



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 08:53 PM UTC

PDB ID : 7QV3 / pdb_00007qv3
EMDB ID : EMD-14159
Title : Bacillus subtilis MutS2-collided disome complex (MutS2 conf.2; Leading 70S)
Authors : Filbeck, S.; Pfeffer, S.
Deposited on : 2022-01-19
Resolution : 5.14 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

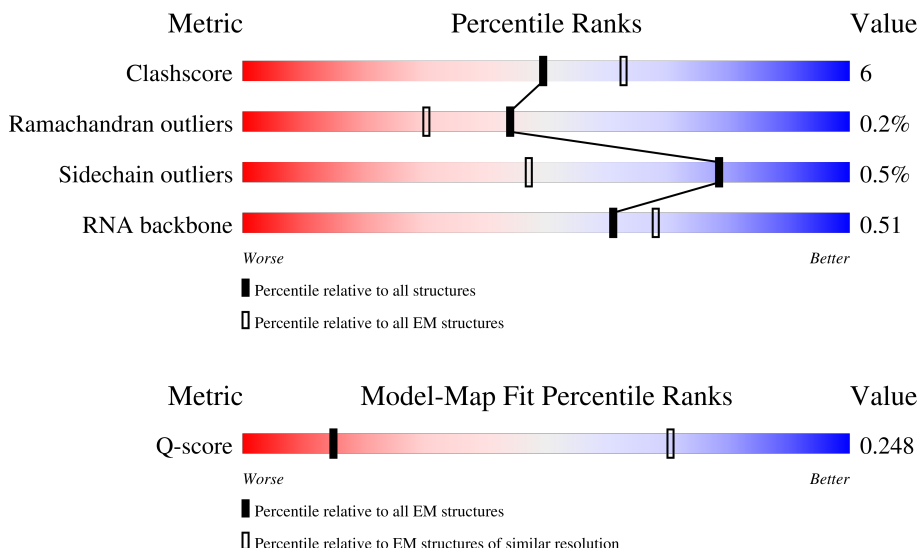
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 5.14 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.



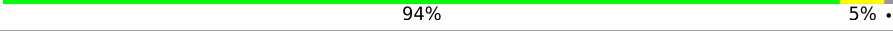
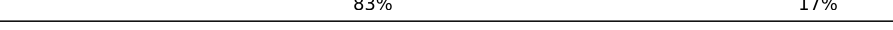
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	700 (4.64 - 5.64)

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	0	59	
2	1	49	
3	2	44	

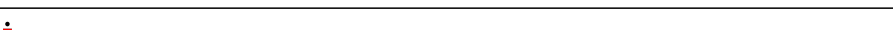
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Mol	Chain	Length	Quality of chain
4	3	66	 83% 14% .
5	4	37	 81% 19%
6	6	66	 5% 86% 9% 5%
7	A	26	 8% 23% 31% 38% 8%
8	B	112	 61% 29% 10%
9	C	277	 85% 13% .
10	D	209	 84% 14% .
11	E	207	 94% 5% .
12	F	179	 86% 12% .
13	G	179	 81% 17% .
14	H	77	 66% 27% 6%
15	I	24	 33% 83% 17%
16	J	145	 85% 13% .
17	K	122	 83% 17%
18	L	146	 86% 14%
19	M	144	 83% 10% 6%
20	N	120	 84% 15% .
21	O	120	 91% 9%
22	P	115	 90% 10%
23	Q	119	 . 87% 11% ..
24	R	102	 82% 17% .
25	S	113	 85% 12% .
26	T	95	 86% 8% 5%
27	U	103	 81% 17% .
28	V	2928	 59% 31% 9% .

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Mol	Chain	Length	Quality of chain
29	W	94	
30	X	149	
31	Y	66	
32	Z	59	
33	a	1533	
34	b	57	
35	c	218	
36	d	200	
37	e	166	
38	f	95	
39	g	156	
40	h	132	
41	i	130	
42	j	102	
43	k	131	
44	l	138	
45	m	121	
46	n	61	
47	o	89	
48	p	90	
49	q	87	
50	r	79	
51	s	92	
52	t	88	
53	u	62	

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Mol	Chain	Length	Quality of chain
54	v	785	
54	w	785	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 149707 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 2 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

- Molecule 6 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	63	Total	C	N	O	S	0	0
			499	312	91	91	5		

- Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	26	Total	C	N	O	P	0	0
			559	251	106	176	26		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	112	Total	C	N	O	P	0	0
			2392	1068	435	778	111		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	272	Total	C	N	O	S	0	0
			2083	1296	408	373	6		

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	176	Total	C	N	O	S	0	0
			1386	882	241	256	7		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 14 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	77	Total	C	N	O	P	0	0
			1643	731	290	545	77		

- Molecule 15 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	I	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 16 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 17 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 19 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	135	Total	C	N	O	S	0	0
			1076	690	205	176	5		

- Molecule 20 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 21 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 22 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	115	Total	C	N	O	S	0	0
			944	600	185	158	1		

- Molecule 23 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 24 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	101	Total	C	N	O		0	0
			786	501	139	146			

- Molecule 25 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 26 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	90	Total	C	N	O	S	0	0
			725	452	134	136	3		

- Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 28 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	2887	Total	C	N	O	P	0	0
			61998	27661	11460	19993	2884		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	243	G	A	conflict	GB 1491848961
V	325	A	-	insertion	GB 1491848961
V	326	A	-	insertion	GB 1491848961
V	327	G	-	insertion	GB 1491848961
V	328	G	-	insertion	GB 1491848961
V	640	U	C	conflict	GB 1491848961
V	2232	A	G	conflict	GB 1491848961

- Molecule 29 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	W	82	Total	C	N	O	0	0
			630	390	123	117		

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	149	Total	C	N	O	S	0	0
			1151	726	205	219	1		

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 33 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	1533	Total	C	N	O	P	0	0
			32891	14667	6034	10657	1533		

- Molecule 34 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	57	Total	C	N	O	S	0	0
			476	295	97	83	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	30	ALA	GLN	conflict	UNP P21478

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	206	Total	C	N	O	S	0	0
			1619	1011	304	301	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	195	Total	C	N	O	S	0	0
			1568	991	291	284	2		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	164	Total	C	N	O	S	0	0
			1218	767	225	224	2		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	92	Total	C	N	O	S	0	0
			755	476	132	146	1		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	151	Total	C	N	O	S	0	0
			1203	755	224	218	6		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	131	Total	C	N	O	S	0	0
			1036	655	191	187	3		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	103	Total	C	N	O	S	0	0
			784	485	151	148			

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	95	Total	C	N	O	S	0	0
			761	479	139	141	2		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	118	Total	C	N	O	S	0	0
			871	537	171	161	2		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	136	Total	C	N	O	S	0	0
			1052	653	211	186	2		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	92	Total	C	N	O	S	0	0
			740	459	145	136			

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	60	Total	C	N	O	S	0	0
			497	317	98	77	5		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	85	Total	C	N	O	S	0	0
			710	436	144	129	1		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	88	Total	C	N	O	S	0	0
			695	441	128	124	2		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	84	Total	C	N	O	S	0	0
			691	435	128	126	2		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	64	Total	C	N	O	S	0	0
			518	332	96	88	2		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	77	Total	C	N	O	S	0	0
			624	403	110	109	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	83	Total	C	N	O	S	0	0
			637	390	130	116	1		

- Molecule 53 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 54 is a protein called Endonuclease MutS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	548	Total	C	N	O	S	0	0
			4289	2680	743	850	16		
54	w	593	Total	C	N	O	S	0	0
			4644	2904	804	919	17		

3 Residue-property plots [i](#)

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

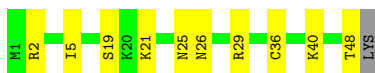
- Molecule 1: 50S ribosomal protein L32

Chain 0:  81% 8% 8%



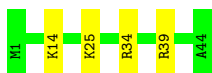
- Molecule 2: 50S ribosomal protein L33 1

Chain 1:  78% 20% .



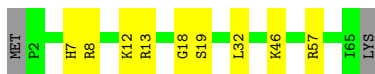
- Molecule 3: 50S ribosomal protein L34

Chain 2:  91% 9%



- Molecule 4: 50S ribosomal protein L35

Chain 3:  83% 14% .

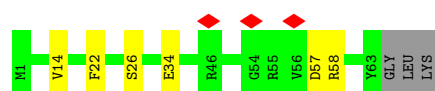
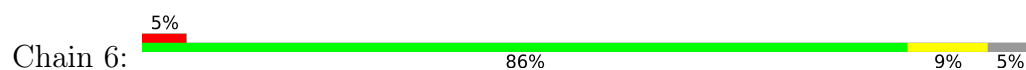


- Molecule 5: 50S ribosomal protein L36

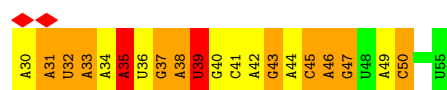
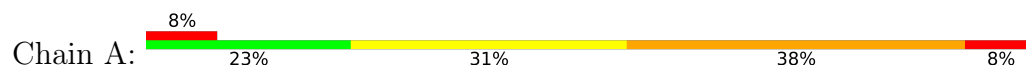
Chain 4:  81% 19%



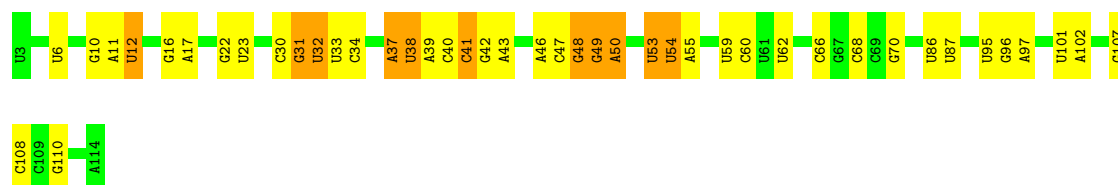
- Molecule 6: 50S ribosomal protein L31



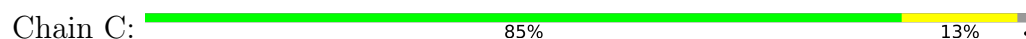
- Molecule 7: mRNA



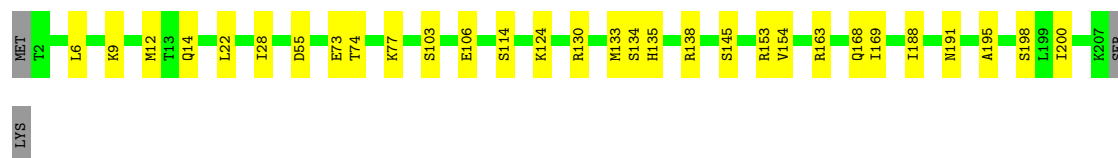
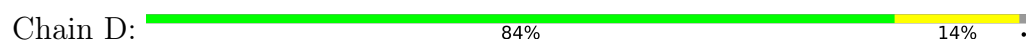
- Molecule 8: 5S ribosomal RNA



- Molecule 9: 50S ribosomal protein L2



- Molecule 10: 50S ribosomal protein L3



- Molecule 11: 50S ribosomal protein L4



- Molecule 12: 50S ribosomal protein L5

Chain F:  86% 12%



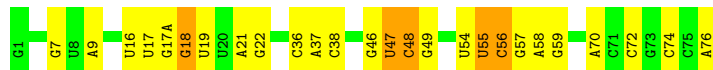
- Molecule 13: 50S ribosomal protein L6

Chain G:  81% 17%



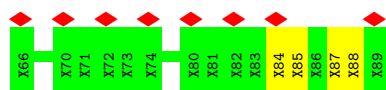
- Molecule 14: P-site tRNA

Chain H:  66% 27% 6%



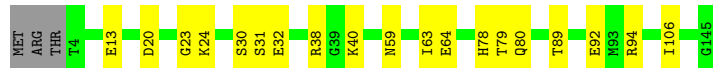
- Molecule 15: Nascent chain

Chain I:  33% 83% 17%



- Molecule 16: 50S ribosomal protein L13

Chain J:  85% 13%



- Molecule 17: 50S ribosomal protein L14

Chain K:  83% 17%



- Molecule 18: 50S ribosomal protein L15

Chain L:  86% 14%



- Molecule 19: 50S ribosomal protein L16

Chain M:  83% 10% 6%



- Molecule 20: 50S ribosomal protein L17

Chain N:  84% 15% .



- Molecule 21: 50S ribosomal protein L18

Chain O:  91% 9%



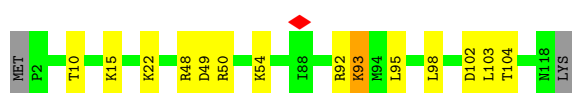
- Molecule 22: 50S ribosomal protein L19

Chain P:  90% 10%



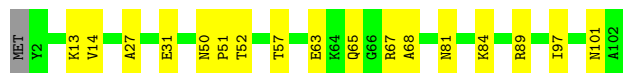
- Molecule 23: 50S ribosomal protein L20

Chain Q:  87% 11% ..



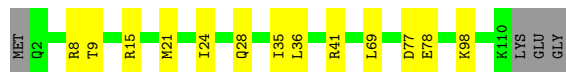
- Molecule 24: 50S ribosomal protein L21

Chain R:  82% 17% .



- Molecule 25: 50S ribosomal protein L22

Chain S:  85% 12% .



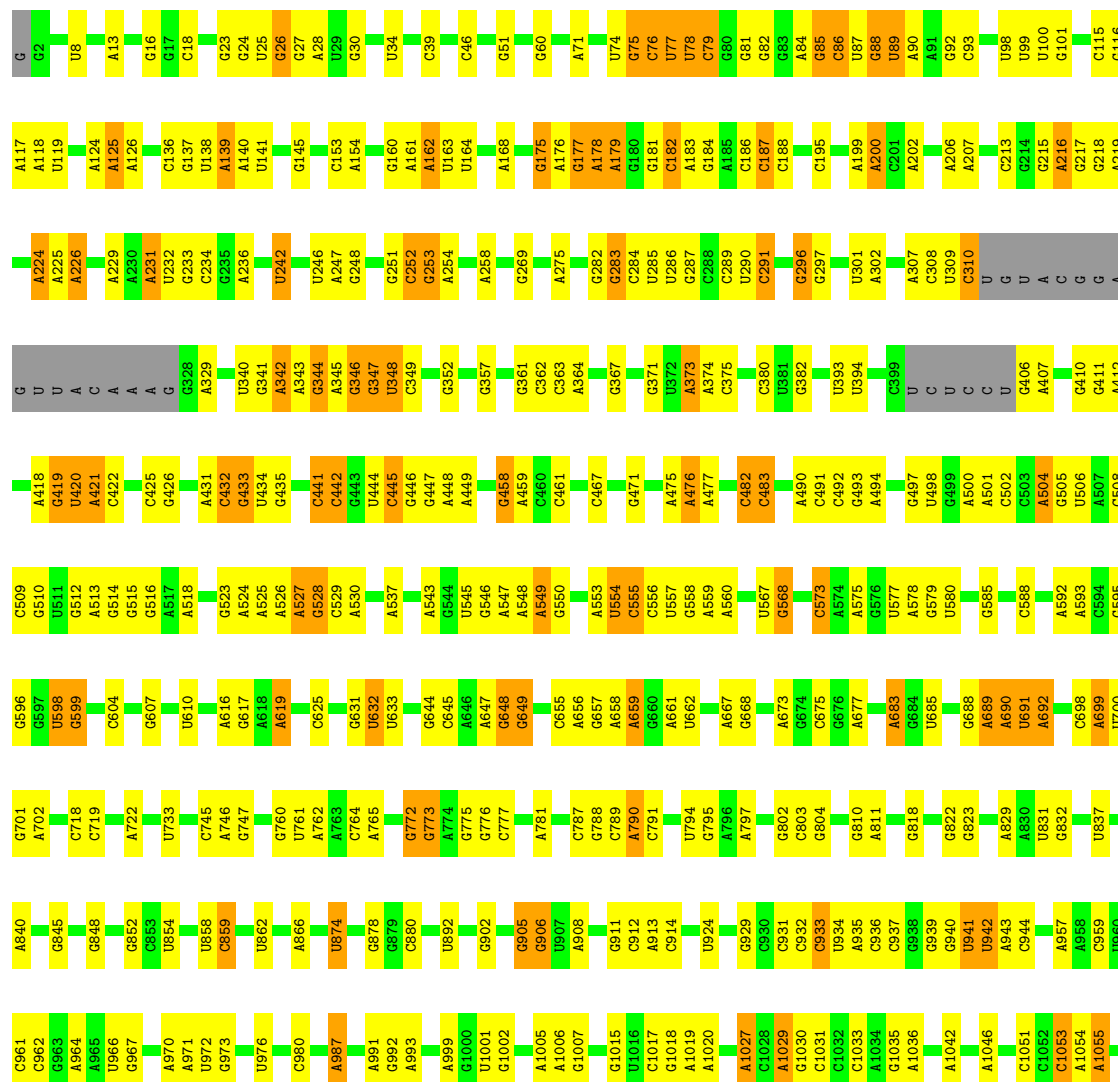
- Molecule 26: 50S ribosomal protein L23

Sequence logo for the 1000bp upstream region of the human HNF1A gene. The y-axis represents information content in bits, ranging from 0.00 to 0.25. The x-axis shows amino acid positions from MET to ALA. The logo shows a strong conservation of Lysine (K) at position 2, Arginine (R) at position 5, and Glutamine (Q) at position 33. Other positions show lower conservation, with some specific residues like Aspartate (D) at 31, Valine (V) at 32, and Glutamine (Q) at 34 also showing some conservation.

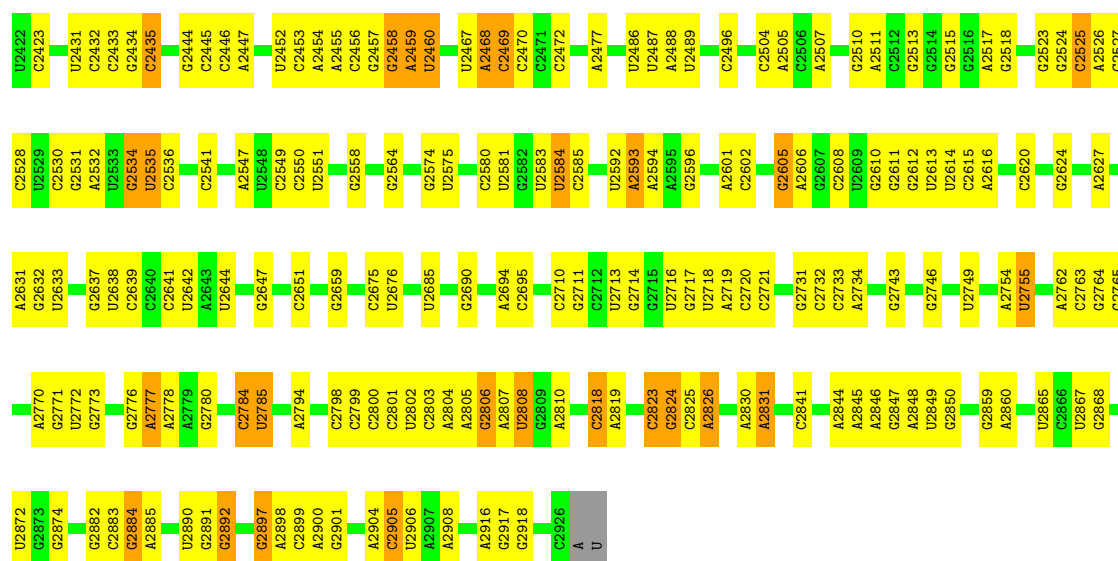
- Chain U:  81% 17%



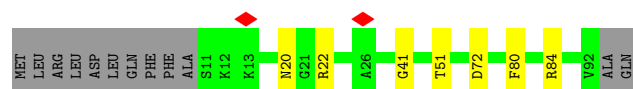
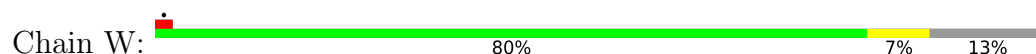
- Chain V: 59% 31% 9%



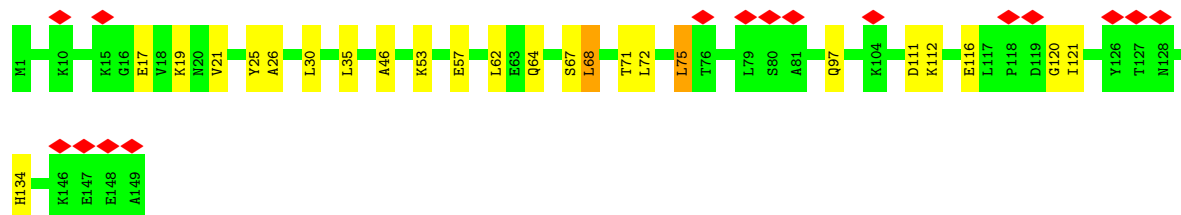
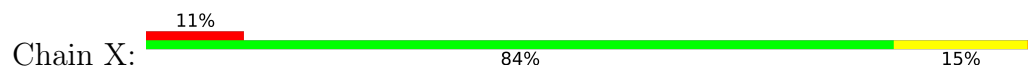




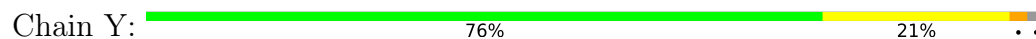
- Molecule 29: 50S ribosomal protein L27



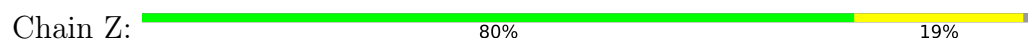
- Molecule 30: 50S ribosomal protein L9



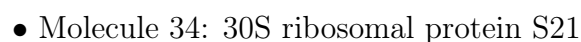
- Molecule 31: 50S ribosomal protein L29

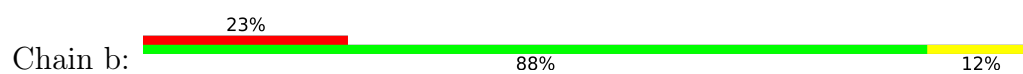


- Molecule 32: 50S ribosomal protein L30

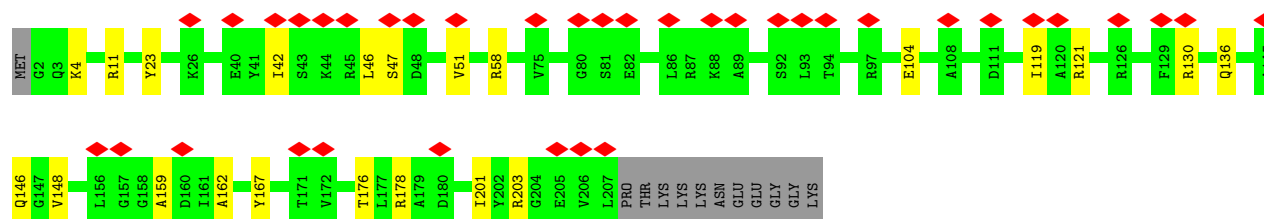
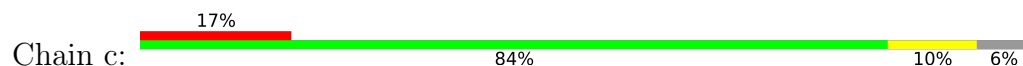


Chain a: 64% 29% 7%

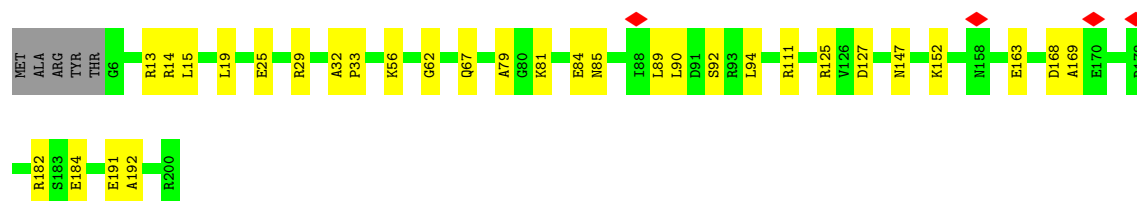
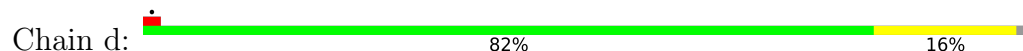




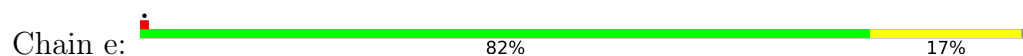
- Molecule 35: 30S ribosomal protein S3



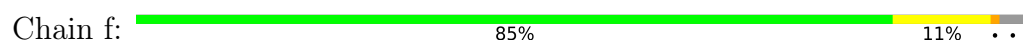
- Molecule 36: 30S ribosomal protein S4



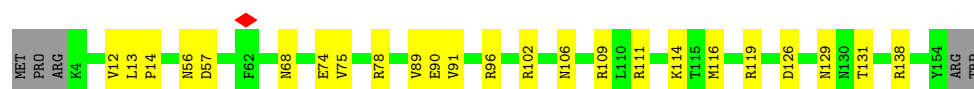
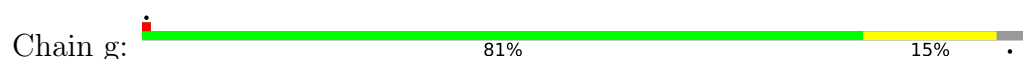
- Molecule 37: 30S ribosomal protein S5



- Molecule 38: 30S ribosomal protein S6

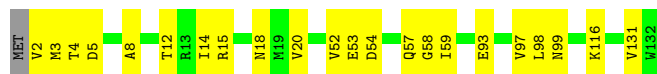


- Molecule 39: 30S ribosomal protein S7



- Molecule 40: 30S ribosomal protein S8

Chain h:  83% 17% .



- Molecule 41: 30S ribosomal protein S9

Chain i:  65% 15% 21%



- Molecule 42: 30S ribosomal protein S10

Chain j:  82% 11% 7%



- Molecule 43: 30S ribosomal protein S11

Chain k:  82% 8% 10%



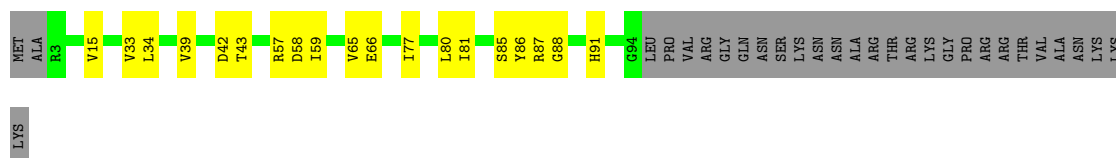
- Molecule 44: 30S ribosomal protein S12

Chain l:  86% 13% .



- Molecule 45: 30S ribosomal protein S13

Chain m:  60% 16% 24%



- Molecule 46: 30S ribosomal protein S14

Chain n:  84% 13%



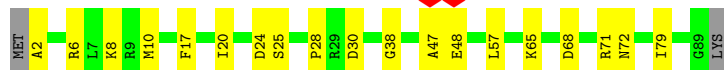
- Molecule 47: 30S ribosomal protein S15

Chain o:  70% 26%



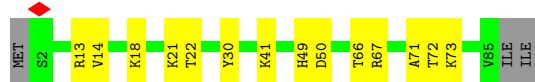
- Molecule 48: 30S ribosomal protein S16

Chain p:  77% 21%



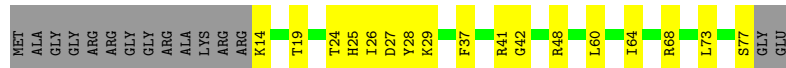
- Molecule 49: 30S ribosomal protein S17

Chain q:  80% 16%



- Molecule 50: 30S ribosomal protein S18

Chain r:  59% 22% 19%



- Molecule 51: 30S ribosomal protein S19

Chain s:  74% 10% 16%



- Molecule 52: 30S ribosomal protein S20

Chain t:  80% 15% 6%



-
- | Category | Item | Value |
|----------|------|-------|
| H1 | | 1 |
| S7 | | 1 |
| A8 | | 1 |
| H12 | | 1 |
| E16 | | 1 |
| G20 | | 1 |
| H21 | | 1 |
| S25 | | 1 |
| I56 | | 1 |
| I57 | | 1 |
| R60 | | 1 |
| A63 | | 1 |
| P64 | | 1 |
| P65 | | 1 |
| G66 | | 1 |
| G67 | | 1 |
| L68 | | 1 |
| V69 | | 1 |
| D70 | | 1 |
| L75 | | 1 |
| A78 | | 1 |
| E79 | | 1 |
| I80 | | 1 |
| G81 | | 1 |
| S82 | | 1 |
| S83 | | 1 |
| L84 | | 1 |
| R85 | | 1 |
| P86 | | 1 |
| S87 | | 1 |
| V99 | | 1 |
| M102 | | 1 |
| M109 | | 1 |
| V114 | | 1 |
| D115 | | 1 |
| I116 | | 1 |
| I119 | | 1 |
| E124 | | 1 |
| Q125 | | 1 |
| L126 | | 1 |
| I140 | | 1 |
| D141 | | 1 |
| D142 | | 1 |

VAL	SER	ILE	ILE	HIS	GLY	LYS	GLY	THR	GLY	ALA	GLY	ALA	LEU	ARG	GLY	VAL	VAL	GLN	ASP	LEU	LEU	LEU	ASN	HIS	ARG	SER	SER	VAL	LYS	SER	SER	ARG	PHE	GLY	GLY	GLU	ASP	ALA	GLY	GLY	ARG	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY</
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5078	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46.5	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.341	Depositor
Minimum map value	-0.207	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0172	Depositor
Map size (Å)	590.64, 590.64, 590.64	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.605, 1.605, 1.605	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.12	0/433	0.28	0/574
2	1	0.14	0/406	0.27	0/540
3	2	0.18	0/370	0.31	0/483
4	3	0.13	0/519	0.34	0/680
5	4	0.15	0/299	0.25	0/393
6	6	0.12	0/509	0.24	0/678
7	A	0.66	4/627 (0.6%)	0.85	5/975 (0.5%)
8	B	0.08	0/2675	0.21	0/4170
9	C	0.13	0/2120	0.30	0/2845
10	D	0.15	0/1591	0.34	0/2132
11	E	0.11	0/1580	0.28	0/2132
12	F	0.38	0/1405	0.79	5/1887 (0.3%)
13	G	0.10	0/1360	0.24	0/1832
14	H	0.07	0/1834	0.21	0/2858
16	J	0.13	0/1146	0.28	0/1542
17	K	0.15	0/927	0.29	0/1245
18	L	0.13	0/1093	0.28	0/1457
19	M	0.12	0/1099	0.25	0/1468
20	N	0.12	0/960	0.28	0/1284
21	O	0.23	0/921	0.42	0/1236
22	P	0.14	0/957	0.29	0/1279
23	Q	0.15	0/952	0.34	0/1266
24	R	0.11	0/797	0.29	0/1070
25	S	0.13	0/851	0.32	0/1146
26	T	0.12	0/731	0.24	0/974
27	U	0.13	0/772	0.27	0/1032
28	V	0.15	0/69444	0.32	23/108334 (0.0%)
29	W	0.13	0/638	0.31	0/847
30	X	0.12	0/1162	0.38	0/1551
31	Y	0.14	0/531	0.25	0/707
32	Z	0.11	0/457	0.29	0/613
33	a	0.09	0/36826	0.22	0/57450
34	b	0.16	0/480	0.33	0/628
35	c	0.13	0/1641	0.30	0/2208

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
36	d	0.13	0/1598	0.31	0/2147
37	e	0.12	0/1230	0.27	0/1655
38	f	0.12	0/766	0.28	0/1031
39	g	0.11	0/1220	0.29	0/1637
40	h	0.14	0/1048	0.33	0/1407
41	i	0.12	0/794	0.30	0/1074
42	j	0.11	0/773	0.28	0/1044
43	k	0.13	0/885	0.30	0/1196
44	l	0.14	0/1069	0.33	0/1435
45	m	0.14	0/744	0.35	0/994
46	n	0.12	0/507	0.32	0/672
47	o	0.12	0/718	0.30	0/960
48	p	0.13	0/708	0.32	0/950
49	q	0.12	0/699	0.30	0/933
50	r	0.13	0/526	0.34	0/705
51	s	0.11	0/640	0.27	0/861
52	t	0.12	0/639	0.34	0/852
53	u	0.13	0/448	0.30	0/596
54	v	0.64	0/4341	1.09	0/5847
54	w	0.64	0/4703	1.12	1/6337 (0.0%)
All	All	0.20	4/162169 (0.0%)	0.38	34/241849 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
28	V	0	16
54	w	0	2
All	All	0	18

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	41	C	C1'-N1	5.46	1.56	1.48
7	A	42	A	C1'-N9	-5.36	1.40	1.48
7	A	39	U	C1'-N1	5.35	1.55	1.47
7	A	50	C	C1'-N1	5.22	1.56	1.48

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	V	138	U	OP1-P-O3'	-29.77	18.68	108.00
7	A	32	U	P-O3'-C3'	-7.69	108.67	120.20
28	V	2336	G	C4'-C3'-O3'	7.11	120.07	109.40
28	V	1449	C	P-O3'-C3'	-6.97	109.74	120.20
7	A	37	G	P-O3'-C3'	-6.92	109.82	120.20

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
28	V	2323	C	Sidechain
28	V	2326	C	Sidechain
28	V	2327	A	Sidechain
28	V	2329	A	Sidechain
28	V	924	U	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	426	0	445	4	0
2	1	401	0	413	6	0
3	2	367	0	410	4	0
4	3	512	0	564	12	0
5	4	296	0	342	6	0
6	6	499	0	491	4	0
7	A	559	0	281	20	0
8	B	2392	0	1213	30	0
9	C	2083	0	2168	31	0
10	D	1569	0	1637	20	0
11	E	1561	0	1647	8	0
12	F	1386	0	1446	12	0
13	G	1342	0	1388	23	0
14	H	1643	0	831	14	0
15	I	120	0	28	3	0
16	J	1123	0	1162	17	0
17	K	920	0	977	18	0
18	L	1081	0	1132	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	M	1076	0	1145	10	0
20	N	953	0	983	13	0
21	O	912	0	947	7	0
22	P	944	0	1020	11	0
23	Q	940	0	1005	10	0
24	R	786	0	826	13	0
25	S	842	0	899	11	0
26	T	725	0	770	5	0
27	U	762	0	821	11	0
28	V	61998	0	31207	570	0
29	W	630	0	644	7	0
30	X	1151	0	1222	16	0
31	Y	530	0	568	10	0
32	Z	455	0	491	8	0
33	a	32891	0	16559	321	0
34	b	476	0	521	6	0
35	c	1619	0	1658	14	0
36	d	1568	0	1604	19	0
37	e	1218	0	1300	20	0
38	f	755	0	746	8	0
39	g	1203	0	1251	18	0
40	h	1036	0	1095	19	0
41	i	784	0	803	14	0
42	j	761	0	795	8	0
43	k	871	0	895	10	0
44	l	1052	0	1112	18	0
45	m	740	0	787	15	0
46	n	497	0	531	8	0
47	o	710	0	735	16	0
48	p	695	0	721	14	0
49	q	691	0	728	11	0
50	r	518	0	555	13	0
51	s	624	0	636	8	0
52	t	637	0	696	10	0
53	u	444	0	487	8	0
54	v	4289	0	4345	24	0
54	w	4644	0	4700	21	0
All	All	149707	0	102383	1366	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 6.

The worst 5 of 1366 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)
28:V:310:C:O2	28:V:406:G:N2	1.93	1.01
33:a:890:C:H5''	44:l:9:ARG:NH1	1.74	1.00
7:A:50:C:N4	33:a:1406:C:O2'	1.95	1.00
28:V:28:A:N6	28:V:558:G:O2'	2.00	0.93
33:a:474:A:O2'	33:a:475:A:O5'	1.87	0.92

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	52/59 (88%)	50 (96%)	2 (4%)	0	100	100
2	1	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
3	2	42/44 (96%)	42 (100%)	0	0	100	100
4	3	62/66 (94%)	60 (97%)	2 (3%)	0	100	100
5	4	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
6	6	61/66 (92%)	60 (98%)	1 (2%)	0	100	100
9	C	270/277 (98%)	260 (96%)	10 (4%)	0	100	100
10	D	204/209 (98%)	193 (95%)	11 (5%)	0	100	100
11	E	203/207 (98%)	193 (95%)	10 (5%)	0	100	100
12	F	174/179 (97%)	161 (92%)	13 (8%)	0	100	100
13	G	173/179 (97%)	165 (95%)	8 (5%)	0	100	100
16	J	140/145 (97%)	133 (95%)	7 (5%)	0	100	100
17	K	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
18	L	144/146 (99%)	139 (96%)	5 (4%)	0	100	100
19	M	133/144 (92%)	132 (99%)	1 (1%)	0	100	100
20	N	117/120 (98%)	113 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	O	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
22	P	113/115 (98%)	108 (96%)	5 (4%)	0	100	100
23	Q	115/119 (97%)	107 (93%)	6 (5%)	2 (2%)	7	34
24	R	99/102 (97%)	88 (89%)	11 (11%)	0	100	100
25	S	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
26	T	88/95 (93%)	87 (99%)	1 (1%)	0	100	100
27	U	99/103 (96%)	92 (93%)	7 (7%)	0	100	100
29	W	80/94 (85%)	76 (95%)	4 (5%)	0	100	100
30	X	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
31	Y	63/66 (96%)	62 (98%)	1 (2%)	0	100	100
32	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
34	b	55/57 (96%)	53 (96%)	2 (4%)	0	100	100
35	c	204/218 (94%)	194 (95%)	10 (5%)	0	100	100
36	d	193/200 (96%)	176 (91%)	17 (9%)	0	100	100
37	e	162/166 (98%)	155 (96%)	7 (4%)	0	100	100
38	f	90/95 (95%)	87 (97%)	3 (3%)	0	100	100
39	g	149/156 (96%)	144 (97%)	5 (3%)	0	100	100
40	h	129/132 (98%)	116 (90%)	13 (10%)	0	100	100
41	i	101/130 (78%)	95 (94%)	6 (6%)	0	100	100
42	j	93/102 (91%)	87 (94%)	6 (6%)	0	100	100
43	k	116/131 (88%)	110 (95%)	6 (5%)	0	100	100
44	l	134/138 (97%)	124 (92%)	10 (8%)	0	100	100
45	m	90/121 (74%)	85 (94%)	5 (6%)	0	100	100
46	n	58/61 (95%)	52 (90%)	5 (9%)	1 (2%)	7	34
47	o	83/89 (93%)	79 (95%)	4 (5%)	0	100	100
48	p	86/90 (96%)	81 (94%)	5 (6%)	0	100	100
49	q	82/87 (94%)	76 (93%)	6 (7%)	0	100	100
50	r	62/79 (78%)	56 (90%)	5 (8%)	1 (2%)	7	36
51	s	75/92 (82%)	69 (92%)	6 (8%)	0	100	100
52	t	81/88 (92%)	79 (98%)	2 (2%)	0	100	100
53	u	56/62 (90%)	54 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	v	544/785 (69%)	527 (97%)	15 (3%)	2 (0%)	30	66
54	w	589/785 (75%)	569 (97%)	16 (3%)	4 (1%)	18	55
All	All	6293/7048 (89%)	5986 (95%)	297 (5%)	10 (0%)	44	77

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
54	v	384	SER
54	w	384	SER
23	Q	103	LEU
50	r	28	TYR
54	w	382	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	48/53 (91%)	46 (96%)	2 (4%)	26	48
2	1	46/47 (98%)	46 (100%)	0	100	100
3	2	39/39 (100%)	39 (100%)	0	100	100
4	3	54/56 (96%)	54 (100%)	0	100	100
5	4	35/35 (100%)	35 (100%)	0	100	100
6	6	53/55 (96%)	53 (100%)	0	100	100
9	C	220/225 (98%)	219 (100%)	1 (0%)	81	82
10	D	167/170 (98%)	167 (100%)	0	100	100
11	E	169/170 (99%)	168 (99%)	1 (1%)	78	81
12	F	151/154 (98%)	149 (99%)	2 (1%)	61	73
13	G	148/151 (98%)	148 (100%)	0	100	100
16	J	120/123 (98%)	120 (100%)	0	100	100
17	K	101/101 (100%)	101 (100%)	0	100	100
18	L	110/110 (100%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	M	109/116 (94%)	108 (99%)	1 (1%)	70	77
20	N	99/100 (99%)	98 (99%)	1 (1%)	68	77
21	O	93/93 (100%)	93 (100%)	0	100	100
22	P	100/100 (100%)	100 (100%)	0	100	100
23	Q	96/98 (98%)	96 (100%)	0	100	100
24	R	83/84 (99%)	83 (100%)	0	100	100
25	S	90/93 (97%)	90 (100%)	0	100	100
26	T	81/85 (95%)	81 (100%)	0	100	100
27	U	85/87 (98%)	85 (100%)	0	100	100
29	W	64/74 (86%)	64 (100%)	0	100	100
30	X	124/124 (100%)	121 (98%)	3 (2%)	43	63
31	Y	56/57 (98%)	55 (98%)	1 (2%)	51	67
32	Z	52/53 (98%)	52 (100%)	0	100	100
34	b	51/51 (100%)	51 (100%)	0	100	100
35	c	168/178 (94%)	168 (100%)	0	100	100
36	d	169/173 (98%)	167 (99%)	2 (1%)	63	74
37	e	128/130 (98%)	127 (99%)	1 (1%)	73	78
38	f	81/84 (96%)	78 (96%)	3 (4%)	30	51
39	g	127/132 (96%)	127 (100%)	0	100	100
40	h	111/112 (99%)	111 (100%)	0	100	100
41	i	81/102 (79%)	81 (100%)	0	100	100
42	j	86/92 (94%)	86 (100%)	0	100	100
43	k	90/100 (90%)	90 (100%)	0	100	100
44	l	114/116 (98%)	114 (100%)	0	100	100
45	m	80/104 (77%)	80 (100%)	0	100	100
46	n	53/54 (98%)	53 (100%)	0	100	100
47	o	80/83 (96%)	79 (99%)	1 (1%)	61	73
48	p	74/76 (97%)	74 (100%)	0	100	100
49	q	77/80 (96%)	77 (100%)	0	100	100
50	r	56/64 (88%)	56 (100%)	0	100	100
51	s	69/81 (85%)	68 (99%)	1 (1%)	59	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	t	66/70 (94%)	66 (100%)	0	100	100
53	u	47/50 (94%)	47 (100%)	0	100	100
54	v	472/674 (70%)	467 (99%)	5 (1%)	65	75
54	w	513/674 (76%)	509 (99%)	4 (1%)	73	78
All	All	5386/5933 (91%)	5357 (100%)	29 (0%)	78	82

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	e	120	VAL
54	w	230	ILE
38	f	89	ILE
54	v	596	THR
38	f	52	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
54	v	143	HIS
54	v	409	ASN
54	w	555	GLN
54	v	160	GLN
54	v	271	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	H	76/77 (98%)	14 (18%)	2 (2%)
28	V	2881/2928 (98%)	634 (22%)	64 (2%)
33	a	1532/1533 (99%)	266 (17%)	0
7	A	25/26 (96%)	12 (48%)	5 (20%)
8	B	111/112 (99%)	28 (25%)	4 (3%)
All	All	4625/4676 (98%)	954 (20%)	75 (1%)

5 of 954 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	33	A

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Mol	Chain	Res	Type
7	A	34	A
7	A	35	A
7	A	37	G
7	A	38	A

5 of 75 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
28	V	2155	A
28	V	2710	C
28	V	2254	A
28	V	2452	U
28	V	1093	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 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.

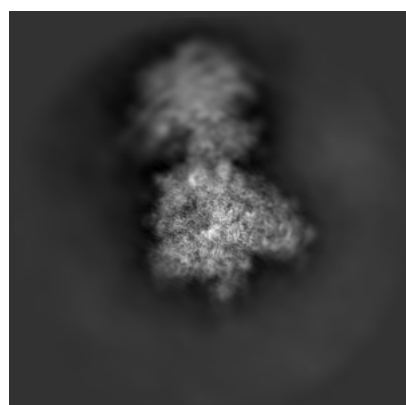
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14159. These allow visual inspection of the internal detail of the map and identification of artifacts.

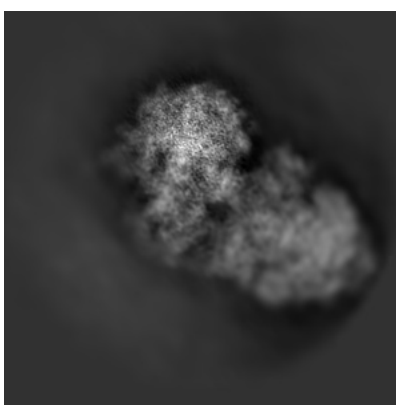
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

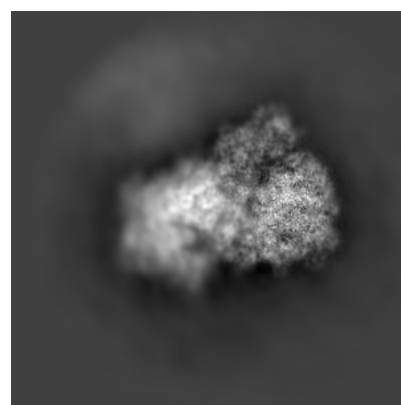
6.1.1 Primary map



X



Y

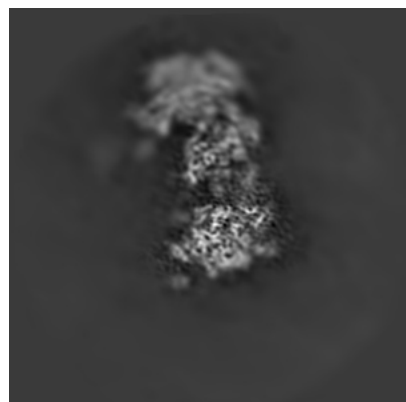


Z

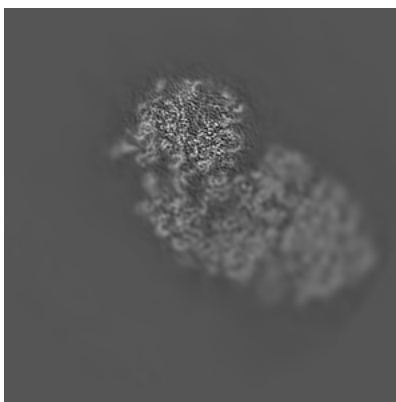
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

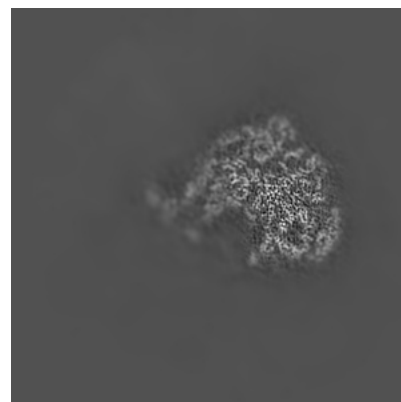
6.2.1 Primary map



X Index: 184



Y Index: 184

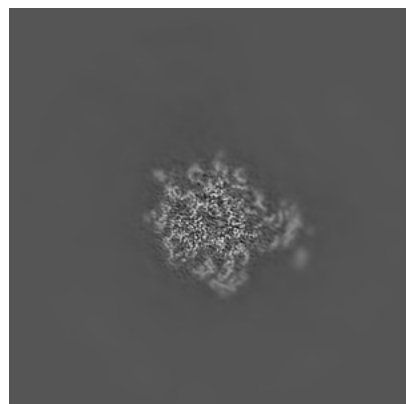


Z Index: 184

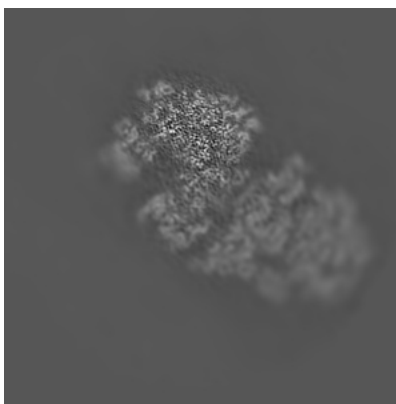
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

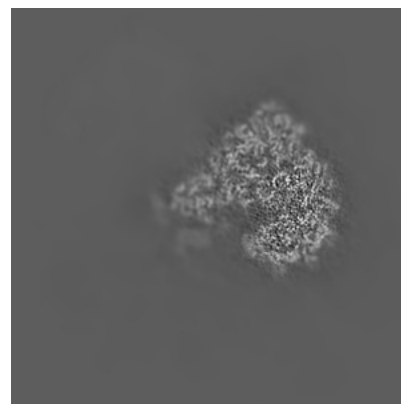
6.3.1 Primary map



X Index: 254



Y Index: 196

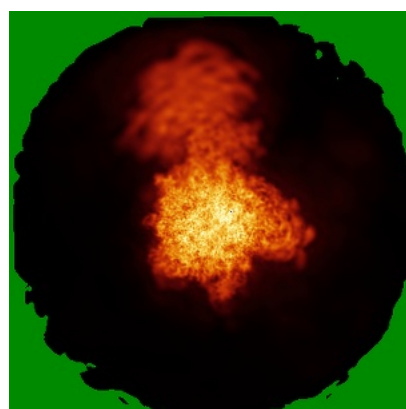


Z Index: 169

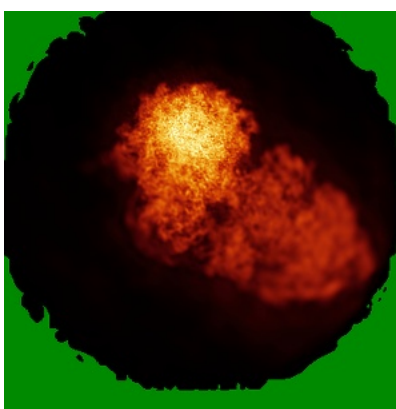
The images above show the largest variance slices of the map in three orthogonal directions.

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

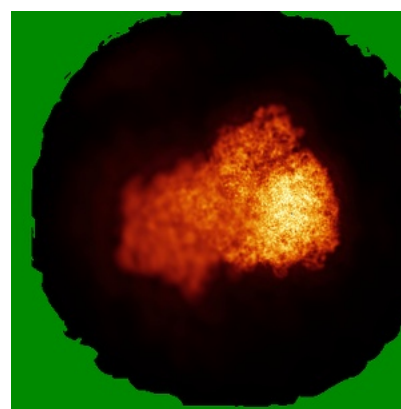
6.4.1 Primary map



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

This section was not generated.

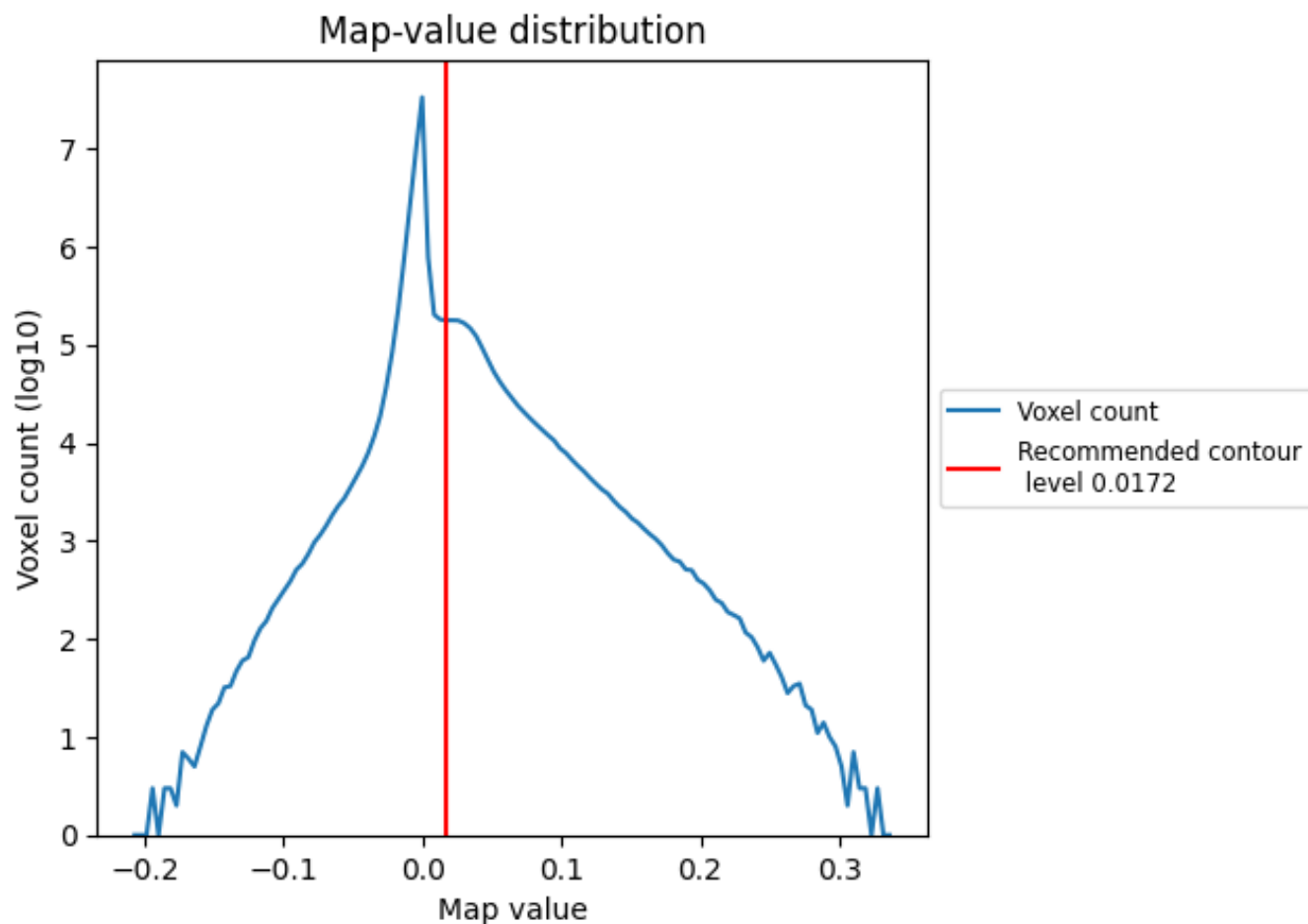
6.6 Mask visualisation

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

7 Map analysis [i](#)

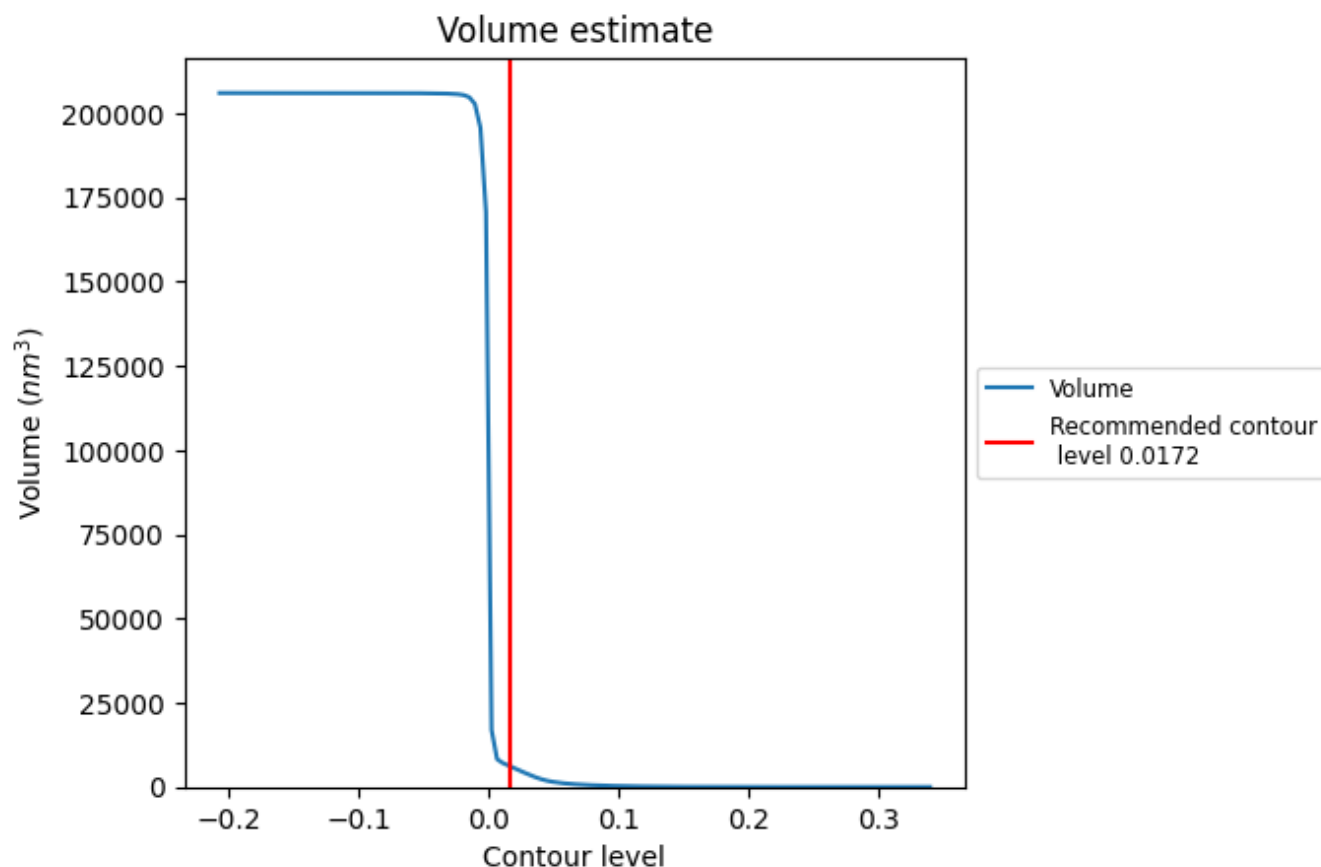
This section contains the results of statistical analysis of the map.

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.

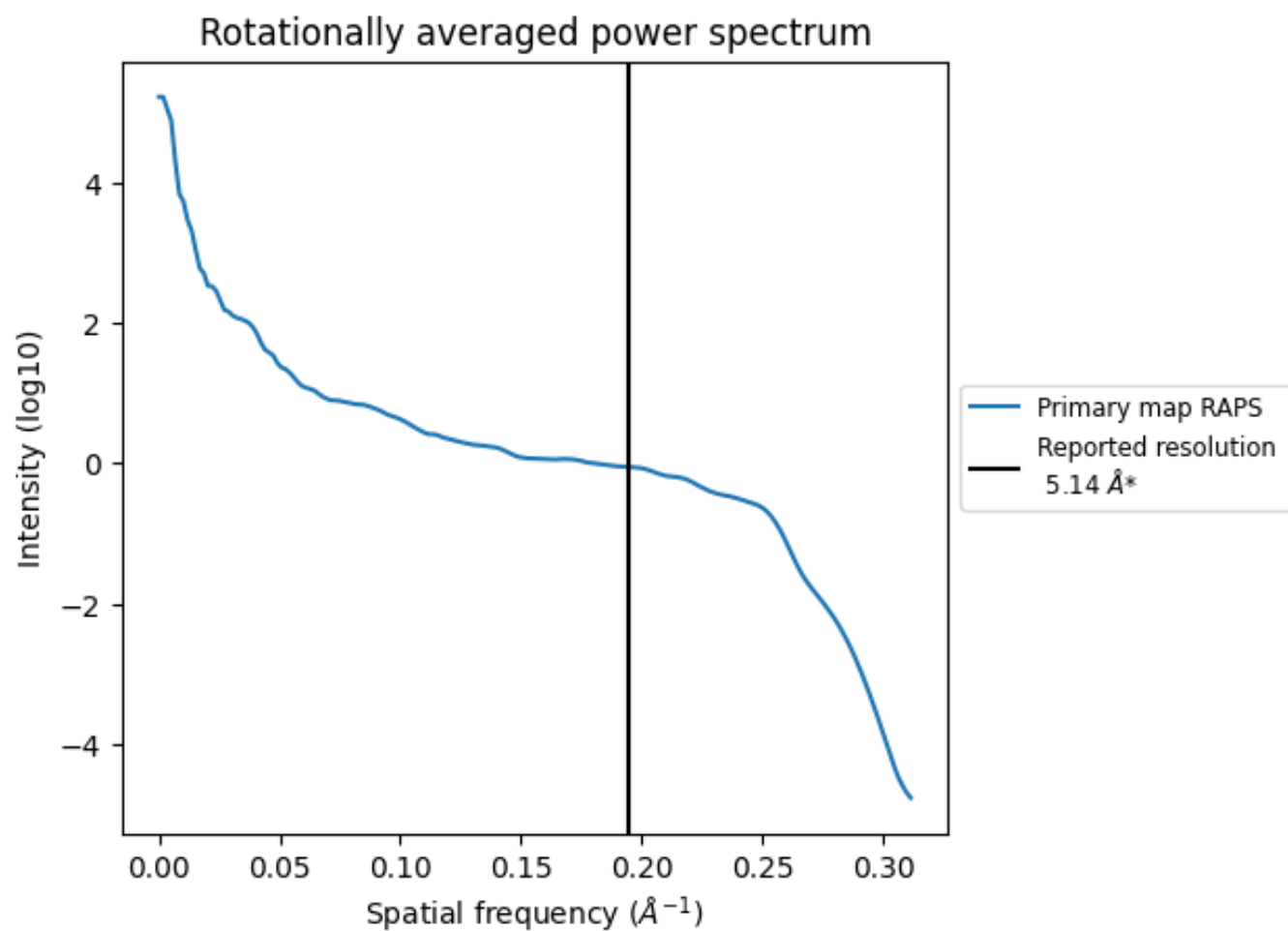
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6043 nm^3 ; this corresponds to an approximate mass of 5459 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 0.195 Å⁻¹

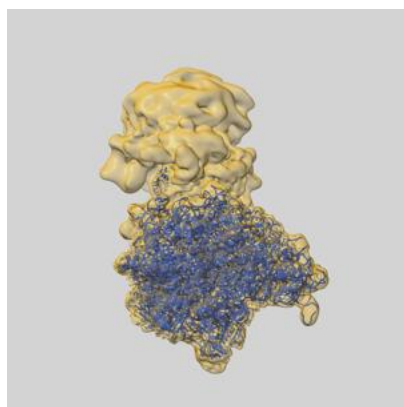
8 Fourier-Shell correlation

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

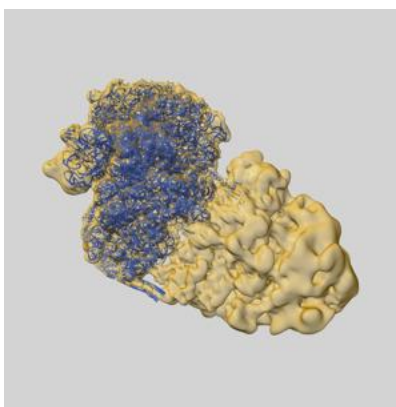
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14159 and PDB model 7QV3. Per-residue inclusion information can be found in section [3](#) on page [15](#).

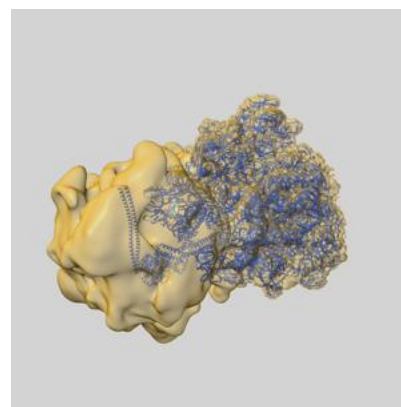
9.1 Map-model overlay [i](#)



X



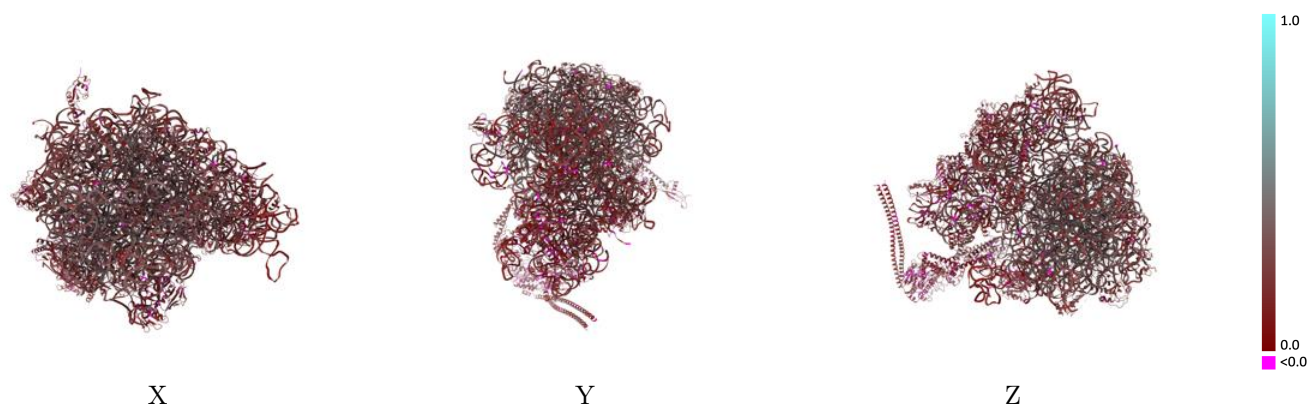
Y



Z

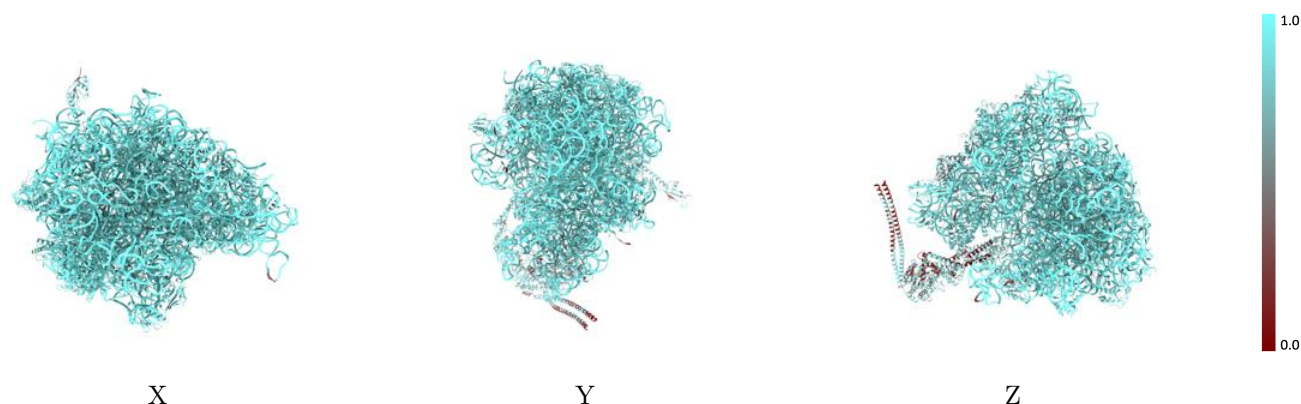
The images above show the 3D surface view of the map at the recommended contour level 0.0172 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



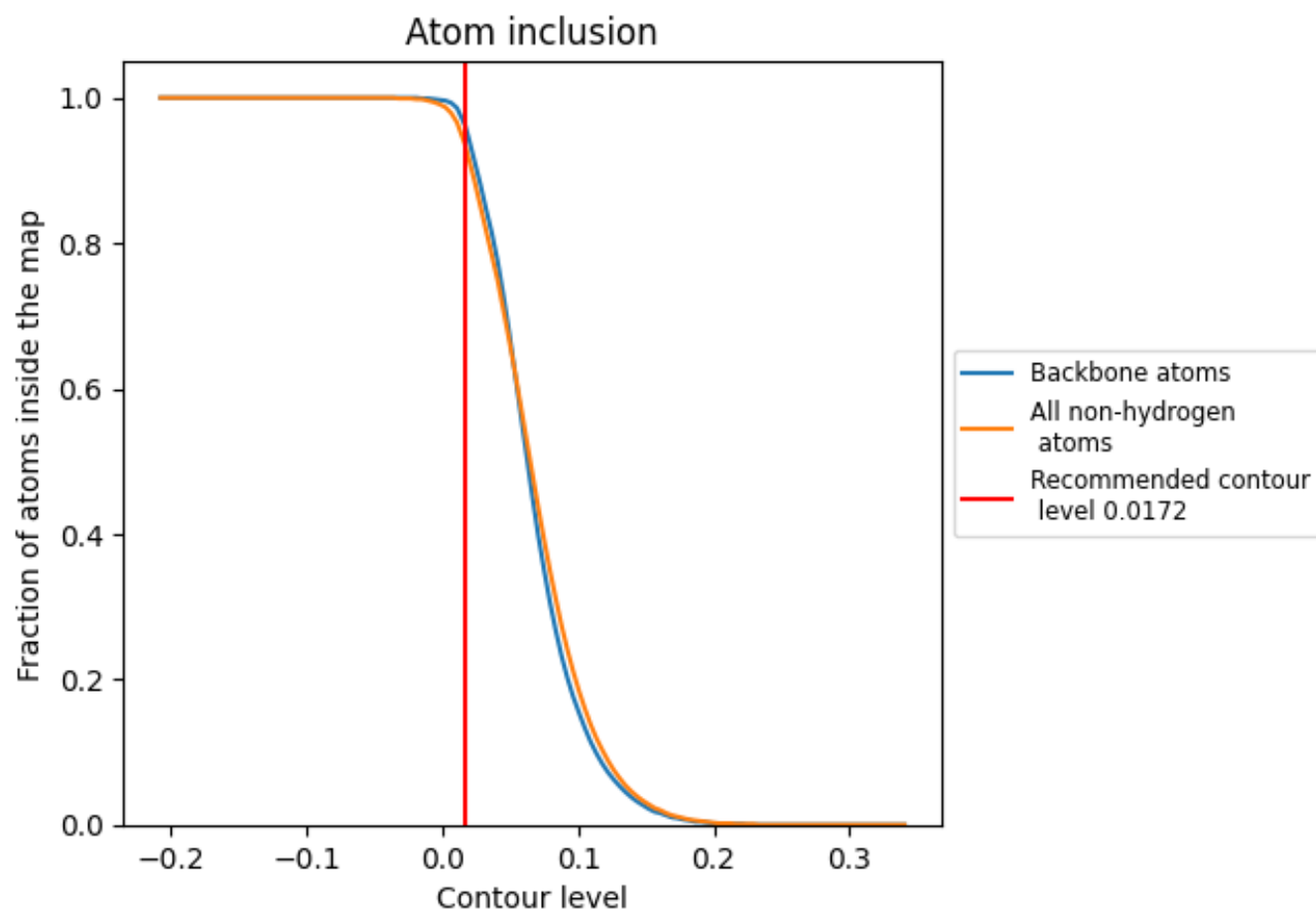
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0172).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% 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 (0.0172) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9340	 0.2480
0	 0.9080	 0.3000
1	 0.9220	 0.2440
2	 0.8960	 0.3180
3	 0.9000	 0.3550
4	 0.8550	 0.2090
6	 0.9300	 0.1610
A	 0.7980	 0.1250
B	 0.9940	 0.2530
C	 0.8930	 0.3170
D	 0.9070	 0.3090
E	 0.9200	 0.2620
F	 0.9030	 0.1500
G	 0.9260	 0.1810
H	 0.9700	 0.2330
I	 0.6500	 0.1160
J	 0.9230	 0.2970
K	 0.8720	 0.3210
L	 0.9260	 0.2840
M	 0.9100	 0.2600
N	 0.9120	 0.2830
O	 0.9260	 0.1790
P	 0.8950	 0.2790
Q	 0.9150	 0.2940
R	 0.9560	 0.2990
S	 0.8960	 0.2950
T	 0.9030	 0.2850
U	 0.9440	 0.2500
V	 0.9780	 0.3050
W	 0.8800	 0.2850
X	 0.7510	 0.1500
Y	 0.9530	 0.1900
Z	 0.9240	 0.2580
a	 0.9880	 0.2230
b	 0.6450	 0.1060



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Chain	Atom inclusion	Q-score
c	 0.6960	 0.1140
d	 0.8750	 0.1380
e	 0.8590	 0.1790
f	 0.8440	 0.1720
g	 0.8630	 0.1620
h	 0.8830	 0.1770
i	 0.9120	 0.1440
j	 0.9070	 0.1250
k	 0.8780	 0.2000
l	 0.8990	 0.1720
m	 0.9100	 0.1630
n	 0.8380	 0.1000
o	 0.8880	 0.1610
p	 0.8790	 0.1400
q	 0.8990	 0.1600
r	 0.8530	 0.1970
s	 0.9610	 0.1090
t	 0.8920	 0.1630
u	 0.8840	 0.2900
v	 0.4980	 0.0920
w	 0.7590	 0.1080