



wwPDB EM Validation Summary Report ⓘ

Dec 17, 2024 – 05:11 AM EST

PDB ID : 6D9J
EMDB ID : EMD-7836
Title : Mammalian 80S ribosome with a double translocated CrPV-IRES, P-sitetRNA and eRF1.
Authors : Pisareva, V.P.; Pisarev, A.V.; Fernandez, I.S.
Deposited on : 2018-04-30
Resolution : 3.20 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:

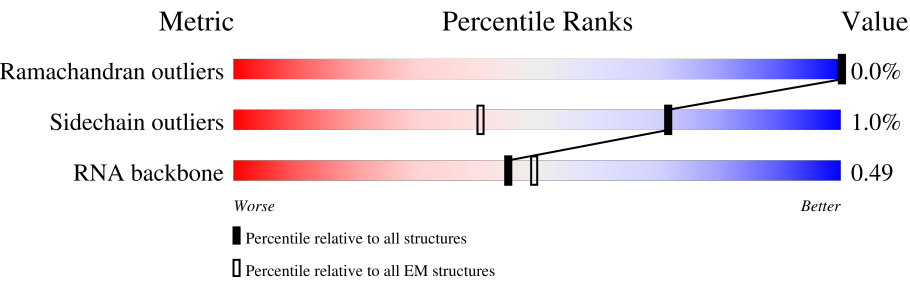
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 Å.

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



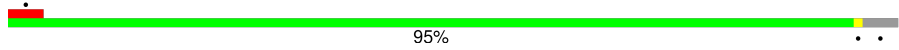
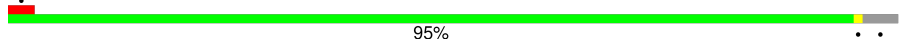
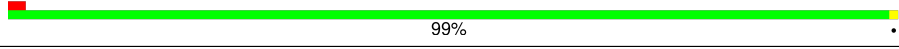

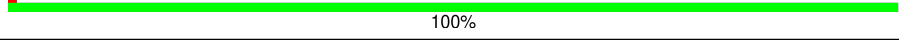
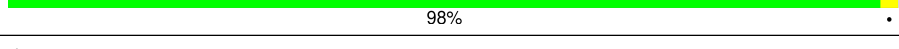
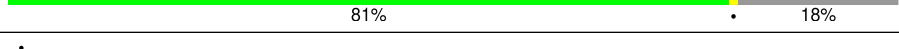
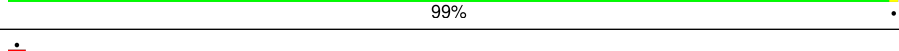
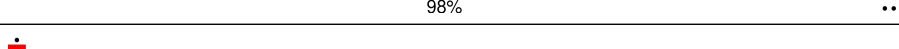
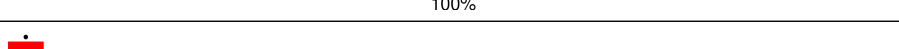
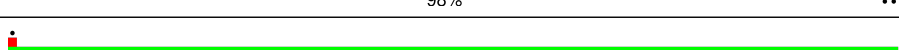
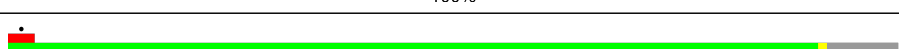
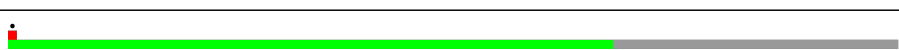

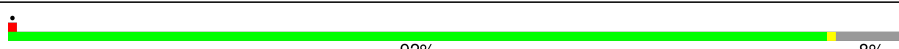
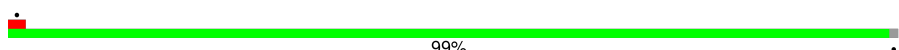
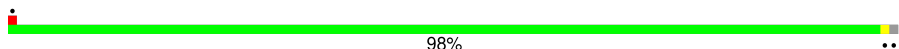



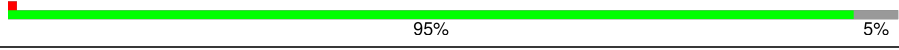
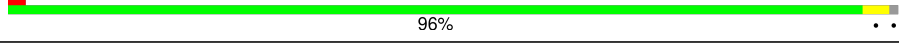

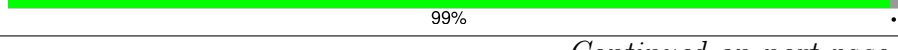

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	257	<div><div>91%</div><div>7%</div></div>
2	B	403	<div><div>97%</div><div>2%</div></div>
3	C	392	<div><div>90%</div><div>8%</div></div>
4	D	297	<div><div>98%</div><div>2%</div></div>
5	E	291	<div><div>74%</div><div>26%</div></div>
6	F	249	<div><div>90%</div><div>10%</div></div>
7	G	242	<div><div>95%</div><div>5%</div></div>
8	H	192	<div><div>96%</div><div>4%</div></div>

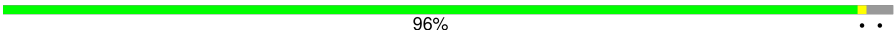

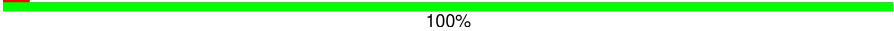
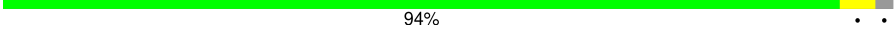
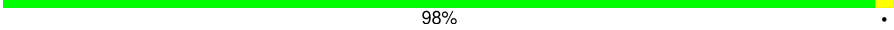
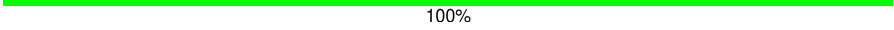
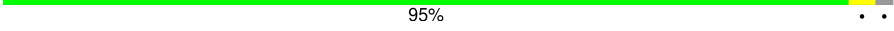
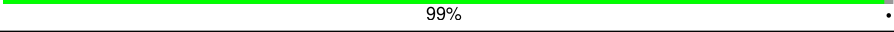



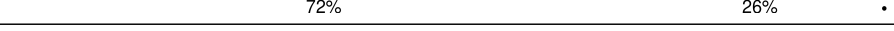


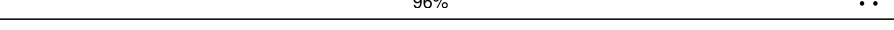

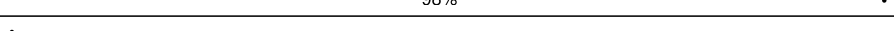

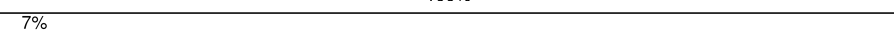
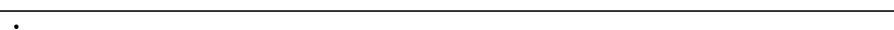

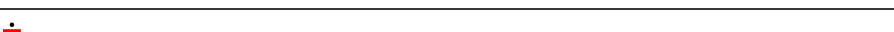
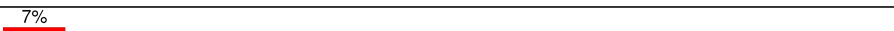


Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	198	
13	N	204	
14	O	198	
15	P	187	
16	Q	187	
17	R	181	
18	S	176	
19	T	160	
20	U	99	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	226	
28	c	115	
29	d	125	
30	e	135	
31	f	110	
32	g	126	
33	h	123	

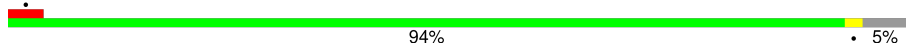

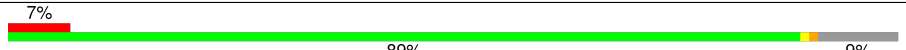


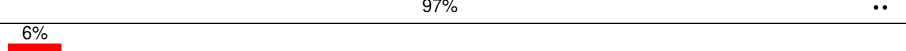
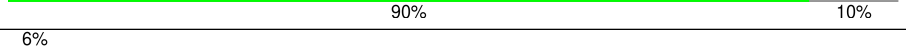


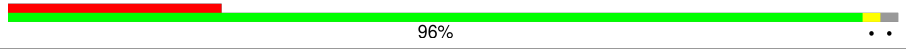
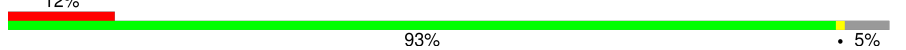
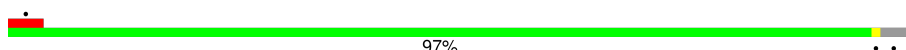
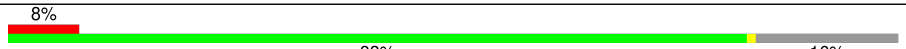

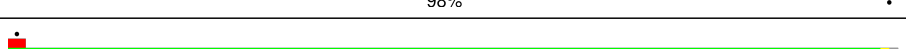
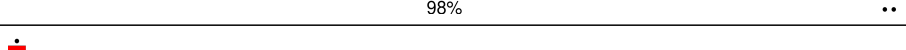
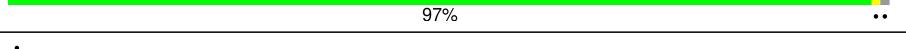
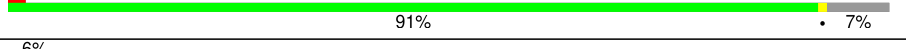

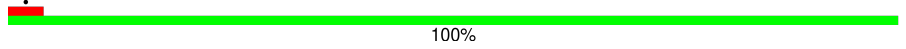
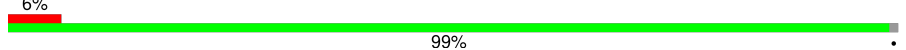


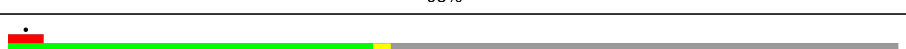
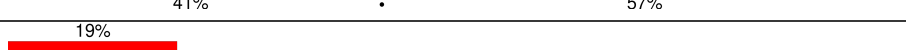
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	i	105	 96%
35	j	97	 88% 11%
36	k	69	 100%
37	l	51	 94%
38	m	52	 8% 98%
39	n	25	 100%
40	o	106	 95%
41	p	92	 99%
42	r	137	 90% 9%
43	s	303	 7% 64% 35%
44	t	195	 21% 78% 22%
45	5	3594	 72% 26%
46	7	119	 84% 16%
47	8	151	 72% 27%
48	K	217	 35% 96%
49	2	1697	 72% 26%
50	BB	217	 8% 98%
51	CC	264	 79% 19%
52	DD	221	 100%
53	EE	281	 7% 79% 19%
54	FF	262	 100%
55	GG	204	 90% 9%
56	HH	249	 95% 5%
57	II	194	 7% 95% 5%
58	JJ	206	 100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	KK	194	
60	LL	149	
61	MM	158	
62	NN	132	
63	OO	151	
64	PP	151	
65	QQ	145	
66	RR	172	
67	SS	135	
68	TT	152	
69	UU	145	
70	VV	119	
71	WW	83	
72	XX	130	
73	YY	143	
74	ZZ	134	
75	aa	125	
76	bb	101	
77	cc	84	
78	dd	69	
79	ee	56	
80	ff	133	
81	gg	156	
82	hh	317	
83	3	87	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
84	9	856	<div><div></div><div>10%</div><div></div><div>99%</div><div></div></div>
85	4	190	<div><div></div><div>41%</div><div></div><div>33%</div><div></div><div>46%</div><div></div><div>14%</div><div></div><div>7%</div><div></div></div>

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 227188 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 Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	239	Total	C	N	O	S	0	0
			1777	1110	361	300	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 3 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	LYS	-	expression tag	UNP P19949

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called Ribosomal protein L11.

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

- Molecule 11 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	137	Total	C	N	O	S	0	0
			1130	722	220	181	7		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	PRO	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	PRO	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLY	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12

- Molecule 13 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	198	Total	C	N	O	S	0	0
			1623	1046	318	254	5		

- Molecule 15 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 21 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 23 is a protein called eL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 30 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called eL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL41.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	262	LEU	ALA	conflict	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	266	THR	ALA	conflict	UNP A0A1U7UFL5
s	267	LEU	PHE	conflict	UNP A0A1U7UFL5
s	269	ILE	ALA	conflict	UNP A0A1U7UFL5
s	270	ILE	ASP	conflict	UNP A0A1U7UFL5
s	?	-	SER	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	PHE	deletion	UNP A0A1U7UFL5
s	?	-	VAL	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	PRO	deletion	UNP A0A1U7UFL5
s	?	-	VAL	deletion	UNP A0A1U7UFL5
s	272	VAL	ALA	conflict	UNP A0A1U7UFL5
s	273	ARG	ALA	conflict	UNP A0A1U7UFL5
s	274	ASP	ALA	conflict	UNP A0A1U7UFL5
s	275	SER	ALA	conflict	UNP A0A1U7UFL5
s	276	THR	PRO	conflict	UNP A0A1U7UFL5
s	278	ASP	ALA	conflict	UNP A0A1U7UFL5
s	282	ALA	LEU	conflict	UNP A0A1U7UFL5
s	284	GLN	ALA	conflict	UNP A0A1U7UFL5
s	286	SER	ALA	conflict	UNP A0A1U7UFL5
s	290	PRO	ALA	conflict	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	?	-	SER	deletion	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	294	ASN	ASP	conflict	UNP A0A1U7UFL5

- Molecule 44 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5	3594	Total	C	N	O	P	0	0
			77073	34324	14116	25039	3594		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 47 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 48 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	K	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

- Molecule 49 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 50 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BB	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CC	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 52 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	DD	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 53 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	EE	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 54 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	FF	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 55 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	GG	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	HH	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	II	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	JJ	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JJ	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 59 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	KK	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 60 is a protein called S10_ plectin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LL	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 61 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	MM	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	NN	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 63 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	OO	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 64 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	PP	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 65 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	QQ	115	Total	C	N	O	S	0	0
			956	610	176	163	7		

- Molecule 66 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	RR	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 67 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 68 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	TT	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 69 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	UU	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 70 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	VV	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 71 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	WW	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 72 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	XX	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 73 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	YY	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	ZZ	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 75 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	aa	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 76 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	bb	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	cc	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	dd	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 79 is a protein called eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	ee	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	ff	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 81 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	gg	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 82 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	hh	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 83 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	3	87	Total	C	N	O	P	0	0
			1860	829	333	612	86		

- Molecule 84 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	9	856	Total	C	N	O	S	0	0
			6673	4234	1148	1247	44		

- Molecule 85 is a RNA chain called CrPV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	4	190	Total	C	N	O	P	0	0
			4020	1802	689	1339	190		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	6217	C	-	expression tag	GB 8895506
4	6218	U	-	expression tag	GB 8895506
4	6219	U	-	expression tag	GB 8895506

- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	p	1	Total	Zn	0
			1	1	
86	2	1	Total	Zn	0
			1	1	
86	bb	1	Total	Zn	0
			1	1	
86	gg	1	Total	Zn	0
			1	1	


- Molecule 87 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	5	2	Total	Mg	0
			2	2	

3 Residue-property plots

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

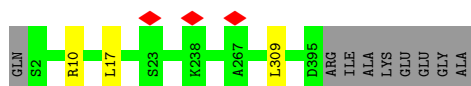
- Molecule 1: Ribosomal protein L8

Chain A: 



- Molecule 2: uL3

Chain B: 



- Molecule 3: Ribosomal protein L4

Chain C: 



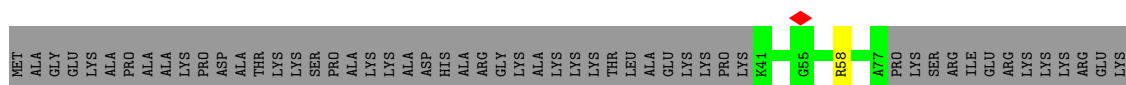
- Molecule 4: Large ribosomal subunit protein uL18

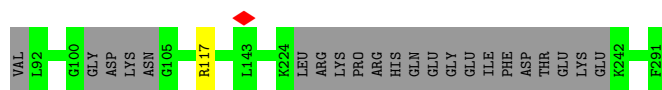
Chain D: 



- Molecule 5: 60S ribosomal protein L6

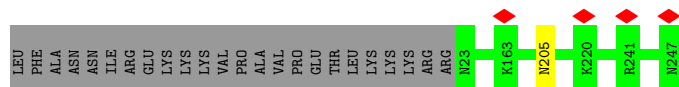
Chain E: 





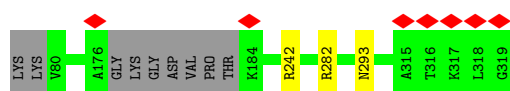
- Molecule 6: uL30

Chain F: 90% 10%



- Molecule 7: eL8

Chain G: 95%



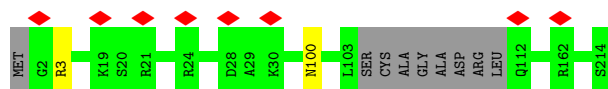
- Molecule 8: 60S ribosomal protein L9

Chain H: 96%



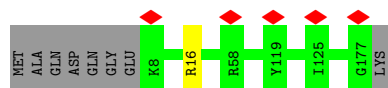
- Molecule 9: 60S ribosomal protein L10

Chain I: 95%



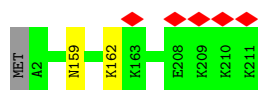
- Molecule 10: Ribosomal protein L11

Chain J: 95%

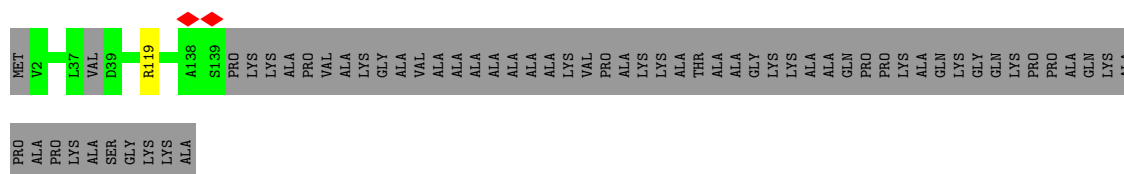


- Molecule 11: 60S ribosomal protein L13

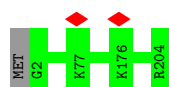
Chain L: 99%



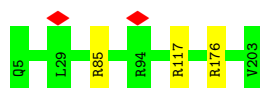
- Molecule 12: Large ribosomal subunit protein eL14



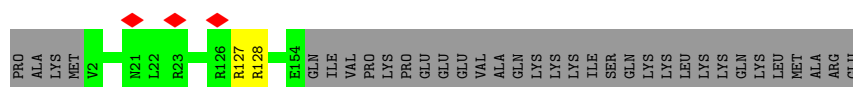
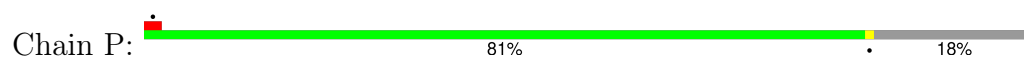
- Molecule 13: Ribosomal protein L15



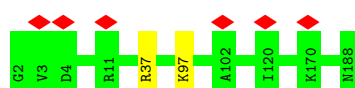
- Molecule 14: uL13



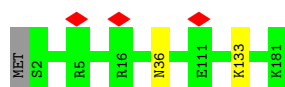
- Molecule 15: Large ribosomal subunit protein uL22



- Molecule 16: eL18

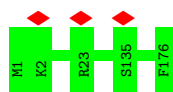


- Molecule 17: eL19

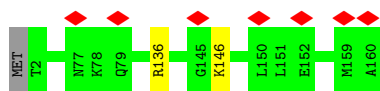


- Molecule 18: eL20





- Molecule 19: eL21



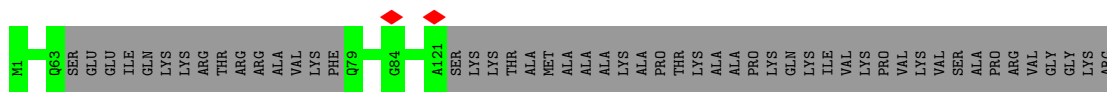
- Molecule 20: eL22



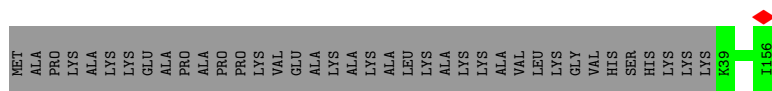
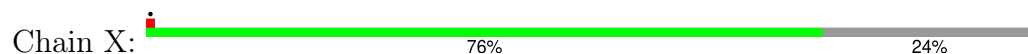
- Molecule 21: Ribosomal protein L23



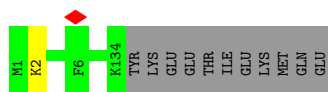
- Molecule 22: eL24



- Molecule 23: eL23



- Molecule 24: uL24

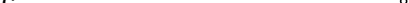


- Molecule 25: 60S ribosomal protein L27

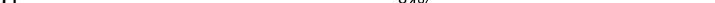
- Chain a: 

- Chain b: 45% 5% 50%

Position	Residue	Conservation	Phylogenetic Information
1	ALA	0.00	0.00
2	LYS	0.00	0.00
3	PRO	0.00	0.00
4	LYS	0.00	0.00
5	ALA	0.00	0.00
6	GLN	0.00	0.00
7	ALA	0.00	0.00
8	GLN	0.00	0.00
9	THR	0.00	0.00
10	LYS	0.00	0.00
11	PRO	0.00	0.00
12	LYS	0.00	0.00
13	ALA	0.00	0.00
14	ALA	0.00	0.00
15	THR	0.00	0.00
16	PRO	0.00	0.00
17	ALA	0.00	0.00
18	GLN	0.00	0.00
19	ALA	0.00	0.00
20	GLN	0.00	0.00
21	GLY	0.00	0.00
22	LYS	0.00	0.00
23	PRO	0.00	0.00
24	ALA	0.00	0.00
25	GLN	0.00	0.00
26	GLN	0.00	0.00
27	GLY	0.00	0.00
28	LYS	0.00	0.00
29	PRO	0.00	0.00
30	LYS	0.00	0.00
31	ALA	0.00	0.00
32	GLN	0.00	0.00
33	ALA	0.00	0.00
34	GLN	0.00	0.00
35	LYS	0.00	0.00
36	PRO	0.00	0.00
37	GLN	0.00	0.00
38	ALA	0.00	0.00
39	GLN	0.00	0.00
40	ALA	0.00	0.00
41	GLN	0.00	0.00
42	LYS	0.00	0.00
43	PRO	0.00	0.00
44	GLN	0.00	0.00
45	ALA	0.00	0.00
46	GLN	0.00	0.00
47	LYS	0.00	0.00
48	PRO	0.00	0.00
49	GLN	0.00	0.00
50	ALA	0.00	0.00
51	GLN	0.00	0.00
52	LYS	0.00	0.00
53	PRO	0.00	0.00
54	GLN	0.00	0.00
55	ALA	0.00	0.00
56	GLN	0.00	0.00
57	LYS	0.00	0.00
58	PRO	0.00	0.00
59	GLN	0.00	0.00
60	ALA	0.00	0.00
61	GLN	0.00	0.00
62	LYS	0.00	0.00
63	PRO	0.00	0.00
64	GLN	0.00	0.00
65	ALA	0.00	0.00
66	GLN	0.00	0.00
67	LYS	0.00	0.00
68	PRO	0.00	0.00
69	GLN	0.00	0.00
70	ALA	0.00	0.00
71	GLN	0.00	0.00
72	LYS	0.00	0.00
73	PRO	0.00	0.00
74	GLN	0.00	0.00
75	ALA	0.00	0.00
76	GLN	0.00	0.00
77	LYS	0.00	0.00
78	PRO	0.00	0.00
79	GLN	0.00	0.00
80	ALA	0.00	0.00
81	GLN	0.00	0.00
82	LYS	0.00	0.00
83	PRO	0.00	0.00
84	GLN	0.00	0.00
85	ALA	0.00	0.00
86	GLN	0.00	0.00
87	LYS	0.00	0.00
88	PRO	0.00	0.00
89	GLN	0.00	0.00
90	ALA	0.00	0.00
91	GLN	0.00	0.00
92	LYS	0.00	0.00
93	PRO	0.00	0.00
94	GLN	0.00	0.00
95	ALA	0.00	0.00


- Chain c:  85% 15%

MET	VAL	ALA	ALA	LYS	THR	LYS	LYS	S10	L11	E12	A84	S107	MET	PRO	GLU	GLN	THR	GLY	GLU	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	-----	-----	-----	-----	-----	-----	-----	-----

- Chain d:  84% 14%

MET
 ALA
 PRO
 ALA
 LYS
 LYS
 GLY
 GLY
 GLU
 LYS
 LYS
 GLY
 ARG
 SER
 ALA
 ILE
 N18
 K31
 E124
 ASN

- Chain e:  95% 5%




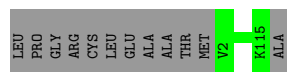
- WORLDWIDE
 PDB
PROTEIN DATA BANK

Chain f:  96% ..



- Molecule 32: Large ribosomal subunit protein eL34

Chain g:  90% 10%



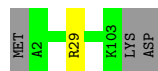
- Molecule 33: eL35

Chain h:  99% .




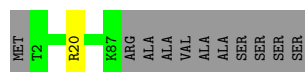
- Molecule 34: 60S ribosomal protein L36

Chain i:  96% ..



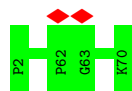
- Molecule 35: Ribosomal protein L37

Chain j:  88% 11%



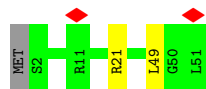
- Molecule 36: eL38

Chain k:  100%

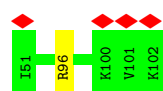


- Molecule 37: eL39

Chain l:  94% ..



- Molecule 38: eL40

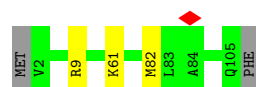


- Molecule 39: eL41



There are no outlier residues recorded for this chain.

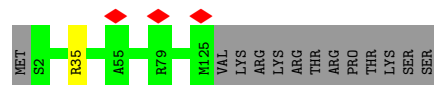
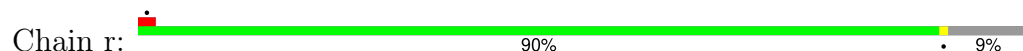
- Molecule 40: Large ribosomal subunit protein eL42



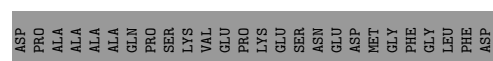
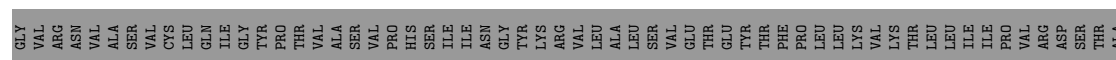
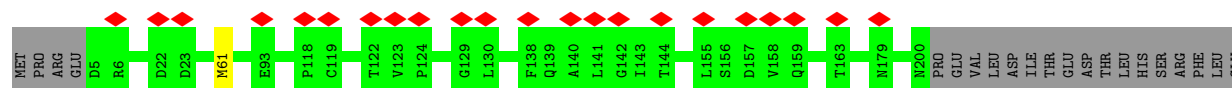
- Molecule 41: eL43



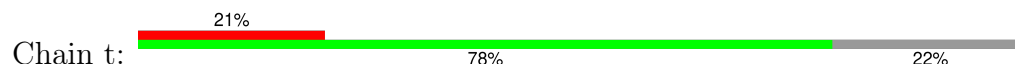
- Molecule 42: eL28

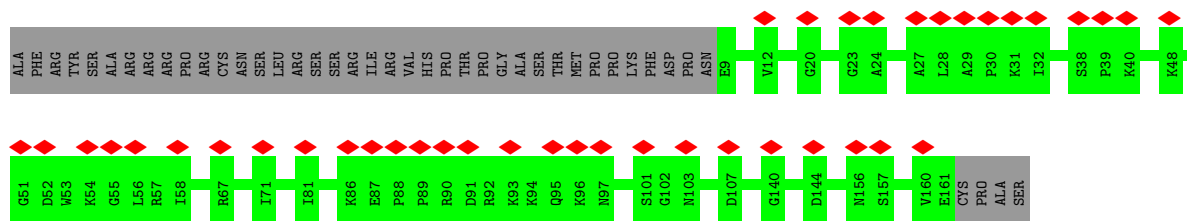


- Molecule 43: 60S acidic ribosomal protein P0



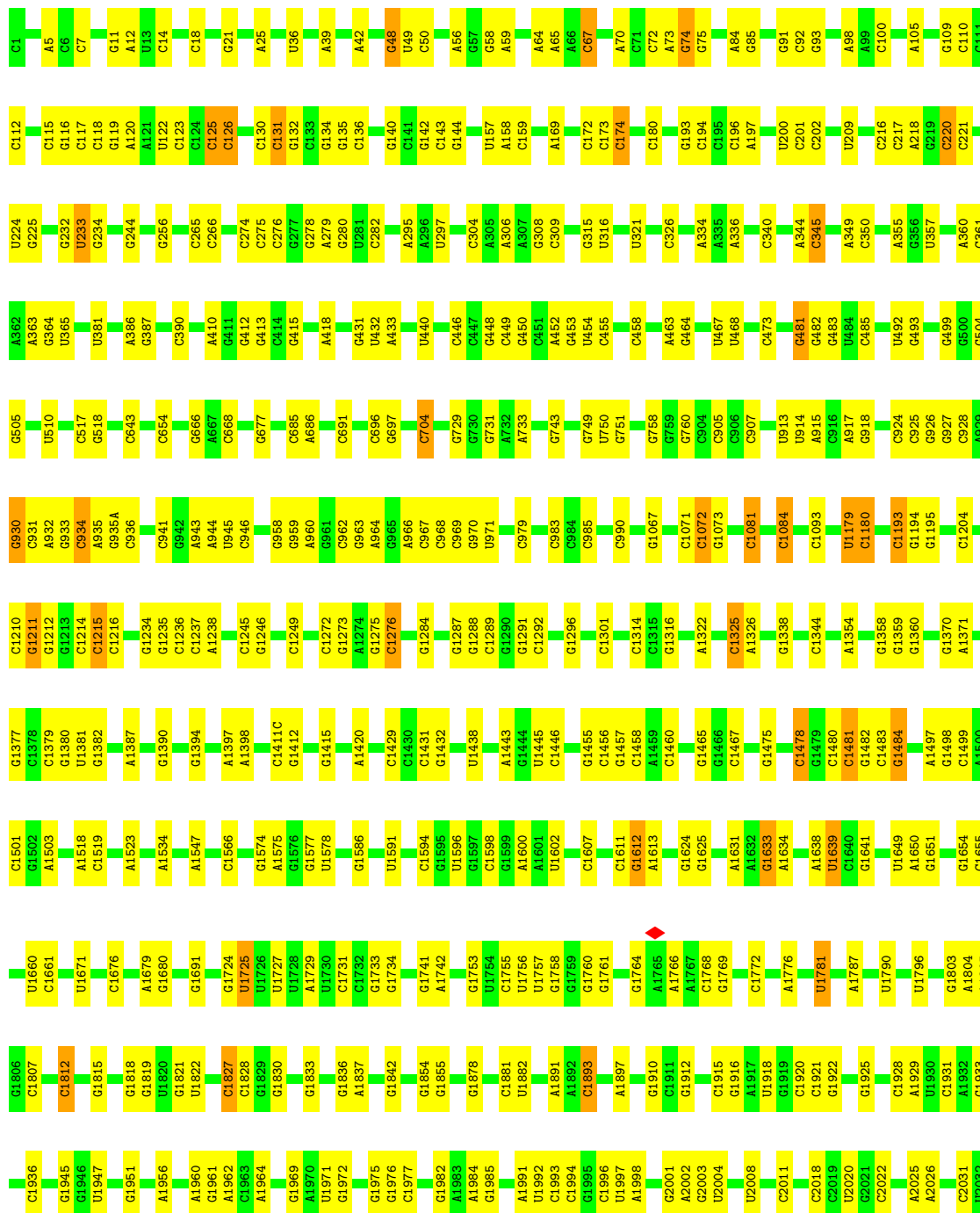
- Molecule 44: Ribosomal protein L12






• Molecule 45: 28S rRNA

Chain 5: 72% 26% .





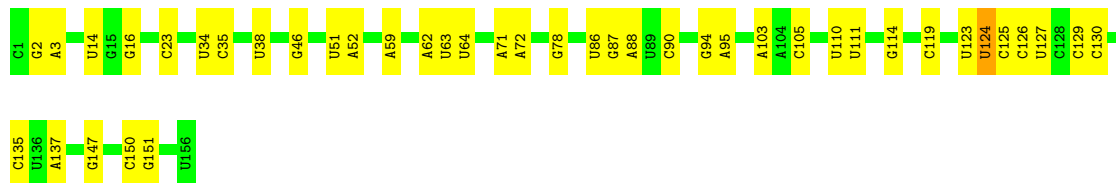
- Molecule 46: 5S rRNA

Chain 7:  84% 16%



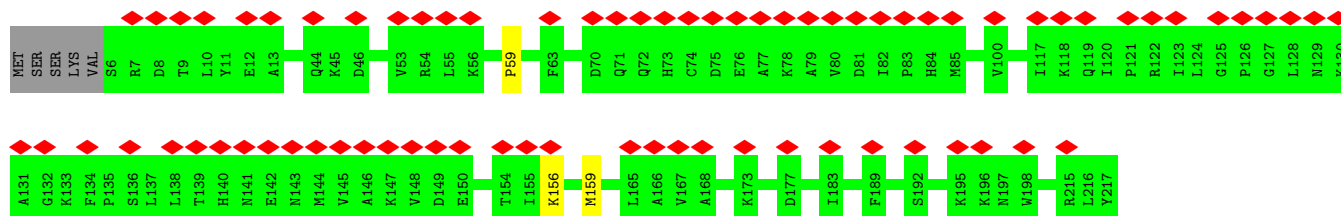
- Molecule 47: 5.8S rRNA

Chain 8:  72% 27%



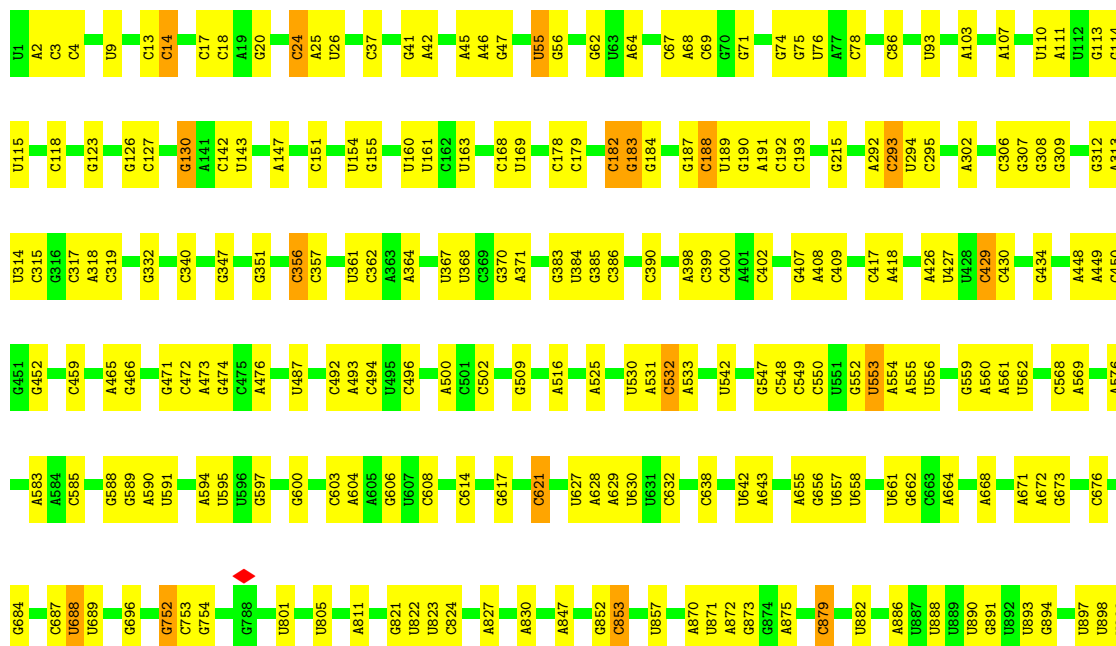
- Molecule 48: Ribosomal protein

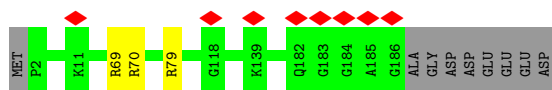
Chain K:  35% 96%



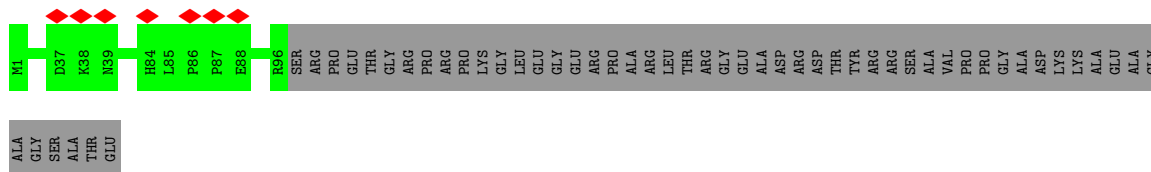
- Molecule 49: 18S rRNA

Chain 2:  72% 26%

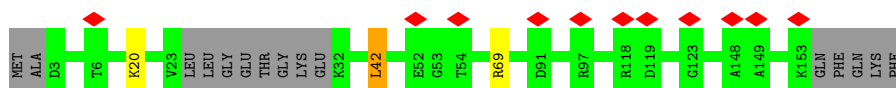
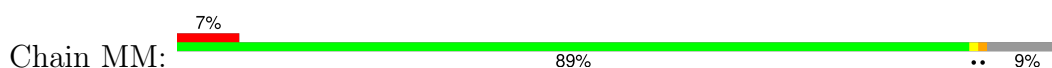




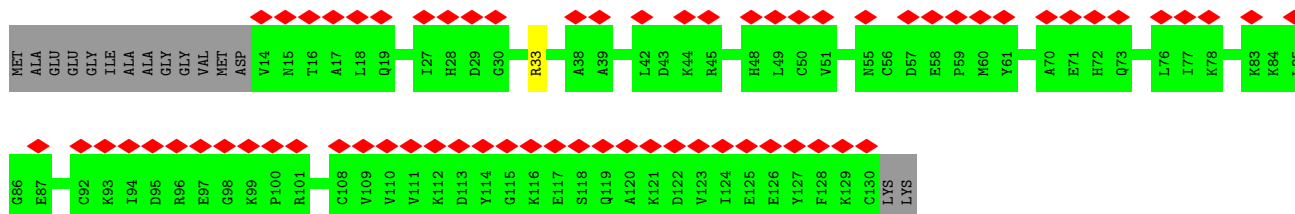
- Molecule 60: S10_pectin domain-containing protein



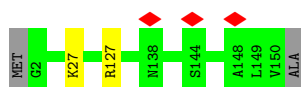
- Molecule 61: Ribosomal protein S11



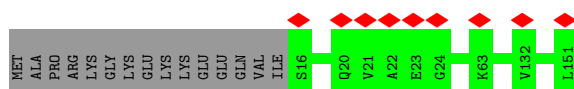
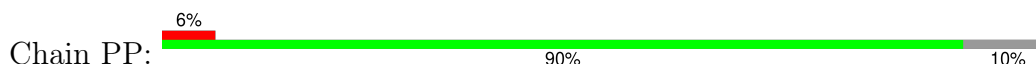
- Molecule 62: 40S ribosomal protein S12



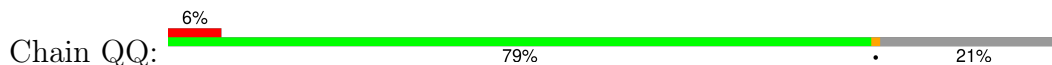
- Molecule 63: Ribosomal protein S13

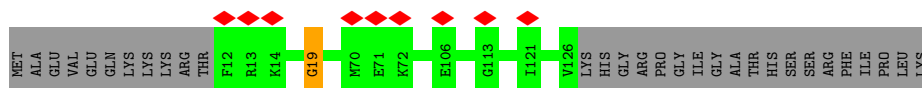


- Molecule 64: Small ribosomal subunit protein uS11

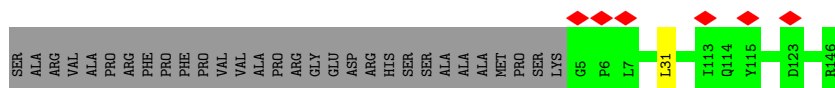
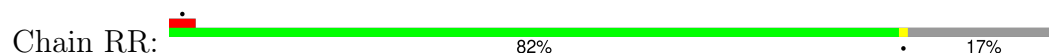


- Molecule 65: uS19

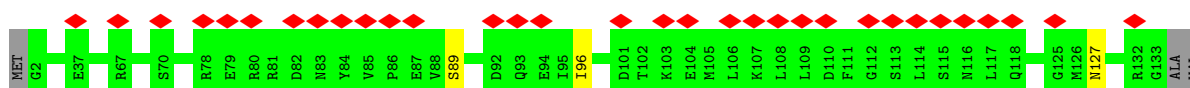




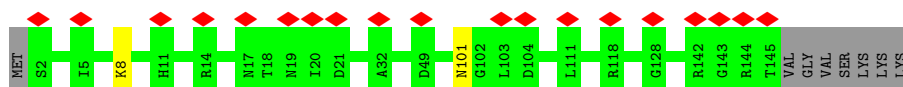
- Molecule 66: Ribosomal protein S16



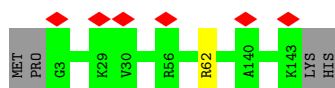
- Molecule 67: eS17



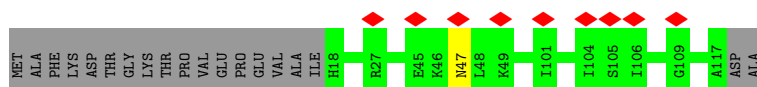
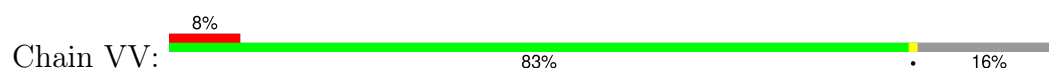
- Molecule 68: uS13



- Molecule 69: eS19



- Molecule 70: uS10

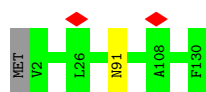


- Molecule 71: eS21



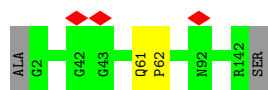
- Molecule 72: Ribosomal protein S15a

Chain XX:  98%



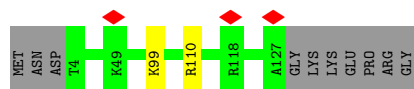
- Molecule 73: Ribosomal protein S23

Chain YY:  97%



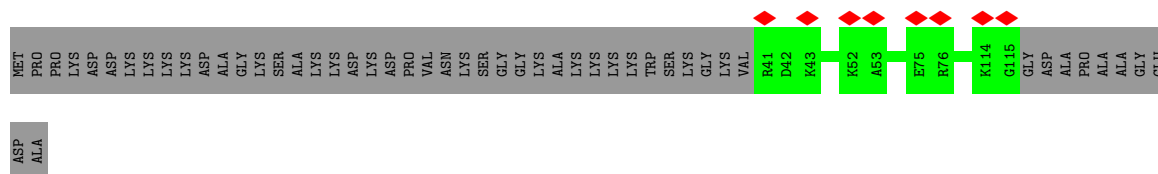
- Molecule 74: 40S ribosomal protein S24

Chain ZZ:  91%



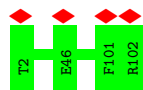
- Molecule 75: eS25

Chain aa:  60%



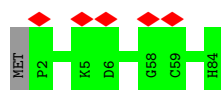
- Molecule 76: eS26

Chain bb:  100%



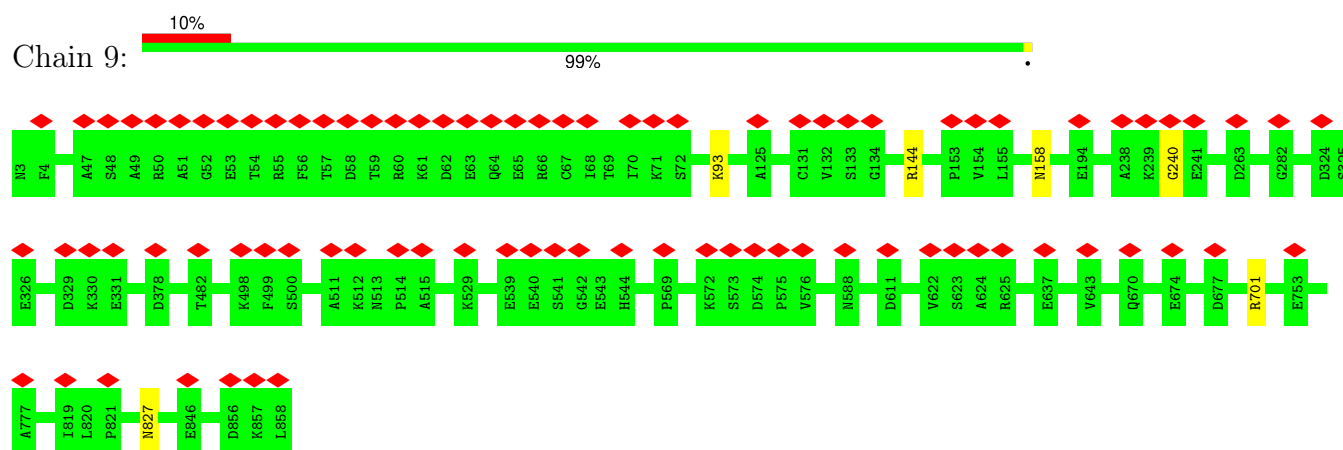
- Molecule 77: 40S ribosomal protein S27

Chain cc:  99%

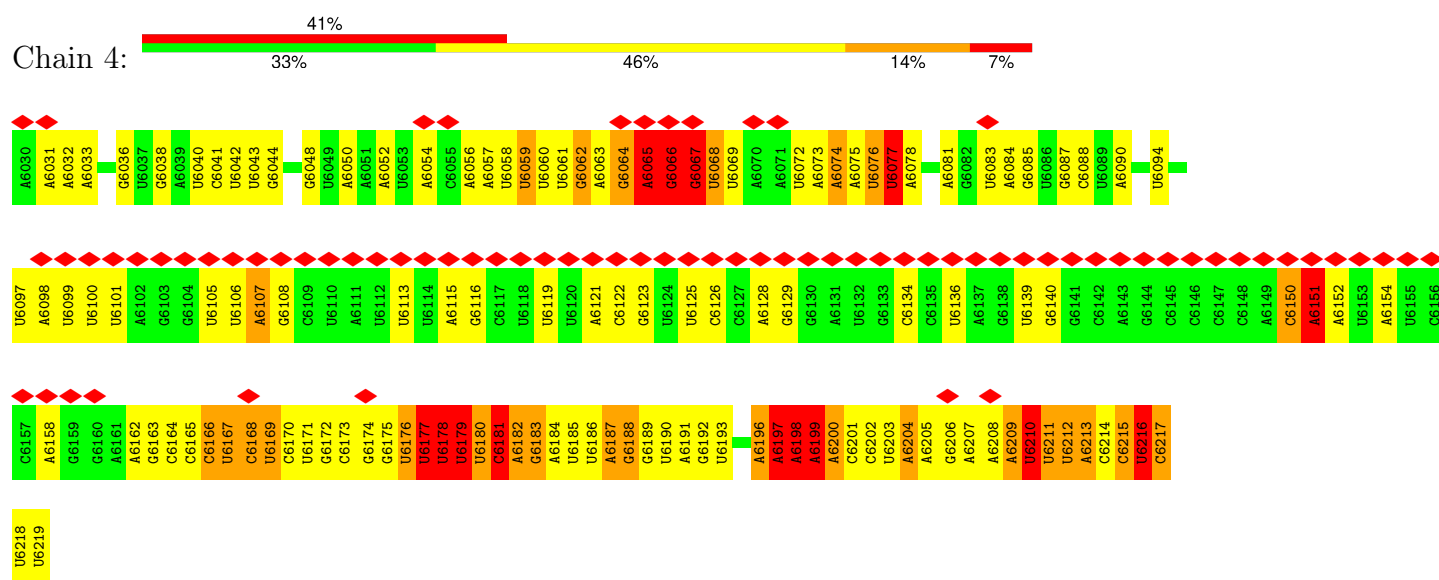


- Molecule 78: Ribosomal protein S28

Chain dd:  90%



● Molecule 85: CrPV IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75654	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.076	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	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

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	0.26	0/1812	0.50	1/2439 (0.0%)
2	B	0.25	0/3240	0.51	2/4339 (0.0%)
3	C	0.24	0/2936	0.45	0/3943
4	D	0.26	0/2437	0.44	0/3264
5	E	0.25	0/1762	0.48	0/2362
6	F	0.25	0/1911	0.44	0/2549
7	G	0.25	0/1910	0.49	0/2569
8	H	0.25	0/1535	0.50	0/2063
9	I	0.26	0/1702	0.45	0/2272
10	J	0.25	0/1385	0.47	0/1852
11	L	0.27	0/1733	0.46	0/2316
12	M	0.25	0/1150	0.44	0/1534
13	N	0.24	0/1746	0.43	0/2338
14	O	0.25	0/1653	0.44	0/2206
15	P	0.24	0/1268	0.47	0/1700
16	Q	0.24	0/1539	0.48	0/2054
17	R	0.24	0/1524	0.44	0/2013
18	S	0.25	0/1501	0.48	0/2012
19	T	0.25	0/1326	0.44	0/1770
20	U	0.26	0/823	0.45	0/1104
21	V	0.26	0/983	0.46	0/1319
22	W	0.25	0/873	0.43	0/1158
23	X	0.24	0/984	0.46	0/1323
24	Y	0.24	0/1132	0.44	0/1504
25	Z	0.26	0/1130	0.46	0/1507
26	a	0.23	0/1191	0.42	0/1590
27	b	0.24	0/861	0.40	0/1138
28	c	0.25	0/771	0.45	0/1034
29	d	0.26	0/903	0.49	0/1216
30	e	0.24	0/1071	0.47	0/1429
31	f	0.25	0/895	0.49	0/1198
32	g	0.25	0/916	0.48	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.25	0/1021	0.42	0/1348
34	i	0.25	0/841	0.43	0/1112
35	j	0.26	0/720	0.45	0/952
36	k	0.24	0/575	0.47	0/761
37	l	0.24	0/459	0.47	1/608 (0.2%)
38	m	0.25	0/435	0.46	0/575
39	n	0.23	0/240	0.40	0/305
40	o	0.24	0/864	0.46	0/1140
41	p	0.24	0/718	0.44	0/953
42	r	0.24	0/1010	0.47	0/1354
43	s	0.27	0/1530	0.47	0/2064
44	t	0.25	0/1174	0.52	0/1582
45	5	0.27	1/86202 (0.0%)	1.01	331/134412 (0.2%)
46	7	0.27	0/2836	1.00	5/4421 (0.1%)
47	8	0.27	0/3581	1.00	10/5577 (0.2%)
48	K	0.28	0/1730	0.55	0/2315
49	2	0.28	0/40500	1.03	194/63092 (0.3%)
50	BB	0.26	0/1747	0.51	0/2374
51	CC	0.26	0/1756	0.50	0/2350
52	DD	0.25	0/1753	0.48	0/2369
53	EE	0.26	0/1796	0.51	0/2417
54	FF	0.25	0/2118	0.47	0/2849
55	GG	0.25	0/1492	0.46	0/2005
56	HH	0.25	0/1946	0.48	0/2590
57	II	0.26	0/1510	0.50	1/2022 (0.0%)
58	JJ	0.25	0/1715	0.46	0/2287
59	KK	0.25	0/1550	0.48	0/2069
60	LL	0.25	0/834	0.48	0/1125
61	MM	0.25	0/1195	0.51	1/1597 (0.1%)
62	NN	0.26	0/918	0.54	0/1233
63	OO	0.24	0/1226	0.45	0/1649
64	PP	0.25	0/1029	0.49	0/1380
65	QQ	0.25	0/974	0.49	0/1301
66	RR	0.25	0/1146	0.48	1/1534 (0.1%)
67	SS	0.25	0/1082	0.50	1/1452 (0.1%)
68	TT	0.25	0/1208	0.47	0/1618
69	UU	0.25	0/1115	0.44	0/1493
70	VV	0.24	0/805	0.48	0/1081
71	WW	0.26	0/643	0.48	0/860
72	XX	0.26	0/1051	0.49	0/1406
73	YY	0.26	0/1116	0.48	0/1490
74	ZZ	0.25	0/1028	0.47	0/1366
75	aa	0.24	0/604	0.50	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	bb	0.24	0/828	0.44	0/1109
77	cc	0.24	0/665	0.47	0/891
78	dd	0.23	0/490	0.45	0/656
79	ee	0.25	0/470	0.41	0/623
80	ff	0.25	0/462	0.44	0/607
81	gg	0.24	0/567	0.46	0/753
82	hh	0.25	0/2492	0.52	0/3391
83	3	0.26	0/2077	0.96	2/3238 (0.1%)
84	9	0.26	0/6804	0.52	0/9189
85	4	0.69	16/4490 (0.4%)	1.54	125/6984 (1.8%)
All	All	0.28	17/243741 (0.0%)	0.86	675/357074 (0.2%)

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
3	C	0	1
50	BB	0	1
65	QQ	0	1
67	SS	0	1
73	YY	0	1
84	9	0	1
85	4	1	14
All	All	1	20

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	4	6178	U	C2-O2	9.15	1.30	1.22
85	4	6065	A	O3'-P	8.59	1.71	1.61
85	4	6078	A	O3'-P	-8.35	1.51	1.61
85	4	6217	C	O3'-P	8.15	1.71	1.61
85	4	6187	A	O3'-P	7.84	1.70	1.61

The worst 5 of 675 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6068	U	OP1-P-O3'	25.71	161.75	105.20
85	4	6068	U	O3'-P-O5'	-20.16	65.70	104.00
85	4	6218	U	O3'-P-O5'	-18.73	68.41	104.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6188	G	O5'-P-OP2	16.39	130.37	110.70
85	4	6218	U	P-O3'-C3'	15.72	138.56	119.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
85	4	6210	U	C1'

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	BB	12	GLU	Peptide
3	C	151	PRO	Peptide
65	QQ	19	GLY	Peptide
67	SS	89	SER	Peptide
73	YY	61	GLN	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	237/257 (92%)	223 (94%)	14 (6%)	0	100	100
2	B	392/403 (97%)	381 (97%)	11 (3%)	0	100	100
3	C	358/392 (91%)	341 (95%)	17 (5%)	0	100	100
4	D	291/297 (98%)	281 (97%)	10 (3%)	0	100	100
5	E	208/291 (72%)	198 (95%)	10 (5%)	0	100	100
6	F	223/249 (90%)	214 (96%)	9 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	229/242 (95%)	218 (95%)	11 (5%)	0	100	100
8	H	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
9	I	201/214 (94%)	192 (96%)	9 (4%)	0	100	100
10	J	168/178 (94%)	165 (98%)	3 (2%)	0	100	100
11	L	208/211 (99%)	198 (95%)	10 (5%)	0	100	100
12	M	133/198 (67%)	128 (96%)	5 (4%)	0	100	100
13	N	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
14	O	194/198 (98%)	186 (96%)	8 (4%)	0	100	100
15	P	151/187 (81%)	147 (97%)	4 (3%)	0	100	100
16	Q	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
17	R	178/181 (98%)	174 (98%)	4 (2%)	0	100	100
18	S	174/176 (99%)	167 (96%)	7 (4%)	0	100	100
19	T	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
20	U	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
21	V	127/140 (91%)	123 (97%)	4 (3%)	0	100	100
22	W	102/157 (65%)	99 (97%)	3 (3%)	0	100	100
23	X	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
24	Y	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
25	Z	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
26	a	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
27	b	100/226 (44%)	99 (99%)	1 (1%)	0	100	100
28	c	96/115 (84%)	94 (98%)	2 (2%)	0	100	100
29	d	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
30	e	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
31	f	107/110 (97%)	98 (92%)	9 (8%)	0	100	100
32	g	112/126 (89%)	109 (97%)	3 (3%)	0	100	100
33	h	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
34	i	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
35	j	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
36	k	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
37	l	48/51 (94%)	45 (94%)	3 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	m	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
41	p	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
42	r	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
43	s	194/303 (64%)	186 (96%)	8 (4%)	0	100	100
44	t	151/195 (77%)	135 (89%)	16 (11%)	0	100	100
48	K	204/217 (94%)	182 (89%)	21 (10%)	1 (0%)	25	60
50	BB	215/217 (99%)	202 (94%)	13 (6%)	0	100	100
51	CC	211/264 (80%)	197 (93%)	14 (7%)	0	100	100
52	DD	219/221 (99%)	216 (99%)	3 (1%)	0	100	100
53	EE	226/281 (80%)	217 (96%)	9 (4%)	0	100	100
54	FF	260/262 (99%)	244 (94%)	16 (6%)	0	100	100
55	GG	181/204 (89%)	173 (96%)	8 (4%)	0	100	100
56	HH	235/249 (94%)	227 (97%)	8 (3%)	0	100	100
57	II	181/194 (93%)	173 (96%)	8 (4%)	0	100	100
58	JJ	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
59	KK	183/194 (94%)	181 (99%)	2 (1%)	0	100	100
60	LL	94/149 (63%)	90 (96%)	4 (4%)	0	100	100
61	MM	139/158 (88%)	132 (95%)	7 (5%)	0	100	100
62	NN	115/132 (87%)	107 (93%)	8 (7%)	0	100	100
63	OO	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
64	PP	134/151 (89%)	126 (94%)	8 (6%)	0	100	100
65	QQ	113/145 (78%)	102 (90%)	10 (9%)	1 (1%)	14	49
66	RR	140/172 (81%)	133 (95%)	7 (5%)	0	100	100
67	SS	130/135 (96%)	119 (92%)	11 (8%)	0	100	100
68	TT	142/152 (93%)	133 (94%)	9 (6%)	0	100	100
69	UU	139/145 (96%)	133 (96%)	6 (4%)	0	100	100
70	VV	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
71	WW	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
72	XX	127/130 (98%)	120 (94%)	7 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	YY	139/143 (97%)	131 (94%)	7 (5%)	1 (1%)	19	54
74	ZZ	122/134 (91%)	120 (98%)	2 (2%)	0	100	100
75	aa	73/125 (58%)	72 (99%)	1 (1%)	0	100	100
76	bb	99/101 (98%)	92 (93%)	7 (7%)	0	100	100
77	cc	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
78	dd	60/69 (87%)	60 (100%)	0	0	100	100
79	ee	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
80	ff	55/133 (41%)	49 (89%)	6 (11%)	0	100	100
81	gg	66/156 (42%)	63 (96%)	3 (4%)	0	100	100
82	hh	310/317 (98%)	292 (94%)	18 (6%)	0	100	100
84	9	854/856 (100%)	801 (94%)	53 (6%)	0	100	100
All	All	12554/14095 (89%)	11964 (95%)	587 (5%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	K	59	PRO
73	YY	62	PRO
65	QQ	19	GLY

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	172/199 (86%)	167 (97%)	5 (3%)	37	67
2	B	342/348 (98%)	341 (100%)	1 (0%)	91	96
3	C	302/323 (94%)	295 (98%)	7 (2%)	45	72
4	D	247/250 (99%)	245 (99%)	2 (1%)	79	90
5	E	190/251 (76%)	188 (99%)	2 (1%)	70	86
6	F	196/218 (90%)	195 (100%)	1 (0%)	86	93

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	200/208 (96%)	197 (98%)	3 (2%)	60	81
8	H	169/171 (99%)	164 (97%)	5 (3%)	36	66
9	I	175/181 (97%)	173 (99%)	2 (1%)	70	86
10	J	143/149 (96%)	142 (99%)	1 (1%)	81	92
11	L	175/176 (99%)	173 (99%)	2 (1%)	70	86
12	M	116/151 (77%)	115 (99%)	1 (1%)	75	89
13	N	171/172 (99%)	171 (100%)	0	100	100
14	O	170/170 (100%)	167 (98%)	3 (2%)	54	77
15	P	134/165 (81%)	132 (98%)	2 (2%)	60	81
16	Q	164/164 (100%)	162 (99%)	2 (1%)	67	85
17	R	159/160 (99%)	157 (99%)	2 (1%)	65	83
18	S	157/157 (100%)	157 (100%)	0	100	100
19	T	139/140 (99%)	137 (99%)	2 (1%)	62	82
20	U	89/89 (100%)	89 (100%)	0	100	100
21	V	100/107 (94%)	98 (98%)	2 (2%)	50	75
22	W	86/126 (68%)	86 (100%)	0	100	100
23	X	106/134 (79%)	106 (100%)	0	100	100
24	Y	124/135 (92%)	123 (99%)	1 (1%)	79	90
25	Z	117/118 (99%)	117 (100%)	0	100	100
26	a	119/120 (99%)	117 (98%)	2 (2%)	56	78
27	b	84/172 (49%)	82 (98%)	2 (2%)	44	71
28	c	84/98 (86%)	84 (100%)	0	100	100
29	d	98/110 (89%)	96 (98%)	2 (2%)	50	75
30	e	114/121 (94%)	114 (100%)	0	100	100
31	f	88/89 (99%)	85 (97%)	3 (3%)	32	63
32	g	98/106 (92%)	98 (100%)	0	100	100
33	h	109/110 (99%)	109 (100%)	0	100	100
34	i	86/89 (97%)	85 (99%)	1 (1%)	67	85
35	j	73/80 (91%)	72 (99%)	1 (1%)	62	82
36	k	64/64 (100%)	64 (100%)	0	100	100
37	l	47/48 (98%)	46 (98%)	1 (2%)	48	74

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	m	48/48 (100%)	47 (98%)	1 (2%)	48	74
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	92/94 (98%)	89 (97%)	3 (3%)	33	64
41	p	74/75 (99%)	74 (100%)	0	100	100
42	r	108/121 (89%)	107 (99%)	1 (1%)	75	89
43	s	164/258 (64%)	163 (99%)	1 (1%)	84	92
44	t	126/163 (77%)	126 (100%)	0	100	100
48	K	190/196 (97%)	188 (99%)	2 (1%)	70	86
50	BB	180/181 (99%)	177 (98%)	3 (2%)	56	78
51	CC	194/231 (84%)	190 (98%)	4 (2%)	48	74
52	DD	187/187 (100%)	187 (100%)	0	100	100
53	EE	190/232 (82%)	184 (97%)	6 (3%)	34	65
54	FF	224/224 (100%)	223 (100%)	1 (0%)	89	94
55	GG	158/170 (93%)	156 (99%)	2 (1%)	65	83
56	HH	207/218 (95%)	206 (100%)	1 (0%)	86	93
57	II	165/174 (95%)	165 (100%)	0	100	100
58	JJ	178/178 (100%)	177 (99%)	1 (1%)	84	92
59	KK	161/168 (96%)	158 (98%)	3 (2%)	52	76
60	LL	87/125 (70%)	87 (100%)	0	100	100
61	MM	130/142 (92%)	127 (98%)	3 (2%)	45	72
62	NN	99/108 (92%)	98 (99%)	1 (1%)	73	87
63	OO	130/131 (99%)	128 (98%)	2 (2%)	60	81
64	PP	106/119 (89%)	106 (100%)	0	100	100
65	QQ	105/130 (81%)	105 (100%)	0	100	100
66	RR	117/140 (84%)	117 (100%)	0	100	100
67	SS	119/121 (98%)	118 (99%)	1 (1%)	79	90
68	TT	125/132 (95%)	123 (98%)	2 (2%)	58	79
69	UU	111/116 (96%)	110 (99%)	1 (1%)	75	89
70	VV	92/107 (86%)	91 (99%)	1 (1%)	70	86
71	WW	67/67 (100%)	65 (97%)	2 (3%)	36	66
72	XX	112/113 (99%)	111 (99%)	1 (1%)	75	89

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	YY	113/114 (99%)	113 (100%)	0	100	100
74	ZZ	107/115 (93%)	105 (98%)	2 (2%)	52	76
75	aa	66/103 (64%)	66 (100%)	0	100	100
76	bb	88/88 (100%)	88 (100%)	0	100	100
77	cc	75/76 (99%)	75 (100%)	0	100	100
78	dd	55/62 (89%)	55 (100%)	0	100	100
79	ee	48/49 (98%)	48 (100%)	0	100	100
80	ff	47/106 (44%)	45 (96%)	2 (4%)	25	57
81	gg	61/140 (44%)	60 (98%)	1 (2%)	58	79
82	hh	272/275 (99%)	270 (99%)	2 (1%)	81	92
84	9	728/728 (100%)	723 (99%)	5 (1%)	81	92
All	All	10937/12018 (91%)	10824 (99%)	113 (1%)	71	87

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	l	21	ARG
84	9	158	ASN
51	CC	162	ARG
84	9	144	ARG
71	WW	82	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 109 such sidechains are listed below:

Mol	Chain	Res	Type
51	CC	232	HIS
60	LL	7	ASN
84	9	64	GLN
52	DD	267	GLN
57	II	91	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	5	3558/3594 (98%)	900 (25%)	29 (0%)
46	7	118/119 (99%)	16 (13%)	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
47	8	149/151 (98%)	37 (24%)	1 (0%)
49	2	1676/1697 (98%)	408 (24%)	14 (0%)
83	3	86/87 (98%)	25 (29%)	0
85	4	188/190 (98%)	123 (65%)	48 (25%)
All	All	5775/5838 (98%)	1509 (26%)	92 (1%)

5 of 1509 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	5	5	A
45	5	7	C
45	5	11	G
45	5	12	A
45	5	14	C

5 of 92 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	4	6151	A
85	4	6180	U
85	4	6164	C
85	4	6172	G
85	4	6184	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
45	5	36
49	2	20
48	K	3
47	8	1
82	hh	1
14	O	1
3	C	1

The worst 5 of 63 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	41.98
1	5	1252:C	O3'	1271:G	P	33.40
1	5	1696:C	O3'	1720:C	P	19.99
1	5	1219:G	O3'	1233:G	P	18.35
1	5	523:C	O3'	638:G	P	18.12

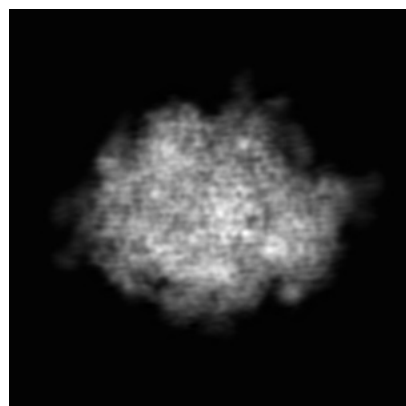
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7836. These allow visual inspection of the internal detail of the map and identification of artifacts.

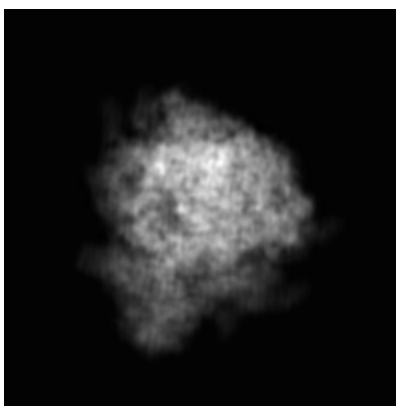
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

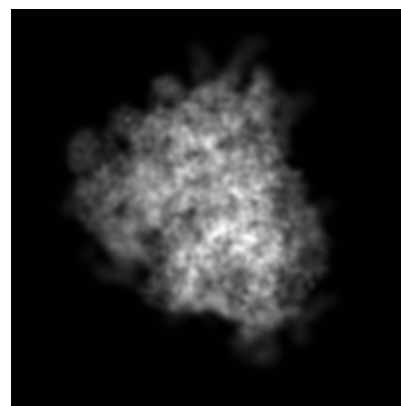
6.1.1 Primary map



X

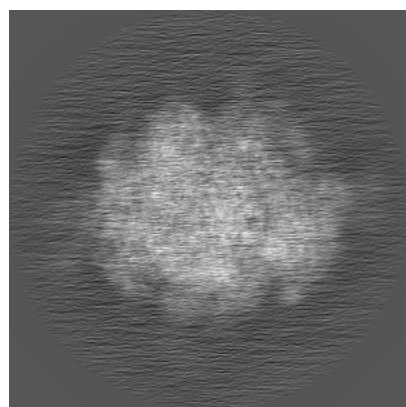


Y

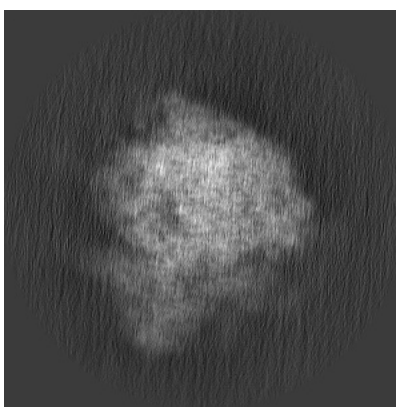


Z

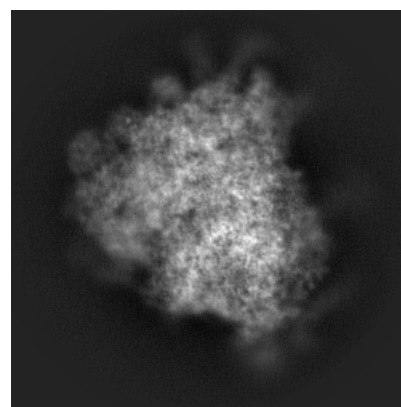
6.1.2 Raw map



X



Y

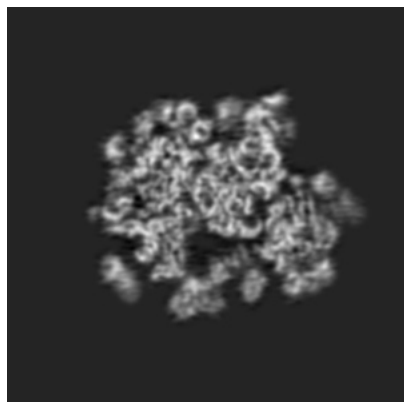


Z

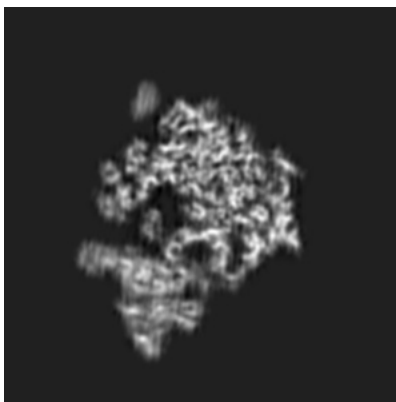
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

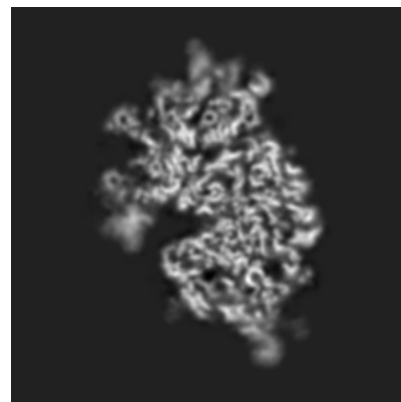
6.2.1 Primary map



X Index: 200

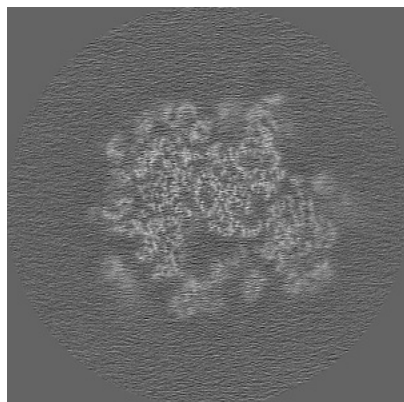


Y Index: 200

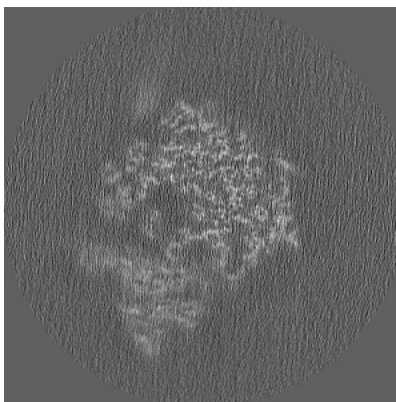


Z Index: 200

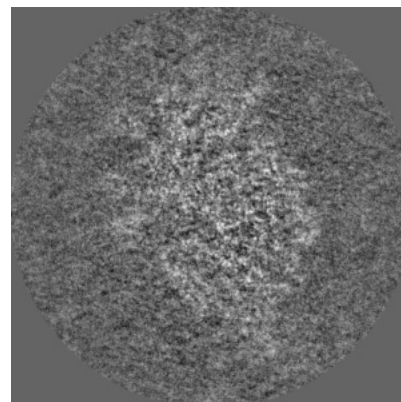
6.2.2 Raw map



X Index: 200



Y Index: 200

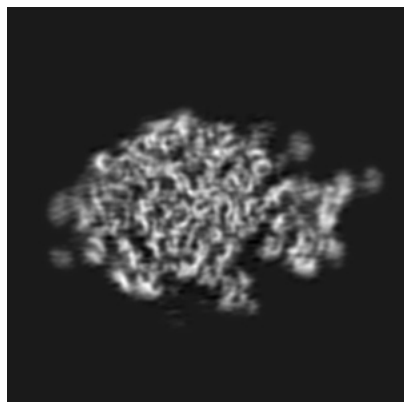


Z Index: 200

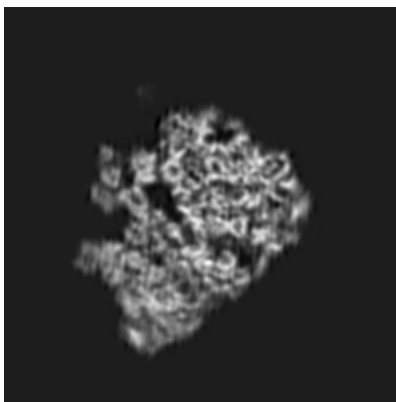
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

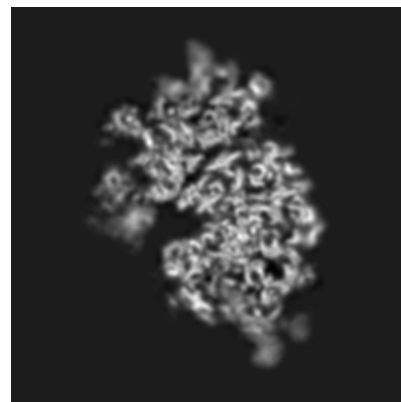
6.3.1 Primary map



X Index: 248

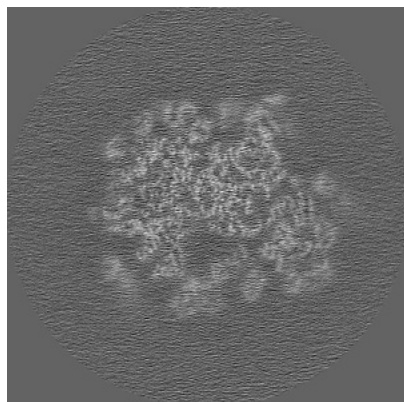


Y Index: 213

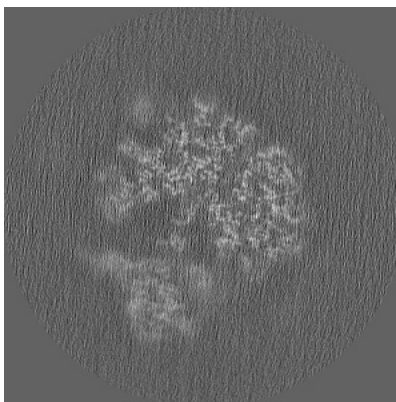


Z Index: 197

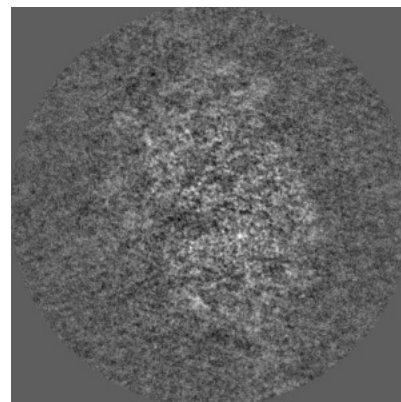
6.3.2 Raw map



X Index: 201



Y Index: 189

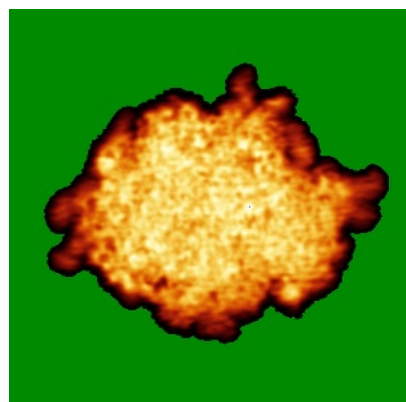


Z Index: 198

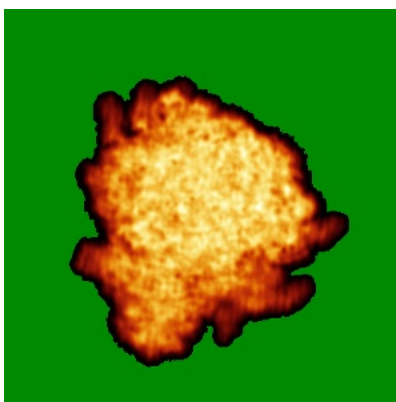
The images above show the largest variance slices of the map in three orthogonal directions.

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

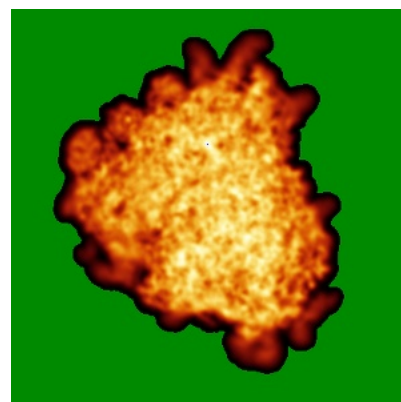
6.4.1 Primary map



X

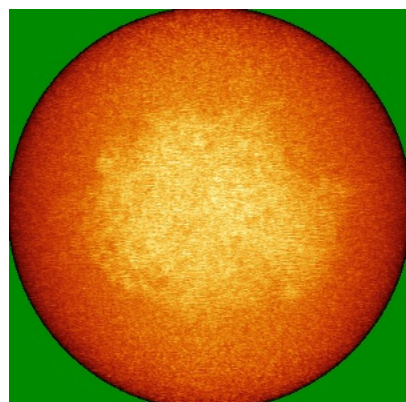


Y

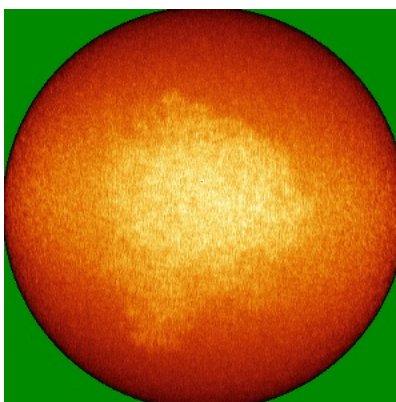


Z

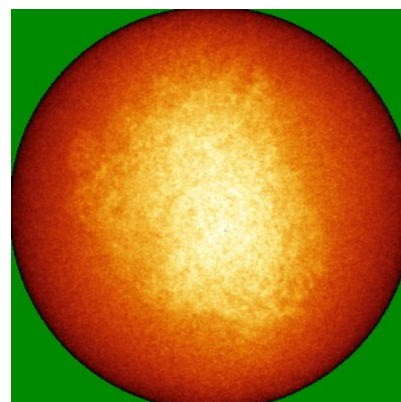
6.4.2 Raw map



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.

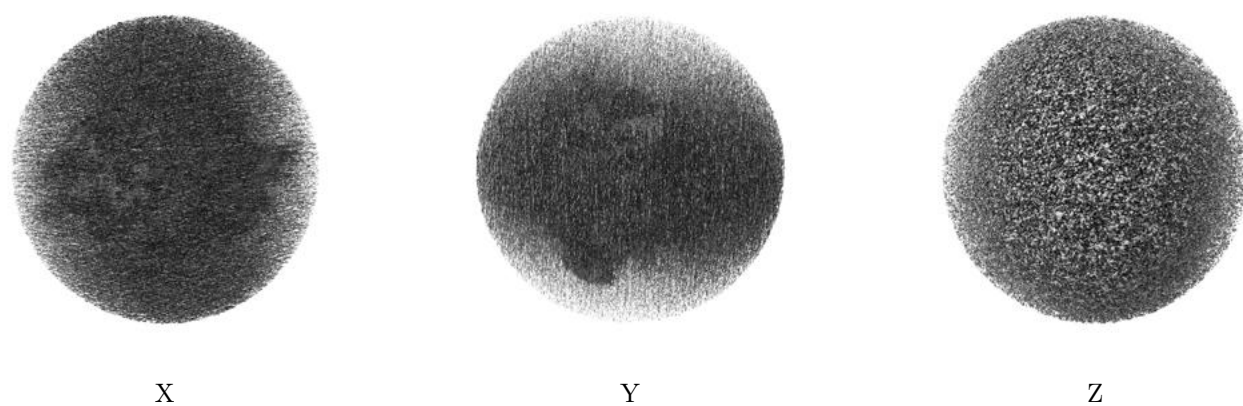
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

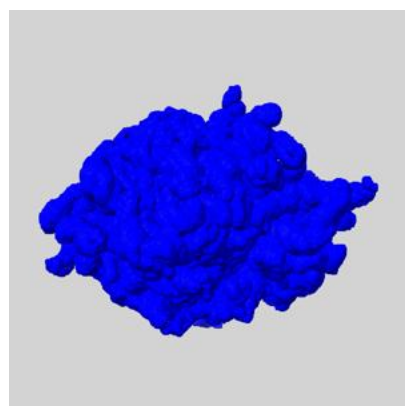
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

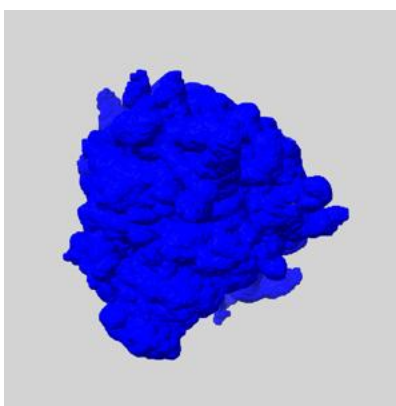
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

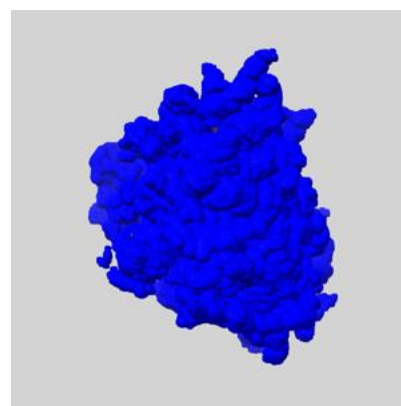
6.6.1 emd_7836_msk_1.map [i](#)



X



Y

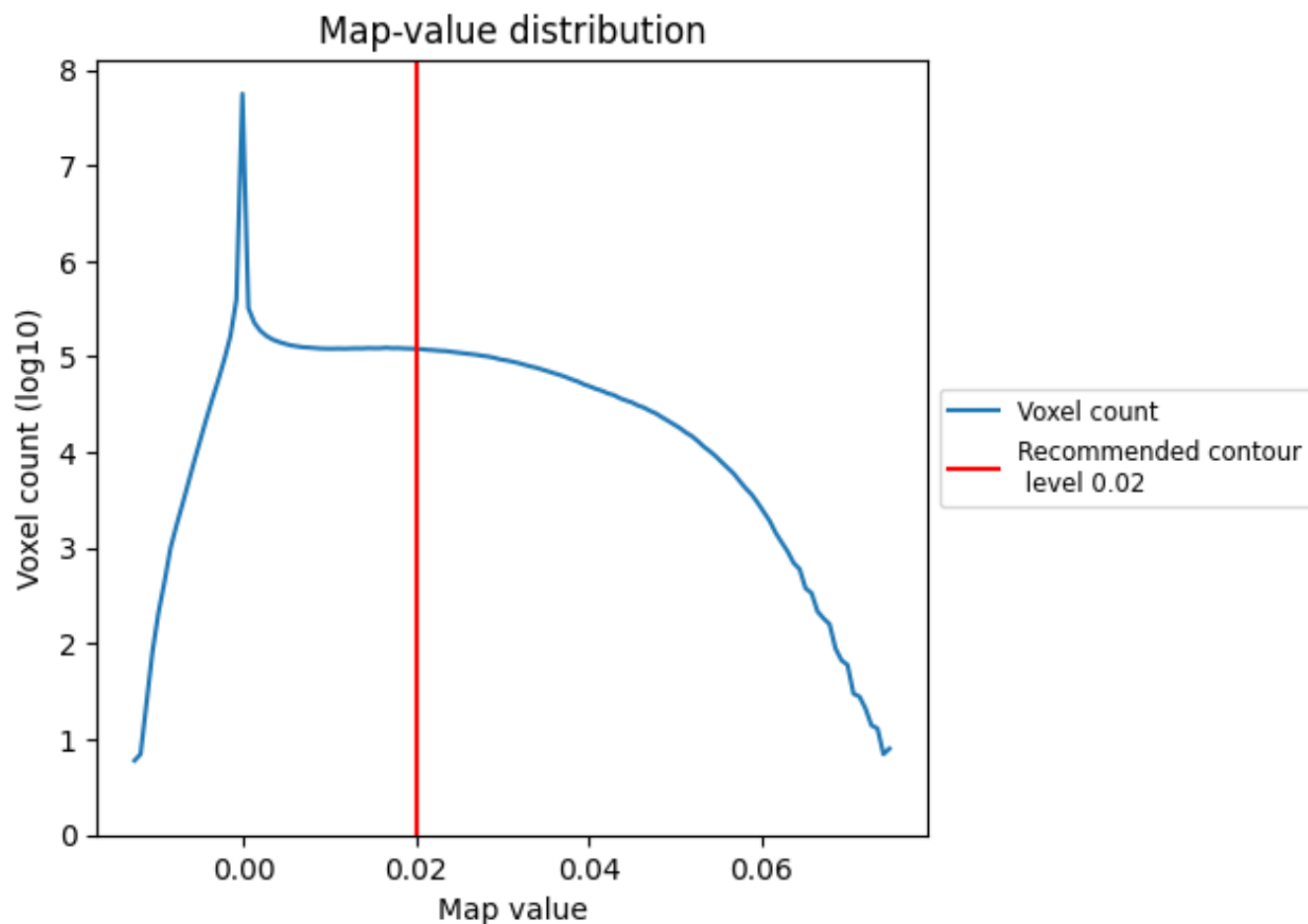


Z

7 Map analysis [i](#)

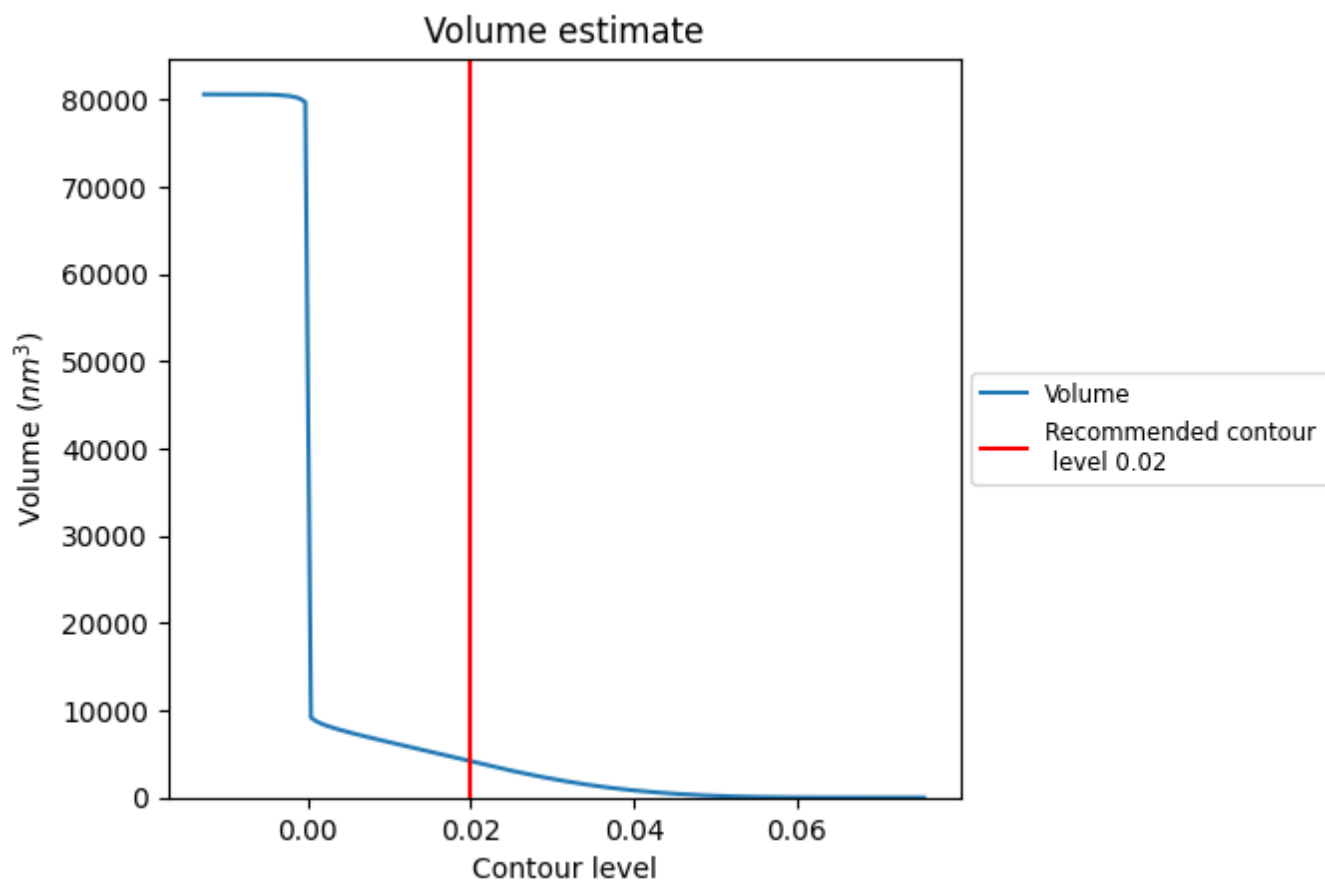
This section contains the results of statistical analysis of the map.

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.

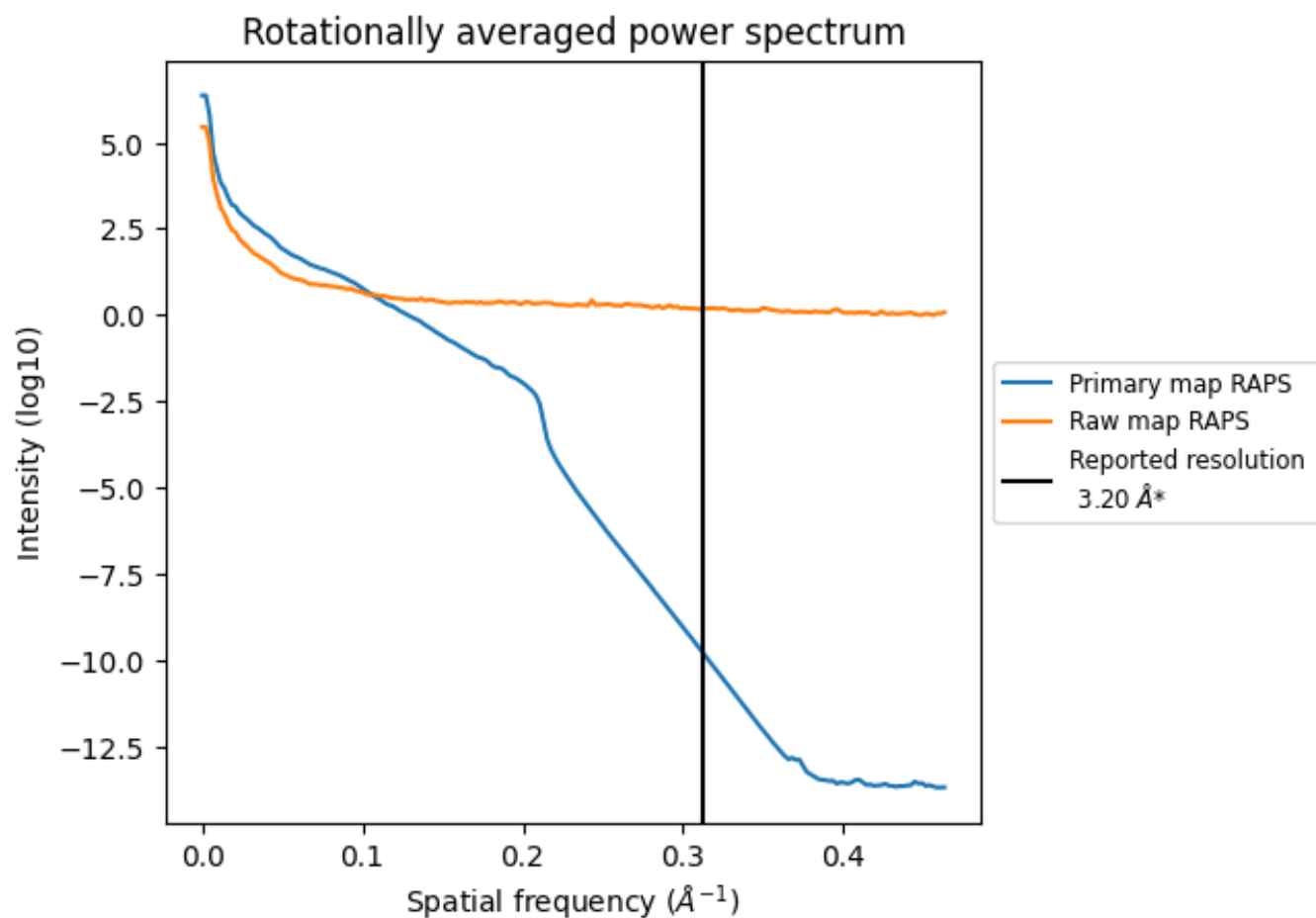
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4136 nm³; this corresponds to an approximate mass of 3736 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 ⓘ

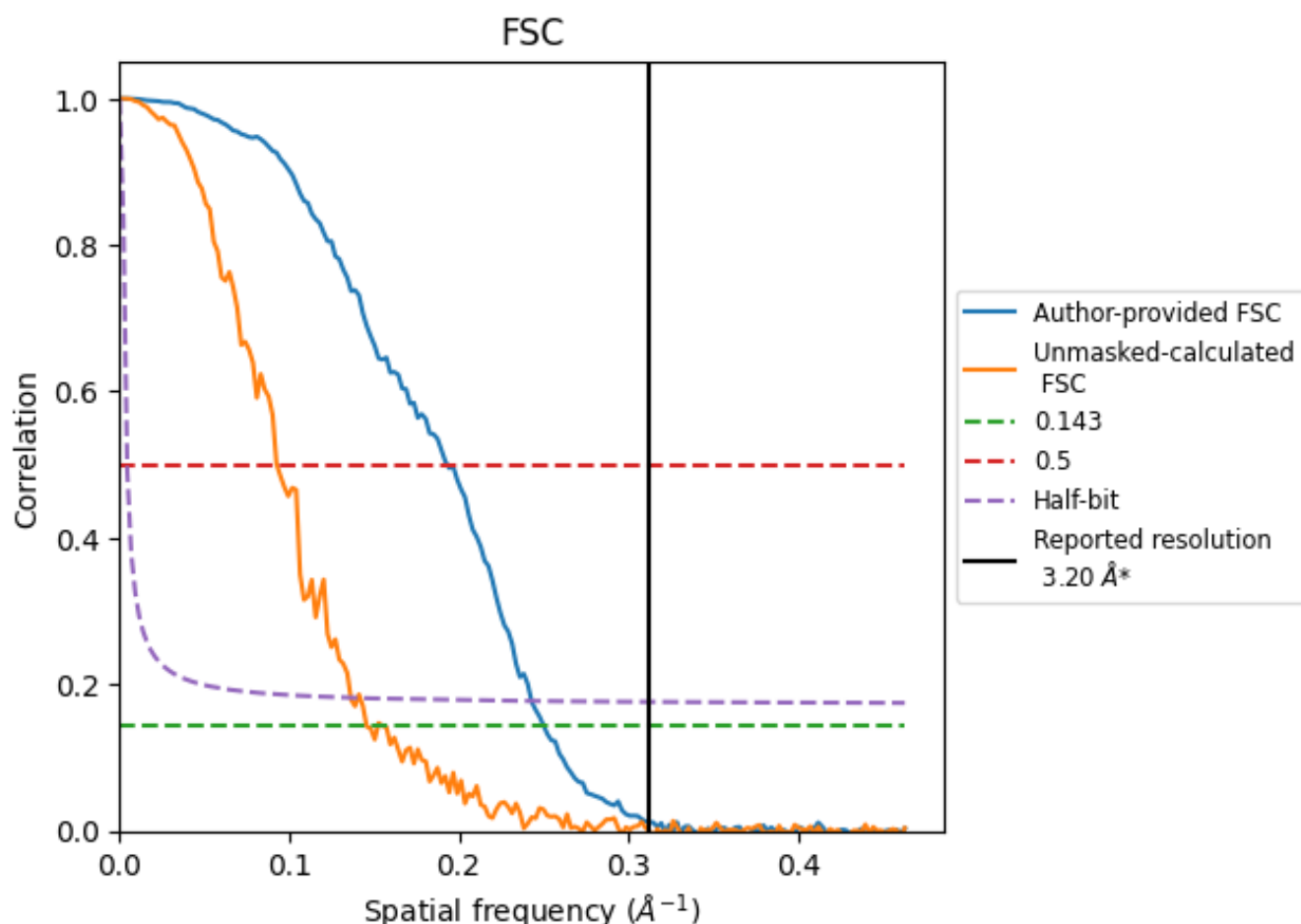


*Reported resolution corresponds to spatial frequency of 0.312 \AA^{-1}

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 0.312 \AA^{-1}

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	4.00	5.17	4.12
Unmasked-calculated*	6.86	10.79	7.33

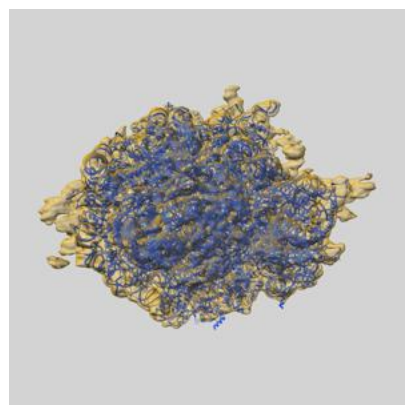
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.00 differs from the reported value 3.2 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.86 differs from the reported value 3.2 by more than 10 %

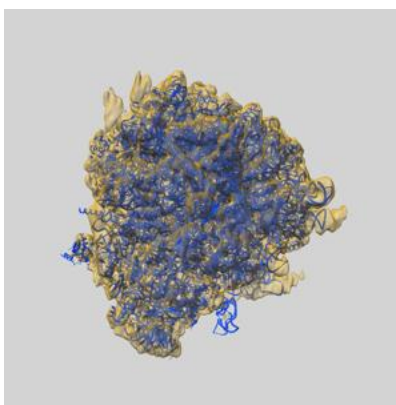
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7836 and PDB model 6D9J. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

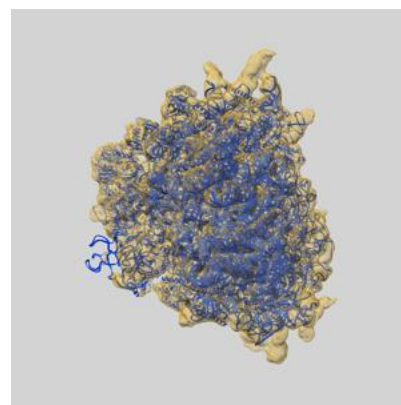
9.1 Map-model overlay [i](#)



X



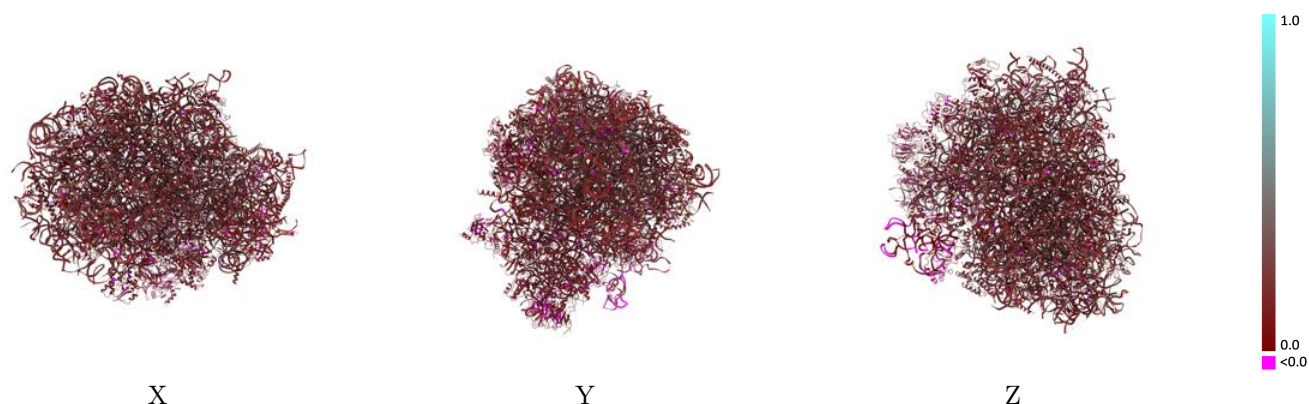
Y



Z

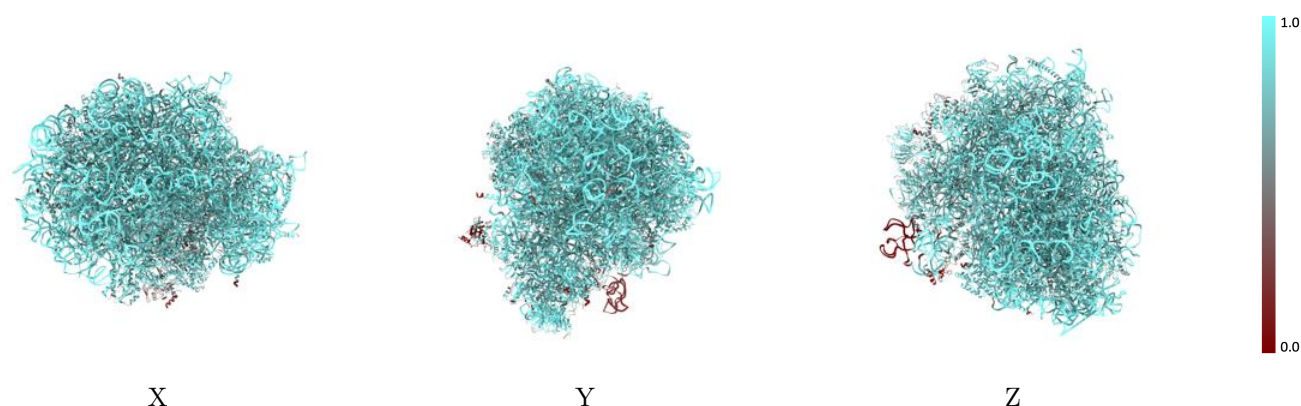
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



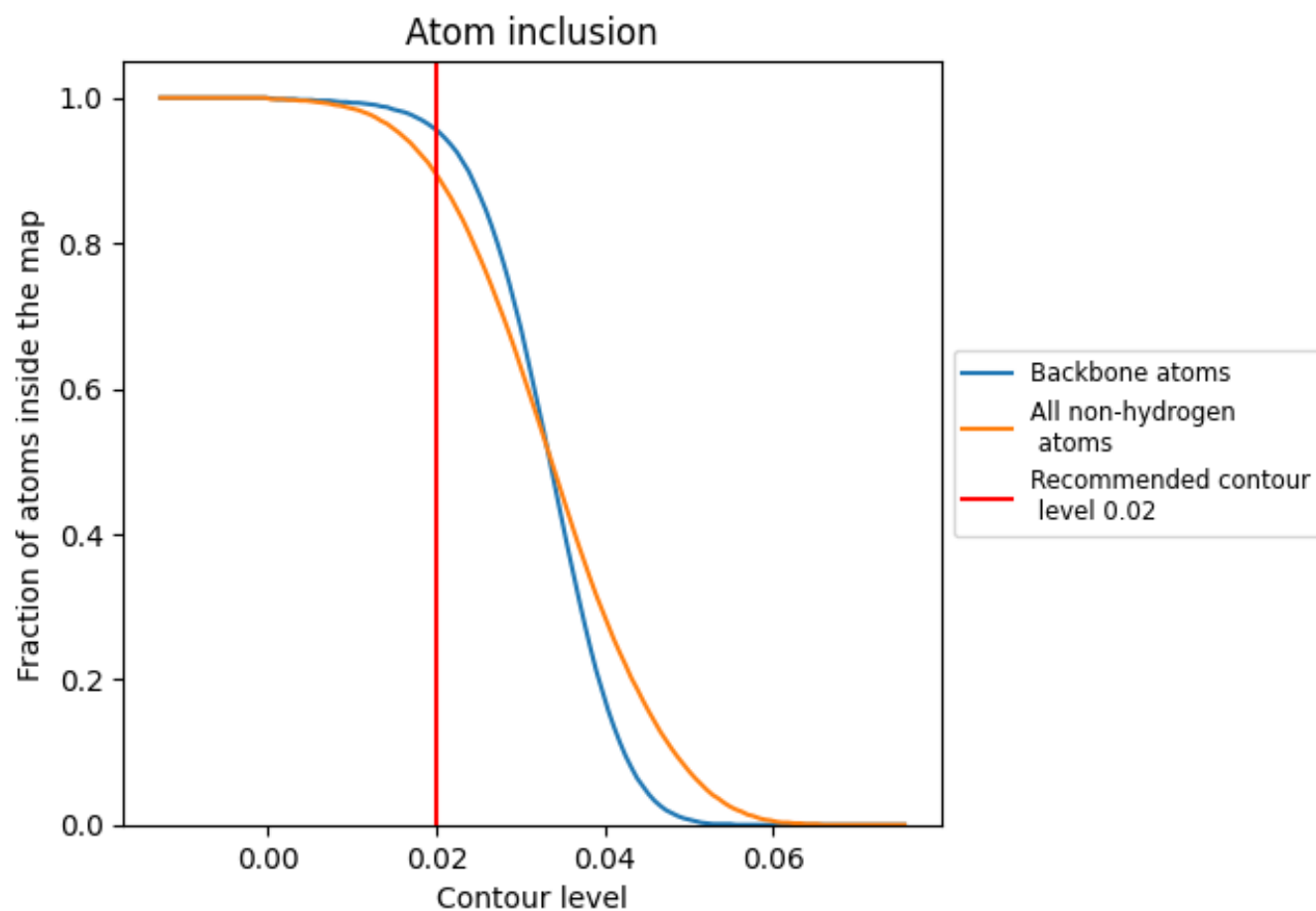
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 90% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8950	 0.1880
2	 0.9770	 0.2060
3	 0.7770	 0.1720
4	 0.5300	 0.0620
5	 0.9830	 0.2280
7	 0.9960	 0.2340
8	 0.9800	 0.2140
9	 0.7330	 0.1480
A	 0.8350	 0.1770
B	 0.8230	 0.1750
BB	 0.7880	 0.1530
C	 0.8350	 0.1610
CC	 0.8570	 0.1640
D	 0.8940	 0.1680
DD	 0.8000	 0.1630
E	 0.8520	 0.1690
EE	 0.7810	 0.1540
F	 0.7990	 0.1610
FF	 0.8580	 0.1500
G	 0.8270	 0.1690
GG	 0.8030	 0.1470
H	 0.8070	 0.1740
HH	 0.8570	 0.1460
I	 0.8200	 0.1700
II	 0.7960	 0.1670
J	 0.8450	 0.1570
JJ	 0.8490	 0.1540
K	 0.5690	 0.0670
KK	 0.8150	 0.1510
L	 0.8350	 0.1780
LL	 0.8610	 0.1400
M	 0.9020	 0.1660
MM	 0.8120	 0.1870
N	 0.8410	 0.1420
NN	 0.3300	 0.0790





















Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
O	 0.8030	 0.1710
OO	 0.8120	 0.1750
P	 0.8720	 0.1570
PP	 0.8460	 0.1530
Q	 0.8000	 0.1630
QQ	 0.8200	 0.1090
R	 0.8240	 0.1720
RR	 0.8210	 0.1110
S	 0.8490	 0.1750
SS	 0.5970	 0.0840
T	 0.8040	 0.1790
TT	 0.7460	 0.1390
U	 0.8410	 0.1780
UU	 0.8590	 0.1220
V	 0.7690	 0.1790
VV	 0.7840	 0.1220
W	 0.8390	 0.1680
WW	 0.7910	 0.1510
X	 0.8170	 0.1620
XX	 0.8150	 0.1770
Y	 0.8820	 0.1560
YY	 0.7550	 0.1600
Z	 0.8910	 0.1650
ZZ	 0.8790	 0.1410
a	 0.8810	 0.1550
aa	 0.7500	 0.1480
b	 0.8070	 0.1590
bb	 0.8250	 0.1560
c	 0.8670	 0.1750
cc	 0.8140	 0.1780
d	 0.8480	 0.1750
dd	 0.7400	 0.1430
e	 0.8280	 0.1830
ee	 0.9050	 0.1340
f	 0.8300	 0.1700
ff	 0.7840	 0.1470
g	 0.8480	 0.1460
gg	 0.5010	 0.0810
h	 0.8320	 0.1750
hh	 0.8710	 0.1260
i	 0.8130	 0.1780
j	 0.8720	 0.1320

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
k	 0.8260	 0.1720
l	 0.8340	 0.1610
m	 0.8070	 0.1570
n	 0.7660	 0.1230
o	 0.8750	 0.1730
p	 0.8200	 0.1710
r	 0.8450	 0.1740
s	 0.7700	 0.1380
t	 0.6520	 0.0890