



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:58 PM UTC

PDB ID : 4V5Z / pdb_00004v5z
EMDB ID : EMD-1480
Title : Structure of a mammalian 80S ribosome obtained by docking homology models of the RNA and proteins into an 8.7 Å cryo-EM map
Authors : Chandramouli, P.; Akey, C.W.
Deposited on : 2008-03-27
Resolution : 8.70 Å (reported)
Based on initial models : 1J5E, 1IGV, 1I6U, 1G1X, 1K7K, 1RQ6, 1FJG, 1VI6, 2AVY

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:

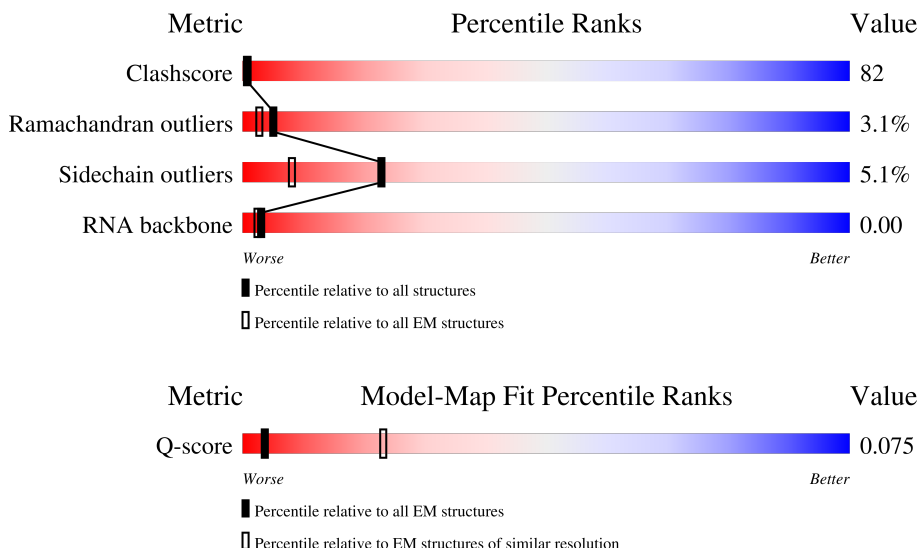
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 8.70 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	282 (8.20 - 9.20)

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	AA	1563	10% 88% 11%
2	AB	35	14% 91% 9%
3	AC	32	6% 91% 9%

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Mol	Chain	Length	Quality of chain
4	AD	42	
5	AE	32	
6	AF	31	
7	AG	14	
8	AH	41	
9	Aa	317	
10	Ab	295	
11	Ac	243	
12	Ad	209	
13	Ae	179	
14	Ag	204	
15	Ah	130	
16	Ai	146	
17	Aj	119	
18	Ak	151	
19	Al	143	
20	Am	152	
21	An	56	
22	Ao	89	
23	Aq	158	
24	As	145	
25	B1	123	
26	B0	2903	
27	BA	21	
28	BB	27	

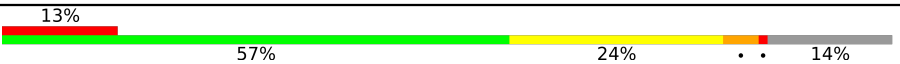
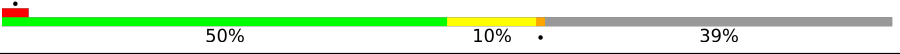
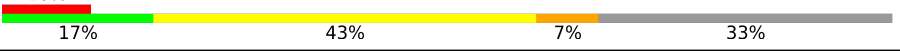
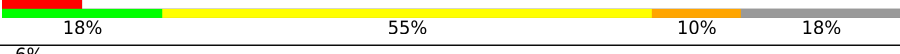
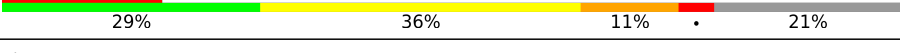
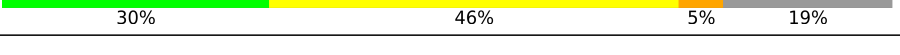
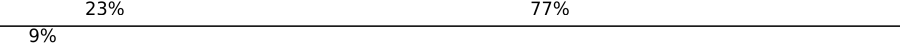
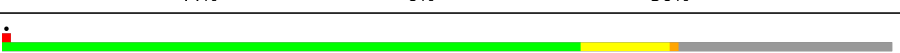
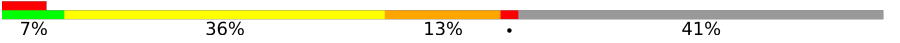
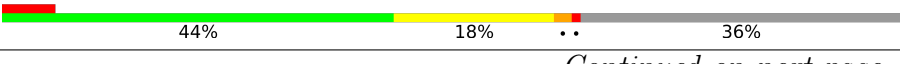
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Mol	Chain	Length	Quality of chain
29	BC	17	12% 100%
30	BD	16	12% 100%
31	BE	54	13% 100%
32	BF	120	8% 100%
33	BG	48	23% 100%
34	BH	25	24% 92% 8%
35	BI	72	10% 100%
36	BJ	30	17% 100%
37	BK	26	46% 96% .
38	BL	20	100%
39	BM	19	16% 89% 11%
40	BN	78	35% 100%
41	BO	20	5% 100%
42	BP	15	27% 100%
43	BQ	30	13% 100%
44	BR	30	17% 100%
45	BS	38	11% 100%
46	BT	30	13% 100%
47	BU	16	12% 100%
48	BV	22	27% 95% 5%
49	BW	16	44% 88% 12%
50	BX	113	10% 100%
51	BY	115	25% 92% 8%
52	BZ	72	14% 99% .
53	Ba	257	10% 83% 11% . 5%

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Mol	Chain	Length	Quality of chain
54	Bb	403	
55	Bc	421	
56	Bd	178	
57	Be	192	
58	Bf	266	
59	Bg	317	
60	Bh	214	
61	Bi	165	
62	Bj	203	
63	Bk	140	
64	Bl	148	
65	Bm	204	
66	Bn	297	
67	Bo	188	
68	Bp	196	
69	B7	13	
70	Bq	160	
71	Br	184	
72	Bs	156	
73	Bt	145	
74	Bu	157	
75	Bv	123	
76	B8	10	
77	Bw	270	
78	Bx	125	

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Mol	Chain	Length	Quality of chain
79	By	135	
80	B9	58	
81	Bz	92	
82	B2	97	
83	B3	51	
84	B4	106	
85	B5	212	
86	B6	115	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 55531 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 RNA chain called 18S Ribosomal RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	AA	1391	Total	P	0	1391
			1391	1391		

- Molecule 2 is a RNA chain called RNA Expansion segment ES3.

Mol	Chain	Residues	Atoms		AltConf	Trace
2	AB	32	Total	P	0	32
			32	32		

- Molecule 3 is a RNA chain called RNA Expansion segment ES4.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	AC	29	Total	P	0	29
			29	29		

- Molecule 4 is a RNA chain called RNA Expansion segment ES6 part I.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	AD	42	Total	P	0	42
			42	42		

- Molecule 5 is a RNA chain called RNA Expansion segment ES6 part II.

Mol	Chain	Residues	Atoms		AltConf	Trace
5	AE	32	Total	P	0	32
			32	32		

- Molecule 6 is a RNA chain called RNA Expansion segment ES9.

Mol	Chain	Residues	Atoms		AltConf	Trace
6	AF	31	Total	P	0	31
			31	31		

- Molecule 7 is a RNA chain called RNA helix.

Mol	Chain	Residues	Atoms		AltConf	Trace
7	AG	14	Total	P	0	14
			14	14		

- Molecule 8 is a RNA chain called RNA helix.

Mol	Chain	Residues	Atoms		AltConf	Trace
8	AH	41	Total	P	0	41
			41	41		

- Molecule 9 is a protein called 40S Ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Aa	306	Total	C	N	O	S	0	0
			2380	1501	414	453	12		

- Molecule 10 is a protein called 40S Ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Ab	192	Total	C	N	O	S	0	0
			1521	972	271	271	7		

- Molecule 11 is a protein called 40S Ribosomal protein S3e.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Ac	192	Total	C	N	O	S	0	0
			1498	953	274	264	7		

- Molecule 12 is a protein called 40S Ribosomal protein S9e.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	Ad	103	Total	C	N	O	0	0
			845	527	172	146		

- Molecule 13 is a protein called 40S Ribosomal protein S2e.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Ae	148	Total	C	N	O	S	0	0
			1096	697	202	191	6		

- Molecule 14 is a protein called 40S Ribosomal protein S5e.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Ag	163	Total	C	N	O	S	0	0
			1277	795	241	234	7		

- Molecule 15 is a protein called 40S Ribosomal protein S15ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Ah	127	Total	C	N	O	S	0	0
			1016	648	188	174	6		

- Molecule 16 is a protein called 40S Ribosomal protein S16e.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Ai	138	Total	C	N	O	S	0	0
			1102	699	209	191	3		

- Molecule 17 is a protein called 40S Ribosomal protein S20e.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Aj	97	Total	C	N	O	S	0	0
			772	483	147	138	4		

- Molecule 18 is a protein called 40S Ribosomal protein S14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Ak	125	Total	C	N	O	S	0	0
			935	572	181	176	6		

- Molecule 19 is a protein called 40S Ribosomal protein S23e.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Al	115	Total	C	N	O	S	0	0
			871	557	162	150	2		

- Molecule 20 is a protein called 40S Ribosomal protein S18e.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Am	140	Total	C	N	O	S	0	0
			1150	717	236	196	1		

- Molecule 21 is a protein called 40S Ribosomal protein S29e.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	An	49	Total	C	N	O	S	0	0
			410	258	84	63	5		

- Molecule 22 is a protein called 40S Ribosomal protein S13e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ao	85	Total	C	N	O	S	0	0
			710	445	141	122	2		

- Molecule 23 is a protein called 40S Ribosomal protein S11e.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Aq	76	Total	C	N	O	S	0	0
			629	401	121	102	5		

- Molecule 24 is a protein called 40S Ribosomal protein S15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	As	88	Total	C	N	O	S	0	0
			721	459	139	118	5		

- Molecule 25 is a RNA chain called 5.8S Ribosomal RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
25	B1	97	Total	P	0	97
			97	97		

- Molecule 26 is a RNA chain called 28S Ribosomal RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
26	B0	2407	Total	P	0	2407
			2407	2407		

- Molecule 27 is a RNA chain called RNA Expansion segment ES3.

Mol	Chain	Residues	Atoms		AltConf	Trace
27	BA	21	Total	P	0	21
			21	21		

- Molecule 28 is a RNA chain called RNA Expansion segment ES4.

Mol	Chain	Residues	Atoms		AltConf	Trace
28	BB	27	Total	P	0	27
			27	27		

- Molecule 29 is a RNA chain called RNA Expansion segment ES5.

Mol	Chain	Residues	Atoms		AltConf	Trace
29	BC	17	Total	P	0	17
			17	17		

- Molecule 30 is a RNA chain called RNA Expansion segment ES7 part I.

Mol	Chain	Residues	Atoms		AltConf	Trace
30	BD	16	Total	P	0	16
			16	16		

- Molecule 31 is a RNA chain called RNA Expansion segment ES7 part II.

Mol	Chain	Residues	Atoms		AltConf	Trace
31	BE	54	Total	P	0	54
			54	54		

- Molecule 32 is a RNA chain called RNA Expansion segment ES7 part III.

Mol	Chain	Residues	Atoms		AltConf	Trace
32	BF	120	Total	P	0	120
			120	120		

- Molecule 33 is a RNA chain called RNA Expansion segment ES9.

Mol	Chain	Residues	Atoms		AltConf	Trace
33	BG	48	Total	P	0	48
			48	48		

- Molecule 34 is a RNA chain called RNA Expansion segment ES12.

Mol	Chain	Residues	Atoms		AltConf	Trace
34	BH	25	Total	P	0	25
			25	25		

- Molecule 35 is a RNA chain called RNA Expansion segment ES15 part I.

Mol	Chain	Residues	Atoms		AltConf	Trace
35	BI	72	Total	P	0	72
			72	72		

- Molecule 36 is a RNA chain called RNA Expansion segment ES15 part II.

Mol	Chain	Residues	Atoms		AltConf	Trace
36	BJ	30	Total	P	0	30
			30	30		

- Molecule 37 is a RNA chain called RNA Expansion segment ES19.

Mol	Chain	Residues	Atoms		AltConf	Trace
37	BK	25	Total	P	0	25
			25	25		

- Molecule 38 is a RNA chain called RNA Expansion segment ES20.

Mol	Chain	Residues	Atoms		AltConf	Trace
38	BL	20	Total	P	0	20
			20	20		

- Molecule 39 is a RNA chain called RNA Expansion segment ES24.

Mol	Chain	Residues	Atoms		AltConf	Trace
39	BM	19	Total	P	0	19
			19	19		

- Molecule 40 is a RNA chain called RNA Expansion segment ES27.

Mol	Chain	Residues	Atoms		AltConf	Trace
40	BN	78	Total	P	0	78
			78	78		

- Molecule 41 is a RNA chain called RNA Expansion segment ES30.

Mol	Chain	Residues	Atoms		AltConf	Trace
41	BO	20	Total	P	0	20
			20	20		

- Molecule 42 is a RNA chain called RNA Expansion segment ES31 part I.

Mol	Chain	Residues	Atoms		AltConf	Trace
42	BP	15	Total	P	0	15
			15	15		

- Molecule 43 is a RNA chain called RNA Expansion segment ES31 part II.

Mol	Chain	Residues	Atoms		AltConf	Trace
43	BQ	30	Total	P	0	30
			30	30		

- Molecule 44 is a RNA chain called RNA Expansion segment ES39 part I.

Mol	Chain	Residues	Atoms		AltConf	Trace
44	BR	30	Total	P	0	30
			30	30		

- Molecule 45 is a RNA chain called RNA Expansion segment ES39 part II.

Mol	Chain	Residues	Atoms		AltConf	Trace
45	BS	38	Total	P	0	38
			38	38		

- Molecule 46 is a RNA chain called RNA Expansion segment ES39 part III.

Mol	Chain	Residues	Atoms		AltConf	Trace
46	BT	30	Total	P	0	30
			30	30		

- Molecule 47 is a RNA chain called RNA Expansion segment ES41.

Mol	Chain	Residues	Atoms		AltConf	Trace
47	BU	16	Total	P	0	16
			16	16		

- Molecule 48 is a RNA chain called RNA Expansion segment ES9 part2.

Mol	Chain	Residues	Atoms		AltConf	Trace
48	BV	22	Total	P	0	22
			22	22		

- Molecule 49 is a RNA chain called RNA Expansion segment ES10.

Mol	Chain	Residues	Atoms		AltConf	Trace
49	BW	16	Total	P	0	16
			16	16		

- Molecule 50 is a RNA chain called RNA helices.

Mol	Chain	Residues	Atoms		AltConf	Trace
50	BX	113	Total	P	0	113
			113	113		

- Molecule 51 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
51	BY	115	Total	P	0	115
			115	115		

- Molecule 52 is a RNA chain called E site t-RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
52	BZ	72	Total	P	0	72
			72	72		

- Molecule 53 is a protein called 60S Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ba	244	Total	C	N	O	S	0	0
			1867	1172	382	307	6		

- Molecule 54 is a protein called 60S Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Bb	345	Total	C	N	O	S	0	0
			2765	1758	521	474	12		

- Molecule 55 is a protein called 60S Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Bc	257	Total	C	N	O	S	0	0
			2035	1282	399	344	10		

- Molecule 56 is a protein called 60S Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Bd	165	Total	C	N	O	S	0	0
			1325	837	248	234	6		

- Molecule 57 is a protein called 60S Ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Be	175	Total	C	N	O	S	0	0
			1407	889	264	249	5		

- Molecule 58 is a protein called 60S Ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Bf	120	Total	C	N	O	S	0	0
			920	584	172	160	4		

- Molecule 59 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	Bg	48	Total	C	N	O	0	0
			327	206	52	69		

- Molecule 60 is a protein called 60S Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Bh	166	Total	C	N	O	S	0	0
			1331	841	260	218	12		

- Molecule 61 is a protein called 60S Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Bi	74	Total	C	N	O	S	0	0
			573	355	110	106	2		

- Molecule 62 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Bj	136	Total	C	N	O	S	0	0
			1095	707	216	168	4		

- Molecule 63 is a protein called 60S Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bk	124	Total	C	N	O	S	0	0
			927	586	173	163	5		

- Molecule 64 is a protein called 60S Ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Bl	122	Total	C	N	O	S	0	0
			951	601	193	154	3		

- Molecule 65 is a protein called 60S Ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Bm	175	Total	C	N	O	S	0	0
			1454	921	298	231	4		

- Molecule 66 is a protein called 60S Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bn	236	Total	C	N	O	S	0	0
			1912	1209	340	350	13		

- Molecule 67 is a protein called 60S Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bo	120	Total	C	N	O	S	0	0
			956	607	185	160	4		

- Molecule 68 is a protein called 60S Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Bp	159	Total	C	N	O	S	0	0
			1329	817	285	220	7		

- Molecule 69 is a protein called 60S Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	B7	13	Total	C	N	O	S	0	0
			129	80	34	14	1		

- Molecule 70 is a protein called 60S Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bq	96	Total	C	N	O	S	0	0
			773	492	155	121	5		

- Molecule 71 is a protein called 60S Ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Br	150	Total	C	N	O	S	0	0
			1217	760	237	211	9		

- Molecule 72 is a protein called 60S Ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bs	78	Total	C	N	O	S	0	0
			622	401	105	115	1		

- Molecule 73 is a protein called 60S Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bt	110	Total	C	N	O	S	0	0
			916	570	188	156	2		

- Molecule 74 is a protein called 60S Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bu	53	Total	C	N	O	S	0	0
			443	284	83	74	2		

- Molecule 75 is a protein called 60S Ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	Bv	61	Total	C	N	O	0	0
			477	300	93	84		

- Molecule 76 is a protein called 60S Ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	B8	10	Total	C	N	O	0	0
			78	48	15	15		

- Molecule 77 is a protein called 60S Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Bw	158	Total	C	N	O	S	0	0
			1281	823	240	213	5		

- Molecule 78 is a protein called 60S Ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bx	80	Total	C	N	O	S	0	0
			670	418	139	111	2		

- Molecule 79 is a protein called 60S Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	By	60	Total	C	N	O	S	0	0
			514	324	114	75	1		

- Molecule 80 is a protein called 60S Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	B9	58	Total	C	N	O	S	0	0
			460	290	87	79	4		

- Molecule 81 is a protein called 60S Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bz	72	Total	C	N	O	S	0	0
			548	345	102	94	7		

- Molecule 82 is a protein called 60S Ribosomal protein L37e.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	B2	51	Total	C	N	O	S	0	0
			407	250	87	66	4		

- Molecule 83 is a protein called 60S Ribosomal protein L39e.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	B3	48	Total	C	N	O	S	0	0
			429	272	96	60	1		

- Molecule 84 is a protein called 60S Ribosomal protein L44e.

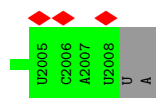
Mol	Chain	Residues	Atoms					AltConf	Trace
84	B4	92	Total	C	N	O	S	0	0
			760	478	154	122	6		

- Molecule 85 is a protein called 60S Ribosomal protein L10a.

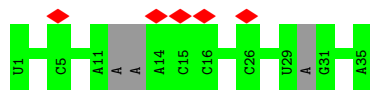
Mol	Chain	Residues	Atoms					AltConf	Trace
85	B5	210	Total	C	N	O	S	0	0
			1621	990	278	347	6		

- Molecule 86 is a protein called 60S Ribosomal protein L30e.

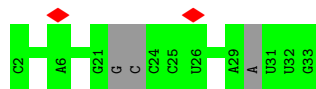
Mol	Chain	Residues	Atoms					AltConf	Trace
86	B6	113	Total	C	N	O	S	0	0
			874	552	154	161	7		



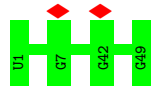
- Molecule 2: RNA Expansion segment ES3



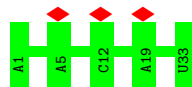
- Molecule 3: RNA Expansion segment ES4



- Molecule 4: RNA Expansion segment ES6 part I



- Molecule 5: RNA Expansion segment ES6 part II



- Molecule 6: RNA Expansion segment ES9

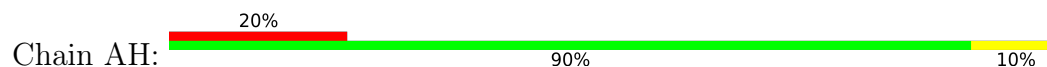


There are no outlier residues recorded for this chain.

- Molecule 7: RNA helix

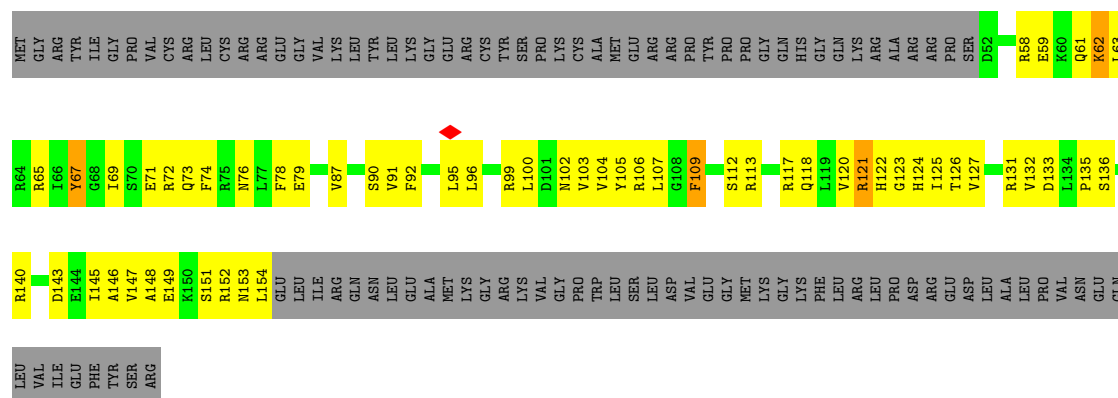


- Molecule 8: RNA helix



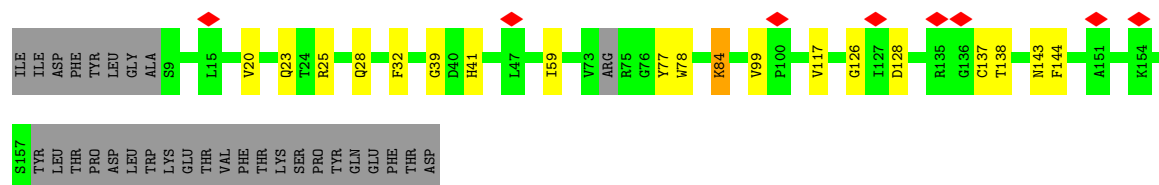
- Molecule 12: 40S Ribosomal protein S9e

Chain Ad:  22% 26% 51%



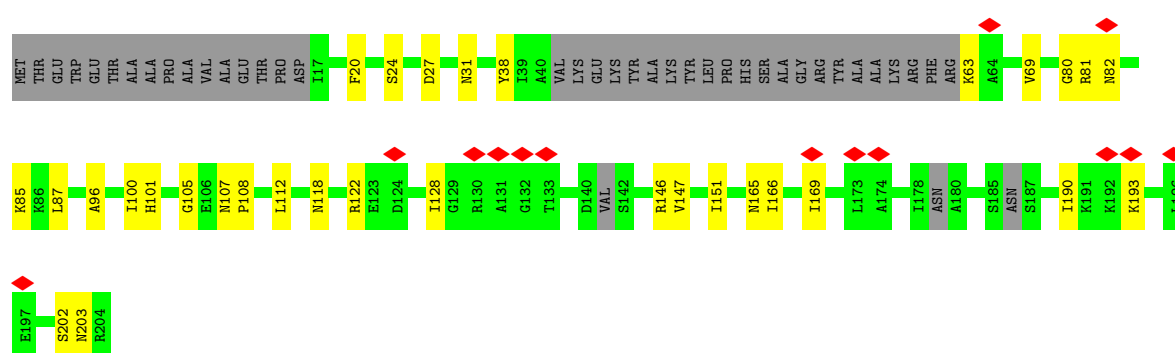
- Molecule 13: 40S Ribosomal protein S2e

Chain Ae:  72% 10% 17%



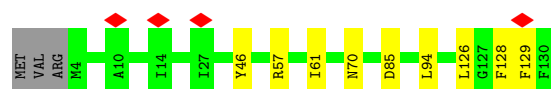
- Molecule 14: 40S Ribosomal protein S5e

Chain Ag:  7% 64% 16% 20%



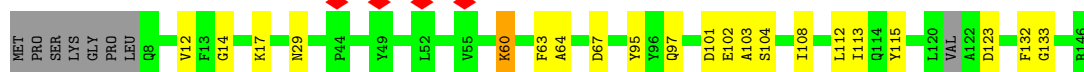
- Molecule 15: 40S Ribosomal protein S15ae

Chain Ah:  91% 7%



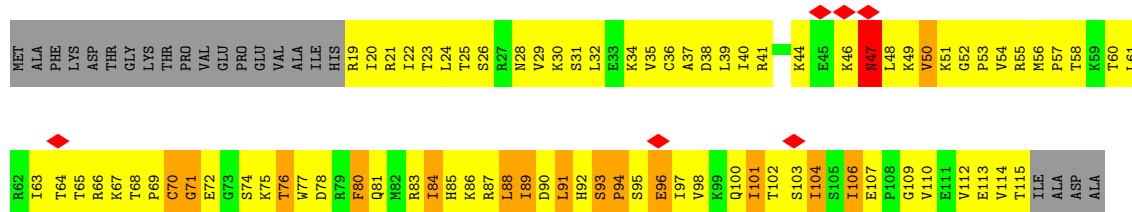
- Molecule 16: 40S Ribosomal protein S16e

Chain Ai:  80% 14% 5%



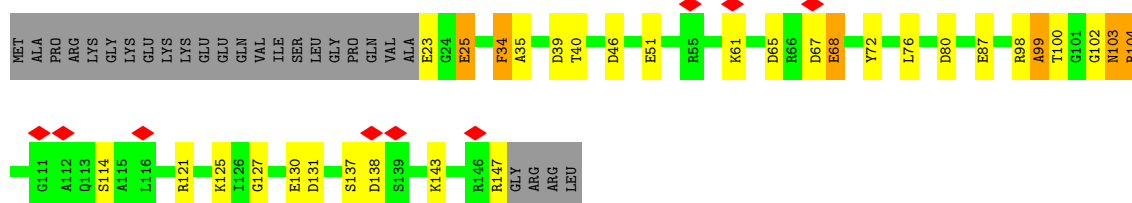
- Molecule 17: 40S Ribosomal protein S20e

Chain Aj:  5% 12% 56% 13% 18%



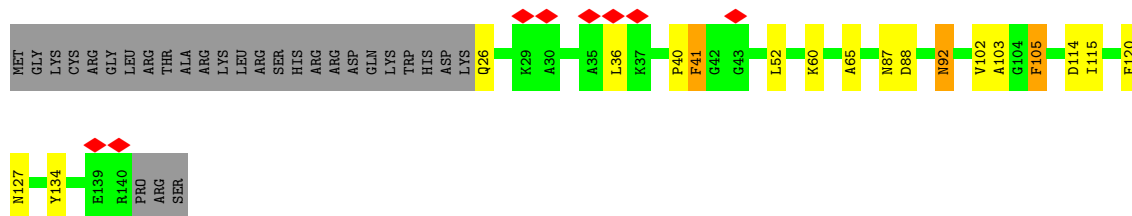
- Molecule 18: 40S Ribosomal protein S14e

Chain Ak:  6% 62% 17% 17%



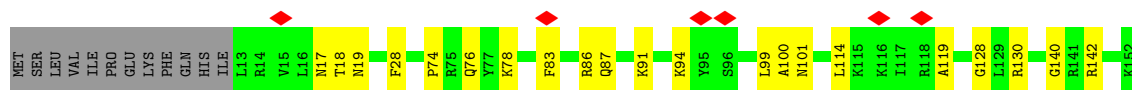
- Molecule 19: 40S Ribosomal protein S23e

Chain Al:  6% 68% 10% 20%

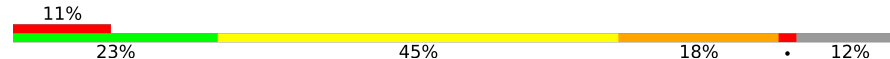


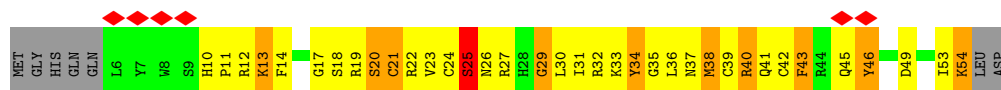
- Molecule 20: 40S Ribosomal protein S18e

Chain Am:  78% 14% 8%

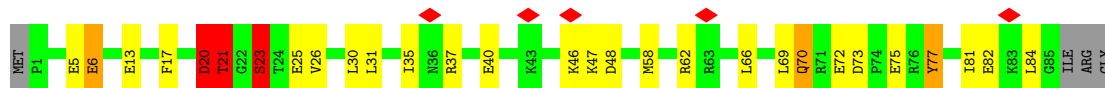


- Molecule 21: 40S Ribosomal protein S29e

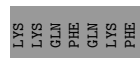
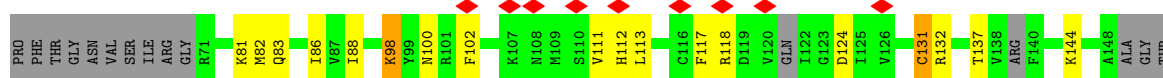
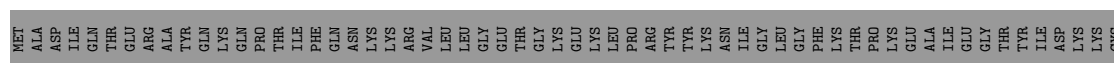
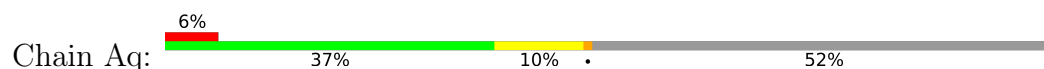
Chain An:  11% 23% 45% 18% 12%



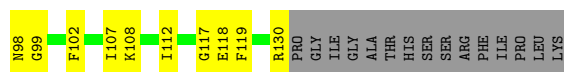
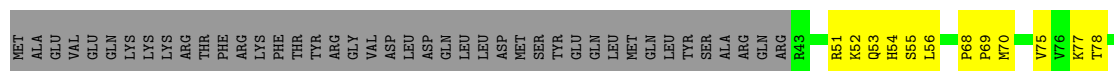
- Molecule 22: 40S Ribosomal protein S13e



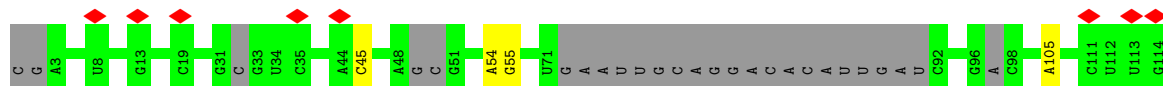
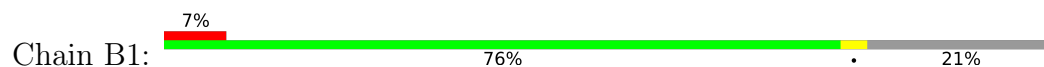
- Molecule 23: 40S Ribosomal protein S11e



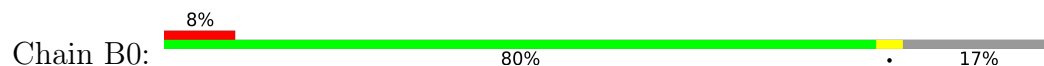
- Molecule 24: 40S Ribosomal protein S15e



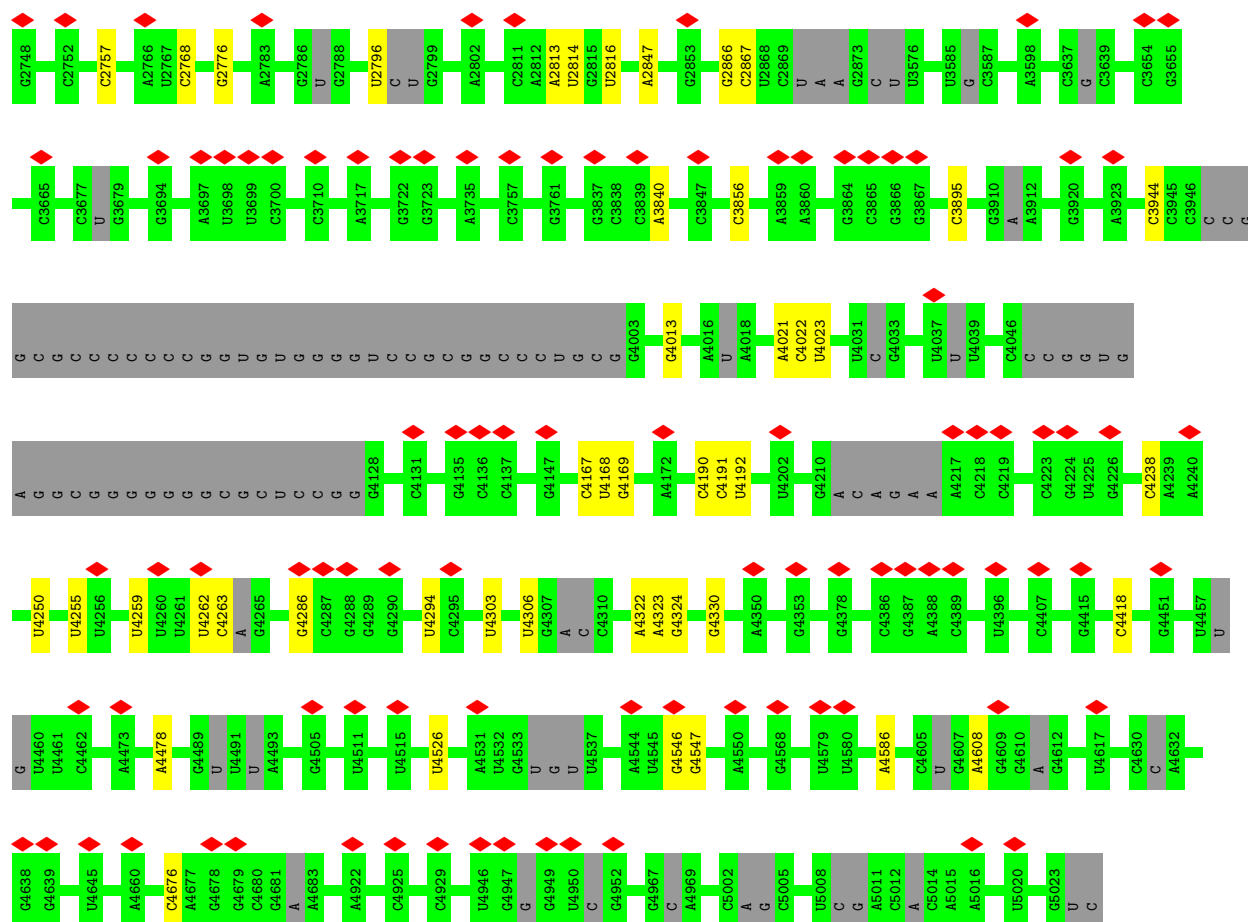
- Molecule 25: 5.8S Ribosomal RNA



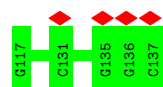
- Molecule 26: 28S Ribosomal RNA







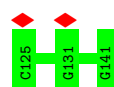
● Molecule 27: RNA Expansion segment ES3



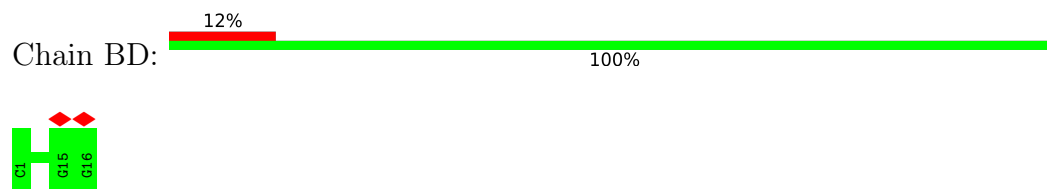
● Molecule 28: RNA Expansion segment ES4



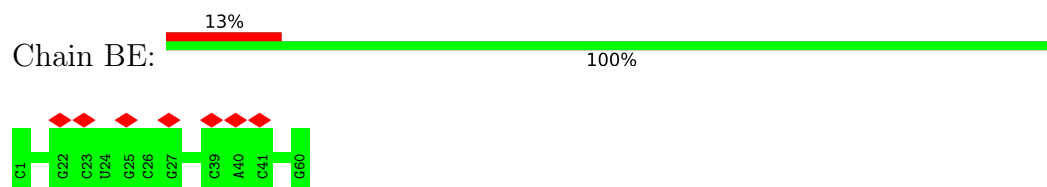
● Molecule 29: RNA Expansion segment ES5



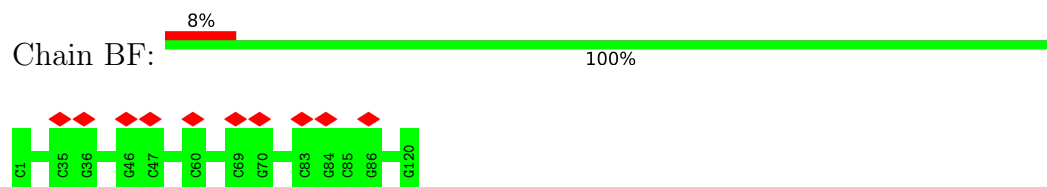
- Molecule 30: RNA Expansion segment ES7 part I



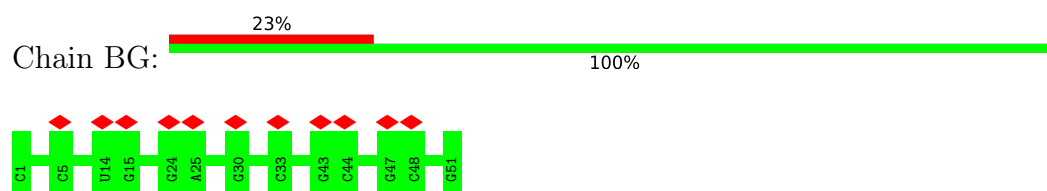
- Molecule 31: RNA Expansion segment ES7 part II



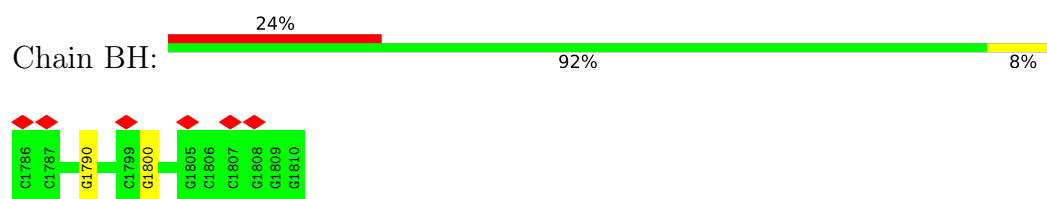
- Molecule 32: RNA Expansion segment ES7 part III



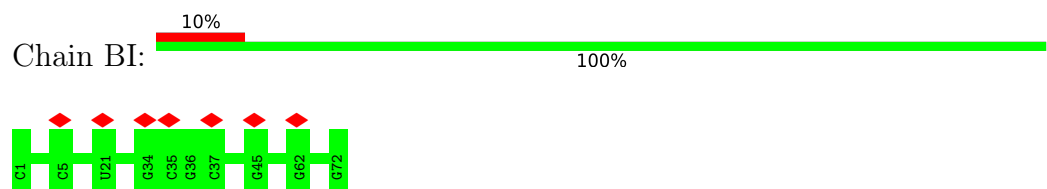
- Molecule 33: RNA Expansion segment ES9



- Molecule 34: RNA Expansion segment ES12

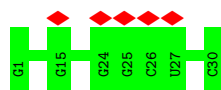


- Molecule 35: RNA Expansion segment ES15 part I

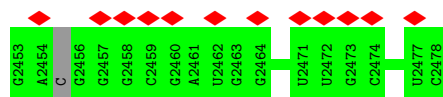


- Molecule 36: RNA Expansion segment ES15 part II





- Molecule 37: RNA Expansion segment ES19

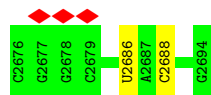


- Molecule 38: RNA Expansion segment ES20

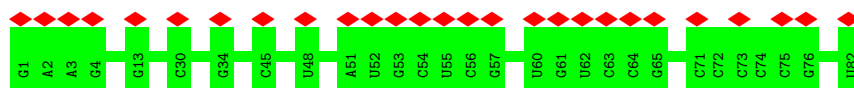


There are no outlier residues recorded for this chain.

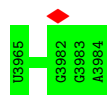
- Molecule 39: RNA Expansion segment ES24



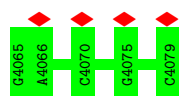
- Molecule 40: RNA Expansion segment ES27



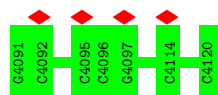
- Molecule 41: RNA Expansion segment ES30



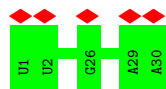
- Molecule 42: RNA Expansion segment ES31 part I



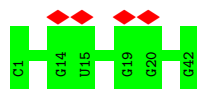
- Molecule 43: RNA Expansion segment ES31 part II



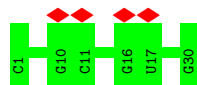
- Molecule 44: RNA Expansion segment ES39 part I



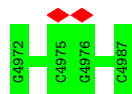
- Molecule 45: RNA Expansion segment ES39 part II



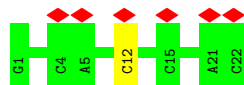
- Molecule 46: RNA Expansion segment ES39 part III



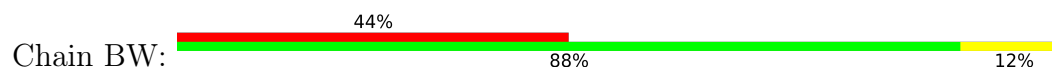
- Molecule 47: RNA Expansion segment ES41

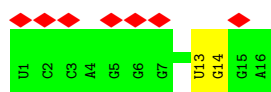


- Molecule 48: RNA Expansion segment ES9 part2

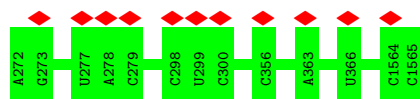


- Molecule 49: RNA Expansion segment ES10

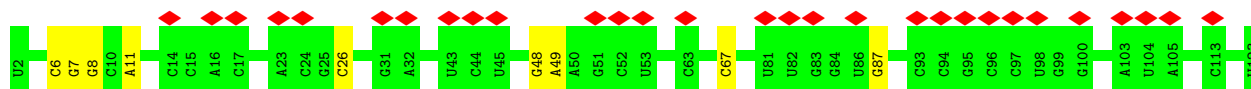




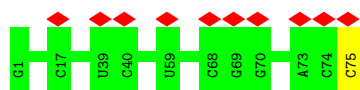
- Molecule 50: RNA helices



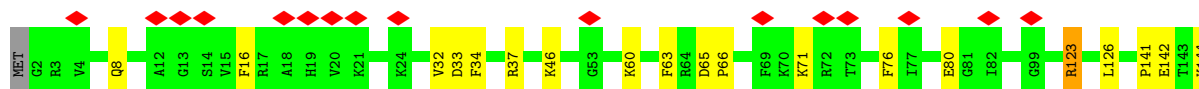
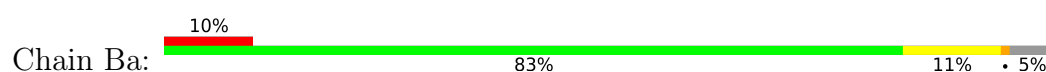
- Molecule 51: 5S Ribosomal RNA



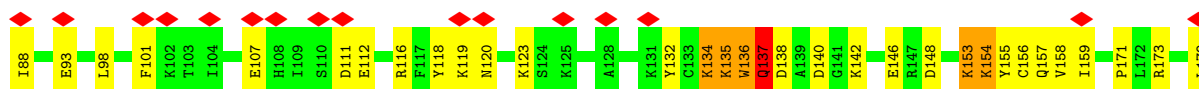
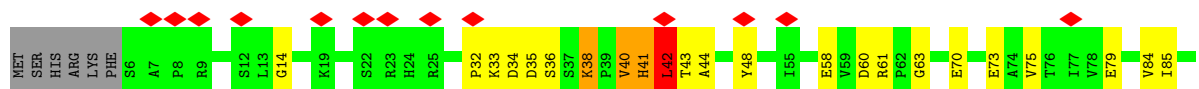
- Molecule 52: E site t-RNA



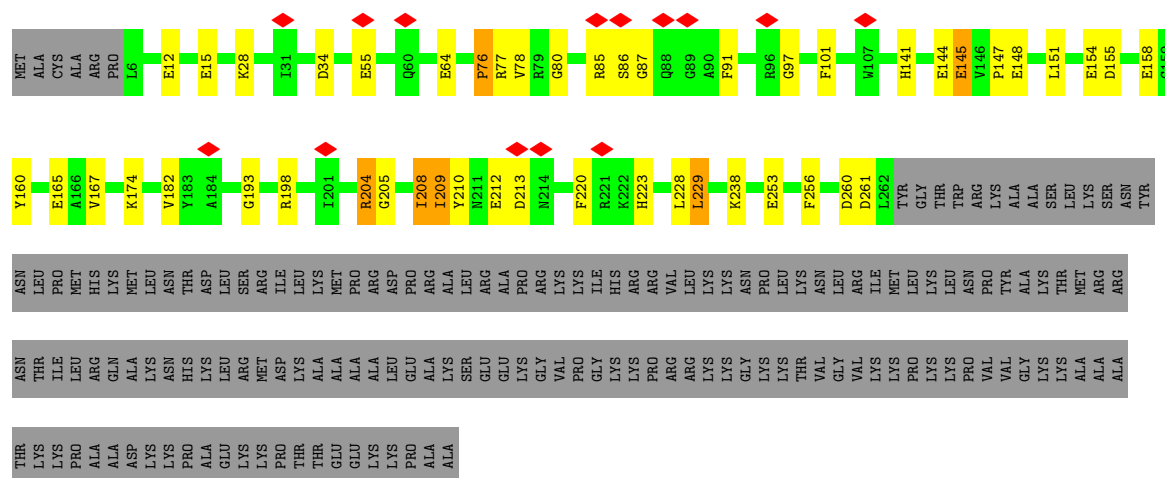
- Molecule 53: 60S Ribosomal protein L8



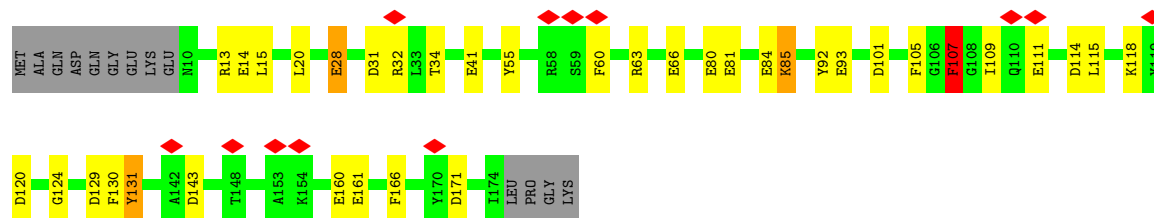
- Molecule 54: 60S Ribosomal protein L3



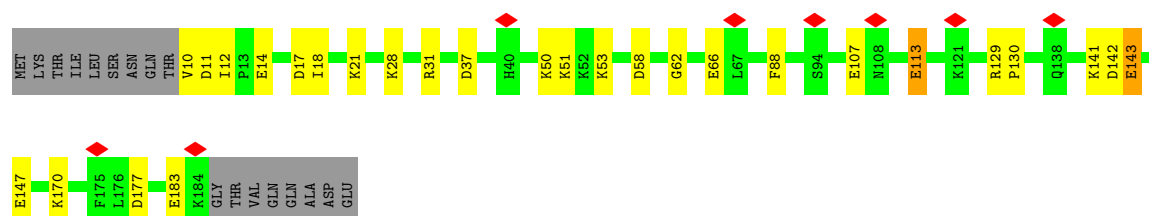
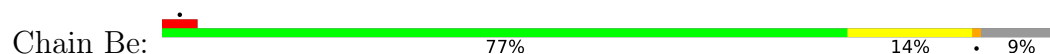
- Molecule 55: 60S Ribosomal protein L4



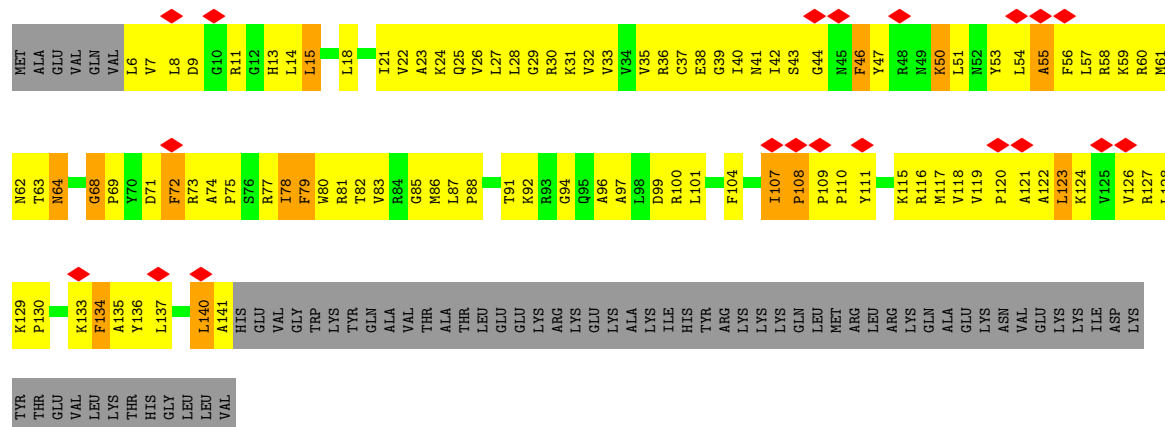
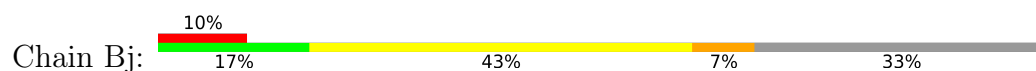
- Molecule 56: 60S Ribosomal protein L11



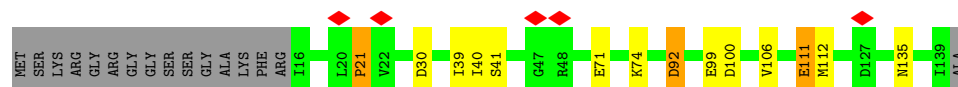
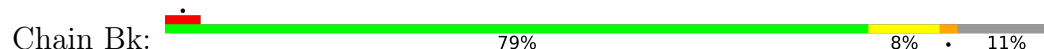
- Molecule 57: 60S Ribosomal protein L9



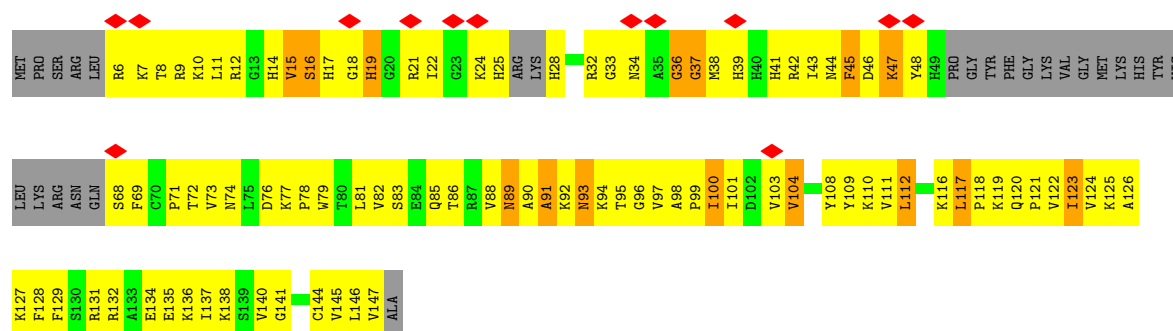
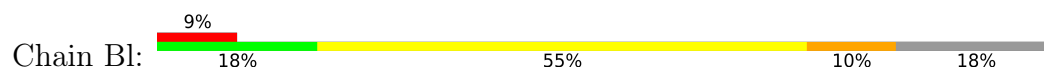
- Molecule 62: 60S ribosomal protein L13a



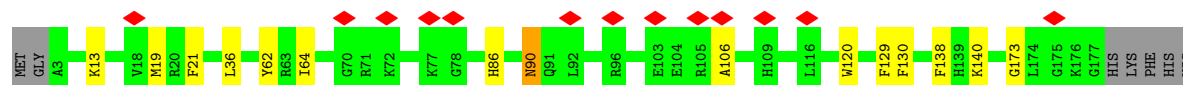
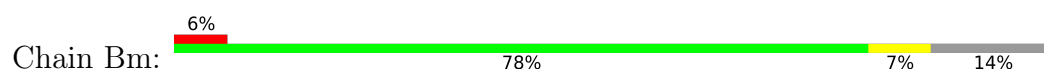
- Molecule 63: 60S Ribosomal protein L23



- Molecule 64: 60S Ribosomal protein L27a

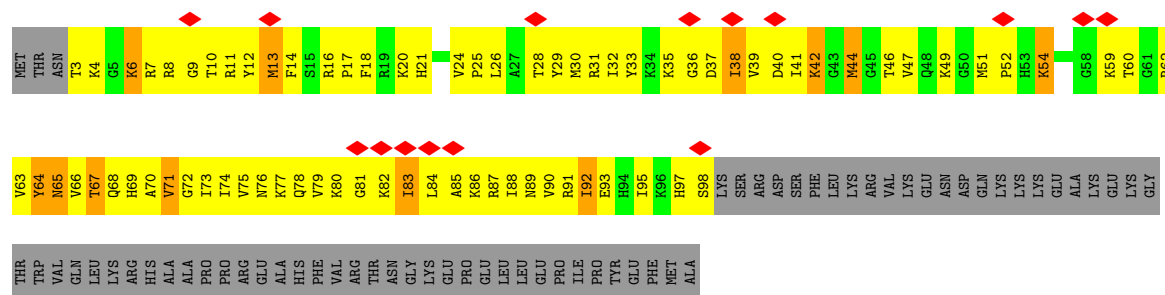


- Molecule 65: 60S Ribosomal protein L15e



R192	M193	R194	I195	L196	R197	R198	L199	L200	R201	R202	Y203	R204
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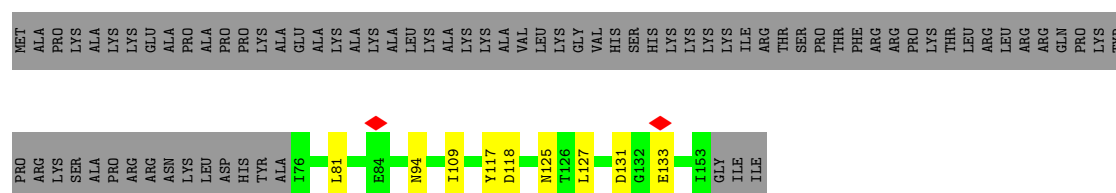
Chain Bq:



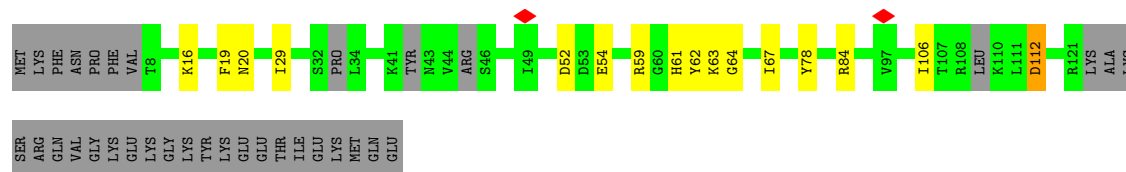
Chain Br: 71% 10% 18%



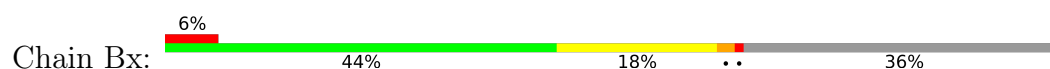
Chain Bs:

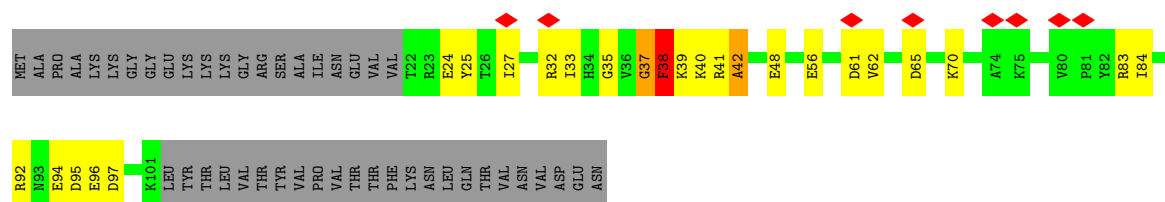


Chain Bt: 65% 10% 24%

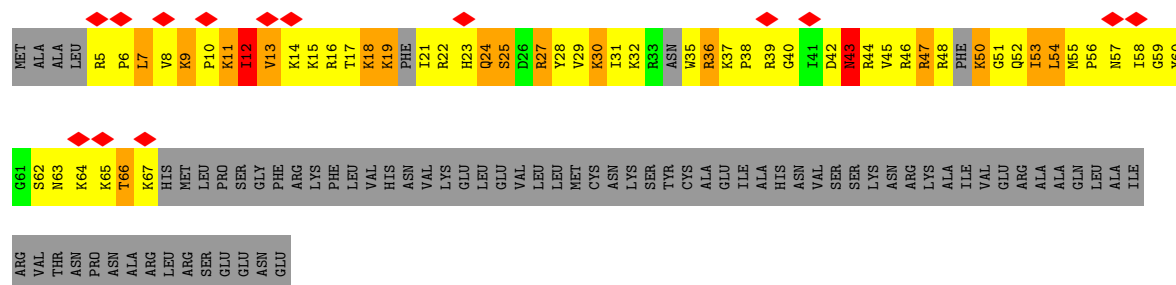
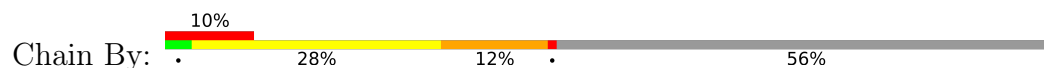


WORLDWIDE
PDB
PROTEIN DATA BANK





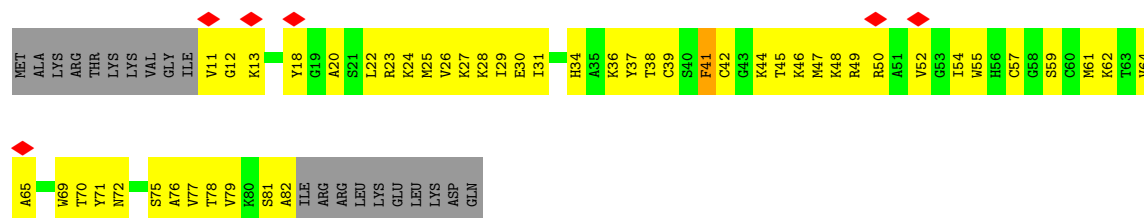
• Molecule 79: 60S Ribosomal protein L32



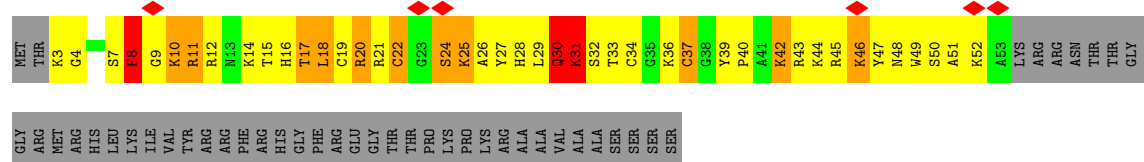
• Molecule 80: 60S Ribosomal protein L32



• Molecule 81: 60S Ribosomal protein L37a



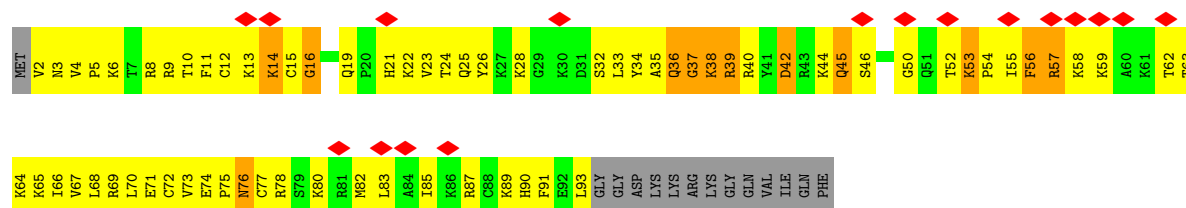
• Molecule 82: 60S Ribosomal protein L37e



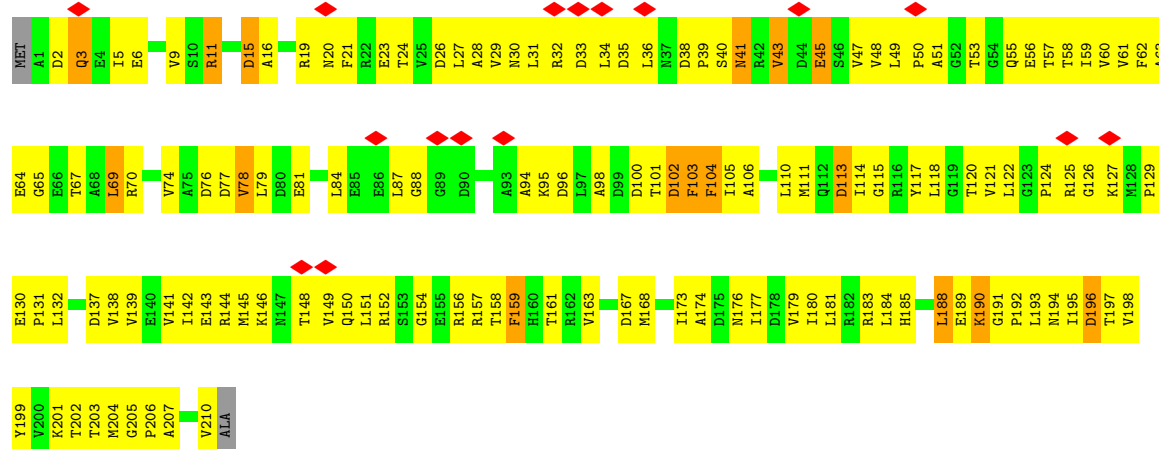
• Molecule 83: 60S Ribosomal protein L39e



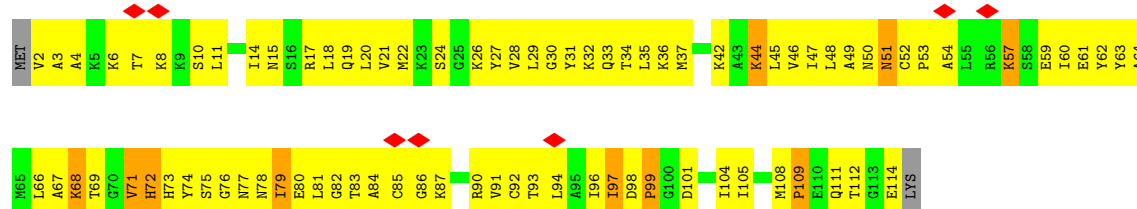
• Molecule 84: 60S Ribosomal protein L44e



• Molecule 85: 60S Ribosomal protein L10a



• Molecule 86: 60S Ribosomal protein L30e



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	78800	Depositor
Resolution determination method	Not provided	
CTF correction method	CTF correction using phase flipping and setsf in EMAN to correct the amplitudes	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	4400	Depositor
Magnification	51000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	23.447	Depositor
Minimum map value	-16.531	Depositor
Average map value	0.178	Depositor
Map value standard deviation	1.378	Depositor
Recommended contour level	1	Depositor
Map size (Å)	458.64, 458.64, 458.64	wwPDB
Map dimensions	168, 168, 168	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	2.73, 2.73, 2.73	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	$\# Z > 5$
9	Aa	1.13	29/2434 (1.2%)	1.74	48/3309 (1.5%)
10	Ab	1.35	0/1556	1.58	17/2115 (0.8%)
11	Ac	0.97	17/1518 (1.1%)	1.29	3/2038 (0.1%)
12	Ad	1.43	0/856	1.44	3/1144 (0.3%)
13	Ae	1.43	0/1115	1.68	16/1505 (1.1%)
14	Ag	1.49	1/1288 (0.1%)	1.77	31/1725 (1.8%)
15	Ah	1.34	0/1033	1.63	5/1382 (0.4%)
16	Ai	1.52	1/1118 (0.1%)	1.72	23/1493 (1.5%)
17	Aj	1.47	0/781	1.76	14/1048 (1.3%)
18	Ak	1.27	17/947 (1.8%)	1.70	13/1271 (1.0%)
19	Al	1.44	0/884	1.65	8/1184 (0.7%)
20	Am	1.51	2/1165 (0.2%)	1.74	17/1555 (1.1%)
21	An	1.55	1/420 (0.2%)	1.88	16/557 (2.9%)
22	Ao	1.32	11/721 (1.5%)	1.71	6/962 (0.6%)
23	Aq	1.53	0/637	1.78	15/849 (1.8%)
24	As	1.46	0/735	1.80	14/980 (1.4%)
53	Ba	1.42	0/1904	1.65	21/2552 (0.8%)
54	Bb	1.29	37/2824 (1.3%)	1.78	42/3786 (1.1%)
55	Bc	1.07	17/2076 (0.8%)	1.51	13/2790 (0.5%)
56	Bd	1.17	22/1347 (1.6%)	1.65	18/1801 (1.0%)
57	Be	1.00	13/1426 (0.9%)	1.40	5/1916 (0.3%)
58	Bf	1.22	12/932 (1.3%)	1.85	17/1256 (1.4%)
59	Bg	1.17	8/332 (2.4%)	1.43	2/454 (0.4%)
60	Bh	1.00	11/1358 (0.8%)	1.58	5/1811 (0.3%)
61	Bi	1.43	0/578	1.62	5/775 (0.6%)
62	Bj	1.47	0/1118	1.66	20/1502 (1.3%)
63	Bk	0.92	6/940 (0.6%)	1.34	3/1264 (0.2%)
64	Bl	1.47	0/972	1.87	29/1299 (2.2%)
65	Bm	1.43	0/1491	1.63	14/1999 (0.7%)
66	Bn	1.31	28/1949 (1.4%)	1.84	50/2615 (1.9%)
67	Bo	1.52	1/965 (0.1%)	1.66	12/1292 (0.9%)
68	Bp	1.42	8/1338 (0.6%)	1.65	12/1766 (0.7%)
69	B7	1.70	0/129	1.44	1/167 (0.6%)
70	Bq	1.47	0/788	1.67	5/1049 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
71	Br	1.44	1/1240 (0.1%)	1.65	15/1660 (0.9%)
72	Bs	1.29	0/630	1.56	8/850 (0.9%)
73	Bt	1.43	0/924	1.68	15/1223 (1.2%)
74	Bu	0.91	2/455 (0.4%)	1.20	0/610
75	Bv	1.42	0/476	1.51	8/632 (1.3%)
76	B8	1.51	0/77	1.43	1/103 (1.0%)
77	Bw	1.49	0/1301	1.88	30/1737 (1.7%)
78	Bx	1.34	14/681 (2.1%)	1.89	9/908 (1.0%)
79	By	1.57	0/519	1.73	11/680 (1.6%)
80	B9	1.43	0/467	1.66	3/626 (0.5%)
81	Bz	1.34	0/558	1.59	4/745 (0.5%)
82	B2	1.57	0/415	2.07	15/547 (2.7%)
83	B3	1.48	0/439	1.56	4/580 (0.7%)
84	B4	1.48	0/773	1.69	14/1022 (1.4%)
85	B5	1.39	1/1638 (0.1%)	1.63	25/2222 (1.1%)
86	B6	1.39	0/885	1.63	7/1186 (0.6%)
All	All	1.34	260/51153 (0.5%)	1.67	692/68542 (1.0%)

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
9	Aa	0	17
11	Ac	0	1
18	Ak	1	5
22	Ao	0	4
23	Aq	0	1
54	Bb	1	19
55	Bc	0	9
56	Bd	0	6
57	Be	0	1
58	Bf	1	6
60	Bh	0	5
63	Bk	1	1
66	Bn	0	9
68	Bp	1	2
74	Bu	0	1
78	Bx	1	6
All	All	6	93

The worst 5 of 260 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	Ag	122	ARG	C-N	18.22	1.56	1.33
16	Ai	12	VAL	CA-CB	-14.34	1.40	1.55
66	Bn	198	ILE	N-CA	12.94	1.62	1.46
66	Bn	197	HIS	CA-C	12.85	1.70	1.52
56	Bd	115	LEU	CB-CG	11.62	1.76	1.53

The worst 5 of 692 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	Bh	20	ARG	N-CA-C	-24.99	79.39	114.12
54	Bb	211	GLY	CA-C-N	19.31	156.47	121.70
54	Bb	211	GLY	C-N-CA	19.31	156.47	121.70
58	Bf	196	ARG	CA-CB-CG	17.78	149.66	114.10
9	Aa	14	HIS	CA-CB-CG	17.34	131.14	113.80

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
18	Ak	99	ALA	CA
54	Bb	137	GLN	CA
58	Bf	197	LYS	CA
63	Bk	21	PRO	CA
68	Bp	191	GLU	CA

5 of 93 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	Aa	14	HIS	Sidechain
9	Aa	34	ALA	Peptide
9	Aa	64	HIS	Sidechain
9	Aa	65	PHE	Sidechain
9	Aa	77	PHE	Sidechain

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	AA	1391	0	0	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AB	32	0	0	0	0
3	AC	29	0	0	0	0
4	AD	42	0	0	0	0
5	AE	32	0	0	0	0
6	AF	31	0	0	0	0
7	AG	14	0	0	0	0
8	AH	41	0	0	13	0
9	Aa	2380	0	2337	221	0
10	Ab	1521	0	1531	0	0
11	Ac	1498	0	1575	0	0
12	Ad	845	0	879	76	0
13	Ae	1096	0	1160	0	0
14	Ag	1277	0	1325	0	0
15	Ah	1016	0	1057	0	0
16	Ai	1102	0	1160	0	0
17	Aj	772	0	839	175	0
18	Ak	935	0	951	0	0
19	Al	871	0	927	0	0
20	Am	1150	0	1202	0	0
21	An	410	0	408	120	0
22	Ao	710	0	743	24	0
23	Aq	629	0	674	0	0
24	As	721	0	759	0	0
25	B1	97	0	0	12	0
26	B0	2407	0	0	238	0
27	BA	21	0	0	0	0
28	BB	27	0	0	0	0
29	BC	17	0	0	0	0
30	BD	16	0	0	0	0
31	BE	54	0	0	0	0
32	BF	120	0	0	0	0
33	BG	48	0	0	0	0
34	BH	25	0	0	3	0
35	BI	72	0	0	0	0
36	BJ	30	0	0	0	0
37	BK	25	0	0	0	0
38	BL	20	0	0	0	0
39	BM	19	0	0	4	0
40	BN	78	0	0	0	0
41	BO	20	0	0	0	0
42	BP	15	0	0	0	0
43	BQ	30	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BR	30	0	0	0	0
45	BS	38	0	0	0	0
46	BT	30	0	0	0	0
47	BU	16	0	0	0	0
48	BV	22	0	0	4	0
49	BW	16	0	0	3	0
50	BX	113	0	0	0	0
51	BY	115	0	0	29	0
52	BZ	72	0	0	4	0
53	Ba	1867	0	1961	0	0
54	Bb	2765	0	2878	24	0
55	Bc	2035	0	2119	0	0
56	Bd	1325	0	1358	0	0
57	Be	1407	0	1481	0	0
58	Bf	920	0	1003	0	0
59	Bg	327	0	323	0	0
60	Bh	1331	0	1384	0	0
61	Bi	573	0	608	0	0
62	Bj	1095	0	1188	283	0
63	Bk	927	0	986	0	0
64	Bl	951	0	985	177	0
65	Bm	1454	0	1498	0	0
66	Bn	1912	0	1887	364	0
67	Bo	956	0	1057	0	0
68	Bp	1329	0	1449	143	0
69	B7	129	0	152	11	0
70	Bq	773	0	829	291	0
71	Br	1217	0	1241	0	0
72	Bs	622	0	661	0	0
73	Bt	916	0	977	0	0
74	Bu	443	0	435	0	0
75	Bv	477	0	546	0	0
76	B8	78	0	84	0	0
77	Bw	1281	0	1362	371	0
78	Bx	670	0	710	0	0
79	By	514	0	578	209	0
80	B9	460	0	481	99	0
81	Bz	548	0	567	88	0
82	B2	407	0	423	151	0
83	B3	429	0	466	85	0
84	B4	760	0	820	147	0
85	B5	1621	0	1559	339	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	B6	874	0	920	215	0
All	All	55531	0	52503	3488	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 82.

The worst 5 of 3488 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)
26:B0:1572:A:P	54:Bb:245:ARG:HD2	1.21	1.75
51:BY:11:A:P	66:Bn:17:VAL:HG23	1.29	1.71
49:BW:13:U:P	64:Bl:131:ARG:HG2	1.18	1.70
26:B0:2251:G:P	77:Bw:186:LYS:HB3	1.25	1.69
8:AH:9:G:P	21:An:13:LYS:HD3	1.31	1.64

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	
9	Aa	300/317 (95%)	256 (85%)	31 (10%)	13 (4%)	2	17
10	Ab	188/295 (64%)	180 (96%)	5 (3%)	3 (2%)	7	38
11	Ac	190/243 (78%)	171 (90%)	12 (6%)	7 (4%)	2	20
12	Ad	101/209 (48%)	100 (99%)	1 (1%)	0	100	100
13	Ae	144/179 (80%)	136 (94%)	6 (4%)	2 (1%)	9	40
14	Ag	153/204 (75%)	147 (96%)	4 (3%)	2 (1%)	9	42
15	Ah	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
16	Ai	134/146 (92%)	120 (90%)	11 (8%)	3 (2%)	5	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Aj	95/119 (80%)	87 (92%)	3 (3%)	5 (5%)	1	15
18	Ak	123/151 (82%)	86 (70%)	31 (25%)	6 (5%)	1	16
19	Al	113/143 (79%)	88 (78%)	17 (15%)	8 (7%)	1	11
20	Am	138/152 (91%)	125 (91%)	9 (6%)	4 (3%)	3	23
21	An	47/56 (84%)	42 (89%)	4 (8%)	1 (2%)	5	30
22	Ao	83/89 (93%)	67 (81%)	15 (18%)	1 (1%)	10	44
23	Aq	70/158 (44%)	65 (93%)	4 (6%)	1 (1%)	9	40
24	As	86/145 (59%)	75 (87%)	7 (8%)	4 (5%)	2	16
53	Ba	240/257 (93%)	219 (91%)	14 (6%)	7 (3%)	3	23
54	Bb	343/403 (85%)	255 (74%)	58 (17%)	30 (9%)	0	9
55	Bc	255/421 (61%)	211 (83%)	33 (13%)	11 (4%)	2	17
56	Bd	163/178 (92%)	140 (86%)	19 (12%)	4 (2%)	4	26
57	Be	173/192 (90%)	155 (90%)	14 (8%)	4 (2%)	5	28
58	Bf	118/266 (44%)	103 (87%)	8 (7%)	7 (6%)	1	13
59	Bg	46/317 (14%)	37 (80%)	8 (17%)	1 (2%)	5	29
60	Bh	164/214 (77%)	154 (94%)	8 (5%)	2 (1%)	10	44
61	Bi	72/165 (44%)	67 (93%)	4 (6%)	1 (1%)	9	40
62	Bj	134/203 (66%)	129 (96%)	4 (3%)	1 (1%)	18	56
63	Bk	122/140 (87%)	114 (93%)	6 (5%)	2 (2%)	7	38
64	Bl	116/148 (78%)	110 (95%)	4 (3%)	2 (2%)	7	36
65	Bm	173/204 (85%)	164 (95%)	8 (5%)	1 (1%)	21	59
66	Bn	232/297 (78%)	186 (80%)	30 (13%)	16 (7%)	1	11
67	Bo	116/188 (62%)	109 (94%)	5 (4%)	2 (2%)	7	36
68	Bp	151/196 (77%)	141 (93%)	6 (4%)	4 (3%)	4	25
69	B7	11/13 (85%)	11 (100%)	0	0	100	100
70	Bq	94/160 (59%)	86 (92%)	7 (7%)	1 (1%)	11	46
71	Br	144/184 (78%)	137 (95%)	6 (4%)	1 (1%)	18	56
72	Bs	76/156 (49%)	74 (97%)	2 (3%)	0	100	100
73	Bt	100/145 (69%)	95 (95%)	3 (3%)	2 (2%)	6	31
74	Bu	51/157 (32%)	49 (96%)	2 (4%)	0	100	100
75	Bv	59/123 (48%)	59 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	B8	8/10 (80%)	8 (100%)	0	0	100	100
77	Bw	152/270 (56%)	119 (78%)	22 (14%)	11 (7%)	1	11
78	Bx	78/125 (62%)	66 (85%)	7 (9%)	5 (6%)	1	12
79	By	52/135 (38%)	39 (75%)	7 (14%)	6 (12%)	0	5
80	B9	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
81	Bz	70/92 (76%)	65 (93%)	5 (7%)	0	100	100
82	B2	49/97 (50%)	33 (67%)	10 (20%)	6 (12%)	0	4
83	B3	46/51 (90%)	46 (100%)	0	0	100	100
84	B4	90/106 (85%)	87 (97%)	2 (2%)	1 (1%)	11	46
85	B5	208/212 (98%)	199 (96%)	7 (3%)	2 (1%)	12	49
86	B6	111/115 (96%)	104 (94%)	5 (4%)	2 (2%)	6	34
All	All	6163/8734 (71%)	5492 (89%)	479 (8%)	192 (3%)	5	22

5 of 192 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	Aa	65	PHE
9	Aa	162	ASN
9	Aa	270	LEU
11	Ac	48	ILE
11	Ac	131	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Aa	265/275 (96%)	262 (99%)	3 (1%)	65	76
10	Ab	160/244 (66%)	153 (96%)	7 (4%)	25	47
11	Ac	157/202 (78%)	148 (94%)	9 (6%)	18	40
12	Ad	89/181 (49%)	87 (98%)	2 (2%)	45	64
13	Ae	117/146 (80%)	111 (95%)	6 (5%)	21	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	Ag	138/170 (81%)	133 (96%)	5 (4%)	31	52
15	Ah	110/113 (97%)	106 (96%)	4 (4%)	31	52
16	Ai	114/121 (94%)	110 (96%)	4 (4%)	32	53
17	Aj	90/107 (84%)	83 (92%)	7 (8%)	11	32
18	Ak	98/119 (82%)	91 (93%)	7 (7%)	13	35
19	Al	90/115 (78%)	85 (94%)	5 (6%)	19	40
20	Am	120/132 (91%)	114 (95%)	6 (5%)	22	43
21	An	43/49 (88%)	41 (95%)	2 (5%)	23	45
22	Ao	77/80 (96%)	72 (94%)	5 (6%)	15	37
23	Aq	72/142 (51%)	67 (93%)	5 (7%)	14	36
24	As	79/130 (61%)	71 (90%)	8 (10%)	7	23
53	Ba	187/199 (94%)	179 (96%)	8 (4%)	26	47
54	Bb	298/348 (86%)	273 (92%)	25 (8%)	10	30
55	Bc	214/351 (61%)	206 (96%)	8 (4%)	30	51
56	Bd	139/149 (93%)	132 (95%)	7 (5%)	22	43
57	Be	156/171 (91%)	148 (95%)	8 (5%)	21	42
58	Bf	100/223 (45%)	86 (86%)	14 (14%)	3	13
59	Bg	29/258 (11%)	29 (100%)	0	100	100
60	Bh	141/181 (78%)	137 (97%)	4 (3%)	38	60
61	Bi	64/137 (47%)	62 (97%)	2 (3%)	35	56
62	Bj	114/174 (66%)	110 (96%)	4 (4%)	32	53
63	Bk	97/107 (91%)	91 (94%)	6 (6%)	16	38
64	Bl	99/122 (81%)	98 (99%)	1 (1%)	68	78
65	Bm	148/172 (86%)	144 (97%)	4 (3%)	39	61
66	Bn	197/251 (78%)	181 (92%)	16 (8%)	11	31
67	Bo	108/165 (66%)	104 (96%)	4 (4%)	30	51
68	Bp	141/175 (81%)	136 (96%)	5 (4%)	32	53
69	B7	13/13 (100%)	13 (100%)	0	100	100
70	Bq	82/139 (59%)	75 (92%)	7 (8%)	10	29
71	Br	131/163 (80%)	123 (94%)	8 (6%)	17	38
72	Bs	69/133 (52%)	67 (97%)	2 (3%)	37	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	Bt	103/135 (76%)	100 (97%)	3 (3%)	37	58
74	Bu	46/126 (36%)	45 (98%)	1 (2%)	45	64
75	Bv	53/110 (48%)	50 (94%)	3 (6%)	18	40
76	B8	9/9 (100%)	9 (100%)	0	100	100
77	Bw	137/234 (58%)	121 (88%)	16 (12%)	5	18
78	Bx	71/110 (64%)	66 (93%)	5 (7%)	14	35
79	By	56/121 (46%)	47 (84%)	9 (16%)	2	11
80	B9	51/51 (100%)	49 (96%)	2 (4%)	28	49
81	Bz	57/75 (76%)	55 (96%)	2 (4%)	32	53
82	B2	42/80 (52%)	38 (90%)	4 (10%)	8	25
83	B3	45/48 (94%)	44 (98%)	1 (2%)	45	64
84	B4	83/94 (88%)	78 (94%)	5 (6%)	17	39
85	B5	177/178 (99%)	175 (99%)	2 (1%)	65	76
86	B6	95/97 (98%)	90 (95%)	5 (5%)	20	41
All	All	5371/7425 (72%)	5095 (95%)	276 (5%)	23	42

5 of 276 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
77	Bw	196	LEU
77	Bw	231	TRP
82	B2	20	ARG
54	Bb	42	LEU
54	Bb	36	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
66	Bn	16	GLN
85	B5	41	ASN
70	Bq	97	HIS
85	B5	30	ASN
86	B6	40	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	0/1563	-	-
2	AB	0/35	-	-
25	B1	0/123	-	-
26	B0	0/2903	-	-
27	BA	0/21	-	-
28	BB	0/27	-	-
29	BC	0/17	-	-
3	AC	0/32	-	-
30	BD	0/16	-	-
31	BE	0/54	-	-
32	BF	0/120	-	-
33	BG	0/48	-	-
34	BH	0/25	-	-
35	BI	0/72	-	-
36	BJ	0/30	-	-
37	BK	0/26	-	-
38	BL	0/20	-	-
39	BM	0/19	-	-
4	AD	0/42	-	-
40	BN	0/78	-	-
41	BO	0/20	-	-
42	BP	0/15	-	-
43	BQ	0/30	-	-
44	BR	0/30	-	-
45	BS	0/38	-	-
46	BT	0/30	-	-
47	BU	0/16	-	-
48	BV	0/22	-	-
49	BW	0/16	-	-
5	AE	0/32	-	-
50	BX	0/113	-	-
51	BY	0/115	-	-
52	BZ	0/72	-	-
6	AF	0/31	-	-
7	AG	0/14	-	-
8	AH	0/41	-	-
All	All	0/5906	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no 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.

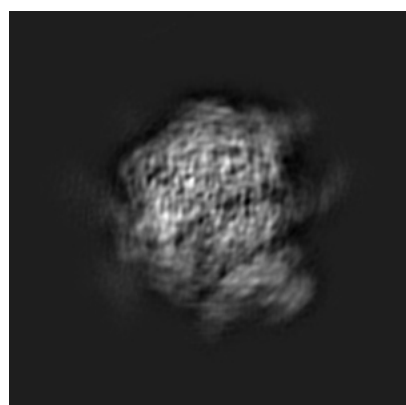
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1480. These allow visual inspection of the internal detail of the map and identification of artifacts.

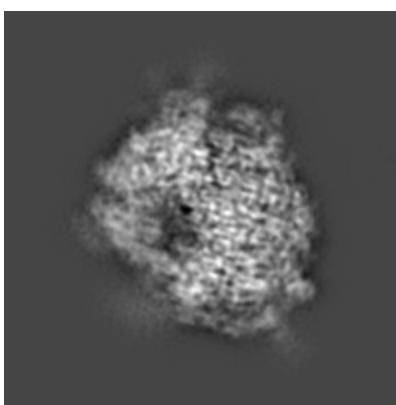
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

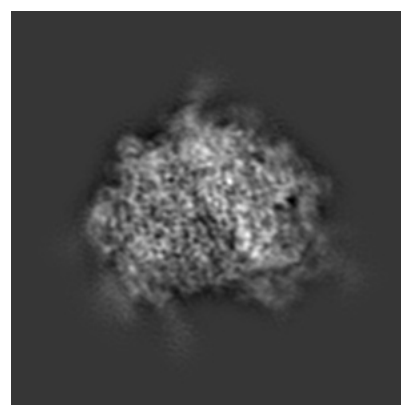
6.1.1 Primary map



X



Y



Z

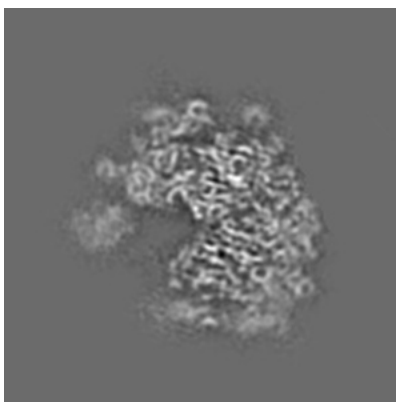
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

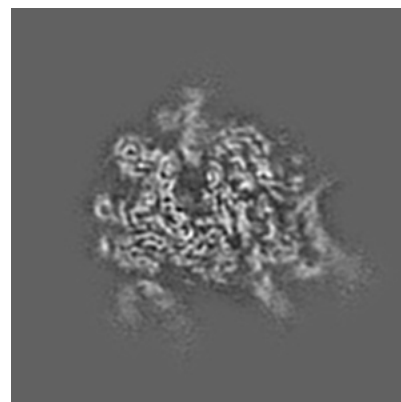
6.2.1 Primary map



X Index: 84



Y Index: 84

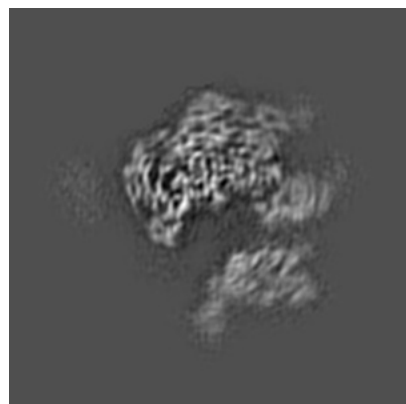


Z Index: 84

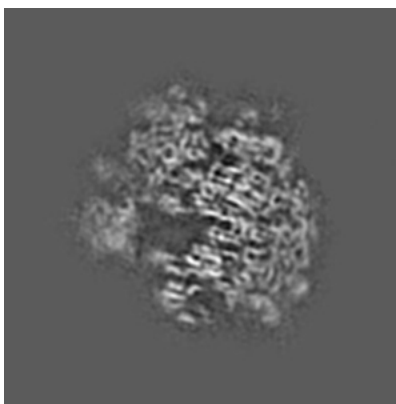
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

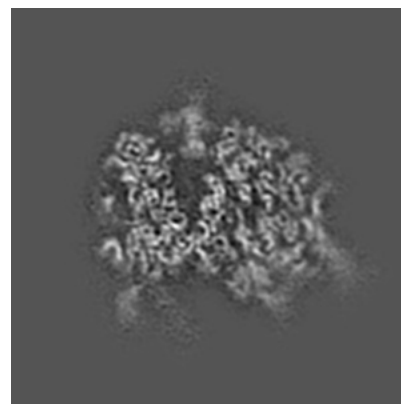
6.3.1 Primary map



X Index: 75



Y Index: 89

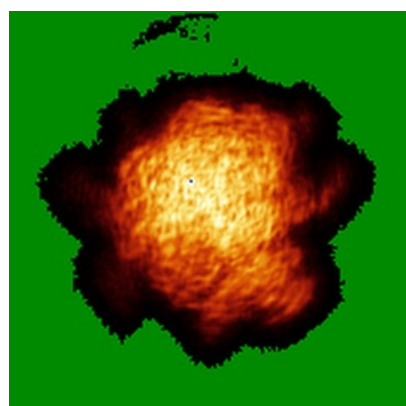


Z Index: 81

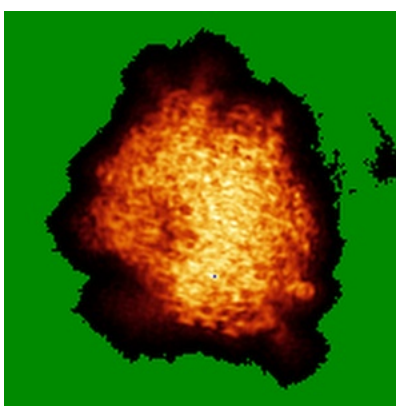
The images above show the largest variance slices of the map in three orthogonal directions.

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

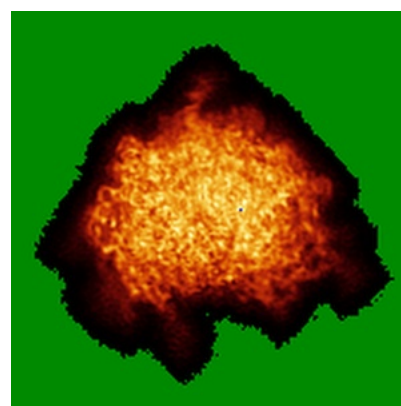
6.4.1 Primary map



X



Y

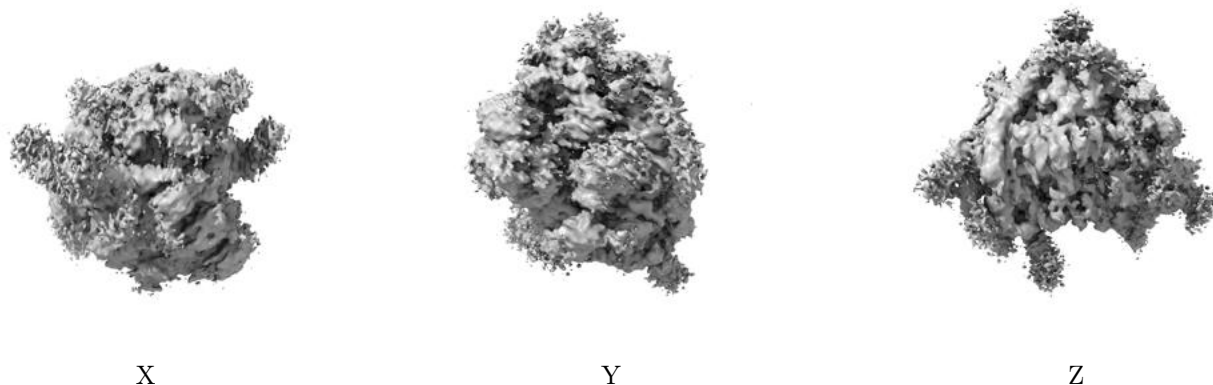


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

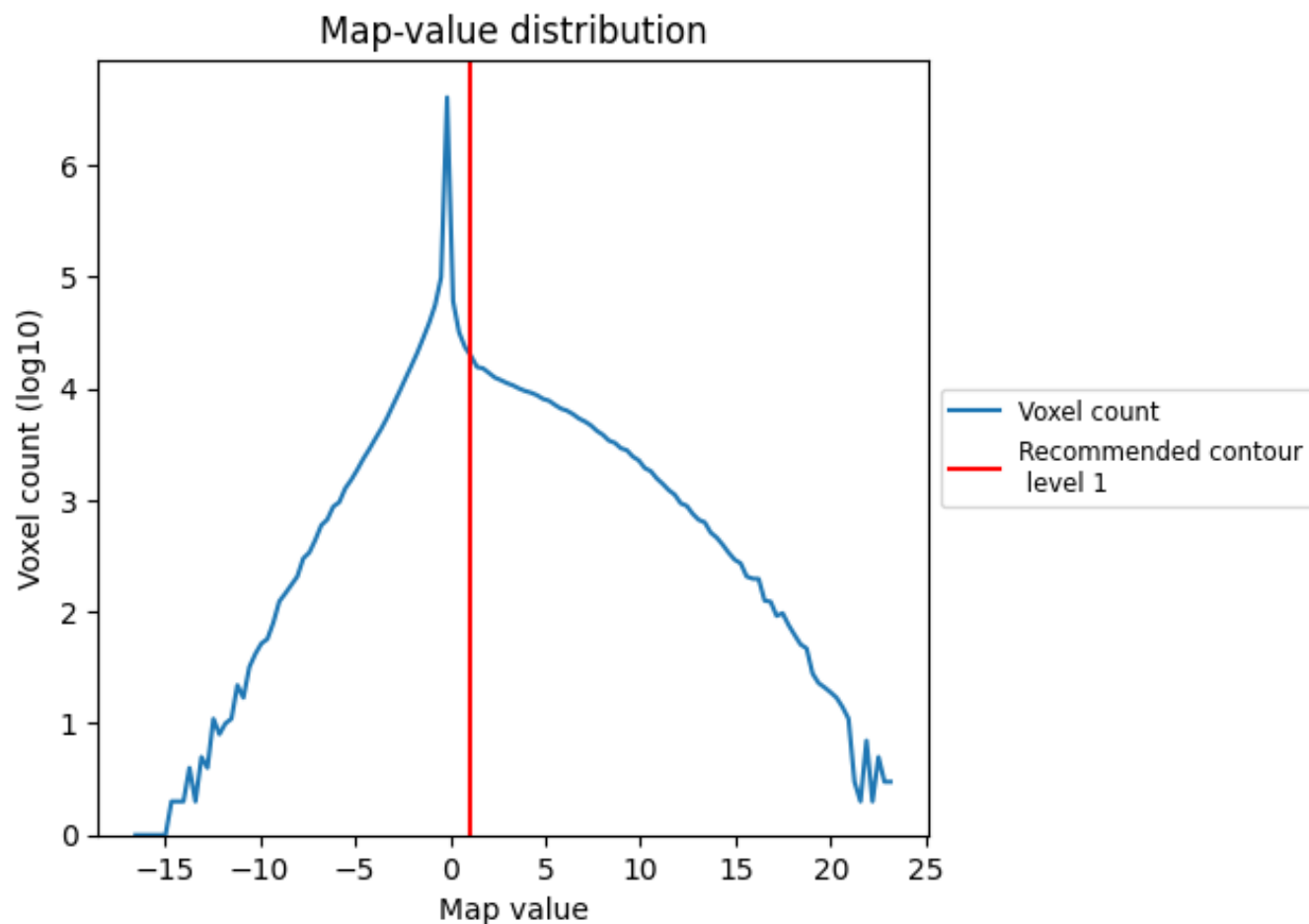
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

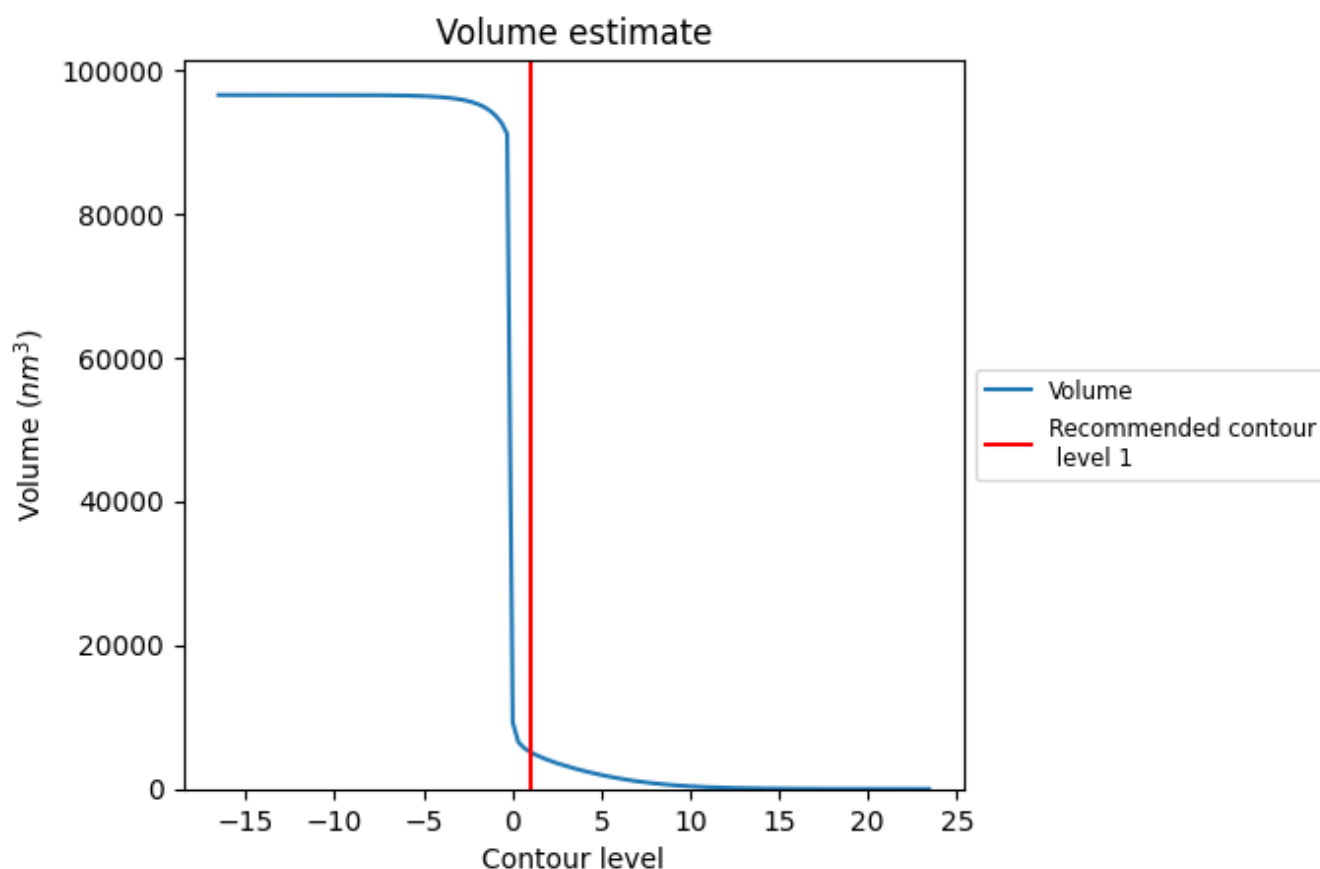
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

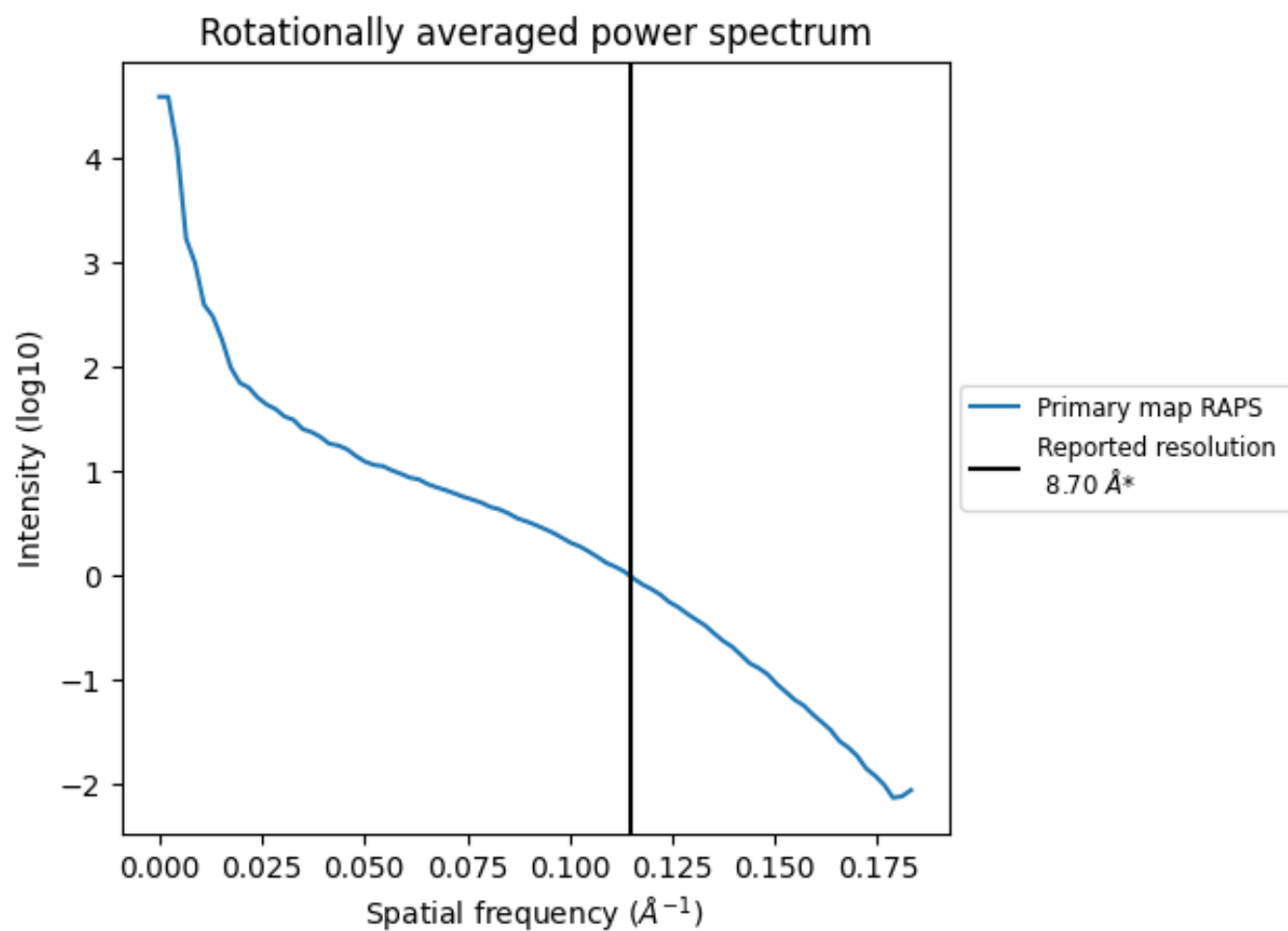
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5149 nm^3 ; this corresponds to an approximate mass of 4651 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 0.115 Å⁻¹

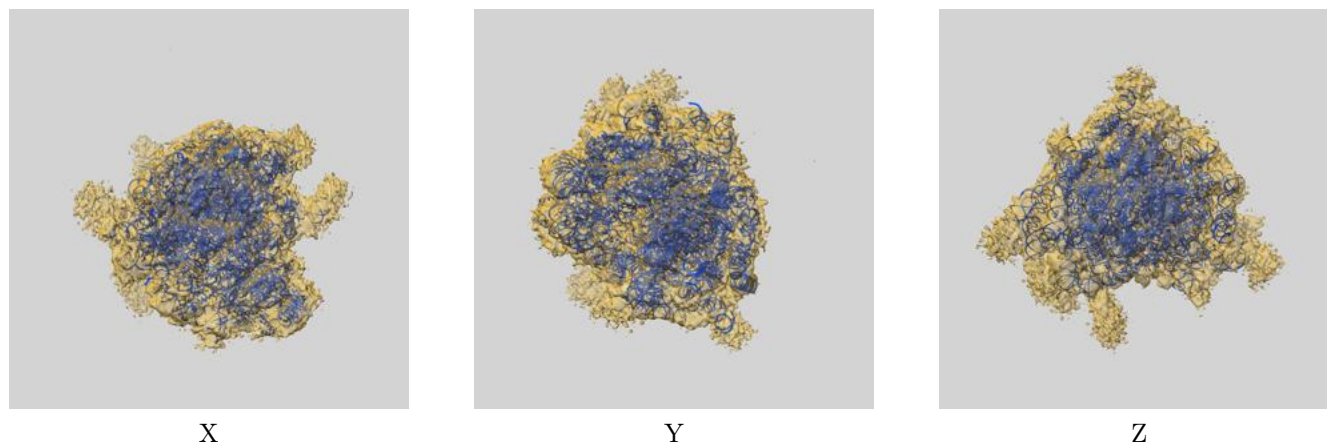
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

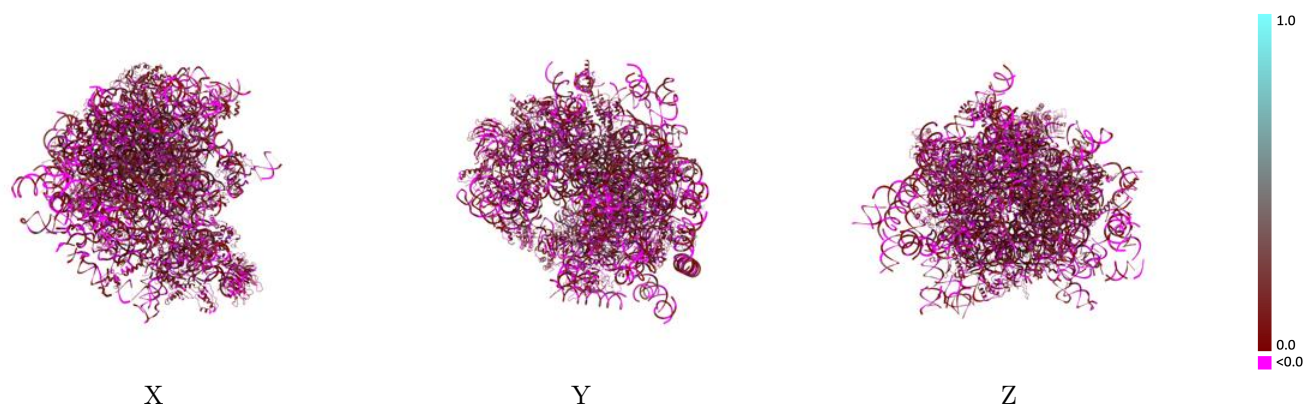
This section contains information regarding the fit between EMDB map EMD-1480 and PDB model 4V5Z. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 1.0 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](#)

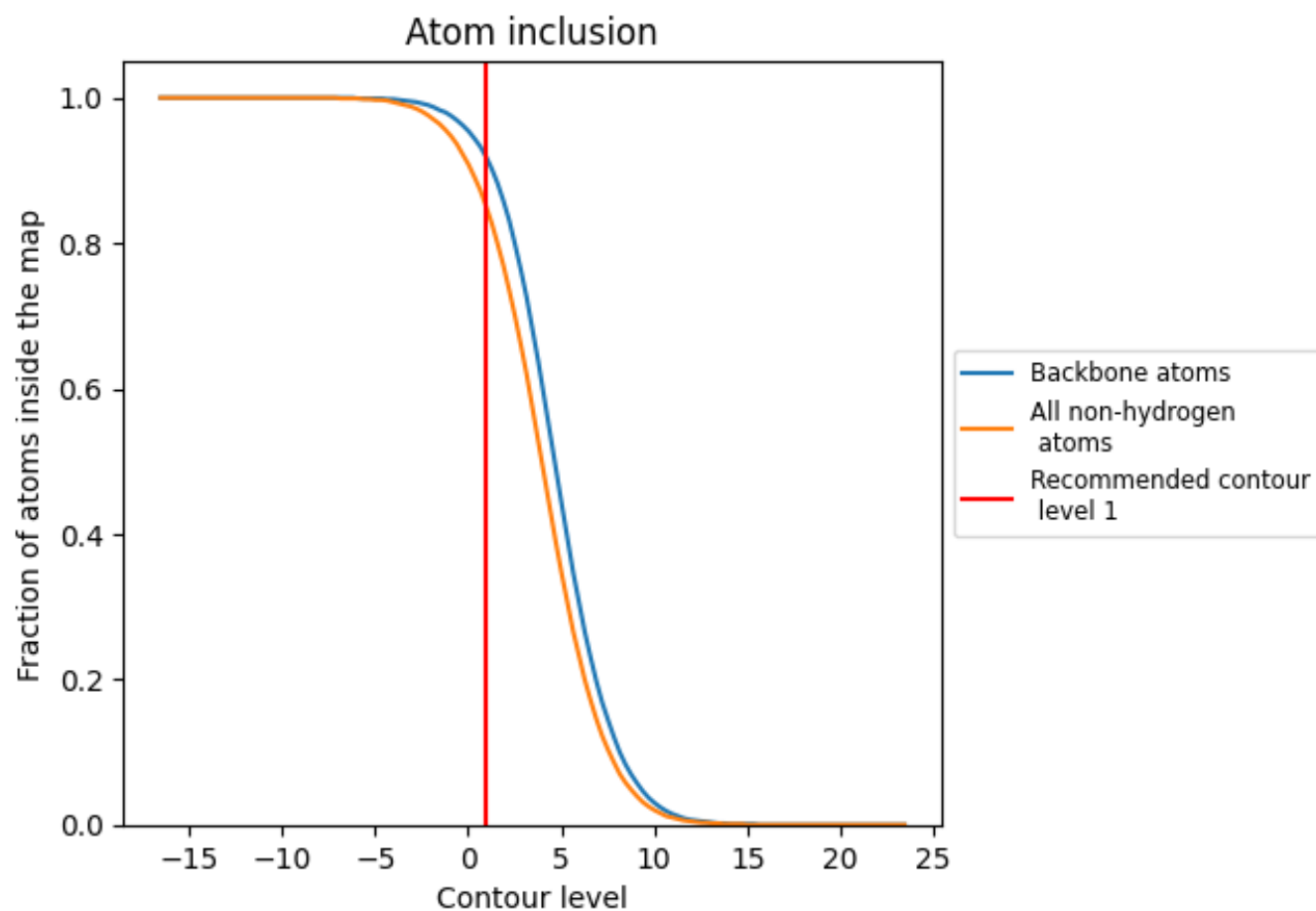


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 85% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8480	 0.0750
AA	 0.8920	 0.0490
AB	 0.8440	 0.0270
AC	 0.9310	 0.0130
AD	 0.9520	 0.0480
AE	 0.9060	 -0.0110
AF	 1.0000	 0.0070
AG	 0.6430	 0.0290
AH	 0.8050	 -0.0040
Aa	 0.9250	 0.0570
Ab	 0.9260	 0.1090
Ac	 0.8790	 0.0870
Ad	 0.9520	 0.0740
Ae	 0.8850	 0.0810
Ag	 0.8940	 0.0520
Ah	 0.8890	 0.0940
Ai	 0.9430	 0.0410
Aj	 0.8920	 0.0370
Ak	 0.8710	 0.0940
Al	 0.8480	 0.0780
Am	 0.9020	 0.0670
An	 0.8470	 0.0030
Ao	 0.7740	 0.1030
Aq	 0.8290	 0.0550
As	 0.9740	 0.0510
B0	 0.9060	 0.0720
B1	 0.9170	 0.0430
B2	 0.8110	 0.0660
B3	 0.7790	 0.0890
B4	 0.7360	 0.0360
B5	 0.8870	 0.0520
B6	 0.8190	 0.0980
B7	 0.8330	 0.1100
B8	 0.9210	 0.1960
B9	 0.8510	 0.0850



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Chain	Atom inclusion	Q-score
BA	 0.8090	 0.0660
BB	 0.8890	 0.0320
BC	 0.8820	 0.0480
BD	 0.8750	 -0.0010
BE	 0.8700	 0.0470
BF	 0.9170	 0.0400
BG	 0.7710	 0.0190
BH	 0.7600	 0.0070
BI	 0.9030	 0.0510
BJ	 0.8330	 0.0430
BK	 0.5200	 0.0340
BL	 1.0000	 0.0490
BM	 0.8420	 0.0050
BN	 0.6540	 -0.0040
BO	 0.9500	 0.0230
BP	 0.7330	 0.0770
BQ	 0.8670	 0.0200
BR	 0.8330	 0.0420
BS	 0.8950	 0.0340
BT	 0.8670	 0.0260
BU	 0.8750	 0.0650
BV	 0.7270	 0.0060
BW	 0.5620	 0.0120
BX	 0.9030	 0.0560
BY	 0.7480	 0.0100
BZ	 0.8610	 0.0440
Ba	 0.7710	 0.1030
Bb	 0.7590	 0.0560
Bc	 0.8320	 0.0730
Bd	 0.8510	 0.0790
Be	 0.8900	 0.1110
Bf	 0.8990	 0.1080
Bg	 0.9850	 0.1320
Bh	 0.8090	 0.0880
Bi	 0.9340	 0.0100
Bj	 0.7050	 0.0620
Bk	 0.8320	 0.1150
Bl	 0.8240	 0.0590
Bm	 0.8270	 0.0560
Bn	 0.7120	 0.0320
Bo	 0.8530	 0.0810
Bp	 0.8690	 0.1260

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Chain	Atom inclusion	Q-score
Bq	 0.7690	 0.0770
Br	 0.8640	 0.1060
Bs	 0.8110	 0.1220
Bt	 0.8900	 0.1040
Bu	 0.8620	 0.1020
Bv	 0.8130	 0.1500
Bw	 0.7930	 0.0960
Bx	 0.8360	 0.0720
By	 0.6480	 0.0340
Bz	 0.7900	 0.0990