WORLDWIDE

wwPDB

PROTEIN DATA BANK

Full wwPDB EM Validation Report (i)

Nov 21, 2022 – 02:38 PM EST

PDB ID	:	8EUI
EMDB ID	:	EMD-24423
Title	:	Ytm1 associated nascent 60S ribosome (-fkbp39) State 3
Authors	:	Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on	:	2022-10-18
Resolution	:	3.10 Å(reported)

This is a Full wwPDB EM Validation 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 (i) 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 (i)) were used in the production of this report:
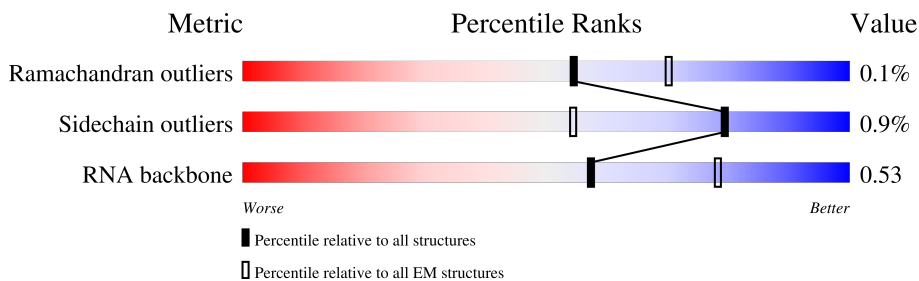
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.10 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	Percentile Ranks	Value
Ramachandran outliers		0.1%
Sidechain outliers		0.9%
RNA backbone		0.53

Worse   *Better*

■ Percentile relative to all structures

▯ Percentile relative to all EM structures

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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	1	3498	65% 17% 18%
2	2	165	75% 21% •
3	3	302	39% • 59%
4	8	51	98% •
5	9	229	45% 6% 48%
6	A	253	96% •
7	B	388	97% •
8	C	363	99% •
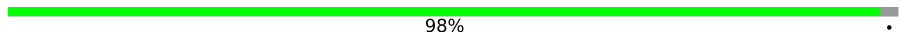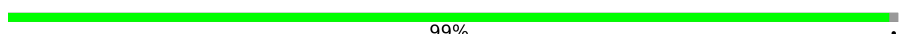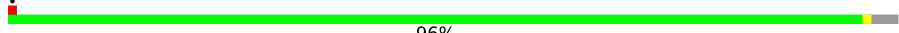
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Mol	Chain	Length	Quality of chain
9	D	294	96%
10	E	195	9% 93% · 6%
11	F	250	85% · 14%
12	G	259	88% · 12%
13	H	190	11% 92% 8%
14	I	221	9% 76% 24%
15	J	174	18% 94% · ·
16	K	94	95% · ·
17	L	208	97% ·
18	M	134	93% 7%
19	N	201	99%
20	O	197	99% ·
21	P	187	92% · 7%
22	Q	187	99% ··
23	R	193	77% 23%
24	S	176	95% 5%
25	T	160	98% ··
26	U	117	13% 82% · 16%
27	V	139	96% ··
28	X	141	82% · 17%
29	Y	126	98% ··
30	Z	136	97% ··
31	a	148	99% ·
32	b	61	90% · 8%
33	c	117	80% · 19%

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Mol	Chain	Length	Quality of chain
34	d	113	86% 14%
35	e	127	91% 8%
36	f	108	98%
37	g	112	93% 5%
38	h	122	99%
39	i	99	96%
40	j	91	91% 9%
41	k	74	5% 91% 5%
42	m	740	14% 57% 43%
43	n	607	17% 59% 41%
44	o	106	92% 8%
45	p	440	53% 65% 35%
46	u	192	29% 69%

2 Entry composition ⓘ

There are 47 unique types of molecules in this entry. The entry contains 122892 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 RNA (2863-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2855	Total 61093	C 27299	N 11065	O 19874	P 2855	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1746	C	U	conflict	GB 157310483
1	2185	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	158	Total 3354	C 1501	N 588	O 1107	P 158	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	123	Total 1042	C 657	N 199	O 180	S 6	0	0

- Molecule 4 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	8	50	Total 437	C 273	N 98	O 65	S 1	0	0

- Molecule 5 is a RNA chain called RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	9	118	Total 2519	C 1124	N 452	O 825	P 118	0	0

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	245	Total 1858	C 1158	N 374	O 321	S 5	0	0

- Molecule 7 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	377	Total 3003	C 1901	N 567	O 525	S 10	0	0

- Molecule 8 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	359	Total 2795	C 1765	N 536	O 491	S 3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L5-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	284	Total 2287	C 1447	N 406	O 430	S 4	0	0

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	183	Total 1415	C 907	N 259	O 245	S 4	0	0

- Molecule 11 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	214	Total 1745	C 1124	N 320	O 298	S 3	0	0

- Molecule 12 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	229	Total 1804	C 1154	N 332	O 315	S 3	0	0

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	H	175	Total 862	C 512	N 175	O 175	0	0

- Molecule 14 is a protein called 60S ribosomal protein L10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	168	Total 1354	C 858	N 251	O 240	S 5	0	0

- Molecule 15 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	169	Total 1359	C 860	N 255	O 239	S 5	0	0

- Molecule 16 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	90	Total 695	C 428	N 144	O 117	S 6	0	0

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	202	Total 1612	C 1008	N 321	O 282	S 1	0	0

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	125	Total 1007	C 644	N 191	O 168	S 4	0	0

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	200	Total 1676	C 1050	N 348	O 275	S 3	0	0

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	196	Total 1557	C 999	N 297	O 257	S 4	0	0

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	173	Total 1369	C 865	N 264	O 237	S 3	0	0

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	186	Total 1487	C 934	N 300	O 252	S 1	0	0

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	149	Total 1229	C 765	N 261	O 198	S 5	0	0

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	168	Total 1408	C 909	N 263	O 231	S 5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	159	Total 1289	C 812	N 248	O 226	S 3	0	0

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	98	Total 791	C 513	N 137	O 141	0	0

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	136	Total 1015	C 638	N 189	O 180	S 8	0	0

- Molecule 28 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	117	Total 939	C 599	N 173	O 166	S 1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	125	Total 998	C 622	N 201	O 173	S 2	0	0

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	134	Total 1072	C 693	N 199	O 178	S 2	0	0

- Molecule 31 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	147	Total 1169	C 740	N 235	O 192	S 2	0	0

- Molecule 32 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	b	56	Total 471	C 284	N 107	O 80	0	0

- Molecule 33 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	95	Total 712	C 453	N 124	O 131	S 4	0	0

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	97	Total 810	C 512	N 159	O 136	S 3	0	0

- Molecule 35 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	117	Total 939	C 588	N 190	O 156	S 5	0	0

- Molecule 36 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	106	Total 839	C 534	N 162	O 140	S 3	0	0

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	106	Total 861	C 540	N 177	O 142	S 2	0	0

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	h	121	Total 999	C 629	N 194	O 176	0	0

- Molecule 39 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	96	Total 767	C 478	N 160	O 128	S 1	0	0

- Molecule 40 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	83	Total 657	C 402	N 141	O 107	S 7	0	0

- Molecule 41 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	70	Total 564	C 357	N 104	O 102	S 1	0	0

- Molecule 42 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	425	Total 3376	C 2168	N 592	O 605	S 11	0	0

- Molecule 43 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	361	Total 2966	C 1933	N 511	O 510	S 12	0	0

- Molecule 44 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	98	Total 796	C 502	N 159	O 130	S 5	0	0

- Molecule 45 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	p	284	Total 1401	C 833	N 284	O 284	0	0

- Molecule 46 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	59	Total 493	C 315	N 100	O 72	S 6	0	0

- Molecule 47 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	j	1	Total 1	Zn 1	0

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: RNA (2863-MER)

U C C C U A C U C U3304 G3307 G3308 G3309 A3310 U3311 U3314 A3317 A3318 G3319 G3329 G3333 A U G A A3338 A3343 A3344 G3345 U3346 G3347 A U U G3355 G3358 U3359 U3370 U3371 C3372 C3373 A3374 U U G A A A U C U

U G G G C G G A A U C G3395 A3396 C3405 A3417 U3418 G3419 U3420 C3425 U3435 A3436 G3441 U3442 A3443 G3444 A3445 G U A G C C U U G U U G U U A C G3462 A3463 U3464 G3470 C3479 U3483 A3490 A3491 G3492

G3497 U3498

• Molecule 2: RNA (152-MER)

Chain 2:

75%   21%

A U U A U U U A8 A9 U31 U42 C43 A67 C70 G71 G83 A87 A88 U89 U90 C91 C92 G93 U94 G95 U98 G103 A112 A113 C114 C115 A119 U120 U121 G122 C123 G124 G131 G132 C135 U136 G156 U159 C162

U165

• Molecule 3: Protein mak16

Chain 3:

39%   59%

MET Q2 V11 G12 H13 M47 E55 K59 D94 Q95 P101 R114 K121 A122 R123 R124 LEU ALA LEU LYS HIS GLN PRO ALA LEU ILE PRO ILE LYS PRO LYS GLN ALA HIS ARG GLU ALA SER ARG GLU ARG LYS ALA LEU ILE ALA ALA LYS LEU GLU LYS ASN

ILE GLU LYS GLU LEU VAL LYS ARG LEU LYS SER GLY VAL TYR GLY ASP GLN PRO LEU ASN VAL ASN GLU GLU ILE TRP ASN LYS VAL LEU ALA ARG GLY GLY LEU ILE ASP GLY GLU GLU GLU ARG GLU GLU ALA GLU LEU GLU PHE VAL SER ASP ASP GLU ASP GLU

GLU GLU ILE SER ASP LEU ASP TRP LEU GLY SER ASP GLN SER MET GLU THR SER GLU SER GLU GLU GLU GLU SER GLU GLU SER GLU ASP SER GLU ASP GLU GLU ASN LYS GLY LYS ILE ARG ARG LYS THR ASP ASP ALA LYS LYS SER ARG LYS LYS ARG ALA PRO

HIS ILE HIS ILE GLU TYR GLU GLN GLU ARG GLU ASN GLU LYS ILE PRO ALA VAL GLN HIS SER TRP

• Molecule 4: 60S ribosomal protein L39

Chain 8:

98%

MET P2 I51

• Molecule 5: RNA (118-MER)

Chain 9:

45%   6%   48%

G U U A A C C U A C U U G A A U A A A C A G A U A A A A A C U U A U U A U U A A C A C A A C A A U G51 G57 A72 U83 A92

A100 U103 A104 G114 U122 U123 A124 C141 A150 G160 G166 G167 C168 U U C C U U U U A U C C U U U U U C G C U U U U U U U C G C U U U U A U U U U A A U U

C U U C G U U U C G A C A U C A A A U C

- Molecule 6: 60S ribosomal protein L2-A

Chain A: 96%

MET G2 D141 R192 R246 GLY ALA ALA ALA VAL GLU ASN
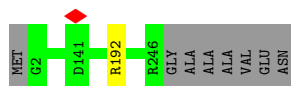
- Molecule 7: 60S ribosomal protein L3-A

Chain B: 97%

MET SER HIS CYS K5 E139 Q378 G381 THR LEU LYS LYS ASP VAL ALA
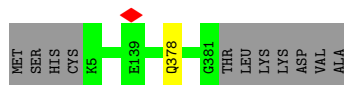
- Molecule 8: 60S ribosomal protein L4-B

Chain C: 99%

MET ALA ALA ALA R5 D156 N363

- Molecule 9: 60S ribosomal protein L5-A

Chain D: 96%

MET PRO PHE ILE LYS A6 W90 D137 R158 E186 D191 D192 E193 D213 D214 D215 D234 K281 E282 R283 A286 K287 V288 I289 GLU ALA GLY ARG ALA
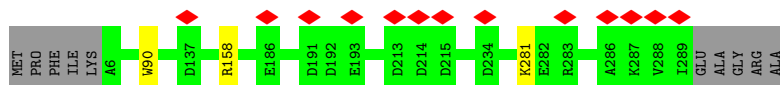
- Molecule 10: 60S ribosomal protein L6

Chain E: 9%   93%   6%

MET SER THR VAL LYS VAL ASN GLY ALA LYS ASN GLY G13 E14 R15 M16 V17 L18 P19 A20 G21 E22 A23 A24 A25 P29 A30 Y31 R129 S130 K135 D136 D161 F195
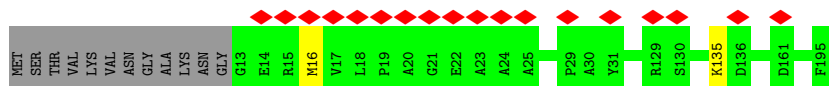
- Molecule 11: 60S ribosomal protein L7-B

Chain F: 85%   14%

MET VAL ALA SER SER THR VAL PRO SER VAL ALA SER ILE PHE ALA PRO GLU SER LEU LEU LYS LYS THR LYS ALA GLN LYS GLN SER ARG GLU GLN ILE VAL ALA ALA A37 A38 E39 K89 D234 L250
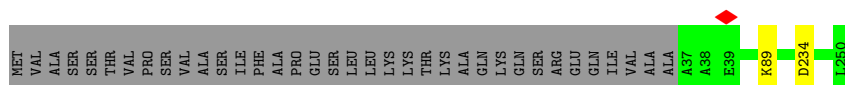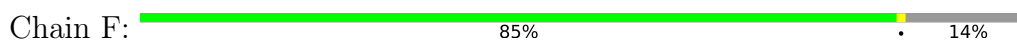
• Molecule 12: 60S ribosomal protein L8

Chain G:

88%   12%

MET ALA PRO LYS SER LYS LYS VAL ALA PRO SER PRO PHE ALA GLN PRO LYS ALA ALA LYS THR THR **K23** **R30** **A117 N118 G119 K120 S121 A122 Q123 D124** **K127** **R204** **K251** ALA ALA ALA ALA THR VAL ARG LEU
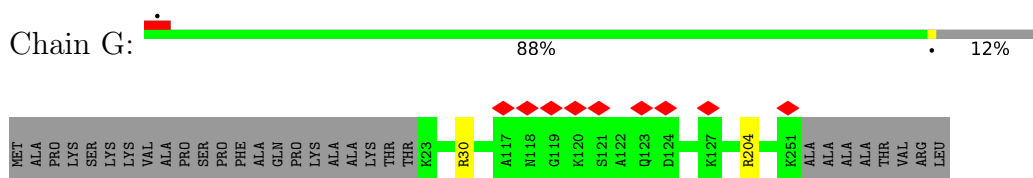
• Molecule 13: 60S ribosomal protein L9-A

Chain H:

11%

92%   8%

MET GLY ARG ASP **I5** **D8 E9** **K15 G16** **V17** **D20** **G30 P31** **G50 N51** **R62** **E105 N106 G107** **P128** **T131 V132 S133 I134** SER SER ALA VAL LYS **D140 E141** **N184** ILE GLU GLU LEU GLU GLU
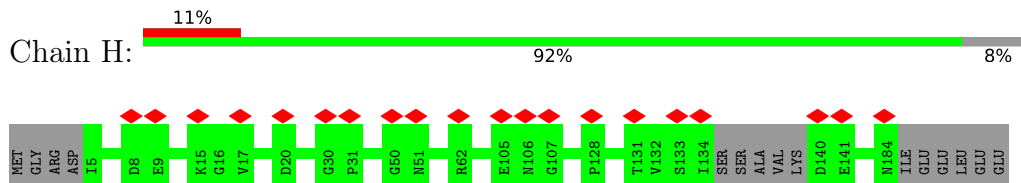
• Molecule 14: 60S ribosomal protein L10-A

Chain I:

9%

76%   24%

MET ALA ARG ARG PRO ALA ARG CYS TYR ARG TYR CYS LYS ASN LYS PRO TYR PRO LYS SER ARG TYR ASN ARG ALA VAL **P27** **D44** **V97** ARG ILE ASN LYS MET LEU SER CYS ALA GLY ALA ASP ARG LEU GLN THR GLY MET ARG HIS ALA PHE GLY LYS PRO **N123** **I182**

R185 S186 R187 G188 E189 I190 **F199** **K202** **E208 K209 L210 D211 L212 F213 P214 E215 A216 S217 F218 N219** LEU ALA
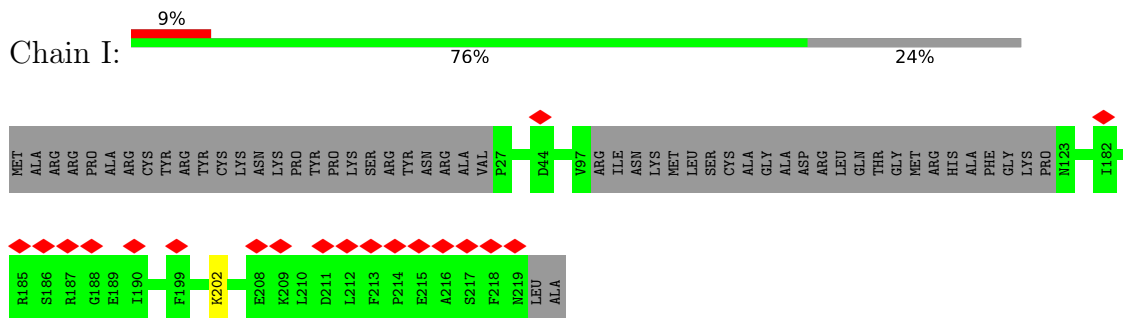
• Molecule 15: 60S ribosomal protein L11-A

Chain J:

18%

94%

MET ALA GLU LYS **A5** **Q6** **N7** **G24 E25 S26 G27 D28 R29** **E38** **Q43** **R55** **G58 I59 R60** **E90** **S97** **Q107 E108 H109 I110 D111 L112 G113 I114 K115 Y116 D117 P118 S119 I120 G121 I122** **M125** **E157** **N161** **D168** **L172 G173** LYS
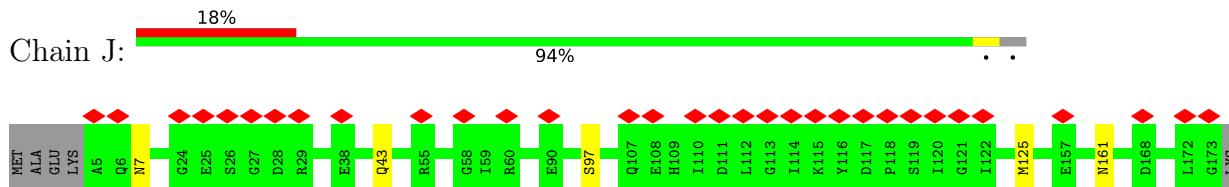
• Molecule 16: 60S ribosomal protein L43-A

Chain K:

95%

MET THR **K3** **S83** **V92** GLU VAL
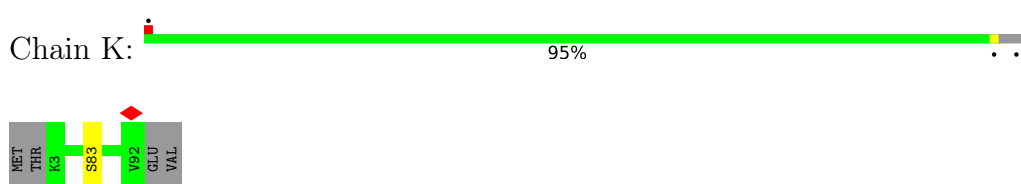
• Molecule 17: 60S ribosomal protein L13

Chain L:

97%

MET **A2** **A203** GLU ALA LYS LYS LYS
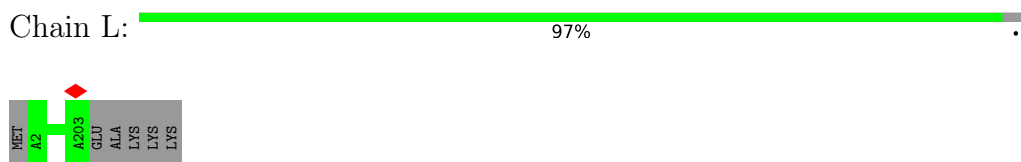
• Molecule 18: 60S ribosomal protein L14

Chain M:

93%   7%

MET GLU GLY F4 N85 V128 ALA LYS ALA LEU LYS ALA
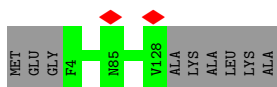
• Molecule 19: 60S ribosomal protein L15-A

Chain N:

99%

MET G2 N122 R201
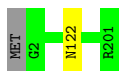
• Molecule 20: 60S ribosomal protein L16-B

Chain O:

99%

MET S2 Y197

• Molecule 21: 60S ribosomal protein L17-A

Chain P:

92%   7%

MET V2 E11 R69 D110 E154 GLU ALA VAL PRO LYS ALA ASN ASP THR V164 A183 ILE THR ALA ALA
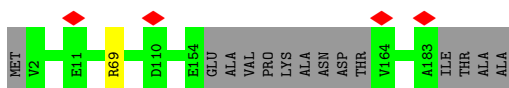
• Molecule 22: 60S ribosomal protein L18-A

Chain Q:

99%

MET G2 A184 V187

• Molecule 23: 60S ribosomal protein L19-A

Chain R:

77%   23%

MET A2 E148 A149 N150 ARG THR LYS LEU ILE GLN GLU GLN GLN ASP ALA ARG ARG ALA ARG ALA LYS ALA ALA ARG GLN ARG ARG ALA LYS ALA VAL GLU GLU LYS ARG GLU GLN LEU TYR THR ALA ALA GLU LYS ILE GLU GLU
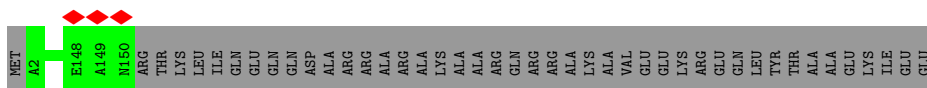
• Molecule 24: 60S ribosomal protein L20-A

Chain S:

95%   5%

MET A2 T156 GLY VAL VAL GLY LEU ALA GLY K164 Y176
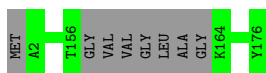
• Molecule 25: 60S ribosomal protein L21-A

Chain T:

98%

MET P2 Q103 G123 K124 T125 S142 T159 I160
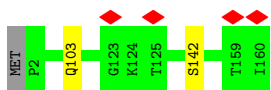
• Molecule 26: 60S ribosomal protein L22

Chain U:

13%

82% 16%

MET VAL LYS LYS ASN THR LYS VAL S9 N21 D22 K23 I24 F25 D26 D36 D41 G45 G48 S49 S50 S54 R55 E56 G57 H66 Y73 Y106 ASN VAL VAL VAL GLY ASN ASP GLU GLU GLU GLN
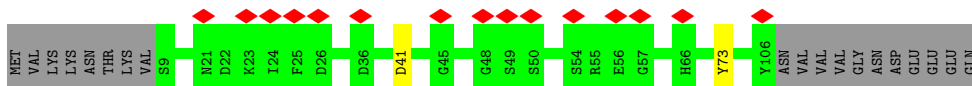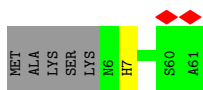
• Molecule 27: 60S ribosomal protein L23-A

Chain V:

96%

MET SER ARG G4 M76 D91 V139
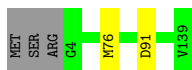
• Molecule 28: 60S ribosomal protein L25-A

Chain X:

82% 17%

MET SER VAL ALA LYS ALA LYS GLY ALA GLN LYS THR VAL GLN LYS GLY ILE HIS ASN LYS VAL ALA LYS LYS V25 D133 L141
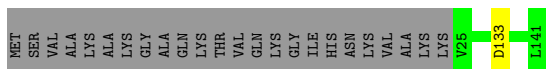
• Molecule 29: 60S ribosomal protein L26

Chain Y:

98%

M1 K2 V125 GLU

• Molecule 30: 60S ribosomal protein L27-A

Chain Z:

97%

MET VAL K3 L26 S33 F136
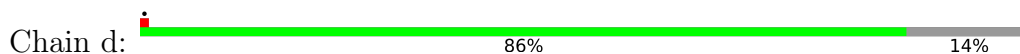
• Molecule 31: 60S ribosomal protein L28-A

Chain a:

99%

MET P2 E96 A148

• Molecule 32: 60S ribosomal protein L29

Chain b:

90%   8%

MET ALA LYS SER LYS N6 H7 S60 A61

• Molecule 33: 60S ribosomal protein L30-2

Chain c:

80%   19%

MET SER ALA ALA PRO THR THR ALA PRO VAL ALA ALA VAL SER LYS LYS GLY LYS LYS SER GLY ASP T23 S50 G110 D111 S112 D113 A116 A117

• Molecule 34: 60S ribosomal protein L31

Chain d:

86%   14%

MET ALA ASN THR LYS LYS SER ALA ILE ASN Q11 D86 GLU ASP ASP LYS ALA L92 E112 GLU

• Molecule 35: 60S ribosomal protein L32-A

Chain e:

91%   8%

MET ALA ALA V4 D20 G120 ALA LYS VAL ARG SER GLN GLU

• Molecule 36: 60S ribosomal protein L33-B

Chain f:

98%

MET PRO A3 I108

• Molecule 37: 60S ribosomal protein L34-A

Chain g:

93%   5%

MET ALA Q3 R4 E97 L108 SER SER GLN LYS

• Molecule 38: 60S ribosomal protein L35

Chain h:

99%

MET A2 A122

• Molecule 39: 60S ribosomal protein L36-B

Chain i:

96%

MET A2 S90 L97 ALA HIS

• Molecule 40: 60S ribosomal protein L37-B

Chain j:

91% 9%

MET T2 A84 ALA ALA VAL ALA ALA SER ALA

• Molecule 41: 60S ribosomal protein L38-1

5%

Chain k:

91% 5%

MET P2 S6 K9 K18 D50 A51 K52 E55 D64 G71 LYS LYS ALA

• Molecule 42: Ribosome biogenesis protein erb1

14%

Chain m:

57% 43%

MET GLU THR GLY MET ASN LYS ARG SER ARG SER LYS ARG ALA ASN SER ASN VAL GLY VAL GLU LYS ASP LYS GLU GLU LYS LYS SER LYS GLY VAL SER ASN VAL PRO ASN GLU VAL THR GLU SER SER HIS GLU PRO PHE LYS LYS ASP VAL ASP GLU ILE PRO

SER LEU THR ALA GLU LEU SER GLU GLU GLU GLU GLY GLU TYR SER SER GLU SER GLY ARG SER THR PRO GLU LEU SER PRO ASP PHE GLU ASP ALA ASP GLU GLU PHE GLU GLU ILE ASP ALA GLY TYR SER SER ASP SER SER THR GLU ASP VAL ALA PRO GLY LEU TYR

GLU SER PRO TYR ASP GLU ASN LEU TYR ILE ASN TYR ILE ASP GLY LYS ILE LYS THR ARG PRO ALA THR PRO ALA LEU ASP SER LEU ILE ALA SER ILE ASP LYS ASP SER GLY TRP THR GLY ILE LEU ASP PRO MET THR GLY LYS PRO VAL ASN LEU THR GLU GLU LEU

GLY LEU LEU LYS ARG LEU ALA GLN LEU SER GLU ILE PRO ASP GLU ASN PHE ASP PRO TYR PRO ASP TYR ASP PHE PHE THR ASN THR VAL ARG GLU THR PRO LEU SER SER ALA PRO GLU PRO LYS ARG ARG PHE ALA **P227 S228** K229 **Q232 K233 R234 I235 L236 A239 Y240** ALA ILE

ARG LYS GLY ARG ILE LEU THR SER GLU GLU GLN ARG ALA GLU ARG GLU GLU SER **Q261 S262** D268 A271 ASP ASP ASP GLN ALA THR VAL ASN ARG LYS LEU ASP TYR A286 H296 E304 E305 Y306 LEU LYS GLN SER SER ASP PHE P314 K315 K316 Y317 K318 S319 L320 R321

V322 V323 P324 A325 Y326 S327 R347 ARG THR LYS LEU ASN ILE ASP P355 E356 S357 L358 L359 P360 K361 L362 P363 T364 E367 L368 R369 P370 F371 R374 I380 G381 H382 K383 S390 L398 A399 S400 D403 V412 M413 T414 G415 R416 K420 C421 S422 L423 ASP SER PHE

GLY ASN ALA HIS ASN ILE ASP SER ASP GLU ASP ALA VAL ASN GLU SER LEU SER HIS SER THR LYS SER SER I451 L460 S461 D462 S463 P464 V465 A469 V470 D471 E472 T473 V474 Y475 P480 I481 F482 E485 Q486 I487 E488 A489 E492 L493 F494 T495 SER ALA PRO TYR GLN

GLU SER S503 R507 R508 GLY ALA LYS GLN SER LEU GLN L516 H517 G518 G519 R539 T549 S561 R562 G563 A564 S570 L601 V602 D644 Y665 R687 V688 Y689 S690 D691 L692 L693 A694 N706 H707 K708 K723 G731 E735 T740

• Molecule 43: Pescadillo homolog

Chain n:

• Molecule 44: 60S ribosomal protein L42

Chain o:

• Molecule 45: Ribosome biogenesis protein ytm1

Chain p:

LYS ASN ALA GLU PHE THR PRO GLN ALA GLY A258 R259 S260 P261 L262 I263 L264 C265 E266 G267 H268 T269 M273 D274 I275 V276 F277 S278 D279 D280 P281 S282 V283 A284 Y285 S286 V287 G288 T292 T295 W296 D297 L298 I299 T300 G301 Q302 N303 V304 D305 S306 K307 I308 T309 K310 A311

L314 C315 V316 E317 K318 L319 T320 D321 L322 H323 L324 V325 I326 S330 A331 R332 H333 H337 D338 P339 R340 ALA GLY SER ASP LYS ILE V347 S348 H349 T350 L351 S352 G353 H354 K355 N356 L357 V358 S359 G360 L361 S362 A363 S364 P365 E366 N367 P368 Y369 M370 F371 A372 S373 V374 T379 C380

R381 V382 W383 D384 V385 R386 A387 T388 S389 G390 S391 I392 Y393 T394 I395 SER ARG ALA GLU LYS THR GLY SER GLN W405 D406 F409 A410 V411 D412 W413 N414 K415 S416 I417 G418 I419 V420 T421 G422 D425 K426 Q427 L428 Q429 I430 N431 Q432 SER SER PHE GLY LYS SER GLU

• Molecule 46: Ribosome biogenesis protein rlp24

Chain u:

29% • 69%

MET R2 V3 H4 Y7 Y55 G60 LYS GLU MET VAL TYR ASP THR ALA LEU ALA VAL THR ALA ALA ARG ARG ASN VAL PRO VAL ARG TYR ASP ARG ASN VAL ILE ALA THR THR LEU ASN ALA MET LYS ARG VAL SER GLN VAL HIS ALA LYS ARG GLU ARG LEU PHE TYR LYS

LYS ARG LEU ALA GLY LYS ARG ALA GLN GLU LEU GLN GLU ALA GLN LYS LEU ILE ALA GLN ASN VAL PRO GLN PHE THR GLU GLU PRO GLU GLY VAL GLU VAL GLU THR ALA GLU VAL GLN GLU GLU PRO GLN ILE ALA VAL SER ASP GLU GLU TYR THR MET GLU GLU GLU VAL ALA GLU PRO VAL LYS ILE

PRO VAL LEU ALA LYS LYS ARG ASN LYS LYS SER SER ARG ASN SER SER SER ALA MET GLN MET ASP

4 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	90	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.589	Depositor
Minimum map value	-0.293	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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

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	1	0.42	0/68374	0.73	0/106528
2	2	0.45	0/3748	0.73	0/5835
3	3	0.35	0/1064	0.56	0/1431
4	8	0.30	0/448	0.58	0/597
5	9	0.26	0/2816	0.69	0/4388
6	A	0.31	0/1896	0.57	0/2556
7	B	0.29	0/3069	0.53	0/4130
8	C	0.30	0/2848	0.52	0/3842
9	D	0.26	0/2336	0.49	0/3142
10	E	0.28	0/1444	0.52	0/1948
11	F	0.30	0/1781	0.50	0/2389
12	G	0.29	0/1833	0.49	0/2467
13	H	0.24	0/860	0.43	0/1193
14	I	0.25	0/1379	0.49	0/1848
15	J	0.28	0/1382	0.53	0/1850
16	K	0.30	0/704	0.60	0/941
17	L	0.29	0/1644	0.53	0/2215
18	M	0.27	0/1024	0.52	0/1375
19	N	0.33	0/1717	0.56	0/2304
20	O	0.31	0/1588	0.50	0/2128
21	P	0.31	0/1393	0.52	0/1866
22	Q	0.30	0/1511	0.55	0/2019
23	R	0.28	0/1248	0.54	0/1661
24	S	0.28	0/1444	0.52	0/1939
25	T	0.32	0/1317	0.53	0/1772
26	U	0.29	0/805	0.49	0/1080
27	V	0.30	0/1031	0.53	0/1388
28	X	0.30	0/955	0.53	0/1285
29	Y	0.28	0/1008	0.58	0/1341
30	Z	0.29	0/1095	0.53	0/1467
31	a	0.31	0/1198	0.55	0/1608
32	b	0.30	0/479	0.57	0/634

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z|$ >5	RMSZ	#$|Z|$ >5
33	c	0.27	0/721	0.47	0/969
34	d	0.29	0/824	0.54	0/1106
35	e	0.31	0/953	0.56	0/1271
36	f	0.31	0/859	0.53	0/1152
37	g	0.35	0/873	0.60	0/1170
38	h	0.29	0/1008	0.52	0/1340
39	i	0.27	0/774	0.56	0/1028
40	j	0.35	0/671	0.57	0/888
41	k	0.30	0/570	0.56	0/762
42	m	0.28	0/3471	0.50	0/4715
43	n	0.26	0/3037	0.47	0/4087
44	o	0.27	0/810	0.50	0/1074
45	p	0.24	0/1396	0.44	0/1935
46	u	0.50	0/509	0.63	0/678
All	All	0.37	0/131915	0.65	0/193342

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
3	3	121/302 (40%)	112 (93%)	7 (6%)	2 (2%)	9	36
4	8	48/51 (94%)	46 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A	243/253 (96%)	234 (96%)	9 (4%)	0	100	100
7	B	375/388 (97%)	362 (96%)	13 (4%)	0	100	100
8	C	357/363 (98%)	338 (95%)	19 (5%)	0	100	100
9	D	282/294 (96%)	278 (99%)	4 (1%)	0	100	100
10	E	181/195 (93%)	167 (92%)	13 (7%)	1 (1%)	25	59
11	F	212/250 (85%)	206 (97%)	6 (3%)	0	100	100
12	G	227/259 (88%)	223 (98%)	4 (2%)	0	100	100
13	H	171/190 (90%)	167 (98%)	4 (2%)	0	100	100
14	I	164/221 (74%)	161 (98%)	3 (2%)	0	100	100
15	J	167/174 (96%)	163 (98%)	4 (2%)	0	100	100
16	K	88/94 (94%)	84 (96%)	4 (4%)	0	100	100
17	L	200/208 (96%)	190 (95%)	10 (5%)	0	100	100
18	M	123/134 (92%)	117 (95%)	6 (5%)	0	100	100
19	N	198/201 (98%)	188 (95%)	10 (5%)	0	100	100
20	O	194/197 (98%)	193 (100%)	1 (0%)	0	100	100
21	P	169/187 (90%)	162 (96%)	7 (4%)	0	100	100
22	Q	184/187 (98%)	173 (94%)	10 (5%)	1 (0%)	29	64
23	R	147/193 (76%)	146 (99%)	1 (1%)	0	100	100
24	S	164/176 (93%)	153 (93%)	11 (7%)	0	100	100
25	T	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
26	U	96/117 (82%)	90 (94%)	6 (6%)	0	100	100
27	V	134/139 (96%)	131 (98%)	3 (2%)	0	100	100
28	X	115/141 (82%)	114 (99%)	1 (1%)	0	100	100
29	Y	123/126 (98%)	119 (97%)	4 (3%)	0	100	100
30	Z	132/136 (97%)	125 (95%)	7 (5%)	0	100	100
31	a	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
32	b	54/61 (88%)	51 (94%)	2 (4%)	1 (2%)	8	33
33	c	93/117 (80%)	90 (97%)	3 (3%)	0	100	100
34	d	93/113 (82%)	92 (99%)	1 (1%)	0	100	100
35	e	115/127 (91%)	113 (98%)	2 (2%)	0	100	100
36	f	104/108 (96%)	99 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	g	104/112 (93%)	98 (94%)	6 (6%)	0	100	100
38	h	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
39	i	94/99 (95%)	90 (96%)	4 (4%)	0	100	100
40	j	81/91 (89%)	78 (96%)	3 (4%)	0	100	100
41	k	68/74 (92%)	66 (97%)	2 (3%)	0	100	100
42	m	409/740 (55%)	386 (94%)	23 (6%)	0	100	100
43	n	351/607 (58%)	331 (94%)	20 (6%)	0	100	100
44	o	96/106 (91%)	93 (97%)	3 (3%)	0	100	100
45	p	274/440 (62%)	265 (97%)	9 (3%)	0	100	100
46	u	57/192 (30%)	55 (96%)	2 (4%)	0	100	100
All	All	7029/8593 (82%)	6760 (96%)	264 (4%)	5 (0%)	54	83

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	3	13	HIS
3	3	11	VAL
22	Q	184	ALA
32	b	7	HIS
10	E	135	LYS

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	
3	3	111/271 (41%)	109 (98%)	2 (2%)	59	82
4	8	46/47 (98%)	46 (100%)	0	100	100
6	A	188/192 (98%)	187 (100%)	1 (0%)	88	94
7	B	316/326 (97%)	315 (100%)	1 (0%)	92	96
8	C	296/297 (100%)	295 (100%)	1 (0%)	92	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	D	234/241 (97%)	231 (99%)	3 (1%)	69	87
10	E	146/155 (94%)	145 (99%)	1 (1%)	84	93
11	F	180/210 (86%)	178 (99%)	2 (1%)	73	89
12	G	191/212 (90%)	189 (99%)	2 (1%)	76	90
14	I	144/187 (77%)	143 (99%)	1 (1%)	84	93
15	J	142/146 (97%)	137 (96%)	5 (4%)	36	68
16	K	71/75 (95%)	70 (99%)	1 (1%)	67	86
17	L	162/167 (97%)	162 (100%)	0	100	100
18	M	108/113 (96%)	108 (100%)	0	100	100
19	N	175/176 (99%)	174 (99%)	1 (1%)	86	94
20	O	161/162 (99%)	161 (100%)	0	100	100
21	P	139/149 (93%)	138 (99%)	1 (1%)	84	93
22	Q	158/159 (99%)	158 (100%)	0	100	100
23	R	127/162 (78%)	127 (100%)	0	100	100
24	S	150/154 (97%)	150 (100%)	0	100	100
25	T	138/139 (99%)	136 (99%)	2 (1%)	67	86
26	U	85/103 (82%)	83 (98%)	2 (2%)	49	76
27	V	104/107 (97%)	102 (98%)	2 (2%)	57	81
28	X	104/122 (85%)	103 (99%)	1 (1%)	76	90
29	Y	110/111 (99%)	109 (99%)	1 (1%)	78	91
30	Z	113/115 (98%)	111 (98%)	2 (2%)	59	82
31	a	121/122 (99%)	121 (100%)	0	100	100
32	b	47/51 (92%)	47 (100%)	0	100	100
33	c	76/91 (84%)	75 (99%)	1 (1%)	69	87
34	d	89/102 (87%)	89 (100%)	0	100	100
35	e	100/107 (94%)	99 (99%)	1 (1%)	76	90
36	f	89/91 (98%)	89 (100%)	0	100	100
37	g	92/97 (95%)	90 (98%)	2 (2%)	52	78
38	h	106/107 (99%)	106 (100%)	0	100	100
39	i	82/84 (98%)	81 (99%)	1 (1%)	71	88
40	j	68/71 (96%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
41	k	63/66 (96%)	60 (95%)	3 (5%)	25	58	
42	m	378/659 (57%)	374 (99%)	4 (1%)	73	89	
43	n	319/532 (60%)	315 (99%)	4 (1%)	69	87	
44	o	88/93 (95%)	88 (100%)	0	100	100	
46	u	52/168 (31%)	48 (92%)	4 (8%)	13	41	
All	All	5669/6739 (84%)	5617 (99%)	52 (1%)	79	91	

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	3	47	ASN
3	3	114	ARG
6	A	192	ARG
7	B	378	GLN
8	C	156	ASP
9	D	90	TRP
9	D	158	ARG
9	D	281	LYS
10	E	16	MET
11	F	89	LYS
11	F	234	ASP
12	G	30	ARG
12	G	204	ARG
14	I	202	LYS
15	J	7	ASN
15	J	43	GLN
15	J	97	SER
15	J	125	MET
15	J	161	ASN
16	K	83	SER
19	N	122	ASN
21	P	69	ARG
25	T	103	GLN
25	T	142	SER
26	U	41	ASP
26	U	73	TYR
27	V	76	MET
27	V	91	ASP
28	X	133	ASP
29	Y	2	LYS

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Mol	Chain	Res	Type
30	Z	26	LEU
30	Z	33	SER
33	c	50	SER
35	e	20	ASP
37	g	4	ARG
37	g	97	GLU
39	i	90	SER
41	k	6	SER
41	k	9	LYS
41	k	18	LYS
42	m	306	TYR
42	m	644	ASP
42	m	665	TYR
42	m	689	TYR
43	n	244	ARG
43	n	248	LYS
43	n	362	ARG
43	n	366	ARG
46	u	2	ARG
46	u	4	HIS
46	u	7	TYR
46	u	55	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
7	B	182	GLN
15	J	68	HIS
21	P	97	ASN
25	T	98	HIS
28	X	136	ASN
32	b	43	GLN
37	g	98	GLN
43	n	190	GLN
46	u	37	HIS

5.3.3　RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2823/3498 (80%)	580 (20%)	10 (0%)

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W O R L D W I D E
wwPDB
PROTEIN DATA BANK

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	2	157/165 (95%)	33 (21%)	1 (0%)
5	9	117/229 (51%)	14 (11%)	0
All	All	3097/3892 (79%)	627 (20%)	11 (0%)

All (627) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	4	U
1	1	5	G
1	1	25	U
1	1	26	A
1	1	30	G
1	1	40	A
1	1	43	A
1	1	49	A
1	1	59	G
1	1	60	A
1	1	63	A
1	1	65	A
1	1	66	A
1	1	68	A
1	1	74	A
1	1	92	G
1	1	96	G
1	1	99	A
1	1	109	A
1	1	110	G
1	1	111	C
1	1	116	A
1	1	122	A
1	1	132	C
1	1	147	C
1	1	153	U
1	1	154	G
1	1	156	A
1	1	161	C
1	1	162	A
1	1	163	A
1	1	167	G
1	1	168	C
1	1	169	U
1	1	170	G

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Mol	Chain	Res	Type
1	1	175	G
1	1	178	U
1	1	181	A
1	1	188	C
1	1	189	G
1	1	190	G
1	1	193	U
1	1	197	U
1	1	198	U
1	1	207	C
1	1	213	G
1	1	217	G
1	1	218	A
1	1	219	G
1	1	220	A
1	1	225	G
1	1	226	A
1	1	227	G
1	1	239	U
1	1	241	G
1	1	243	C
1	1	244	G
1	1	247	U
1	1	252	A
1	1	257	A
1	1	258	U
1	1	259	A
1	1	260	U
1	1	261	A
1	1	266	G
1	1	269	U
1	1	270	U
1	1	274	A
1	1	277	G
1	1	289	G
1	1	292	A
1	1	293	A
1	1	303	A
1	1	305	A
1	1	310	U
1	1	311	G
1	1	312	G

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Mol	Chain	Res	Type
1	1	313	U
1	1	315	A
1	1	319	U
1	1	321	A
1	1	322	U
1	1	324	U
1	1	331	A
1	1	337	U
1	1	339	G
1	1	344	A
1	1	345	G
1	1	346	A
1	1	347	C
1	1	359	A
1	1	360	A
1	1	367	U
1	1	377	A
1	1	378	U
1	1	384	G
1	1	406	U
1	1	410	A
1	1	411	C
1	1	429	G
1	1	430	A
1	1	437	G
1	1	445	G
1	1	449	U
1	1	505	G
1	1	531	A
1	1	532	A
1	1	534	A
1	1	540	A
1	1	544	A
1	1	545	A
1	1	546	G
1	1	547	G
1	1	550	G
1	1	551	C
1	1	577	U
1	1	578	U
1	1	579	A
1	1	581	A

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Mol	Chain	Res	Type
1	1	582	G
1	1	591	G
1	1	592	U
1	1	602	A
1	1	603	C
1	1	616	A
1	1	618	U
1	1	629	G
1	1	634	G
1	1	635	G
1	1	636	A
1	1	646	A
1	1	647	A
1	1	661	C
1	1	672	A
1	1	674	A
1	1	676	G
1	1	685	A
1	1	700	C
1	1	702	A
1	1	706	U
1	1	708	U
1	1	732	A
1	1	739	G
1	1	742	A
1	1	747	A
1	1	765	G
1	1	770	G
1	1	774	C
1	1	775	A
1	1	778	G
1	1	783	A
1	1	786	C
1	1	794	U
1	1	795	G
1	1	796	U
1	1	797	C
1	1	798	A
1	1	802	G
1	1	806	G
1	1	807	G
1	1	808	U

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Mol	Chain	Res	Type
1	1	809	U
1	1	812	A
1	1	813	G
1	1	816	A
1	1	817	G
1	1	833	A
1	1	840	A
1	1	846	U
1	1	848	A
1	1	849	A
1	1	862	A
1	1	877	G
1	1	878	A
1	1	882	U
1	1	889	G
1	1	893	C
1	1	902	A
1	1	903	U
1	1	906	U
1	1	911	U
1	1	912	G
1	1	928	A
1	1	939	G
1	1	940	G
1	1	946	A
1	1	947	A
1	1	948	G
1	1	949	A
1	1	953	A
1	1	955	C
1	1	956	G
1	1	957	A
1	1	958	A
1	1	965	A
1	1	969	G
1	1	976	C
1	1	985	G
1	1	991	C
1	1	992	U
1	1	993	C
1	1	995	G
1	1	1002	A

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Mol	Chain	Res	Type
1	1	1006	A
1	1	1008	U
1	1	1011	G
1	1	1012	A
1	1	1013	U
1	1	1026	G
1	1	1034	A
1	1	1042	G
1	1	1046	U
1	1	1073	U
1	1	1079	A
1	1	1081	C
1	1	1095	G
1	1	1096	A
1	1	1097	C
1	1	1113	U
1	1	1119	G
1	1	1126	A
1	1	1127	U
1	1	1129	G
1	1	1130	A
1	1	1135	G
1	1	1139	U
1	1	1147	G
1	1	1148	G
1	1	1162	G
1	1	1166	A
1	1	1171	G
1	1	1175	U
1	1	1184	A
1	1	1185	A
1	1	1186	C
1	1	1190	A
1	1	1205	G
1	1	1211	A
1	1	1212	U
1	1	1223	C
1	1	1224	A
1	1	1227	C
1	1	1231	A
1	1	1232	G
1	1	1239	U

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Mol	Chain	Res	Type
1	1	1243	A
1	1	1326	G
1	1	1339	A
1	1	1340	U
1	1	1356	U
1	1	1361	A
1	1	1362	U
1	1	1363	A
1	1	1379	U
1	1	1380	A
1	1	1388	G
1	1	1389	A
1	1	1390	A
1	1	1421	G
1	1	1433	U
1	1	1434	G
1	1	1452	A
1	1	1453	A
1	1	1455	A
1	1	1459	U
1	1	1465	G
1	1	1466	C
1	1	1468	G
1	1	1471	C
1	1	1477	G
1	1	1484	G
1	1	1487	A
1	1	1489	U
1	1	1503	C
1	1	1515	A
1	1	1516	A
1	1	1517	G
1	1	1521	G
1	1	1525	A
1	1	1528	U
1	1	1536	G
1	1	1537	A
1	1	1542	C
1	1	1561	C
1	1	1571	A
1	1	1573	A
1	1	1581	G

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Mol	Chain	Res	Type
1	1	1587	U
1	1	1588	A
1	1	1589	U
1	1	1590	G
1	1	1600	C
1	1	1602	A
1	1	1603	U
1	1	1604	U
1	1	1606	U
1	1	1608	C
1	1	1609	G
1	1	1618	A
1	1	1622	A
1	1	1624	A
1	1	1629	A
1	1	1640	A
1	1	1655	G
1	1	1664	A
1	1	1666	C
1	1	1677	A
1	1	1678	A
1	1	1691	A
1	1	1692	C
1	1	1697	G
1	1	1712	A
1	1	1713	G
1	1	1723	U
1	1	1724	U
1	1	1754	A
1	1	1756	U
1	1	1764	U
1	1	1770	G
1	1	1780	G
1	1	1781	G
1	1	1786	U
1	1	1789	A
1	1	1790	A
1	1	1791	G
1	1	1792	A
1	1	1811	A
1	1	1816	G
1	1	1819	G

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Mol	Chain	Res	Type
1	1	1821	G
1	1	1829	C
1	1	1837	G
1	1	1838	A
1	1	1839	A
1	1	1842	U
1	1	1873	U
1	1	1874	U
1	1	1876	U
1	1	1880	A
1	1	1897	A
1	1	1901	C
1	1	1902	A
1	1	1904	C
1	1	1905	A
1	1	1913	A
1	1	1933	G
1	1	1935	U
1	1	1936	A
1	1	1940	C
1	1	1941	A
1	1	1944	G
1	1	1961	G
1	1	1963	A
1	1	1989	G
1	1	1990	G
1	1	1999	U
1	1	2001	A
1	1	2003	G
1	1	2188	A
1	1	2189	C
1	1	2190	U
1	1	2191	U
1	1	2195	A
1	1	2199	G
1	1	2202	C
1	1	2203	G
1	1	2204	G
1	1	2209	G
1	1	2210	G
1	1	2214	A
1	1	2215	U

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Mol	Chain	Res	Type
1	1	2219	A
1	1	2228	U
1	1	2232	A
1	1	2234	C
1	1	2246	A
1	1	2257	G
1	1	2266	A
1	1	2272	U
1	1	2276	A
1	1	2280	C
1	1	2298	G
1	1	2299	U
1	1	2311	A
1	1	2313	U
1	1	2360	G
1	1	2361	G
1	1	2369	A
1	1	2371	G
1	1	2386	U
1	1	2395	G
1	1	2396	C
1	1	2397	A
1	1	2398	U
1	1	2401	A
1	1	2403	G
1	1	2406	U
1	1	2422	U
1	1	2424	U
1	1	2435	U
1	1	2461	A
1	1	2462	C
1	1	2463	G
1	1	2466	C
1	1	2467	C
1	1	2471	C
1	1	2473	A
1	1	2474	A
1	1	2477	C
1	1	2481	G
1	1	2485	A
1	1	2488	G
1	1	2490	A

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Mol	Chain	Res	Type
1	1	2491	G
1	1	2492	A
1	1	2493	C
1	1	2499	U
1	1	2505	U
1	1	2506	G
1	1	2522	U
1	1	2523	G
1	1	2525	G
1	1	2610	U
1	1	2611	A
1	1	2618	G
1	1	2620	A
1	1	2622	C
1	1	2647	U
1	1	2648	C
1	1	2650	A
1	1	2654	U
1	1	2657	A
1	1	2658	A
1	1	2661	U
1	1	2668	C
1	1	2669	G
1	1	2674	G
1	1	2675	A
1	1	2676	U
1	1	2688	A
1	1	2689	C
1	1	2695	C
1	1	2697	G
1	1	2701	G
1	1	2702	G
1	1	2705	G
1	1	2709	G
1	1	2721	A
1	1	2722	C
1	1	2733	A
1	1	2743	G
1	1	2746	G
1	1	2747	U
1	1	2751	A
1	1	2768	A

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Mol	Chain	Res	Type
1	1	2769	A
1	1	2778	U
1	1	2780	G
1	1	2781	A
1	1	2784	A
1	1	2786	A
1	1	2787	A
1	1	2789	A
1	1	2799	A
1	1	2809	G
1	1	2814	U
1	1	2815	G
1	1	2821	C
1	1	2823	G
1	1	2824	U
1	1	2832	C
1	1	2847	U
1	1	2848	G
1	1	2850	C
1	1	2872	G
1	1	2873	A
1	1	2875	A
1	1	2894	A
1	1	2895	G
1	1	2896	A
1	1	2897	A
1	1	2905	C
1	1	2907	C
1	1	2909	G
1	1	2912	A
1	1	2917	U
1	1	2932	A
1	1	2933	A
1	1	2948	G
1	1	2949	U
1	1	2966	G
1	1	2971	C
1	1	2982	A
1	1	2989	C
1	1	3006	A
1	1	3018	U
1	1	3020	C

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Mol	Chain	Res	Type
1	1	3021	A
1	1	3028	A
1	1	3030	U
1	1	3031	A
1	1	3040	G
1	1	3041	A
1	1	3042	G
1	1	3046	G
1	1	3050	U
1	1	3066	A
1	1	3067	G
1	1	3070	U
1	1	3078	C
1	1	3082	A
1	1	3085	G
1	1	3087	U
1	1	3108	A
1	1	3117	A
1	1	3118	G
1	1	3127	G
1	1	3155	G
1	1	3174	A
1	1	3176	G
1	1	3182	G
1	1	3188	U
1	1	3189	C
1	1	3196	C
1	1	3197	G
1	1	3200	U
1	1	3220	G
1	1	3225	A
1	1	3226	A
1	1	3227	U
1	1	3238	A
1	1	3239	A
1	1	3248	U
1	1	3269	A
1	1	3270	U
1	1	3271	G
1	1	3272	U
1	1	3273	A
1	1	3275	A

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Mol	Chain	Res	Type
1	1	3276	A
1	1	3281	A
1	1	3282	G
1	1	3307	U
1	1	3308	G
1	1	3310	A
1	1	3311	U
1	1	3314	U
1	1	3317	A
1	1	3318	A
1	1	3319	G
1	1	3329	G
1	1	3343	A
1	1	3345	G
1	1	3346	U
1	1	3347	G
1	1	3358	U
1	1	3359	U
1	1	3370	U
1	1	3371	U
1	1	3372	C
1	1	3373	C
1	1	3396	A
1	1	3405	C
1	1	3417	A
1	1	3418	U
1	1	3420	U
1	1	3425	C
1	1	3435	U
1	1	3436	A
1	1	3442	U
1	1	3443	A
1	1	3464	U
1	1	3470	G
1	1	3479	C
1	1	3483	U
1	1	3490	A
1	1	3491	A
1	1	3492	G
1	1	3497	G
1	1	3498	U
2	2	9	A

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Mol	Chain	Res	Type
2	2	31	U
2	2	42	U
2	2	43	C
2	2	67	A
2	2	70	C
2	2	71	G
2	2	83	G
2	2	87	A
2	2	89	U
2	2	90	U
2	2	91	C
2	2	92	C
2	2	93	G
2	2	94	U
2	2	95	G
2	2	98	U
2	2	103	G
2	2	112	A
2	2	114	C
2	2	115	G
2	2	119	A
2	2	120	U
2	2	121	U
2	2	122	G
2	2	124	G
2	2	132	G
2	2	135	C
2	2	136	U
2	2	156	G
2	2	159	U
2	2	162	C
2	2	165	U
5	9	57	G
5	9	72	A
5	9	83	U
5	9	92	A
5	9	100	A
5	9	103	U
5	9	104	A
5	9	114	G
5	9	122	U
5	9	124	A

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Mol	Chain	Res	Type
5	9	141	C
5	9	150	A
5	9	160	G
5	9	166	G

All (11) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	269	U
1	1	311	G
1	1	628	U
1	1	805	G
1	1	948	G
1	1	1388	G
1	1	1628	A
1	1	1640	A
1	1	2198	G
1	1	3441	G
2	2	131	G

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-24423. 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 ⓘ

6.1.1 Primary map

| X | Y | Z |
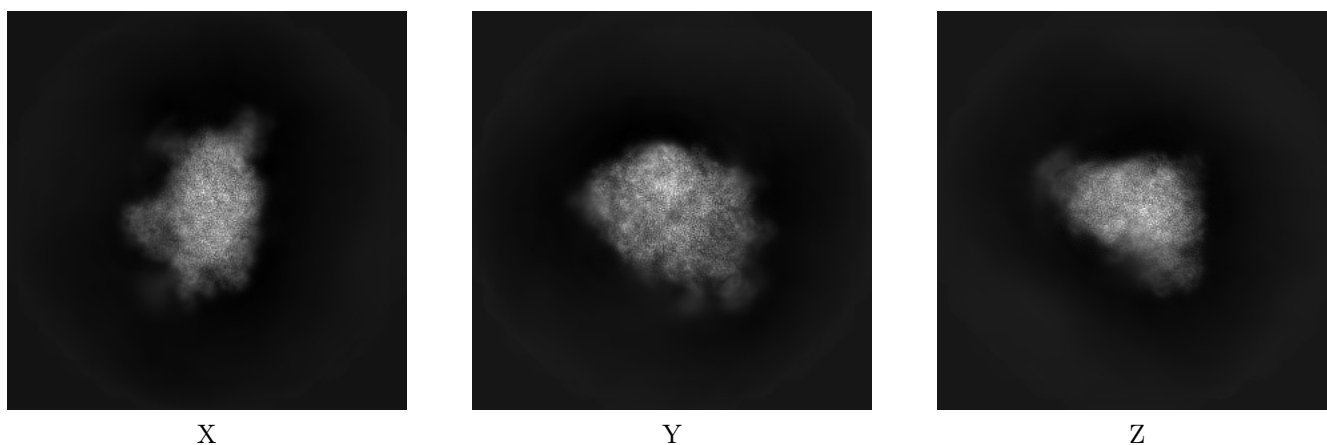
The images above show the map projected in three orthogonal directions.

6.2 Central slices ⓘ

6.2.1 Primary map

X Index: 256   Y Index: 256   Z Index: 256
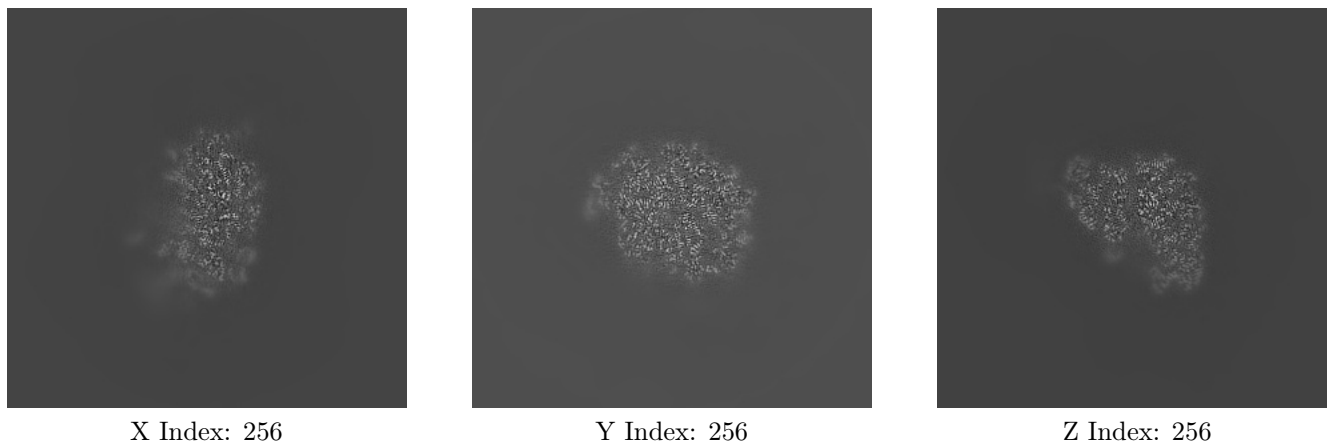
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices ⓘ
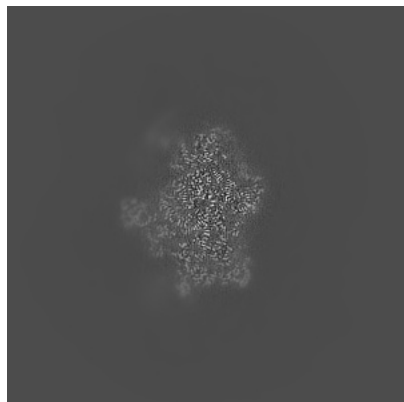
6.3.1 Primary map
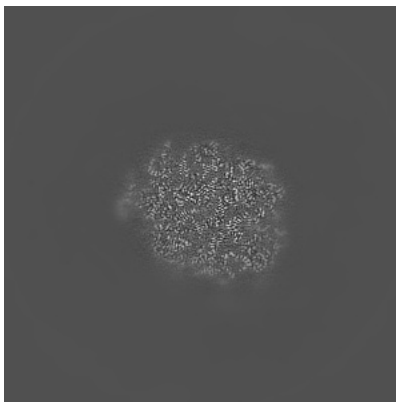
| X Index: 282 | Y Index: 262 | Z Index: 276 |
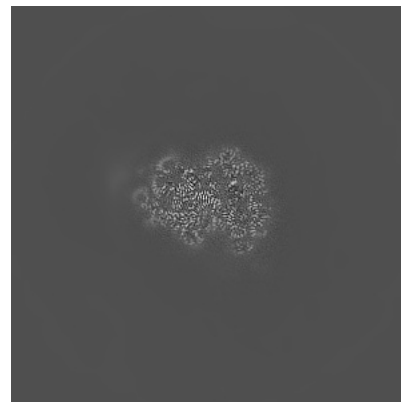
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views ⓘ

6.4.1 Primary map

| X | Y | Z |
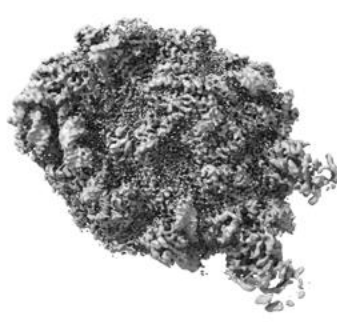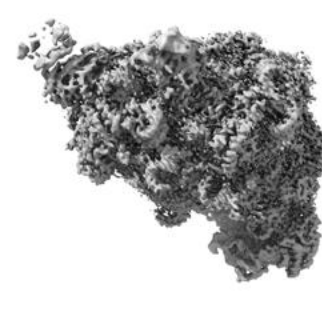
The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

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

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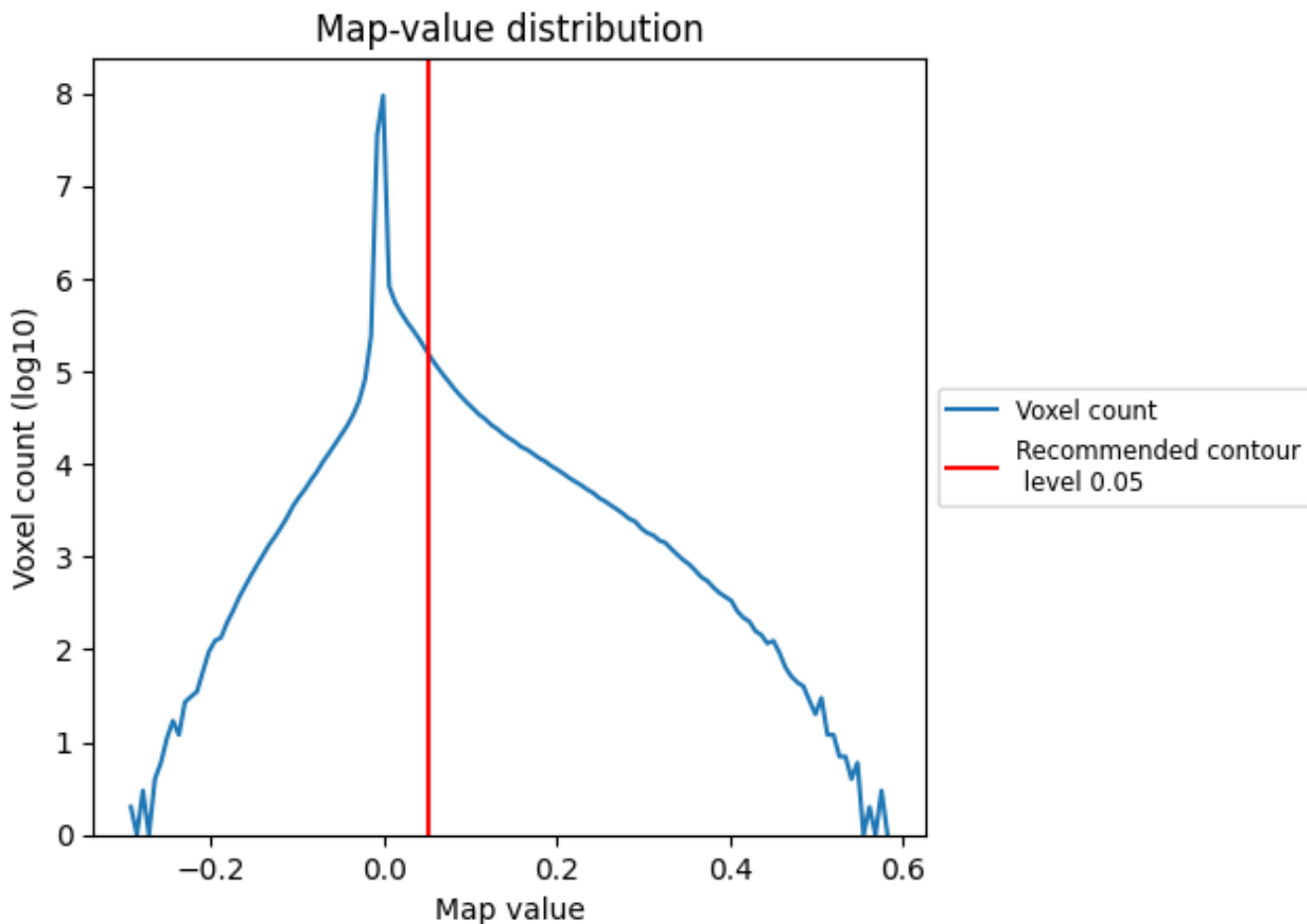
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2　Volume estimate ⓘ
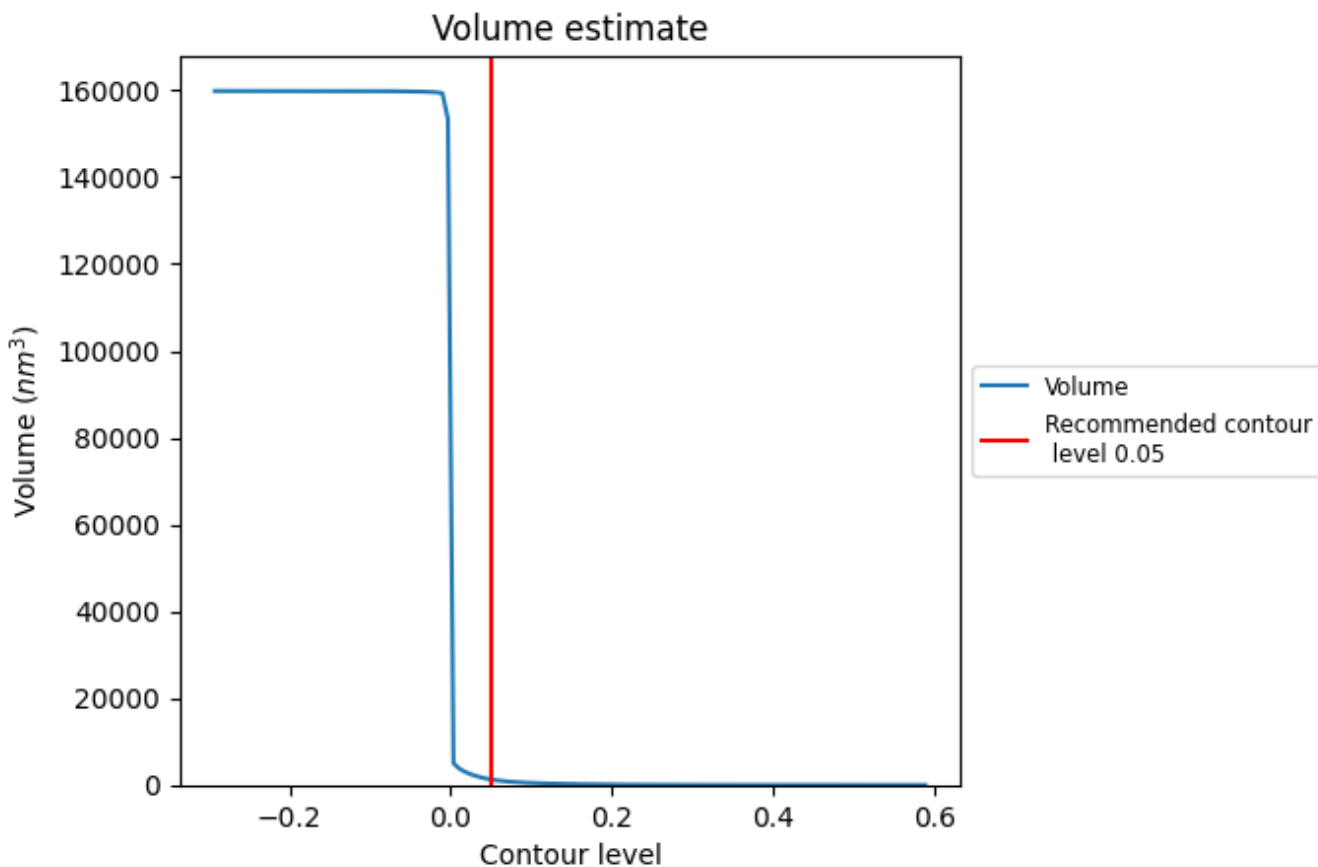
The volume at the recommended contour level is 1266 nm^3; this corresponds to an approximate mass of 1144 kDa.

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 ⓘ
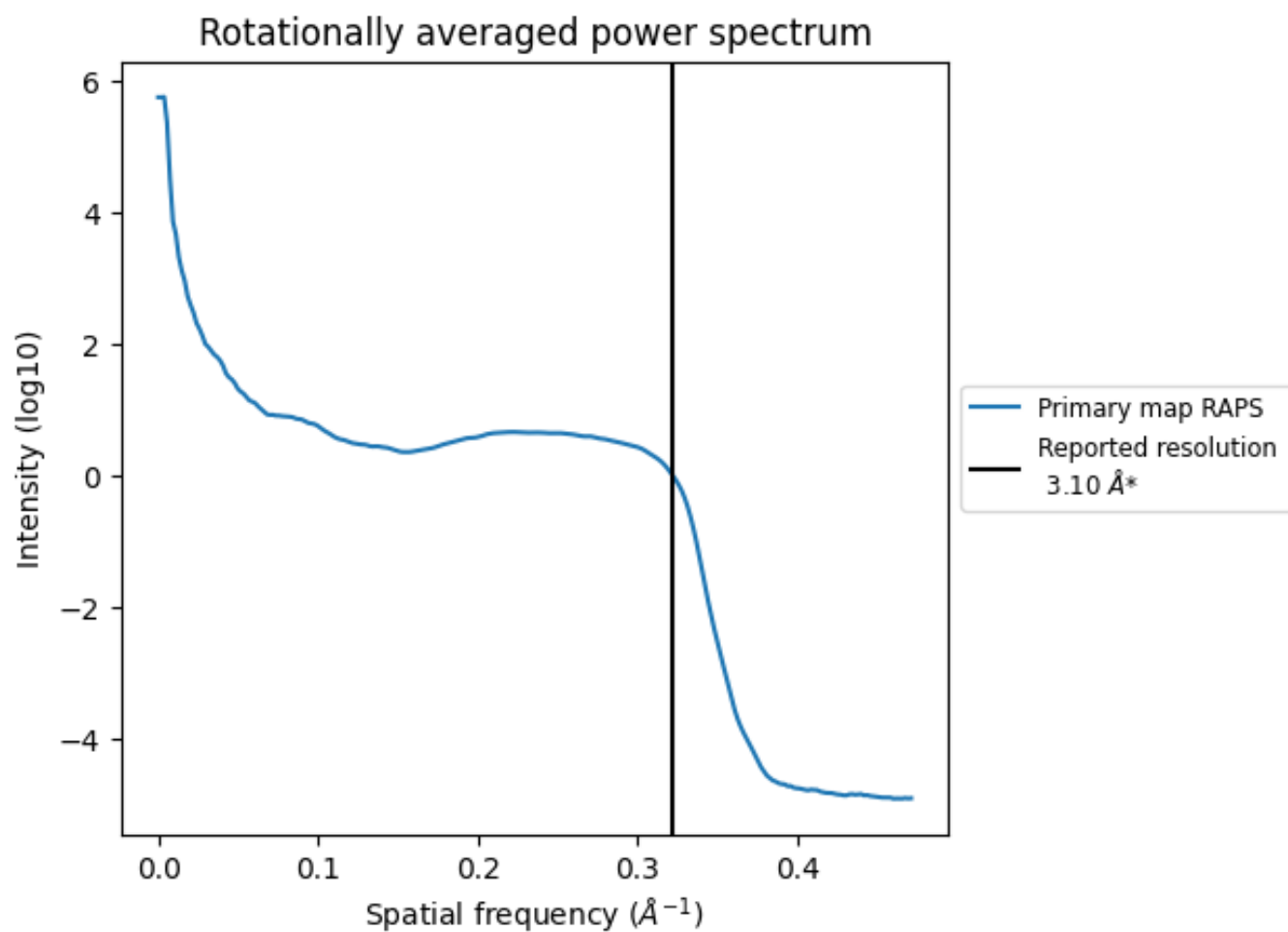
*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8 Fourier-Shell correlation ⓘ

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

9   Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-24423 and PDB model 8EUI. Per-residue inclusion information can be found in section 3 on page 12.

9.1   Map-model overlay ⓘ

| X | Y | Z |
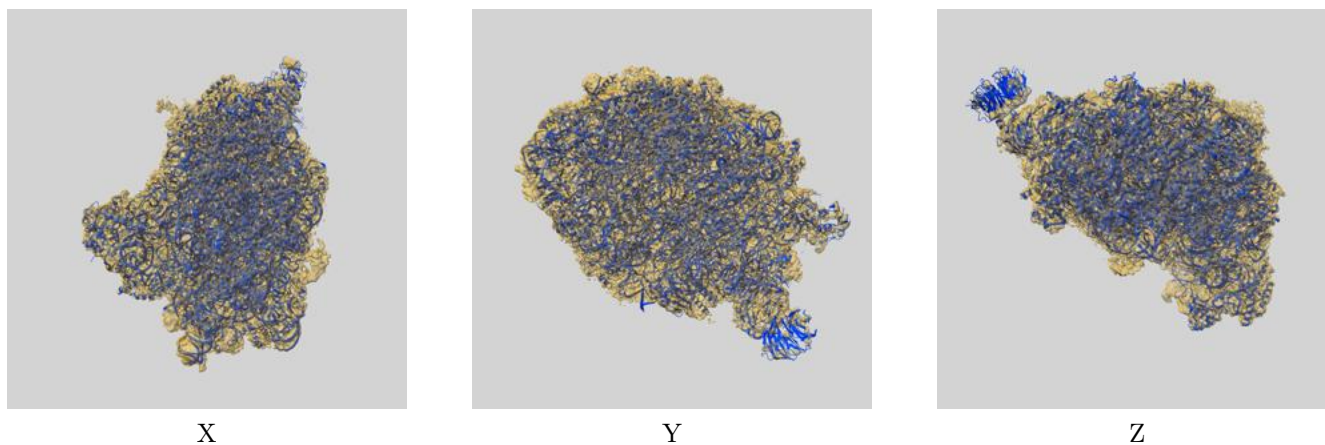
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2　Q-score mapped to coordinate model ⓘ

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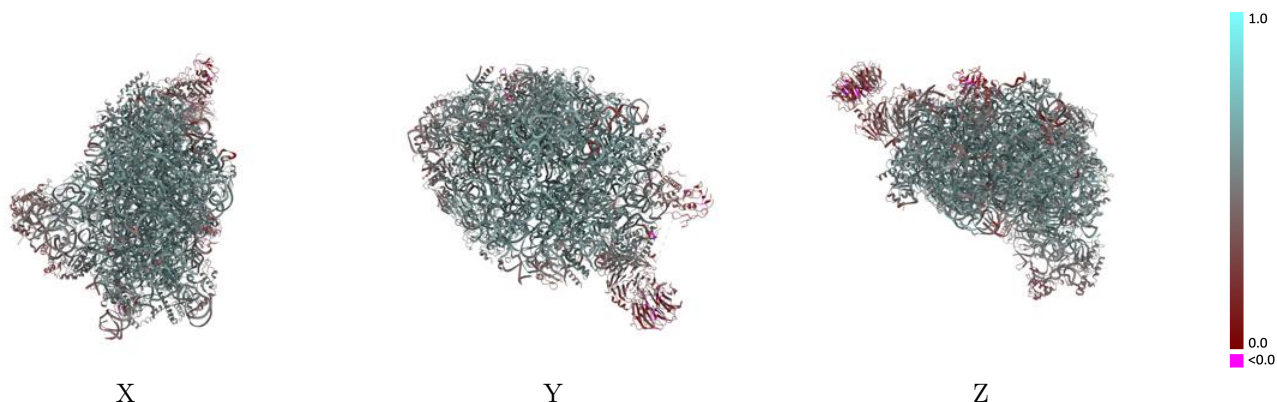
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

X	Y	Z
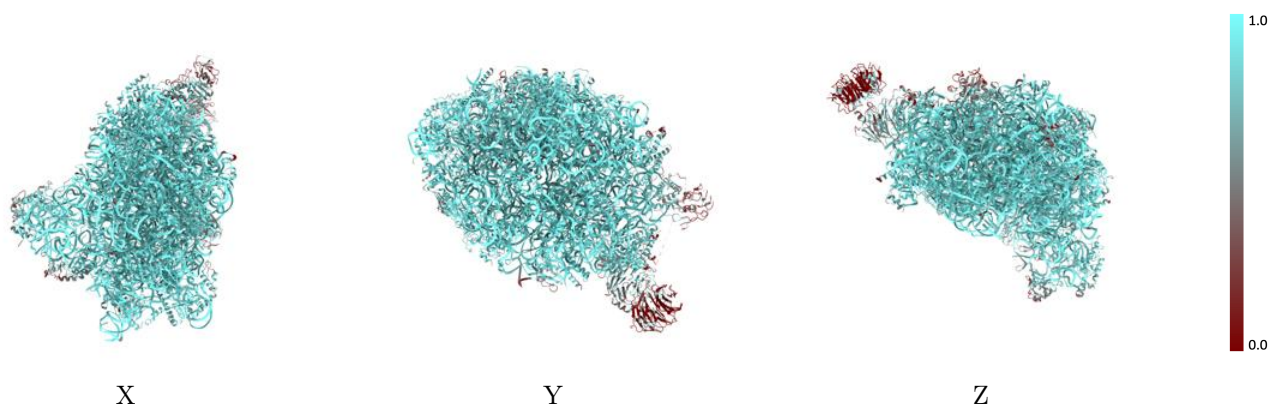
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion ⓘ
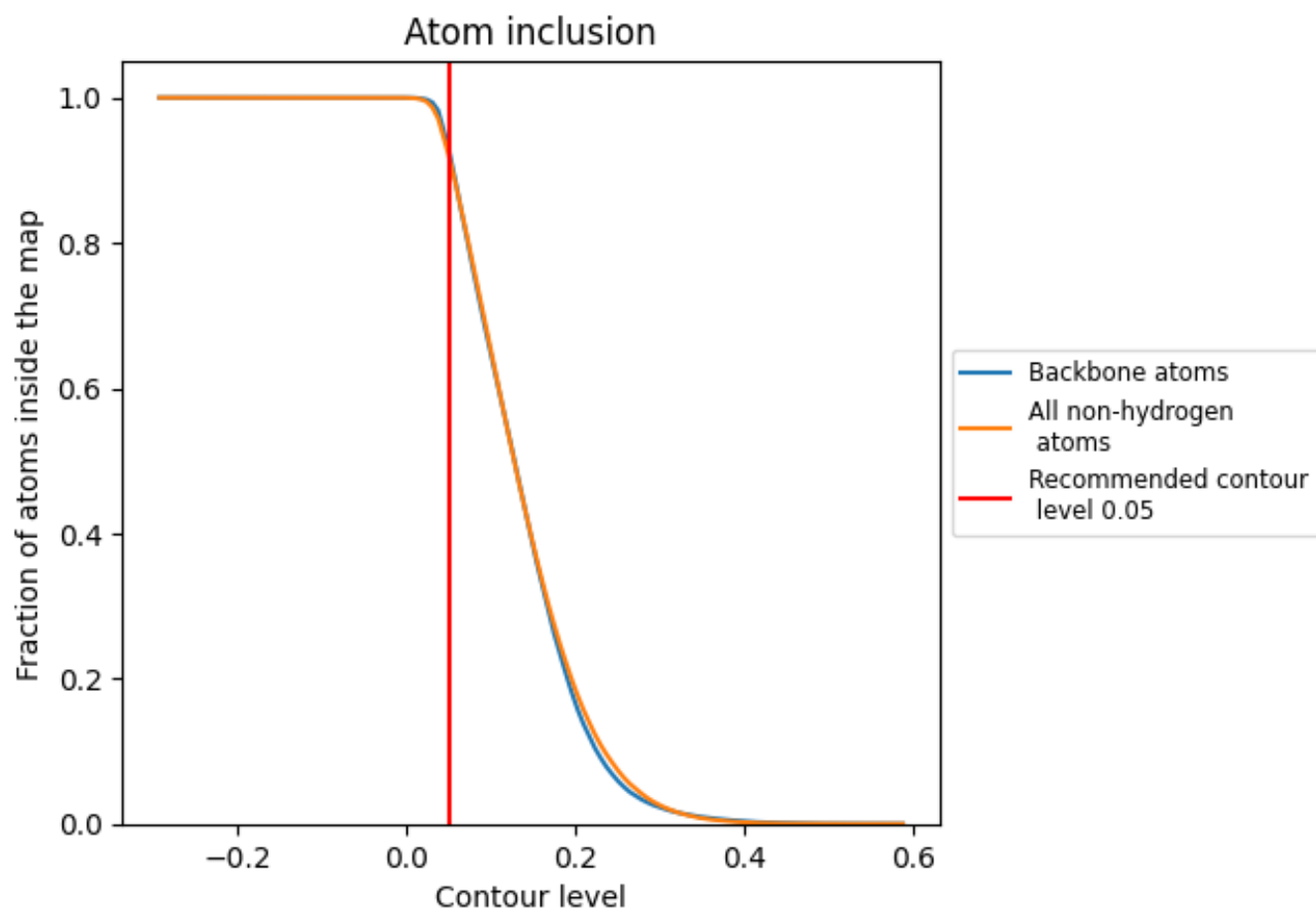
At the recommended contour level, 93% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5　Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9220	0.5360
1	0.9815	0.5650
2	0.9642	0.5680
3	0.7532	0.4160
8	0.9760	0.5880
9	0.9798	0.4840
A	0.9561	0.5800
B	0.9422	0.5610
C	0.9486	0.5700
D	0.8234	0.4530
E	0.7971	0.4580
F	0.9295	0.5540
G	0.8889	0.5290
H	0.8051	0.3970
I	0.7110	0.4400
J	0.6424	0.3590
K	0.9535	0.5710
L	0.9255	0.5650
M	0.9222	0.4980
N	0.9844	0.6080
O	0.9492	0.5530
P	0.9189	0.5520
Q	0.9596	0.5710
R	0.9423	0.5570
S	0.9126	0.5180
T	0.9273	0.5490
U	0.7056	0.4050
V	0.9484	0.5560
X	0.9553	0.5750
Y	0.9293	0.5520
Z	0.9110	0.5250
a	0.9514	0.5850
b	0.9161	0.5410
c	0.8398	0.4990
d	0.9462	0.5760

1.0

0.0
<0.0

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Chain	Atom inclusion	Q-score
e	0.9724	0.5910
f	0.9644	0.5720
g	0.9504	0.5840
h	0.9379	0.5660
i	0.9293	0.5410
j	0.9889	0.6120
k	0.8236	0.4730
m	0.5993	0.3460
n	0.6156	0.3550
o	0.8943	0.5390
p	0.1827	0.2420
u	0.9116	0.4920