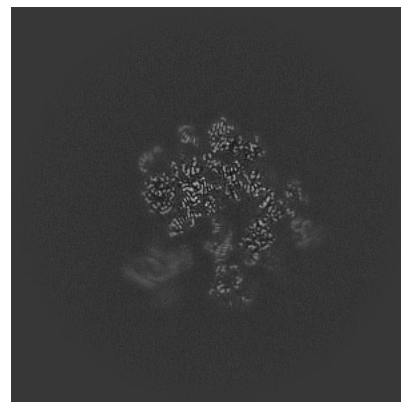
### 6.2.1 Primary map



X Index: 300

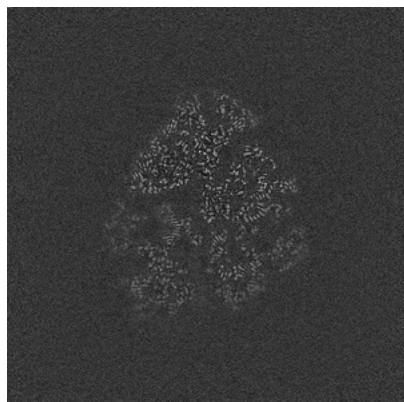


Y Index: 300

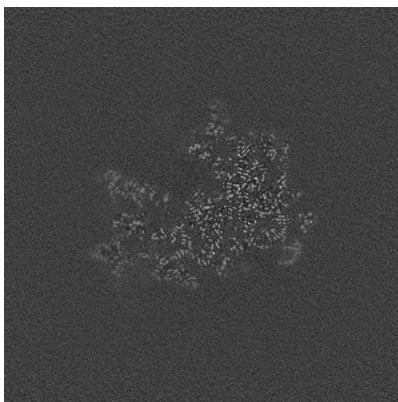


Z Index: 300

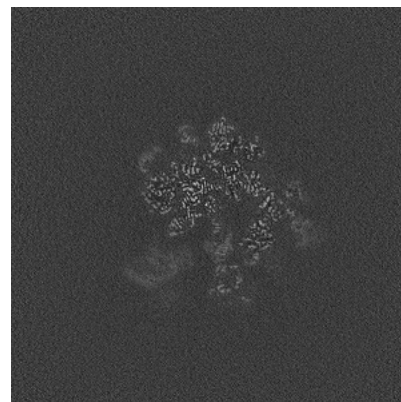
### 6.2.2 Raw map



X Index: 300



Y Index: 300



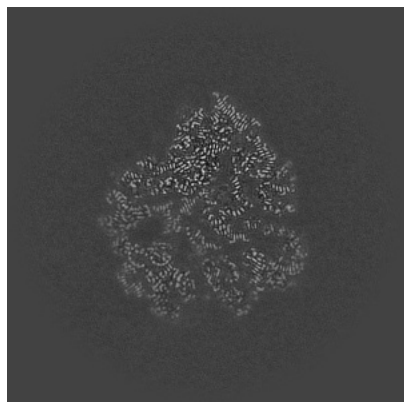
Z Index: 300

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

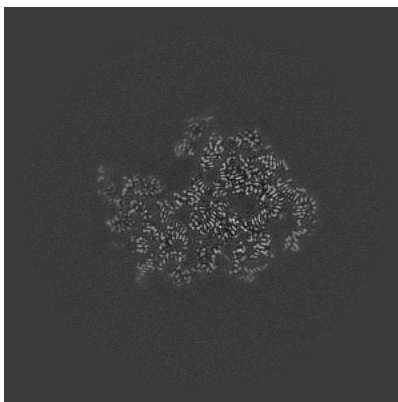


## 6.3 Largest variance slices [i](#)

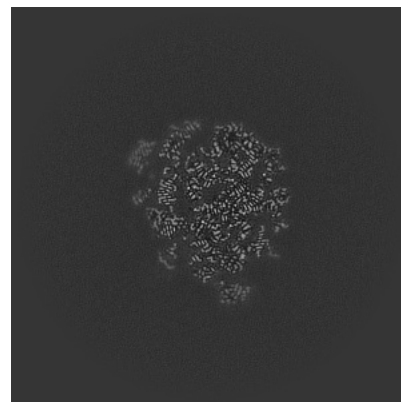
### 6.3.1 Primary map



X Index: 311

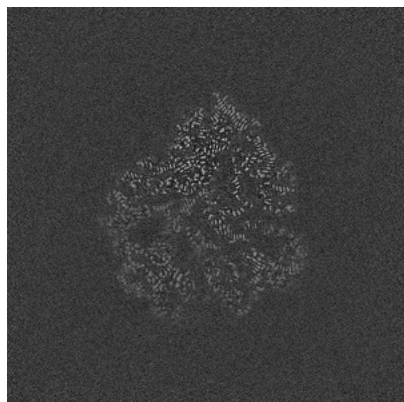


Y Index: 324

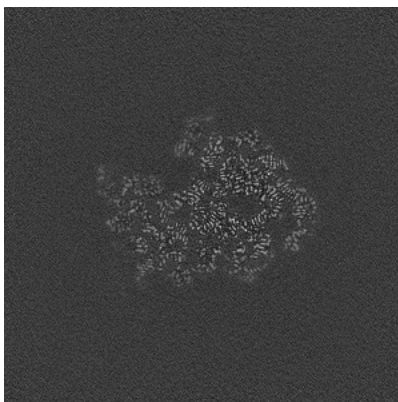


Z Index: 354

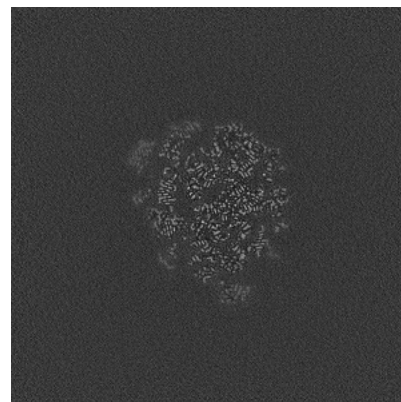
### 6.3.2 Raw map



X Index: 311



Y Index: 324

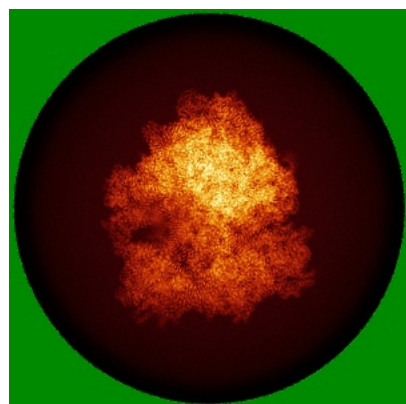


Z Index: 354

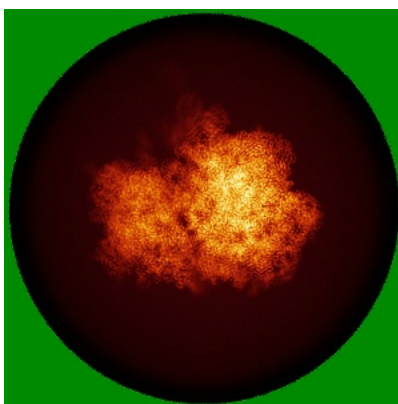
The images above show the largest variance slices of the map in three orthogonal directions.

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

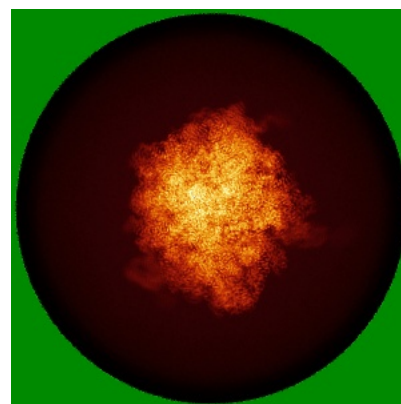
### 6.4.1 Primary map



X

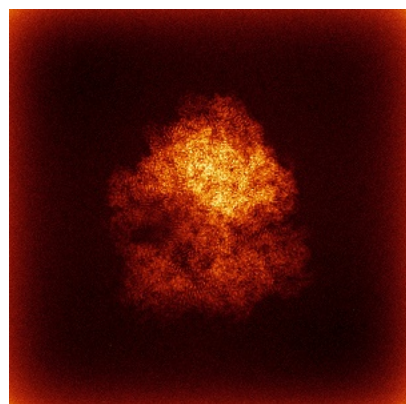


Y

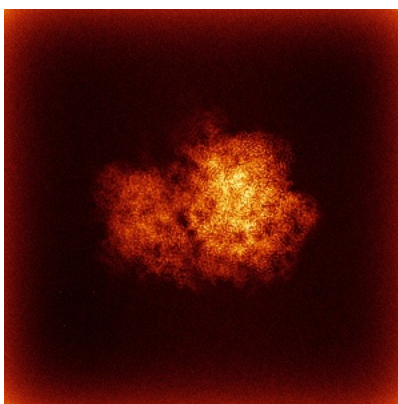


Z

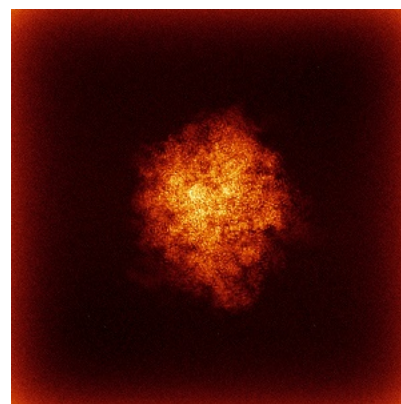
### 6.4.2 Raw map



X



Y



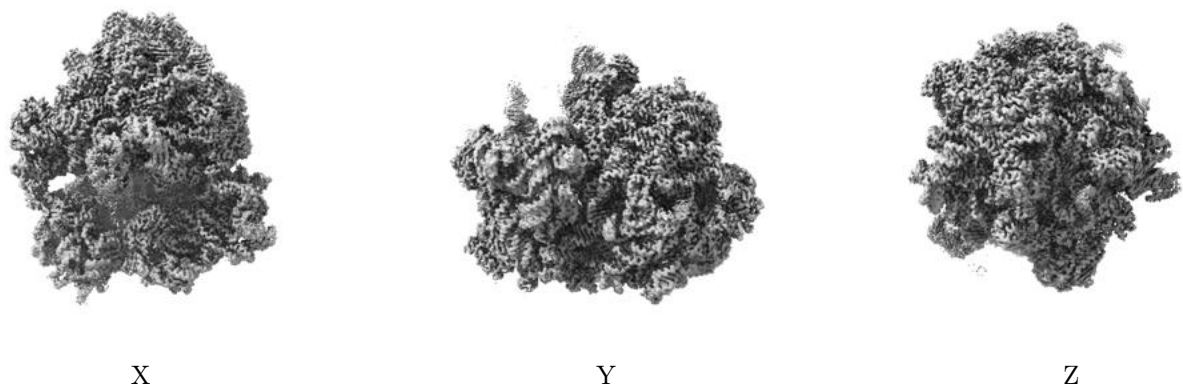
Z

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.



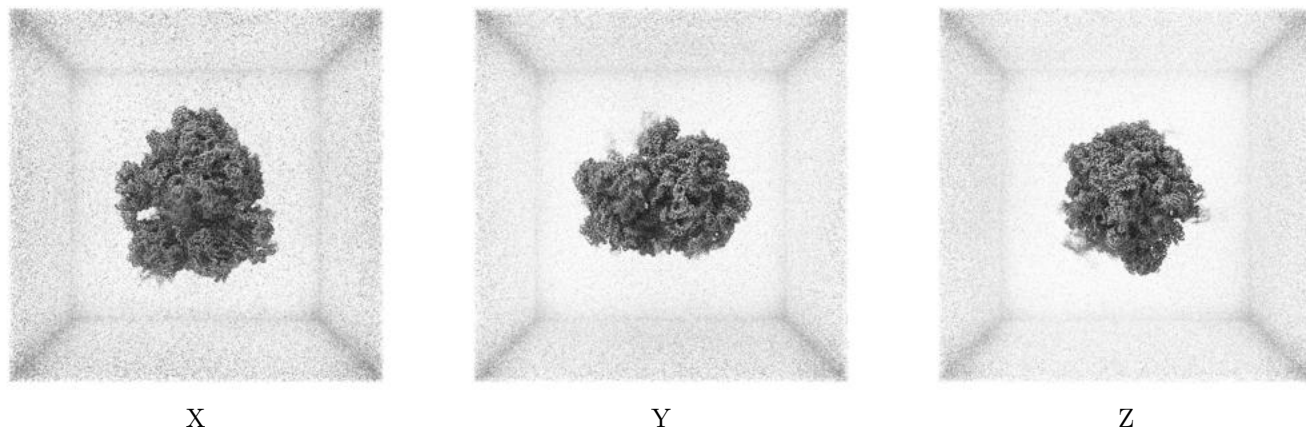
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.078. 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.

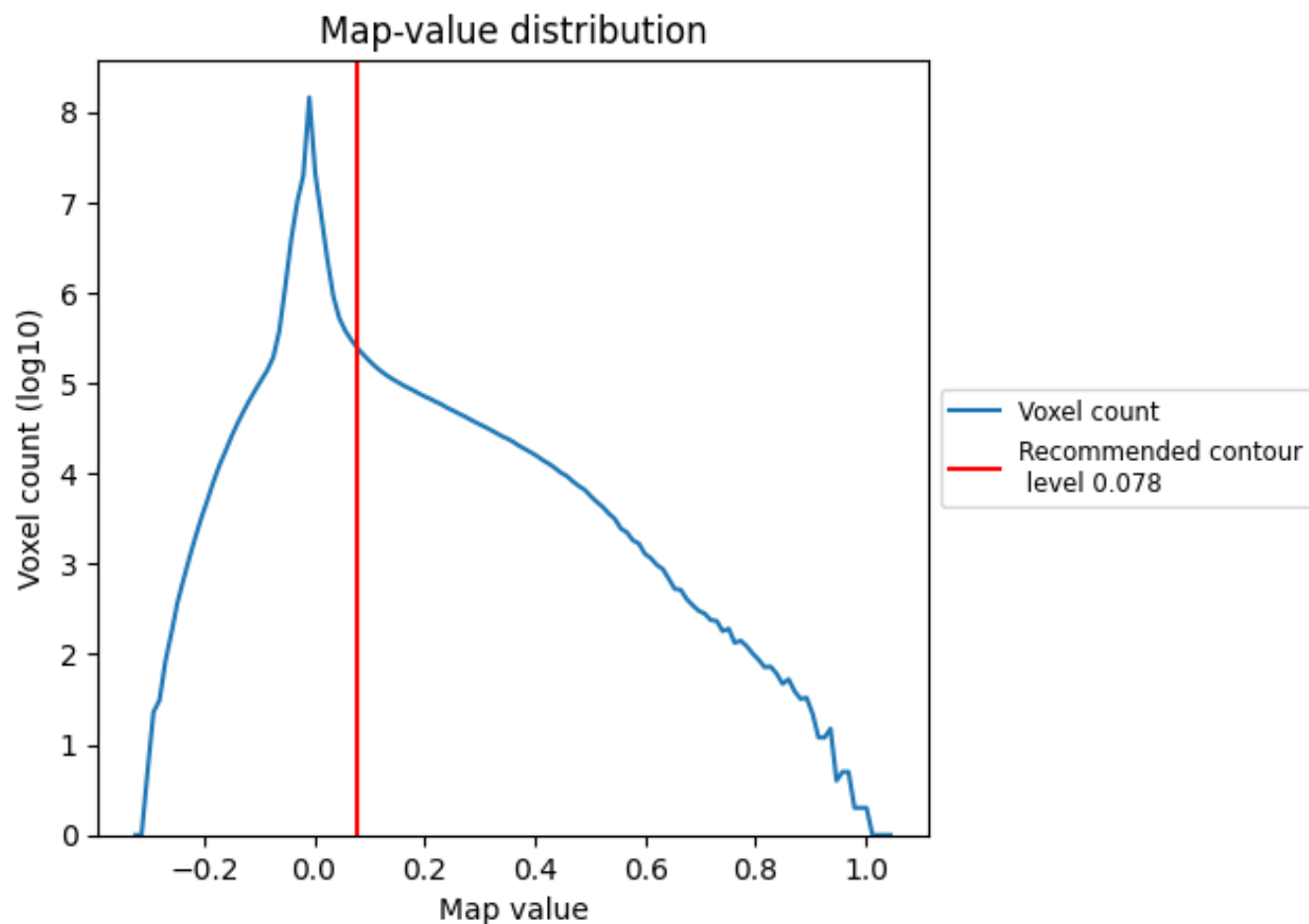
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

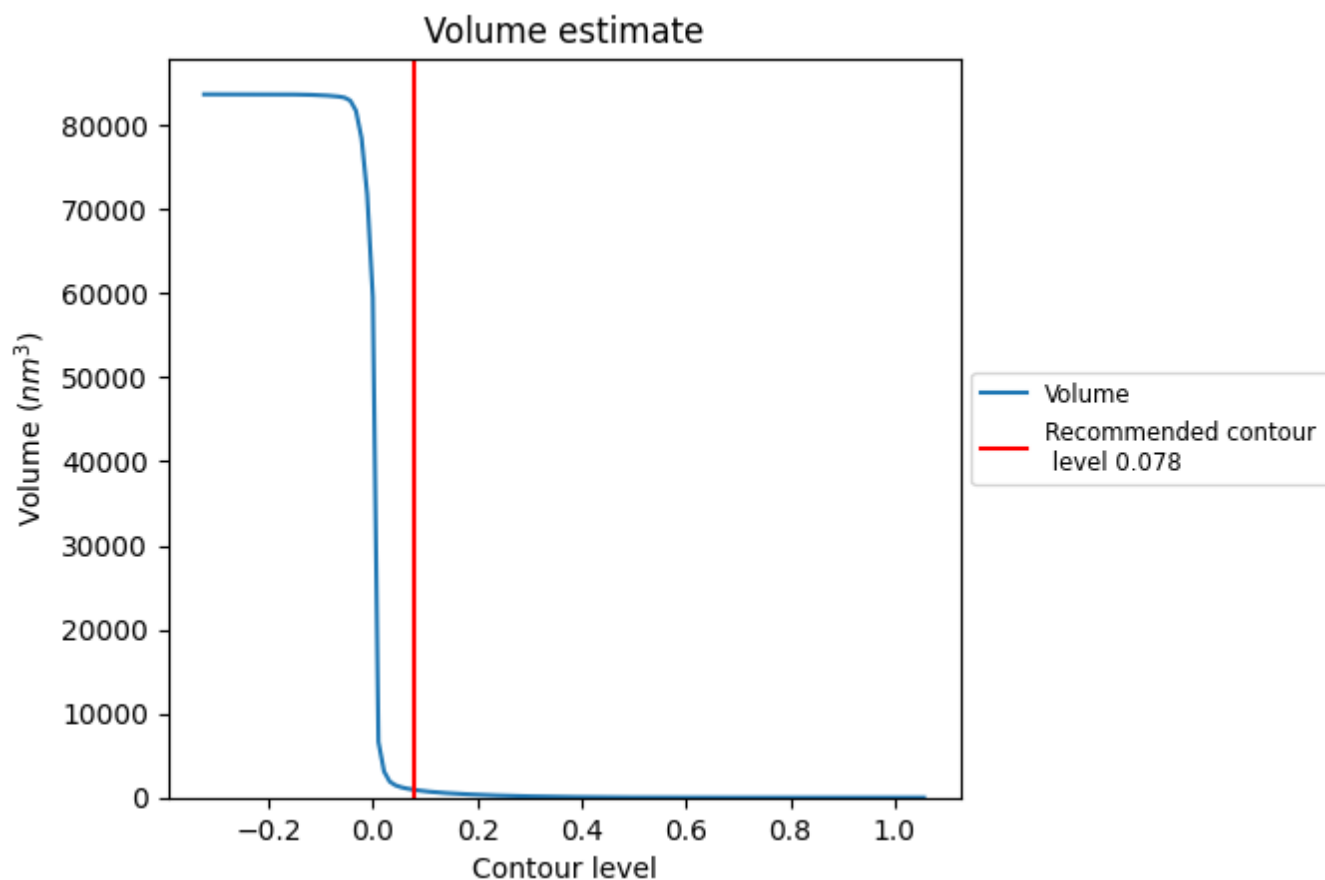
This section contains the results of statistical analysis of the map.

### 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.

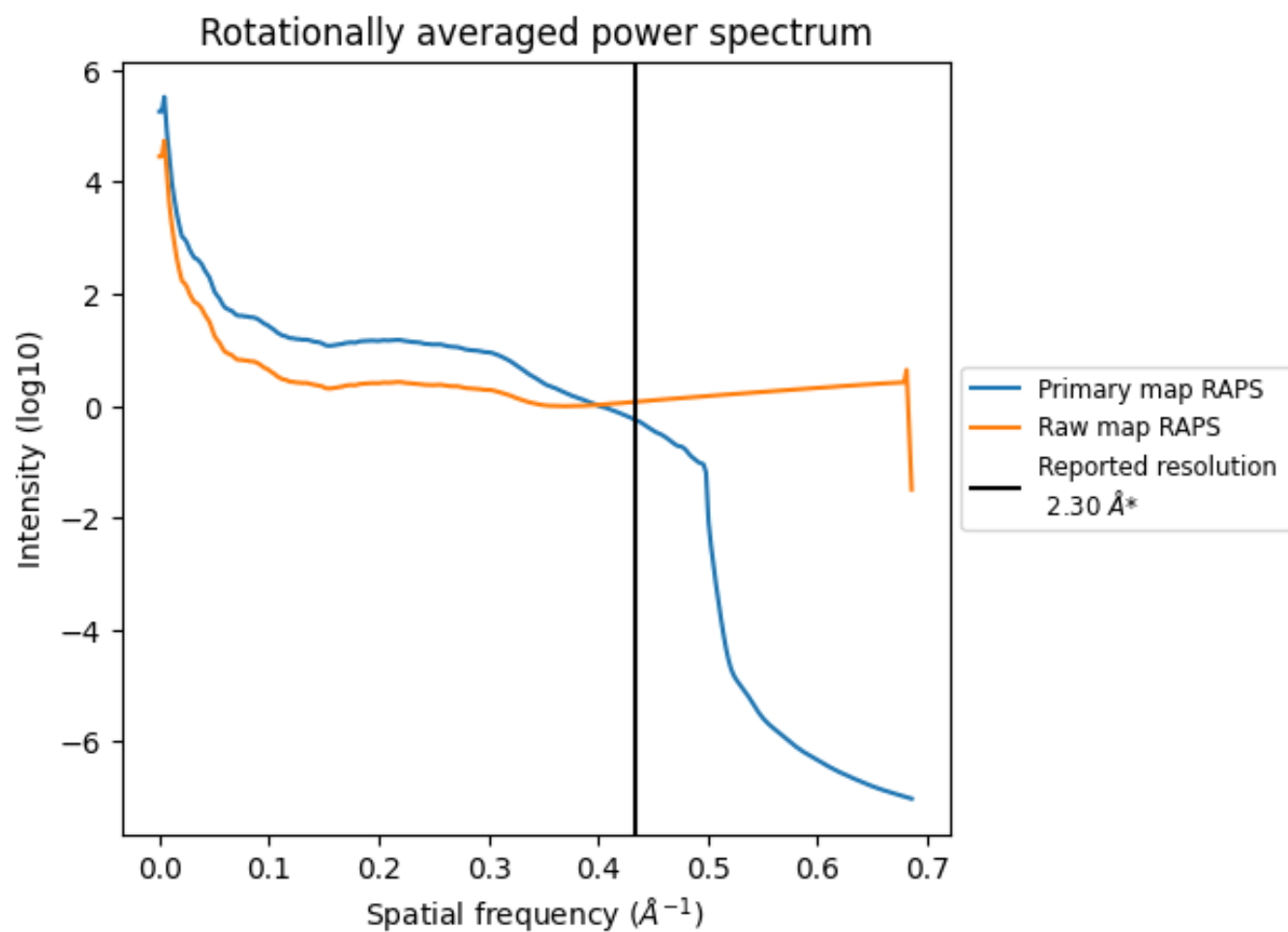
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 928  $\text{nm}^3$ ; this corresponds to an approximate mass of 838 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 ⓘ

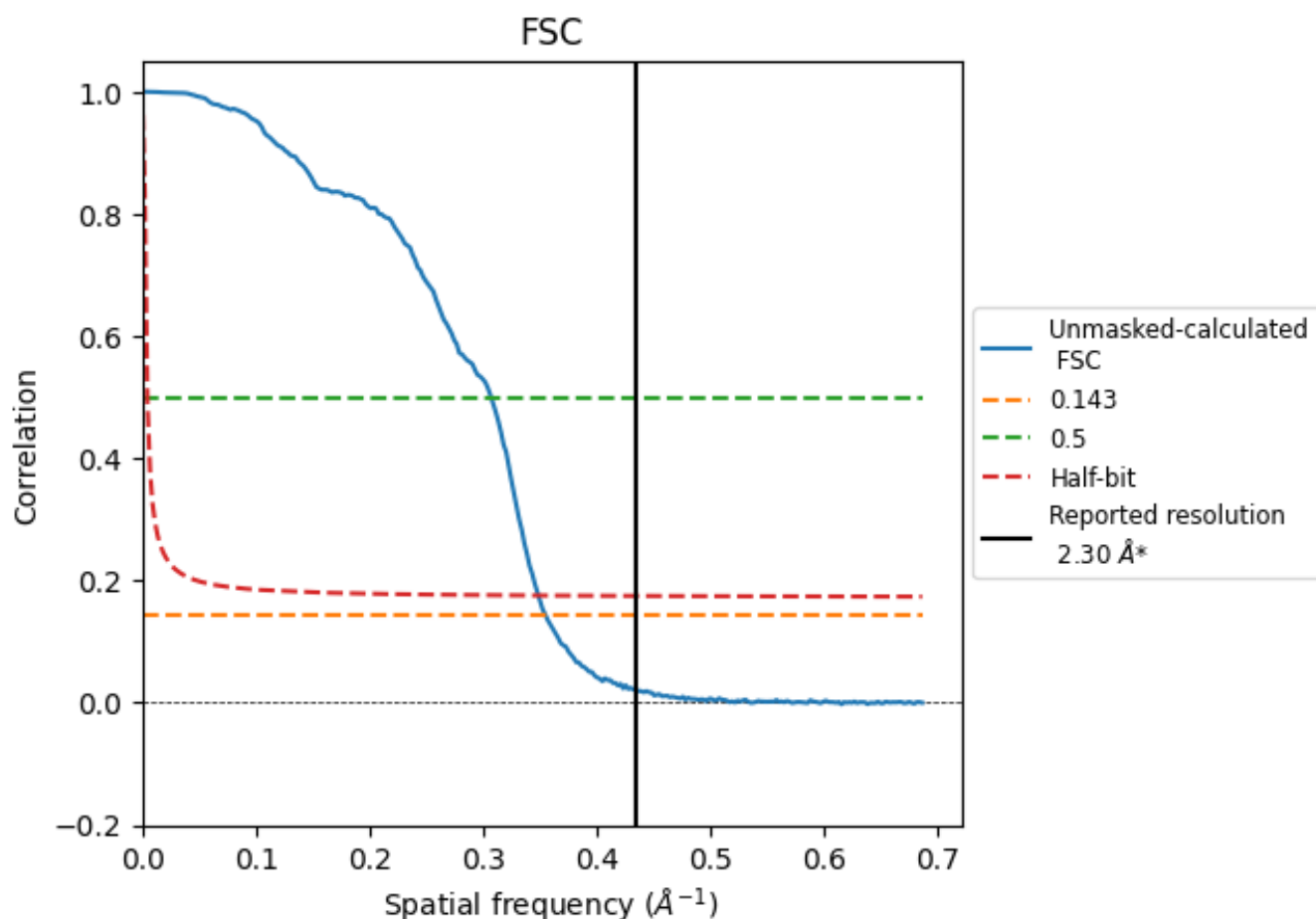


\*Reported resolution corresponds to spatial frequency of 0.435  $\text{\AA}^{-1}$

## 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 0.435 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

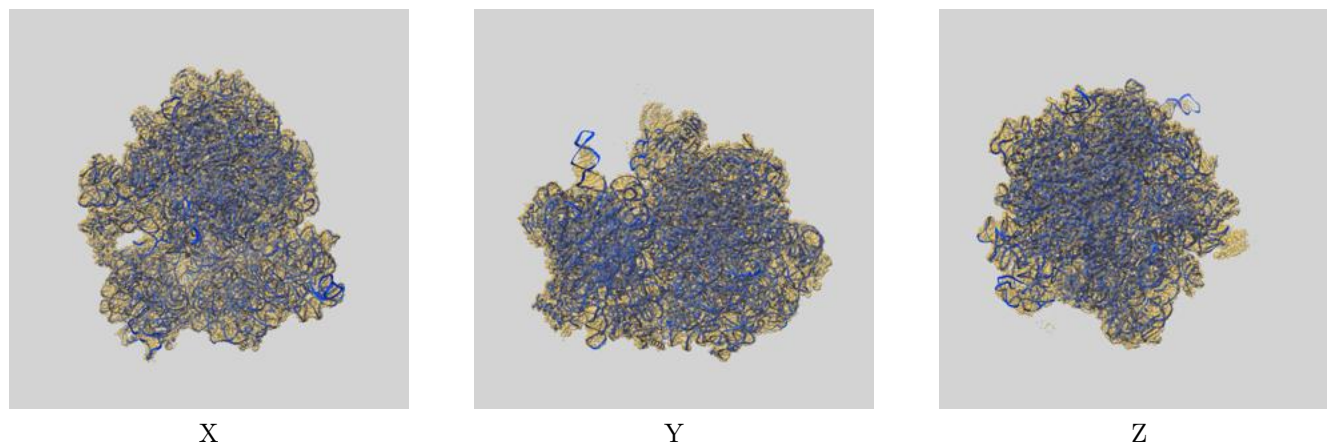
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.82	3.26	2.87

\*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 2.82 differs from the reported value 2.3 by more than 10 %

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

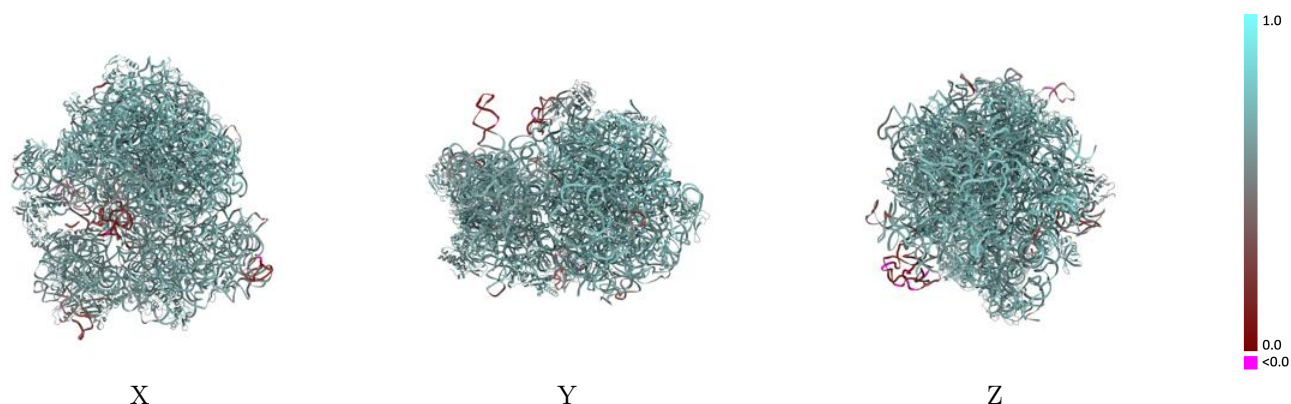
This section contains information regarding the fit between EMDB map EMD-55526 and PDB model 9T4R. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

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



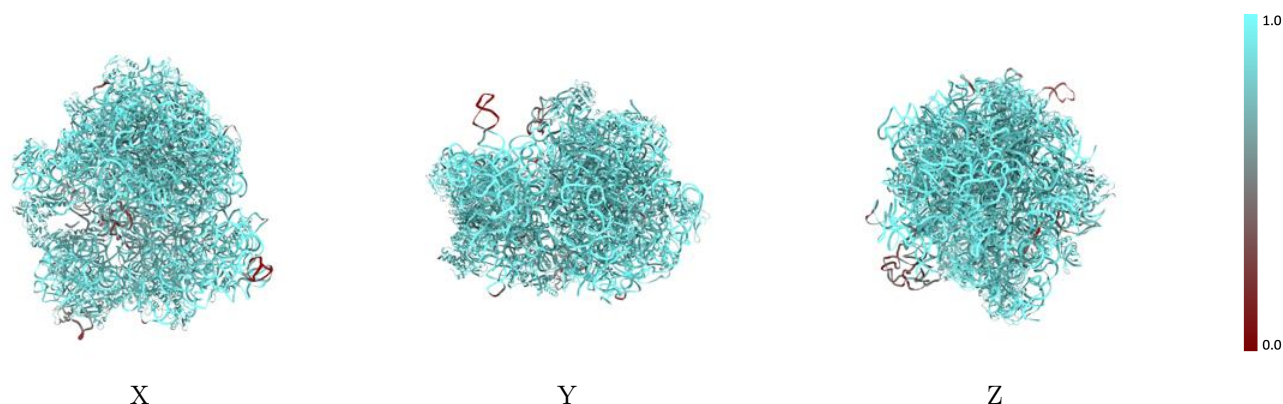
The images above show the 3D surface view of the map at the recommended contour level 0.078 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

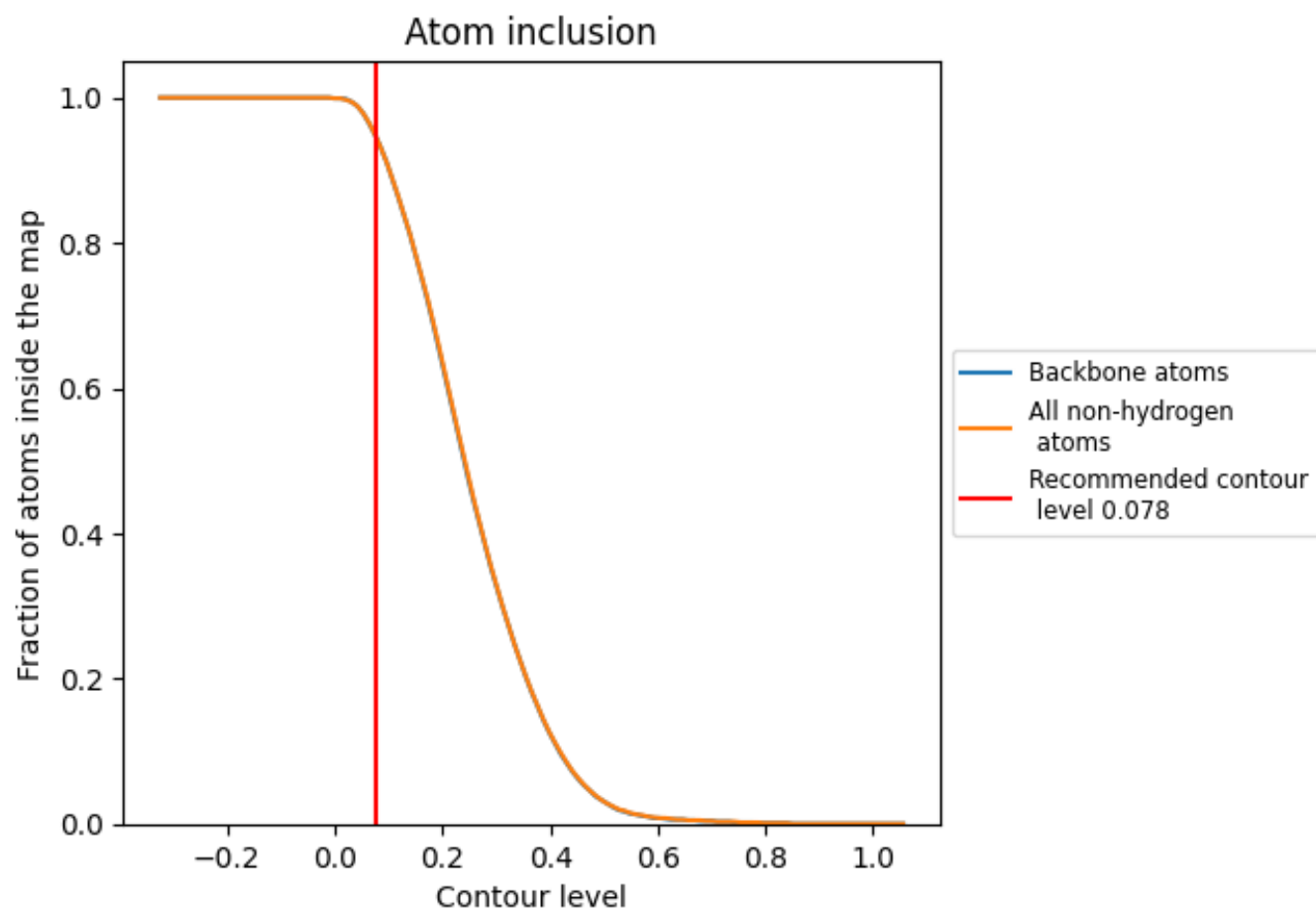
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.078).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% 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 (0.078) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.6480
0	 0.9620	 0.6870
1	 0.9860	 0.7290
2	 0.9880	 0.7180
3	 0.9520	 0.6810
4	 0.8320	 0.5830
A	 0.9630	 0.6310
B	 0.8690	 0.6070
C	 0.8740	 0.6180
D	 0.8950	 0.6270
E	 0.9390	 0.6700
F	 0.9030	 0.6480
G	 0.8710	 0.6050
H	 0.9420	 0.6560
I	 0.9070	 0.6200
J	 0.9720	 0.7040
K	 0.8930	 0.6340
L	 0.9220	 0.6650
M	 0.8820	 0.6190
N	 0.9330	 0.6340
O	 0.9320	 0.6620
P	 0.9080	 0.6380
Q	 0.8860	 0.6380
R	 0.9180	 0.6450
S	 0.8690	 0.6030
T	 0.9100	 0.6380
U	 0.9670	 0.7030
X	 0.7920	 0.5910
Z	 0.9460	 0.6190
a	 0.9590	 0.6530
b	 0.9830	 0.6380
c	 0.9800	 0.7160
d	 0.9690	 0.7070
e	 0.9490	 0.6860
f	 0.8890	 0.6210



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Chain	Atom inclusion	Q-score
g	 0.8440	 0.5800
j	 0.7890	 0.5630
k	 0.9540	 0.6840
l	 0.9510	 0.6910
m	 0.9580	 0.6940
n	 0.9310	 0.6490
o	 0.9640	 0.6940
p	 0.9790	 0.7130
q	 0.9560	 0.6960
r	 0.9580	 0.6980
s	 0.9420	 0.6820
t	 0.9090	 0.6260
u	 0.8940	 0.6440
v	 0.9750	 0.7030
w	 0.9370	 0.6560
x	 0.8960	 0.6420
y	 0.9670	 0.6980
z	 0.9540	 0.6940