



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 03:02 AM UTC

PDB ID : 6XDQ / pdb_00006xdq
EMDB ID : EMD-22141
Title : Cryo-EM structure of an Escherichia coli coupled transcription-translational complex B3 (TTC-B3) containing an mRNA with a 30 nt long spacer, transcription factors NusA and NusG, and fMet-tRNAs at P-site and E-site
Authors : Molodtsov, V.; Ebright, R.H.; Wang, C.; Su, M.
Deposited on : 2020-06-11
Resolution : 3.70 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:

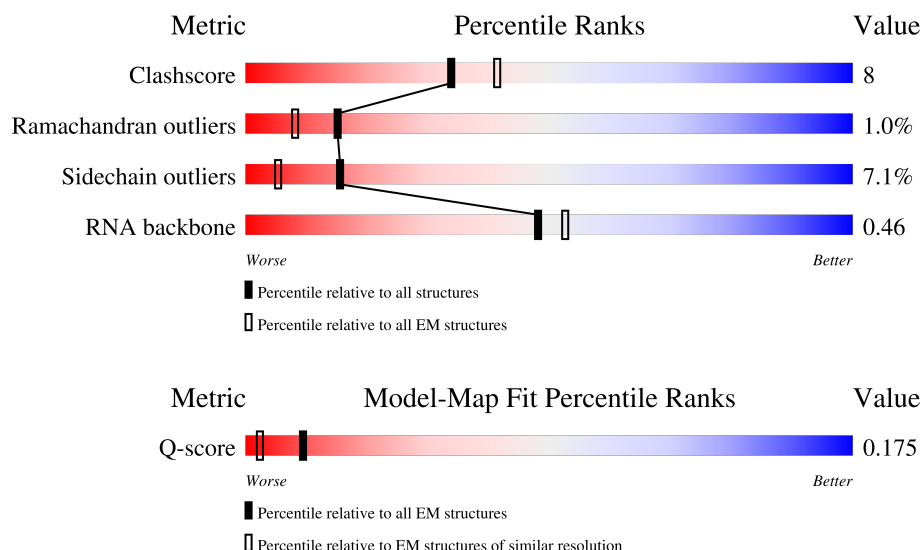
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.70 Å.

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



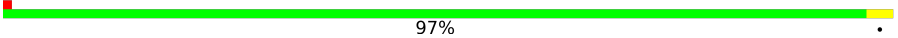
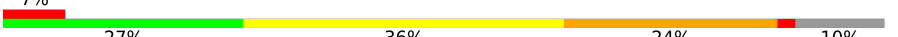
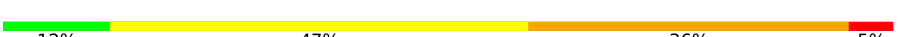
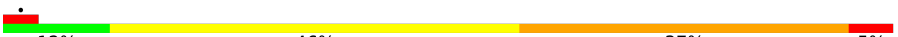
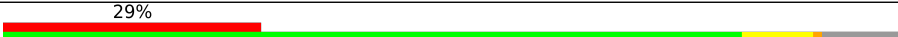
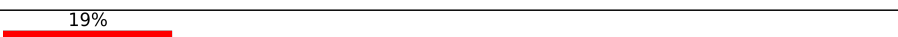
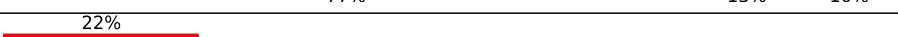
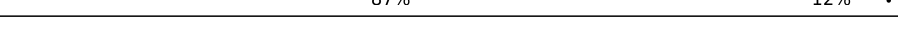
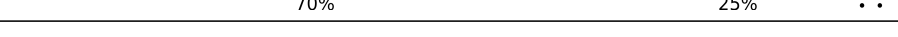
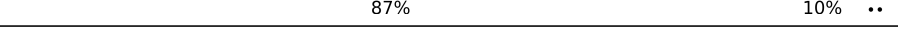
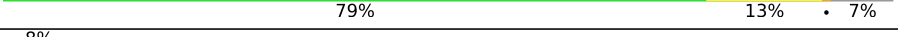
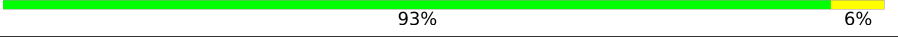
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	0	103	
2	1	110	
3	2	100	

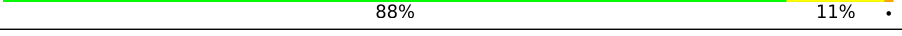
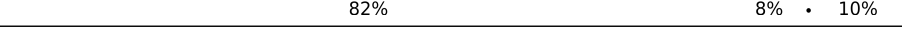
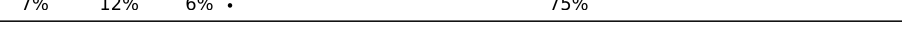
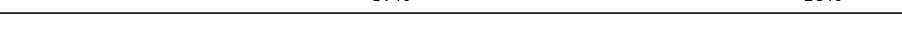
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	36	
7	6	36	
8	7	46	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	

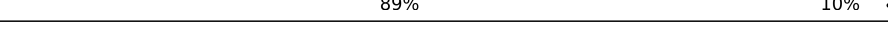
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Mol	Chain	Length	Quality of chain
27	M	179	
28	N	130	
29	O	130	
30	P	103	
31	Q	129	
32	R	124	
33	S	101	
34	T	89	
35	U	82	
36	V	84	
37	W	92	
38	X	118	
39	Y	142	
40	Z	121	
41	a	2904	
42	b	85	
43	c	78	
44	d	120	
45	e	63	
46	f	59	
47	g	70	
48	h	273	
49	i	57	
50	j	209	
51	k	55	

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Mol	Chain	Length	Quality of chain
52	l	201	 85% 13% .
53	m	46	 78% 17% .
54	n	179	 75% 20% ..
55	o	65	 88% 8% ..
56	p	177	 90% 8% .
57	q	38	 89% 8% .
58	r	149	 5% 88% 9% .
59	s	142	 83% 15% .
60	t	123	 80% 18% .
61	u	144	 90% 10%
62	v	136	 91% 8% .
63	w	127	 76% 18% 6%
64	x	117	 84% 15% ..
65	y	115	 89% 10% .
66	z	118	 84% 14% ..

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 290243 atoms, of which 109912 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 L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	94	Total	C	H	N	O	S	0	0
			1557	470	811	140	134	2		

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	103	Total	C	H	N	O	0	0
			1632	498	844	148	142		

- Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	23	Total	C	H	N	O	P	0	0
			732	225	260	87	137	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	27	Total	C	H	N	O	P	0	0
			847	259	305	89	167	27		

- Molecule 8 is a RNA chain called mRNA with 30 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	35	Total	C	H	N	O	P	0	0
			824	325	97	100	267	35		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

- Molecule 10 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
10	B	76	Total	C	H	N	O	P	0	0
			2433	723	813	295	527	75		

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

- Molecule 12 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	161	Total	C	N	O	S	0	0
			1276	813	221	235	7		

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	301	Total	C	N	O	S	0	0
			2091	1295	379	411	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	298	Total	C	N	O	S	0	0
			2073	1284	377	406	6		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AE	1335	Total	C	H	N	O	S	0	0
			21000	6526	10612	1854	1958	50		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	1384	VAL	MET	variant	UNP A0A4S1NBU2

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AF	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 16 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	AG	494	Total	C	N	O	0	0
			2442	1454	494	494		

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	C	66	Total	C	H	N	O	S	0	0
			1103	344	559	102	97	1		

- Molecule 18 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	D	1524	Total	C	H	N	O	P	0	0
			49126	14585	16423	6003	10591	1524		

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	E	86	Total	C	H	N	O	S	0	0
			1388	414	719	138	114	3		

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	F	70	Total	C	H	N	O	S	0	0
			1218	366	629	125	97	1		

- Molecule 21 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	G	225	Total	C	H	N	O	S	0	0
			3545	1113	1785	316	323	8		

- Molecule 22 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	H	259	Total	C	H	N	O	S	0	0
			3184	1073	1454	305	349	3		

- Molecule 23 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	I	208	Total	C	H	N	O	S	0	0
			3346	1036	1710	307	290	3		

- Molecule 24 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	J	205	Total	C	H	N	O	S	0	0
			3350	1026	1707	315	298	4		

- Molecule 25 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	K	156	Total	C	H	N	O	S	0	0
			2348	717	1196	217	212	6		

- Molecule 26 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	L	104	Total	C	H	N	O	S	0	0
			1694	536	846	153	152	7		

- Molecule 27 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	M	151	Total	C	H	N	O	S	0	0
			2416	735	1235	227	215	4		

- Molecule 28 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

- Molecule 29 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	O	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
30	P	99	Total	C	H	N	O	S	0	0
			1621	495	831	151	143	1		

- Molecule 31 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	Q	117	Total	C	H	N	O	S	0	0
			1764	540	887	174	160	3		

- Molecule 32 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	R	121	Total	C	H	N	O	S	0	0
			1940	580	1001	194	161	4		

- Molecule 33 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	S	100	Total	C	H	N	O	S	0	0
			1649	499	844	164	139	3		

- Molecule 34 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	T	88	Total	C	H	N	O	S	0	0
			1448	439	734	144	130	1		

- Molecule 35 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 36 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 37 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 38 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

- Molecule 39 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Y	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 40 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Z	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 41 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	887	A	U	variant	GB 937521852

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	b	76	Total	C	H	N	O	S	0	0
			1181	360	599	117	104	1		

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace	
43	c	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 44 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
44	d	120	Total	C	H	N	O	P	0	0
			3870	1144	1301	468	837	120		

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace	
45	e	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	f	58	Total	C	H	N	O	S	0	0
			936	281	488	87	78	2		

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	g	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 48 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	h	271	Total	C	H	N	O	S	0	0
			4236	1288	2154	423	364	7		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	i	56	Total	C	H	N	O	S	0	0
			903	269	459	94	80	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
50	j	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

- Molecule 51 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	k	52	Total	C	H	N	O		0	0
			890	275	464	78	73			

- Molecule 52 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	l	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	m	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 54 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	n	177	Total	C	H	N	O	S	0	0
			2853	899	1443	249	256	6		

- Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 56 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 58 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 59 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 60 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 61 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 62 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 63 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 64 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	x	116	Total	C	H	N	O		0	0
			1815	552	923	178	162			

- Molecule 65 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

- Molecule 66 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	z	117	Total	C	H	N	O		0	0
			1967	604	1020	192	151			

- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
67	AE	1	Total 1	Mg 1	0

- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

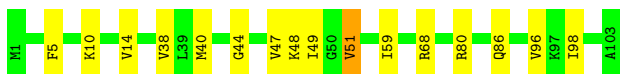
Mol	Chain	Residues	Atoms		AltConf
68	AE	2	Total 2	Zn 2	0

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 L21

Chain 0:  84% 15% .



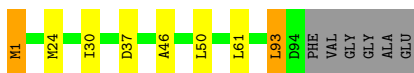
- Molecule 2: 50S ribosomal protein L22

Chain 1:  75% 25%



- Molecule 3: 50S ribosomal protein L23

Chain 2:  86% 6% . 6%

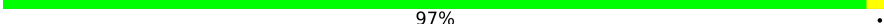


- Molecule 4: 50S ribosomal protein L24

Chain 3:  84% 14% ..



- Molecule 5: 50S ribosomal protein L25

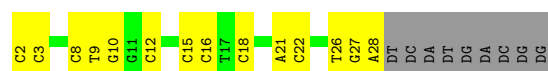
Chain 4:  97% .



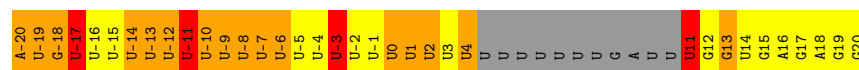
- Molecule 6: NT DNA



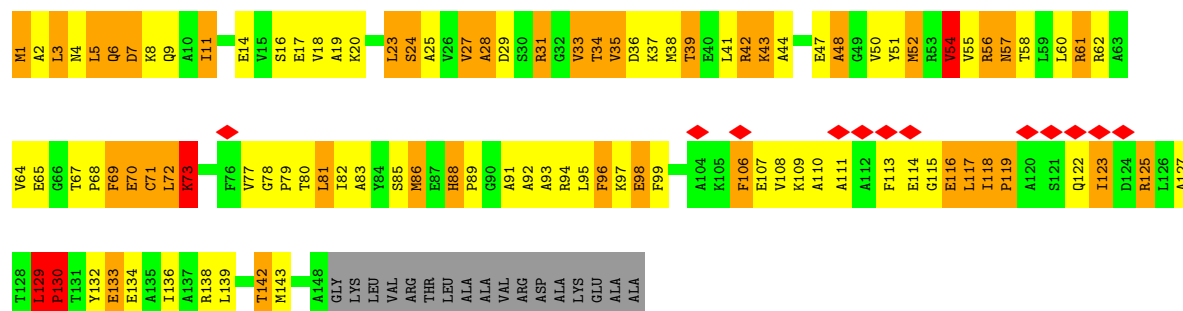
Chain 6: 36% 39% 25%



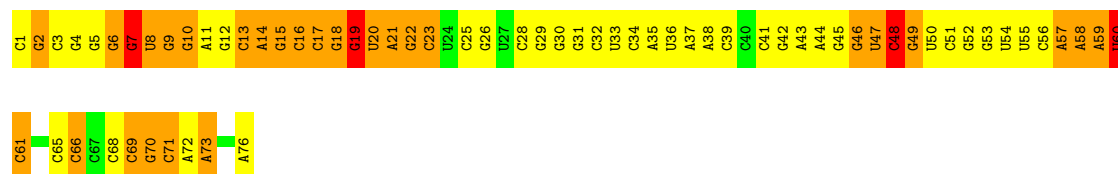
Chain 7:



Chain 9: 7% 27% 36% 24% • 10%



Chain A: 12% 47% 36% 5%



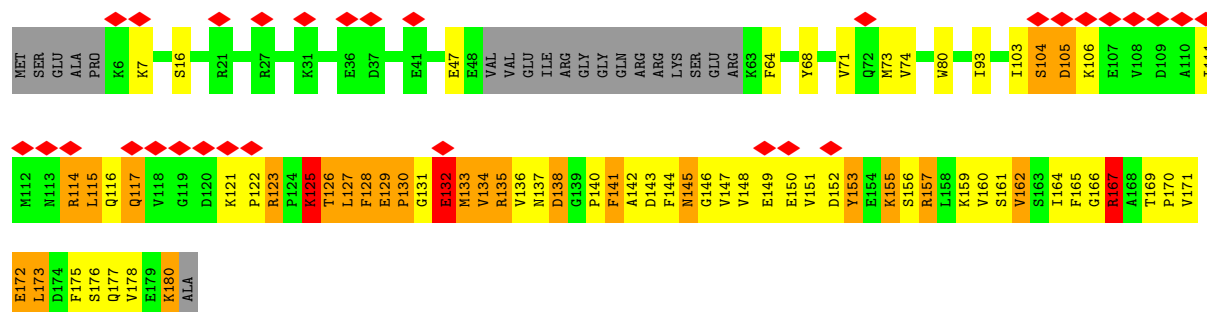
Chain B: 12% 46% 37% 5%



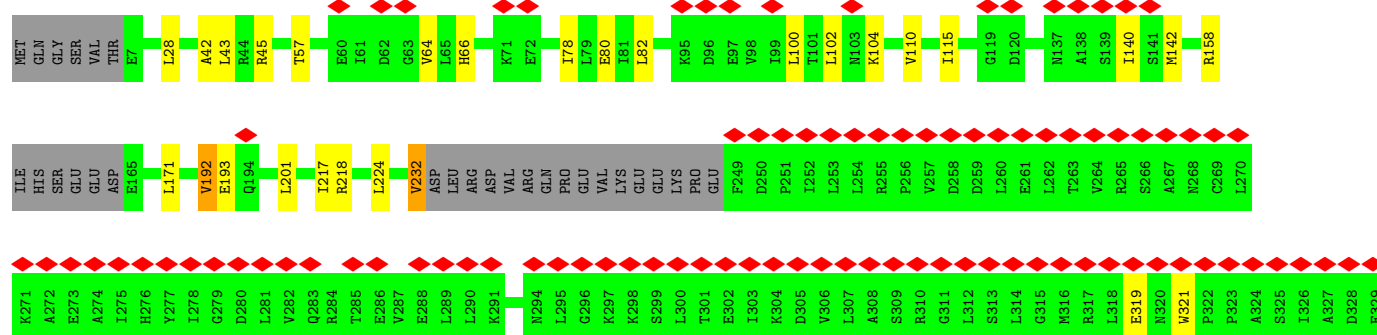
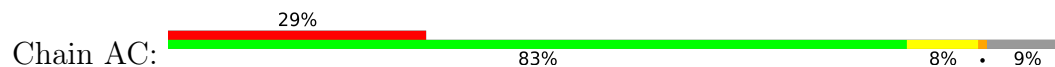




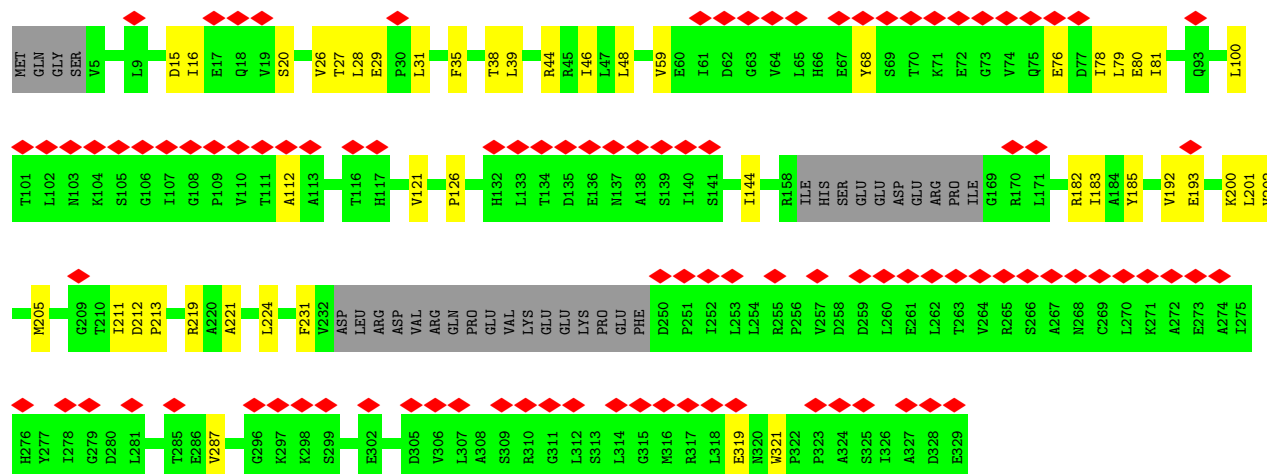
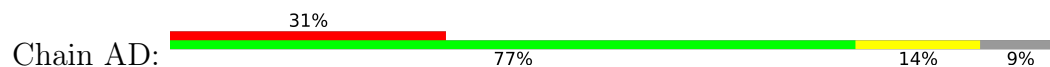
• Molecule 12: Transcription termination/antitermination protein NusG



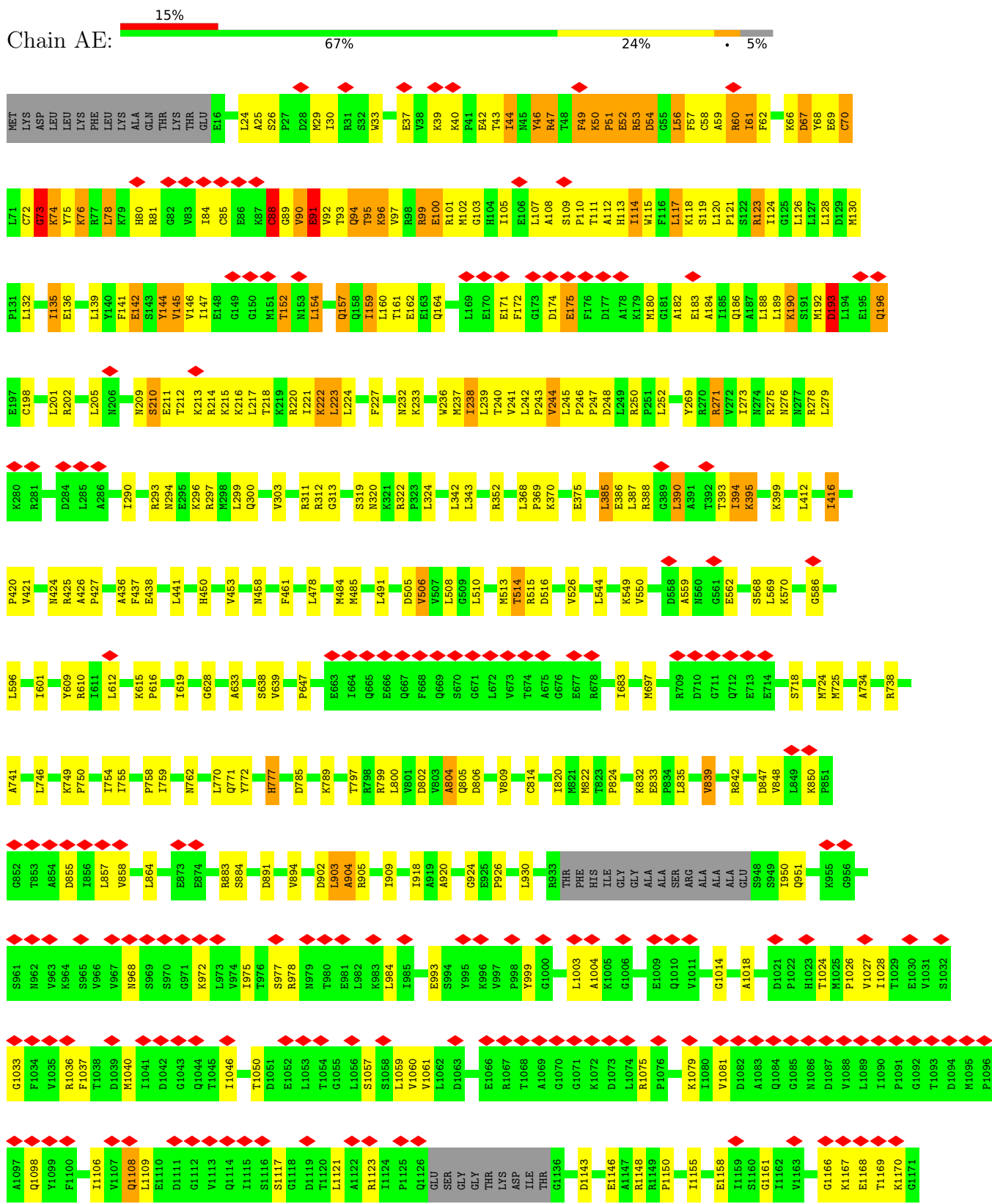
• Molecule 13: DNA-directed RNA polymerase subunit alpha

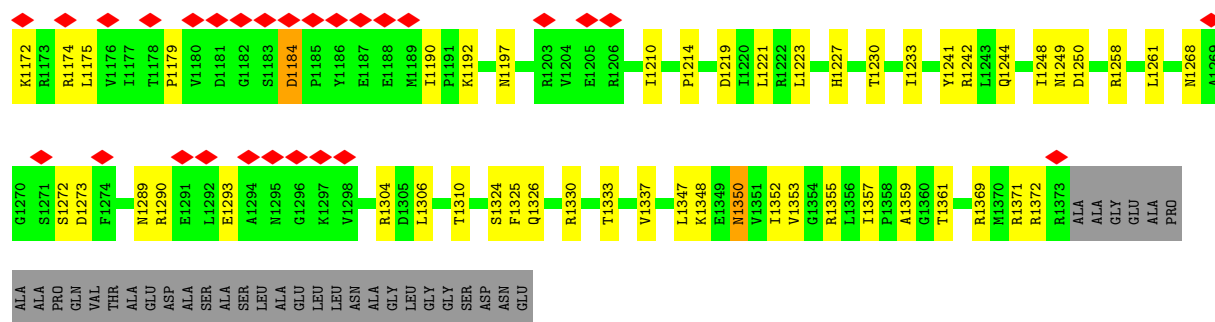


• Molecule 13: DNA-directed RNA polymerase subunit alpha

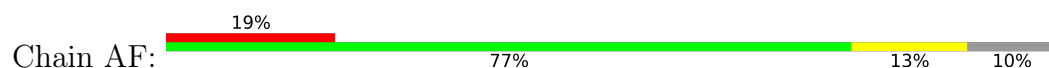


• Molecule 14: DNA-directed RNA polymerase subunit beta'

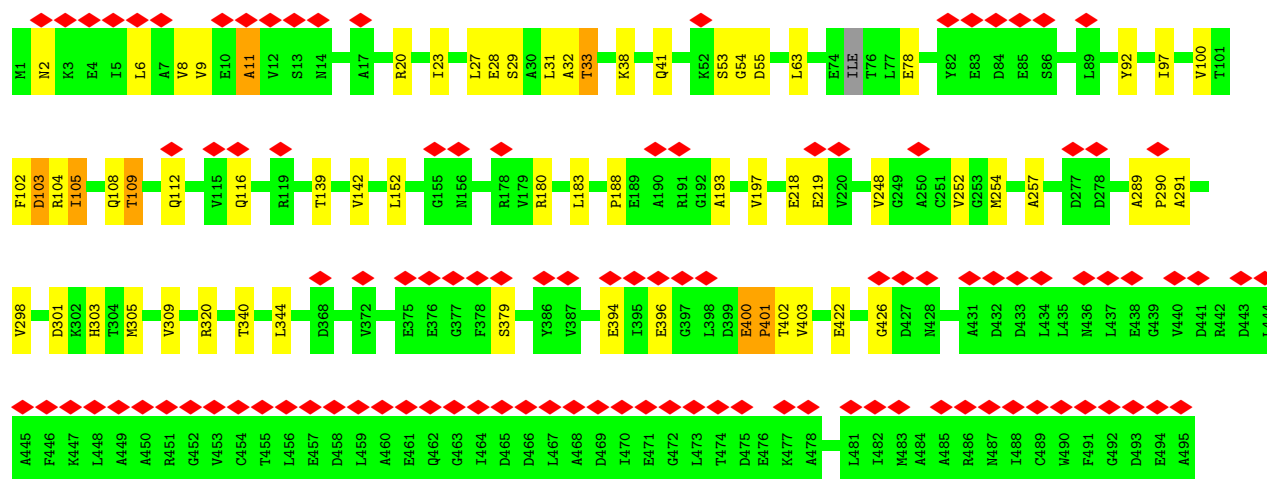
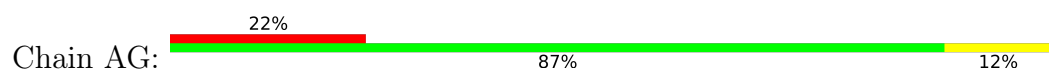




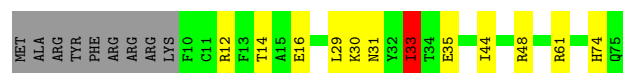
- Molecule 15: DNA-directed RNA polymerase subunit omega



- Molecule 16: Transcription termination/antitermination protein NusA

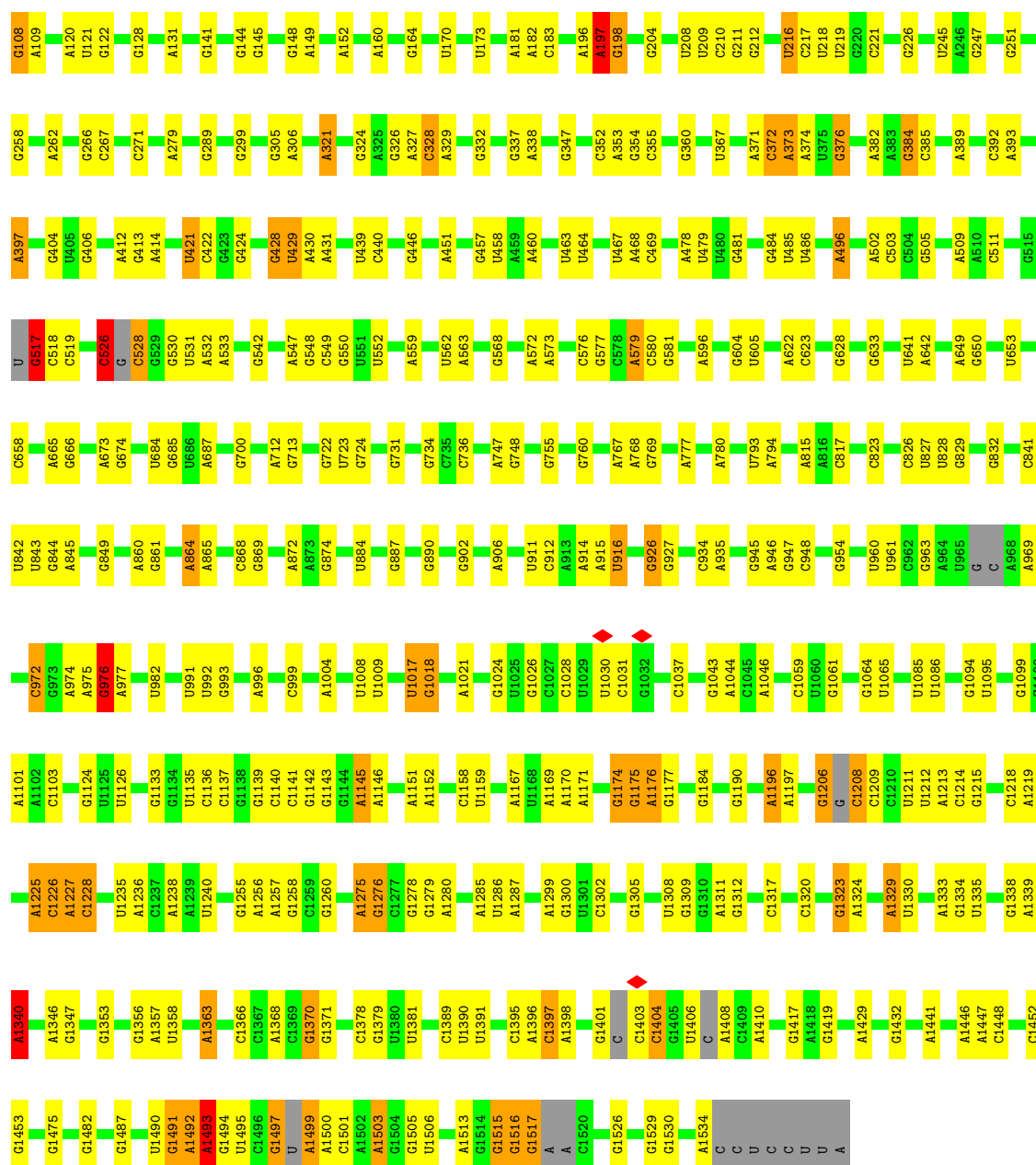


- Molecule 17: 30S ribosomal protein S18



- Molecule 18: 16S rRNA





• Molecule 19: 30S ribosomal protein S20

Chain E: 87% 11% .

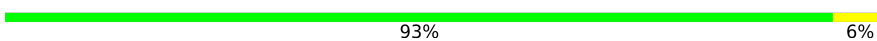


• Molecule 20: 30S ribosomal protein S21

Chain F: 87% 10% ..



- Molecule 24: 30S ribosomal protein S4

Chain J:  93% 6%



- Molecule 25: 30S ribosomal protein S5

Chain K:  76% 14% 7%



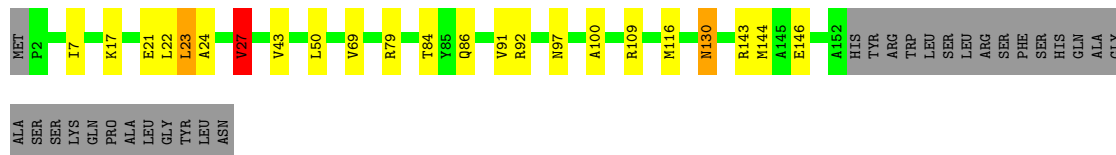
- Molecule 26: 30S ribosomal protein S6

Chain L:  67% 10% 23%



- Molecule 27: 30S ribosomal protein S7

Chain M:  72% 11% 16%



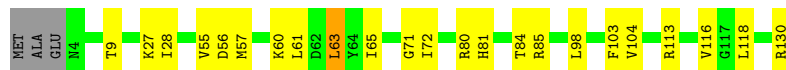
- Molecule 28: 30S ribosomal protein S8

Chain N:  89% 9%



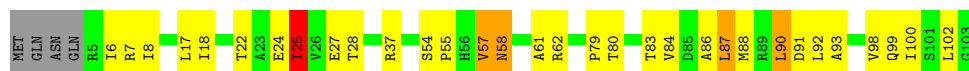
- Molecule 29: 30S ribosomal protein S9

Chain O:  80% 17%



- Molecule 30: 30S ribosomal protein S10

Chain P:  65% 26% . . .



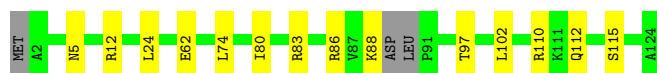
- Molecule 31: 30S ribosomal protein S11

Chain Q:  82% 9% 9%



- Molecule 32: 30S ribosomal protein S12

Chain R:  86% 11% .



- Molecule 33: 30S ribosomal protein S14

Chain S:  89% 8% ...



- Molecule 34: 30S ribosomal protein S15

Chain T:  79% 18% ..



- Molecule 35: 30S ribosomal protein S16

Chain U:  88% 11% .

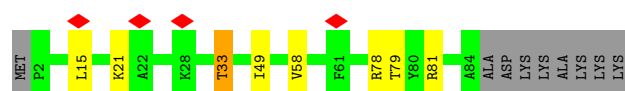


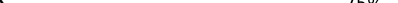
- Molecule 36: 30S ribosomal protein S17

Chain V:  87% 7% . 5%

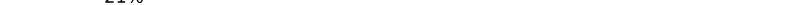


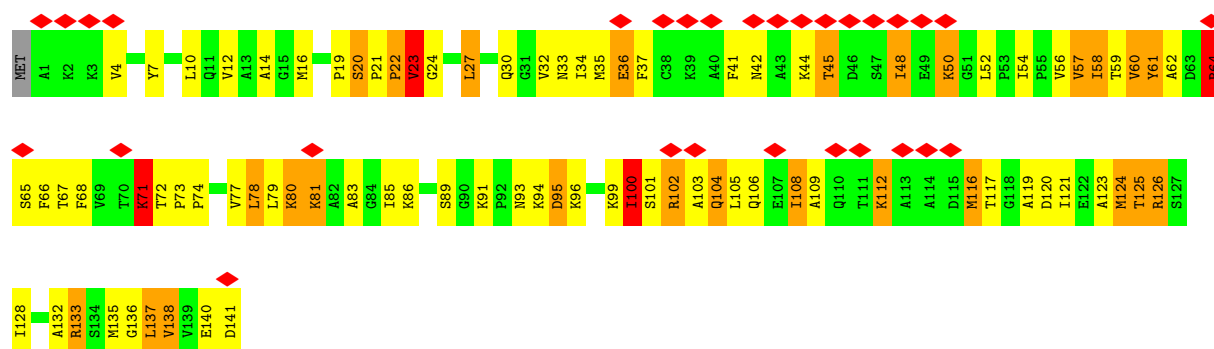
- Molecule 37: 30S ribosomal protein S19

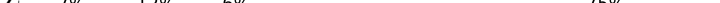


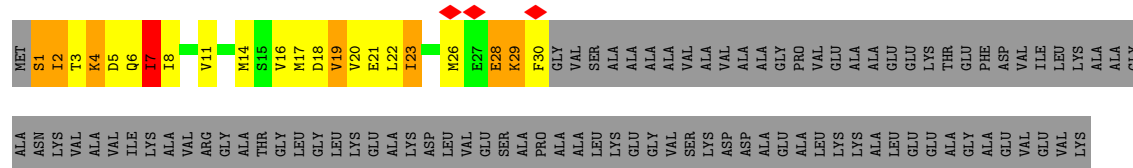
- Chain X:  75% 18% 5%

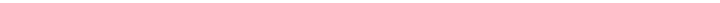


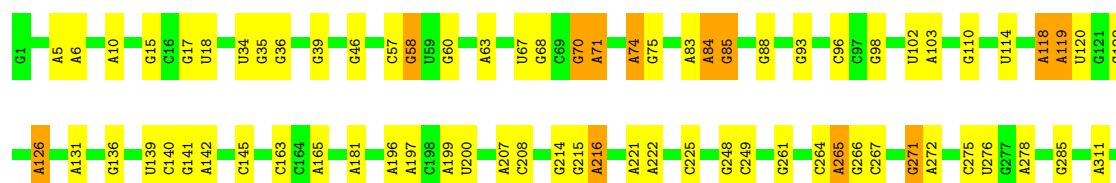
- Chain Y: 



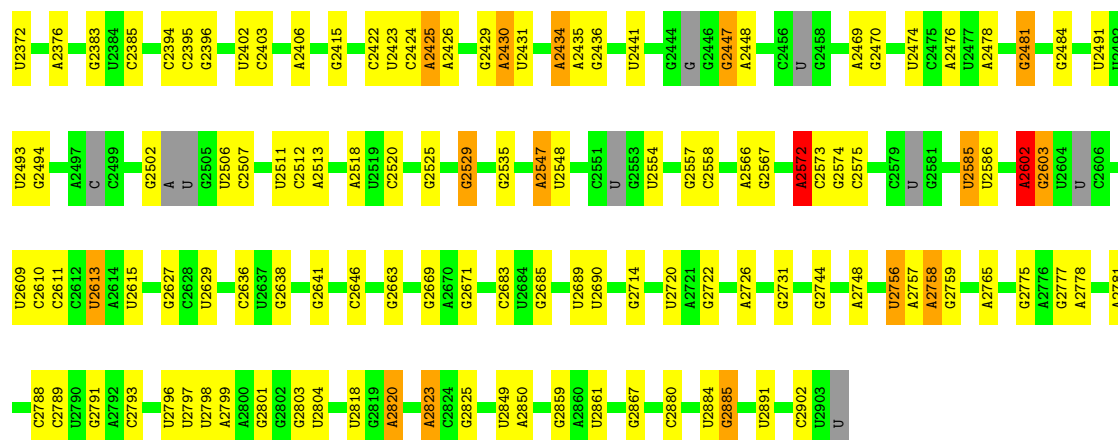
- Chain Z: 



- Chain a:  73% 23% .



U2249	G2146	A2051	A1936	G1817	G1649	A1503	C1345	A1133	G1042	A910	G776	A613	G494	A320
G2250	A2147	A2052	A1937	U1818	A1650	A1508	U1352	A1134	C1045	G914	A782	A614	A501	A324
G2252	A2154	G2055	U1938	G1824	G1651	A1509	U1352	C1136	A1046	C915	A783	U615	A502	A504
G2253	G2157	C2056	U1940	A1829	A1568	G1510	A1365	U1141	G1047	A927	G785	G617	A503	G329
A2268	A2158	G2056	U1955	U1833	G1674	A1515	G1368	A1142	A1054	A928	A800	G618	A505	A330
A2273	G2159	A2060	U1961	C1833	A1677	G1529	A1378	C1153	G1055	U929	G801	G619	C509	A340
A2274	G2162	G2061	C1961	U1834	A1677	G1534	U1379	A1169	G1056	G930	A802	G620	C517	C353
A2278	A2163	C2063	U1963	G1836	U1693	A1535	C1380	C1170	U1060	A941	G805	A627	A522	G359
C2283	C2164	U2068	G1964	G1839	C1694	U1536	A1583	U1173	G1062	C944	U811	A631	C523	U360
A2287	C2165	G	A1966	U1847	G1703	C1537	A1384	U1174	G1063	C945	C812	A637	A945	A362
U2291	U2167	A2070	C1967	A1848	U1714	A1548	A1385	A1175	U1065	C946	U813	A637	A526	A371
U2292	A2170	C2072	U1971	A1848	G1715	A1549	C1386	U1176	A1067	A947	C814	U639	A528	G372
G2293	U2171	U	C1972	U1859	G1715	U1554	A1387	G1177	G1068	C948	A819	C640	A529	U373
C2295	U2172	U2075	G1980	G1862	G1718	U1554	A1392	G1179	A1069	G953	U827	C645	A532	A374
C2296	C2178	A2077	U1981	U1863	G1719	U1559	A1394	U1180	A1070	G954	U828	U646	A532	G375
A2297	G2181	G2083	U1982	G1864	G1721	A1566	U1395	U1181	C1071	U	U828	G647	C540	G375
A2298	U2182	A2087	A1987	G1869	U1729	G1567	U1396	U1183	A1073	C961	A845	A654	G543	C353
U2299	A2183	U2098	U1991	C1870	C1730	G1568	U1406	G1186	C1075	A973	U846	G654	U546	G386
G2303	A2184	U2099	G1992	A1871	G1732	A1570	G1407	U1187	C1076	G974	C851	G664	U547	G396
U2305	U2185	C2100	U1993	A1873	G1738	A1571	G1408	U1189	C1079	A983	G858	A668	G548	A404
G2308	U2188	A2108	C1997	G1905	G1738	U1578	U1411	U1209	U1081	A984	G859	A685	C550	U405
A2309	U2189	U2109	A1998	C1906	G1750	A1579	U1412	U1237	U1082	C985	G869	U686	G551	G411
U2310	A2190	G2110	C1999	G1907	A1755	A1580	A1413	A1237	U1083	C995	U870	A705	U554	A412
A2311	U2192	U2111	C2000	C1908	A1756	G1581	C1414	G1238	A1084	G997	U871	U710	C560	C420
U2194	G2193	C2001	C2001	C1909	G1756	C1582	G1415	U1248	A1085	C998	U872	C717	A563	A423
A2314	U2194	G2002	G2002	G1910	A1757	A1583	C1416	G1249	A1086	U999	U872	A730	C565	G424
G2315	A2198	C2006	C2006	U	U1758	U1584	G1418	G1250	A1087	C1007	U872	G738	U567	C435
U2321	G2204	A2116	A2013	A1912	C1764	G1588	A1419	A1253	A1089	C1005	A878	A742	U568	G450
A2322	U2210	G2116	U2017	A1913	A1773	U1589	A1420	A1256	A1090	C1007	U884	A743	U569	U451
U2210	G2210	U2118	U2017	U	A1773	A1590	G1422	G1256	A1095	U1012	U884	U744	A572	C456
A2211	A2210	G2121	U2017	A1916	U1779	A1591	C1428	G1266	A1096	C1013	U884	U744	A572	C456
U2213	U2213	G2123	A2020	A1918	A1784	A1596	A1433	C1270	A1103	U1019	C888	U744	A572	C456
A2225	G2124	G2125	C2021	A1919	A1789	A1597	A1434	A1271	G1107	A1020	C888	U744	A572	C456
C2226	A2126	G2126	C2023	C1920	C1790	A1603	A1452	A1272	U1108	A1021	C888	U744	A572	C456
U2229	G2127	G2128	U2027	G1922	A1791	A1608	A1453	U1273	G1109	G1022	C888	U744	A572	C456
G2230	U2128	C1925	C2028	C1924	C1800	A1609	U1460	A1274	G1110	U1023	C888	U744	A572	C456
U2231	U2131	U1926	A	C1925	A1901	A1610	U1460	A1275	A1111	G1023	C888	U744	A572	C456
G2345	U2132	U1926	A2031	U1926	A1901	A1614	U1460	A1275	A1111	G1023	C888	U744	A572	C456
A2346	U2133	A1927	A2031	A1927	A1901	A1614	U1460	A1275	A1111	G1023	C888	U744	A572	C456
C2347	G2238	G2032	G2032	A1928	A1901	A1614	U1460	A1275	A1111	G1023	C888	U744	A572	C456
U2347	G2239	A2033	A2033	G1929	A1901	A1614	U1460	A1275	A1111	G1023	C888	U744	A572	C456
C2350	U2243	U2139	G2038	G1930	G1811	C1617	G1482	A1301	U1119	A1027	C888	U744	A572	C456
G2361	U2244	G2140	U2039	U1931	G1814	A	G1619	A1321	G1122	A1028	C888	U744	A572	C456
U2245	U2245	G2141	A1932	A1932	G1815	U1647	G1491	A1321	G1125	U1033	C888	U744	A572	C456
			C2043	G1933	C1816	U1648	U1497	A1327	U1132	G1041	C888	U744	A572	C456



• Molecule 42: 50S ribosomal protein L27

Chain b: 84% 6% 11%



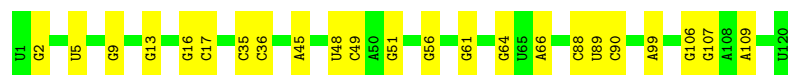
• Molecule 43: 50S ribosomal protein L28

Chain c: 88% 8% 4%



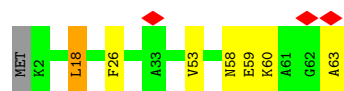
• Molecule 44: 5S rRNA

Chain d: 81% 19% 0%



• Molecule 45: 50S ribosomal protein L29

Chain e: 5% 87% 10% 2%



• Molecule 46: 50S ribosomal protein L30

Chain f: 85% 12% 3%



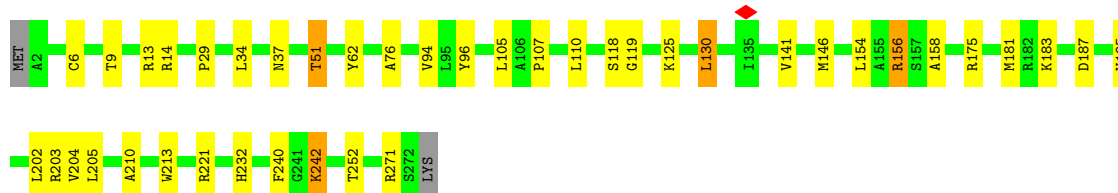
• Molecule 47: 50S ribosomal protein L31

Chain g:  80% 13% • 6%



- Molecule 48: 50S ribosomal protein L2

Chain h:  84% 14% ••



- Molecule 49: 50S ribosomal protein L32

Chain i:  77% 19% ••



- Molecule 50: 50S ribosomal protein L3

Chain j:  88% 11%



- Molecule 51: 50S ribosomal protein L33

Chain k:  89% 5% 5%



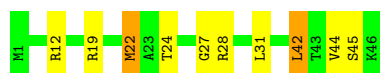
- Molecule 52: 50S ribosomal protein L4

Chain l:  85% 13% •



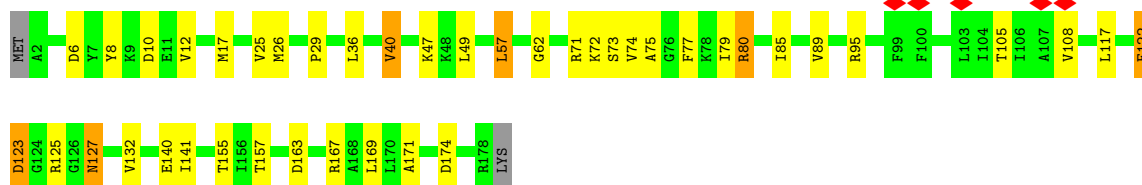
- Molecule 53: 50S ribosomal protein L34

Chain m:  78% 17% •



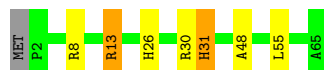
- Molecule 54: 50S ribosomal protein L5

Chain n: 75% 20% . .



- Molecule 55: 50S ribosomal protein L35

Chain o: 88% 8% . .



- Molecule 56: 50S ribosomal protein L6

Chain p: 90% 8% .



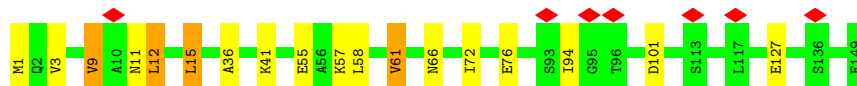
- Molecule 57: 50S ribosomal protein L36

Chain q: 89% 8% .



- Molecule 58: 50S ribosomal protein L9

Chain r: 5% 88% 9% .



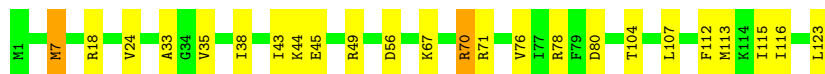
- Molecule 59: 50S ribosomal protein L13

Chain s: 83% 15% .

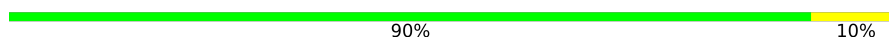


- Molecule 60: 50S ribosomal protein L14

Chain t:  80% 18% .

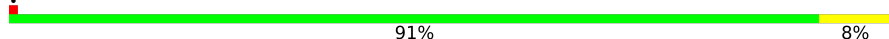


- Molecule 61: 50S ribosomal protein L15

Chain u:  90% 10%



- Molecule 62: 50S ribosomal protein L16

Chain v:  91% 8% .



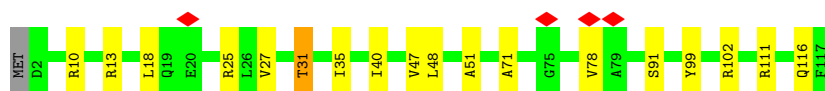
- Molecule 63: 50S ribosomal protein L17

Chain w:  76% 18% 6%



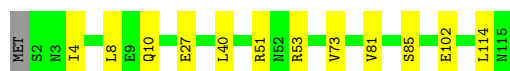
- Molecule 64: 50S ribosomal protein L18

Chain x:  84% 15% ..



- Molecule 65: 50S ribosomal protein L19

Chain y:  89% 10% .



- Molecule 66: 50S ribosomal protein L20

Chain z:  84% 14% ..



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19967	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.039	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00359	Depositor
Map size (Å)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.49	0/829	0.74	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.54	0/752	0.89	0/1005
4	3	0.47	0/796	0.77	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.63	1/528 (0.2%)	0.55	0/810
7	6	0.55	1/603 (0.2%)	0.56	0/926
8	7	0.60	3/805 (0.4%)	0.88	4/1246 (0.3%)
9	9	1.15	3/1131 (0.3%)	1.30	4/1524 (0.3%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.43	0/1810	0.87	9/2821 (0.3%)
11	AA	0.40	0/10736	0.64	0/14487
12	AB	0.72	0/1304	0.93	1/1759 (0.1%)
13	AC	0.35	0/2110	0.61	0/2873
13	AD	0.29	0/2091	0.59	0/2847
14	AE	0.54	9/10545 (0.1%)	0.74	25/14236 (0.2%)
15	AF	0.29	0/652	0.61	0/879
16	AG	0.64	0/2440	0.90	6/3396 (0.2%)
17	C	0.66	0/553	1.14	2/743 (0.3%)
18	D	0.40	9/36610 (0.0%)	0.75	38/57091 (0.1%)
19	E	0.76	0/675	1.32	0/895
20	F	0.71	0/597	1.20	0/792
21	G	0.65	0/1791	1.08	1/2413 (0.0%)
22	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
23	I	0.58	0/1663	0.98	0/2241
24	J	0.63	0/1665	1.08	0/2227
25	K	0.63	0/1165	1.06	2/1568 (0.1%)
26	L	0.58	0/867	0.94	0/1171
27	M	0.68	0/1195	1.19	3/1602 (0.2%)
28	N	0.55	0/989	0.92	0/1326
29	O	0.58	0/1034	1.02	1/1375 (0.1%)
30	P	0.63	0/800	1.14	4/1082 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.55	0/893	0.91	0/1205
32	R	0.49	0/952	0.81	0/1274
33	S	0.64	0/817	1.11	1/1088 (0.1%)
34	T	0.69	0/722	1.21	0/964
35	U	0.58	0/659	0.99	0/884
36	V	0.46	0/657	0.73	0/881
37	W	0.51	0/680	0.83	0/915
38	X	0.67	0/909	1.21	3/1215 (0.2%)
39	Y	1.03	0/1046	1.08	0/1410
40	Z	1.02	0/227	1.13	0/304
41	a	0.40	3/69247 (0.0%)	0.75	56/107985 (0.1%)
42	b	0.51	0/589	0.76	0/779
43	c	0.63	0/635	0.97	0/848
44	d	0.37	0/2872	0.69	0/4478
45	e	0.69	0/502	1.19	0/667
46	f	0.62	0/452	1.02	0/605
47	g	0.55	0/531	0.99	1/709 (0.1%)
48	h	0.54	0/2121	0.85	0/2852
49	i	0.52	0/450	0.94	0/599
50	j	0.60	0/1586	0.87	0/2134
51	k	0.47	0/433	0.80	0/576
52	l	0.61	0/1571	1.03	1/2113 (0.0%)
53	m	0.68	0/380	1.22	0/498
54	n	0.62	0/1434	1.18	10/1926 (0.5%)
55	o	0.64	0/513	1.10	1/676 (0.1%)
56	p	0.58	0/1333	0.89	0/1805
57	q	0.50	0/303	0.88	0/397
58	r	0.63	0/1122	0.97	1/1515 (0.1%)
59	s	0.68	0/1152	1.02	2/1551 (0.1%)
60	t	0.57	0/955	0.88	0/1279
61	u	0.55	0/1062	0.96	1/1413 (0.1%)
62	v	0.60	0/1093	0.97	0/1460
63	w	0.67	0/964	1.13	0/1289
64	x	0.61	0/902	1.09	0/1209
65	y	0.53	0/929	0.79	0/1242
66	z	0.80	0/960	1.25	0/1278
All	All	0.49	33/193575 (0.0%)	0.82	213/284911 (0.1%)

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
10	A	0	2
10	B	0	2
11	AA	0	1
13	AC	0	3
13	AD	0	3
14	AE	0	5
16	AG	0	1
22	H	0	3
38	X	0	1
All	All	0	21

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.15	1.70	1.47
14	AE	93	THR	CA-C	12.17	1.69	1.52
22	H	169	SER	N-CA	11.76	1.61	1.46
18	D	1516	G	O3'-P	-10.73	1.45	1.61
14	AE	70	CYS	CA-CB	-8.81	1.41	1.53

The worst 5 of 213 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	D	1516	G	O3'-P-O5'	17.45	130.18	104.00
22	H	88	LYS	CA-C-N	16.90	143.54	120.38
22	H	88	LYS	C-N-CA	16.90	143.54	120.38
10	B	29	G	C3'-C2'-O2'	15.94	134.61	110.70
9	9	129	LEU	CA-C-N	15.85	139.66	119.84

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
11	AA	910	ALA	Peptide
13	AC	192	VAL	Peptide
13	AC	319	GLU	Peptide

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	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	6	0
4	3	788	844	844	11	0
5	4	753	780	780	0	0
6	5	472	260	260	20	0
7	6	542	305	306	24	0
8	7	727	97	361	106	0
9	9	1117	0	1153	163	0
10	A	1620	826	826	169	0
10	B	1620	813	827	138	0
11	AA	10567	0	10582	280	0
12	AB	1276	0	1244	234	0
13	AC	2091	0	1892	17	0
13	AD	2073	0	1889	30	0
14	AE	10388	10612	10611	364	0
15	AF	650	0	658	13	0
16	AG	2442	0	1177	83	0
17	C	544	559	560	23	0
18	D	32703	16423	16459	220	0
19	E	669	719	719	3	0
20	F	589	629	629	8	0
21	G	1760	1785	1785	51	0
22	H	1730	1454	1454	211	0
23	I	1636	1710	1710	18	0
24	J	1643	1707	1707	15	0
25	K	1152	1196	1196	22	0
26	L	848	846	846	3	0
27	M	1181	1235	1235	33	0
28	N	979	1031	1031	7	0
29	O	1022	1070	1070	12	0
30	P	790	831	831	103	0
31	Q	877	887	887	4	0
32	R	939	1001	1001	7	0
33	S	805	844	844	5	0
34	T	714	734	734	8	0
35	U	649	666	666	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	V	648	691	691	4	0
37	W	663	688	688	2	0
38	X	900	964	964	57	0
39	Y	1032	0	1088	84	0
40	Z	227	0	237	19	0
41	a	61841	31077	31123	299	0
42	b	582	599	599	3	0
43	c	625	652	652	4	0
44	d	2569	1301	1301	3	0
45	e	501	531	531	4	0
46	f	448	488	488	5	0
47	g	522	520	520	11	0
48	h	2082	2154	2154	20	0
49	i	444	459	458	6	0
50	j	1565	1617	1616	15	0
51	k	426	464	464	0	0
52	l	1552	1619	1619	13	0
53	m	377	418	418	10	0
54	n	1410	1443	1444	28	0
55	o	504	572	572	3	0
56	p	1313	1358	1358	7	0
57	q	302	343	343	1	0
58	r	1111	1148	1148	6	0
59	s	1129	1162	1162	12	0
60	t	946	1023	1023	12	0
61	u	1053	1129	1129	7	0
62	v	1074	1157	1157	5	0
63	w	951	994	994	9	0
64	x	892	923	923	8	0
65	y	917	962	962	4	0
66	z	947	1020	1019	13	0
67	AE	1	0	0	0	0
68	AE	2	0	0	0	0
All	All	180331	109912	130191	2521	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 8.

The worst 5 of 2521 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)
22:H:131:LEU:CB	22:H:167:VAL:CA	1.78	1.62
11:AA:902:LEU:CD1	16:AG:27:LEU:CB	1.78	1.58
11:AA:902:LEU:HD13	16:AG:27:LEU:CB	1.23	1.56
17:C:12:ARG:HG3	22:H:264:GLU:CB	1.30	1.54
12:AB:141:PHE:CE2	12:AB:173:LEU:HD11	1.40	1.51

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	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	43
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	12	43
5	4	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	7
11	AA	1338/1342 (100%)	1209 (90%)	126 (9%)	3 (0%)	43	72
12	AB	157/181 (87%)	128 (82%)	22 (14%)	7 (4%)	2	18
13	AC	295/329 (90%)	274 (93%)	19 (6%)	2 (1%)	18	50
13	AD	292/329 (89%)	270 (92%)	22 (8%)	0	100	100
14	AE	1329/1407 (94%)	1198 (90%)	122 (9%)	9 (1%)	18	50
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	AG	490/495 (99%)	421 (86%)	51 (10%)	18 (4%)	2	22
17	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
20	F	68/71 (96%)	68 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
22	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	18
23	I	206/233 (88%)	197 (96%)	8 (4%)	1 (0%)	24	56
24	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
25	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	21	52
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	43
27	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	18	50
28	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	48
29	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	48
30	P	97/103 (94%)	87 (90%)	9 (9%)	1 (1%)	12	43
31	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	34
32	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
35	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	38
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
38	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	6	34
39	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	8
40	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	12
42	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
43	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
45	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
47	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
48	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	60
49	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
51	k	50/55 (91%)	50 (100%)	0	0	100	100
52	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	56
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	11	42
55	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
56	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
59	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
60	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
61	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
63	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
64	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
65	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
66	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	45
All	All	10154/11072 (92%)	9318 (92%)	738 (7%)	98 (1%)	15	43

5 of 98 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
16	AG	6	LEU
16	AG	100	VAL
16	AG	400	GLU
16	AG	401	PRO

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	84/84 (100%)	76 (90%)	8 (10%)	8	31
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	39
3	2	81/84 (96%)	77 (95%)	4 (5%)	22	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	84/85 (99%)	79 (94%)	5 (6%)	17	44
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	53
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1155/1157 (100%)	1135 (98%)	20 (2%)	53	67
12	AB	138/158 (87%)	108 (78%)	30 (22%)	1	7
13	AC	185/286 (65%)	184 (100%)	1 (0%)	81	80
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1120/1168 (96%)	1047 (94%)	73 (6%)	15	43
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	70
17	C	57/65 (88%)	55 (96%)	2 (4%)	32	54
19	E	65/66 (98%)	61 (94%)	4 (6%)	16	44
20	F	60/61 (98%)	57 (95%)	3 (5%)	22	48
21	G	187/199 (94%)	174 (93%)	13 (7%)	14	41
22	H	137/461 (30%)	124 (90%)	13 (10%)	8	31
23	I	171/190 (90%)	162 (95%)	9 (5%)	20	46
24	J	172/173 (99%)	164 (95%)	8 (5%)	23	48
25	K	119/126 (94%)	111 (93%)	8 (7%)	15	42
26	L	91/116 (78%)	84 (92%)	7 (8%)	12	38
27	M	124/147 (84%)	113 (91%)	11 (9%)	9	33
28	N	104/105 (99%)	101 (97%)	3 (3%)	37	57
29	O	105/107 (98%)	99 (94%)	6 (6%)	18	45
30	P	86/90 (96%)	78 (91%)	8 (9%)	8	32
31	Q	90/99 (91%)	88 (98%)	2 (2%)	45	63
32	R	101/104 (97%)	95 (94%)	6 (6%)	18	44
33	S	83/84 (99%)	79 (95%)	4 (5%)	23	48
34	T	76/77 (99%)	65 (86%)	11 (14%)	3	17
35	U	65/65 (100%)	60 (92%)	5 (8%)	12	38
36	V	74/78 (95%)	71 (96%)	3 (4%)	27	52
37	W	72/79 (91%)	66 (92%)	6 (8%)	10	35
38	X	94/96 (98%)	87 (93%)	7 (7%)	13	39
39	Y	109/110 (99%)	69 (63%)	40 (37%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
42	b	58/63 (92%)	57 (98%)	1 (2%)	53	67
43	c	67/68 (98%)	64 (96%)	3 (4%)	24	49
45	e	54/55 (98%)	51 (94%)	3 (6%)	19	46
46	f	48/49 (98%)	43 (90%)	5 (10%)	7	28
47	g	59/62 (95%)	54 (92%)	5 (8%)	10	35
48	h	216/218 (99%)	199 (92%)	17 (8%)	11	37
49	i	47/48 (98%)	41 (87%)	6 (13%)	4	21
50	j	164/164 (100%)	156 (95%)	8 (5%)	22	48
51	k	47/49 (96%)	44 (94%)	3 (6%)	16	43
52	l	165/165 (100%)	151 (92%)	14 (8%)	10	35
53	m	38/38 (100%)	36 (95%)	2 (5%)	20	46
54	n	148/150 (99%)	130 (88%)	18 (12%)	5	22
55	o	51/52 (98%)	47 (92%)	4 (8%)	11	37
56	p	136/138 (99%)	130 (96%)	6 (4%)	25	50
57	q	34/34 (100%)	31 (91%)	3 (9%)	9	33
58	r	114/114 (100%)	102 (90%)	12 (10%)	6	28
59	s	116/116 (100%)	106 (91%)	10 (9%)	10	34
60	t	104/104 (100%)	97 (93%)	7 (7%)	15	42
61	u	103/103 (100%)	96 (93%)	7 (7%)	14	42
62	v	109/109 (100%)	105 (96%)	4 (4%)	30	54
63	w	99/103 (96%)	91 (92%)	8 (8%)	11	36
64	x	86/87 (99%)	80 (93%)	6 (7%)	14	41
65	y	99/100 (99%)	91 (92%)	8 (8%)	11	36
66	z	89/90 (99%)	85 (96%)	4 (4%)	24	49
All	All	7904/8739 (90%)	7344 (93%)	560 (7%)	15	40

5 of 560 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	n	6	ASP
54	n	123	ASP
53	m	42	LEU

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Mol	Chain	Res	Type
60	t	70	ARG
14	AE	395	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
26	L	11	HIS
47	g	33	ASN
26	L	63	ASN
32	R	72	HIS
55	o	28	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	6 (8%)
10	B	75/76 (98%)	35 (46%)	6 (8%)
18	D	1514/1542 (98%)	289 (19%)	34 (2%)
41	a	2859/2904 (98%)	542 (18%)	0
44	d	119/120 (99%)	17 (14%)	0
8	7	34/46 (73%)	21 (61%)	4 (11%)
All	All	4676/4764 (98%)	933 (19%)	50 (1%)

5 of 933 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-18	G
8	7	-17	U
8	7	-16	U
8	7	-14	U
8	7	-13	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	D	531	U
18	D	992	U
18	D	1493	A
18	D	532	A
18	D	722	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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

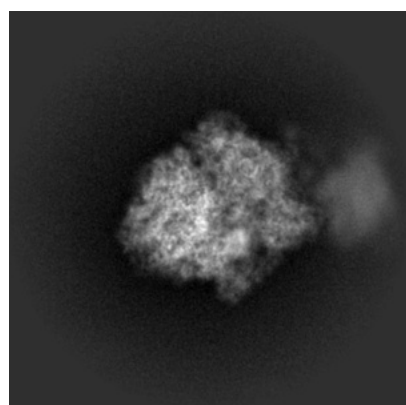
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22141. These allow visual inspection of the internal detail of the map and identification of artifacts.

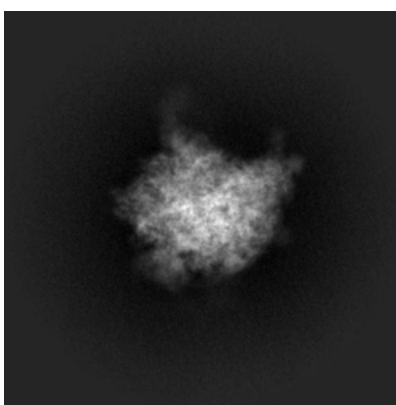
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

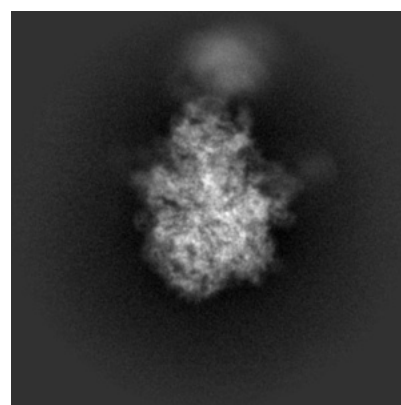
6.1.1 Primary map



X



Y

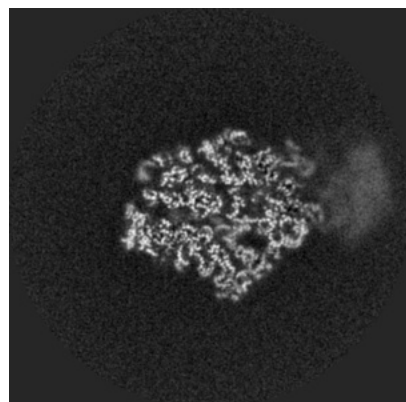


Z

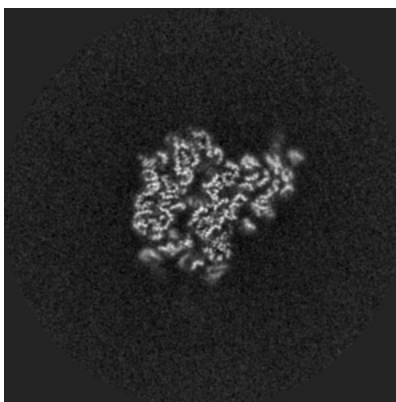
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

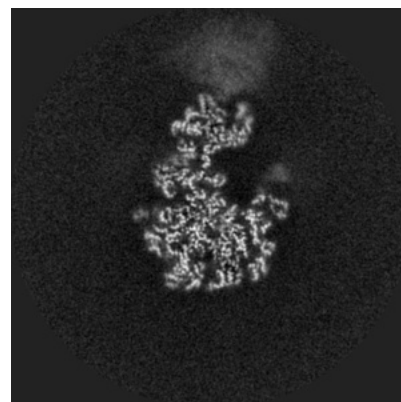
6.2.1 Primary map



X Index: 256



Y Index: 256

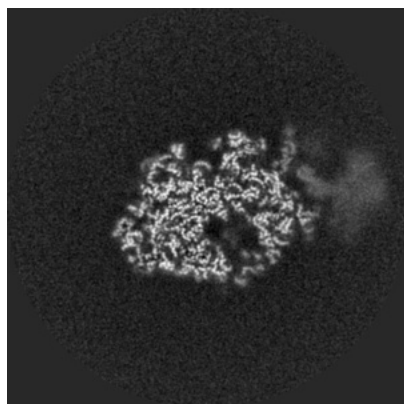


Z Index: 256

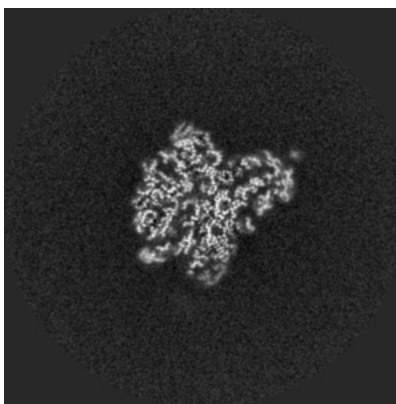
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

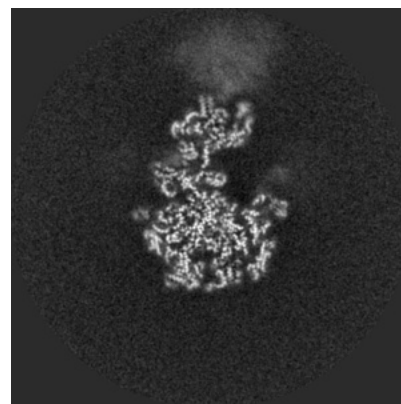
6.3.1 Primary map



X Index: 239



Y Index: 251

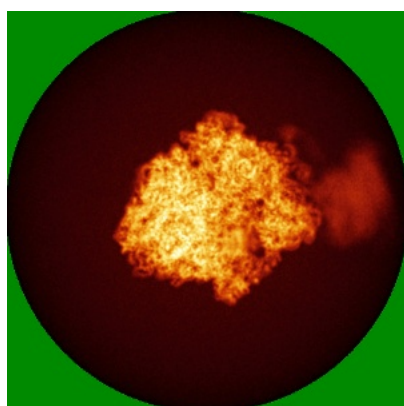


Z Index: 258

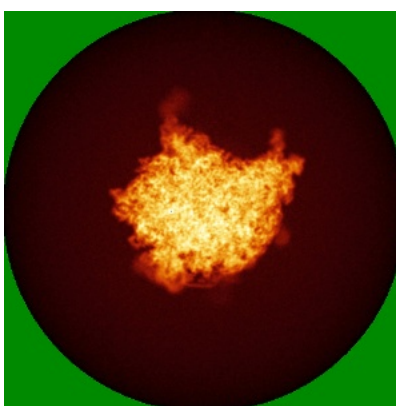
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

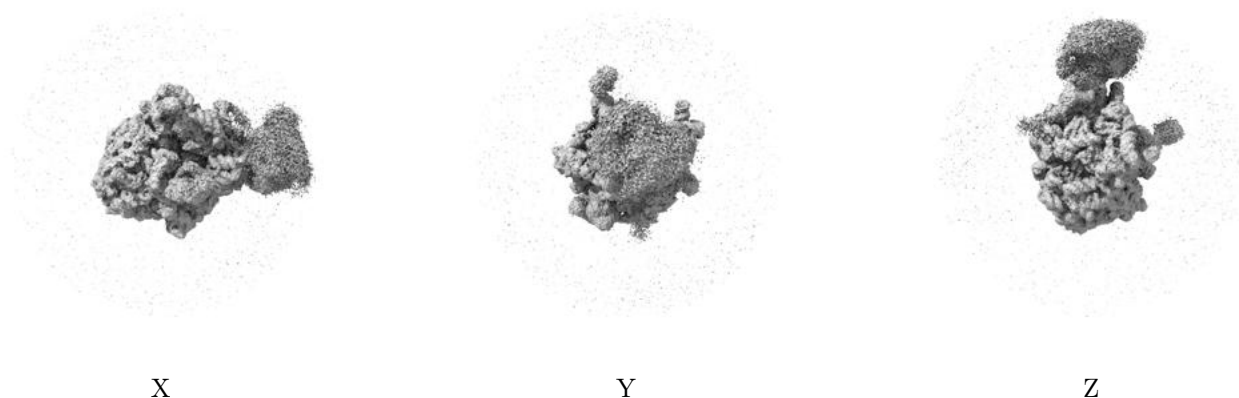


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00359. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

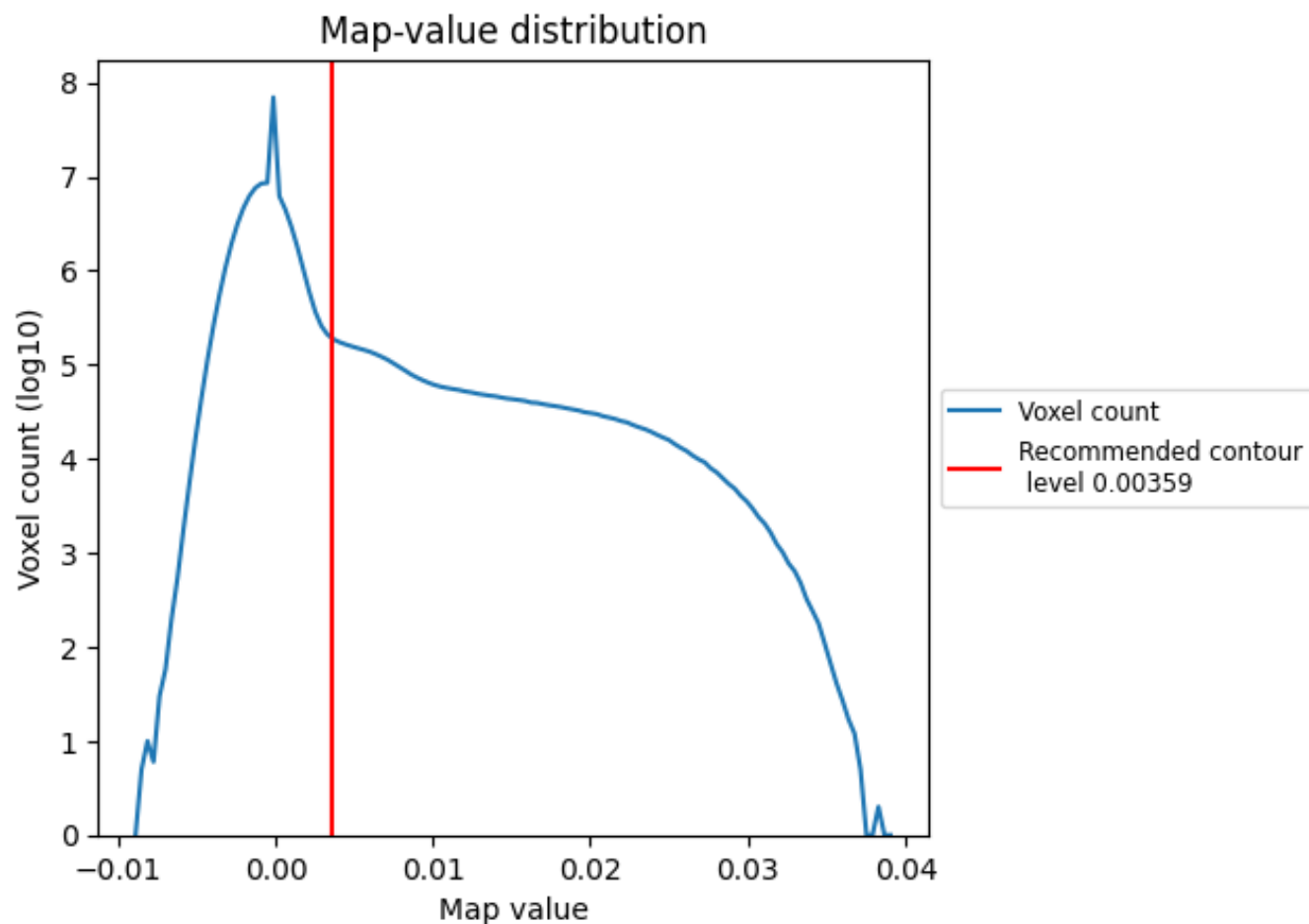
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

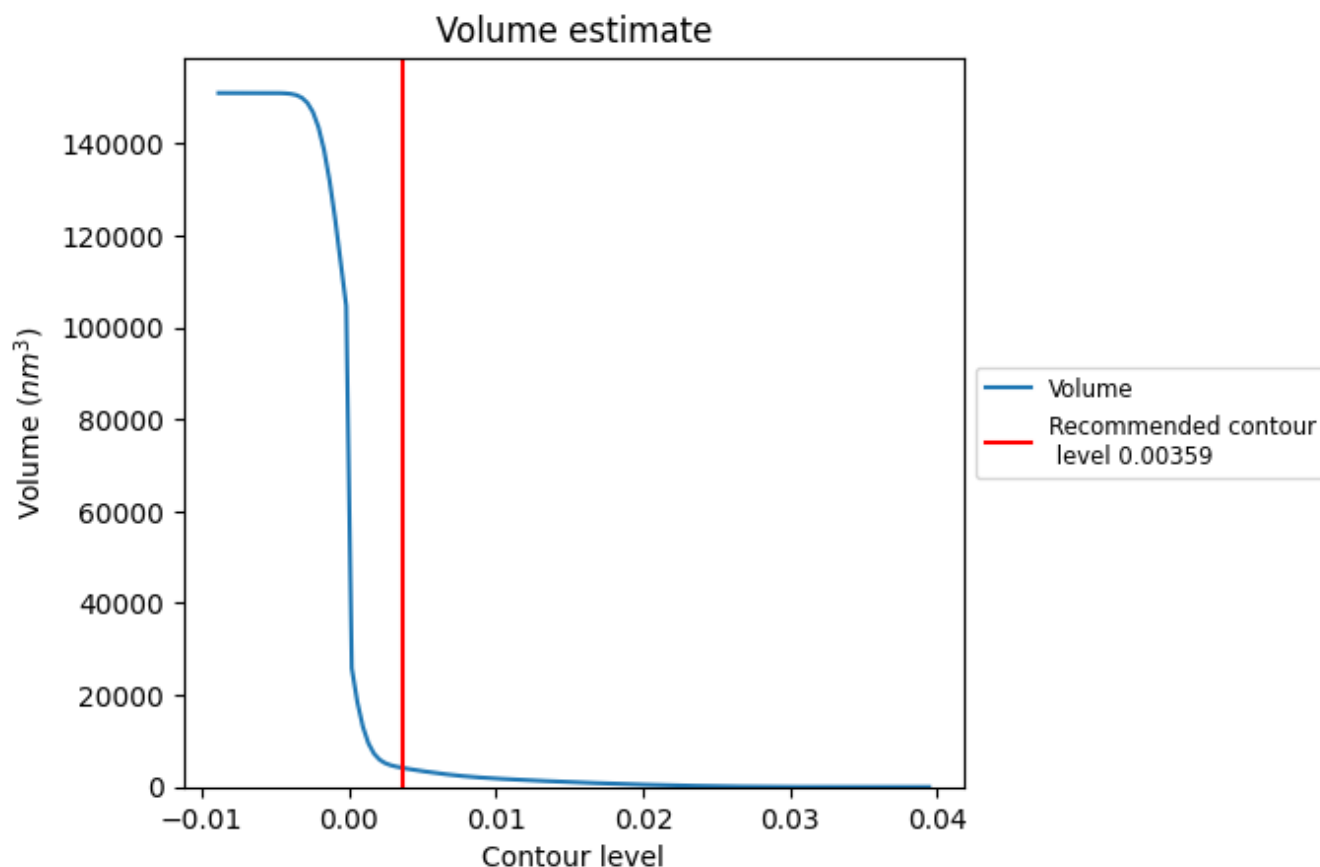
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

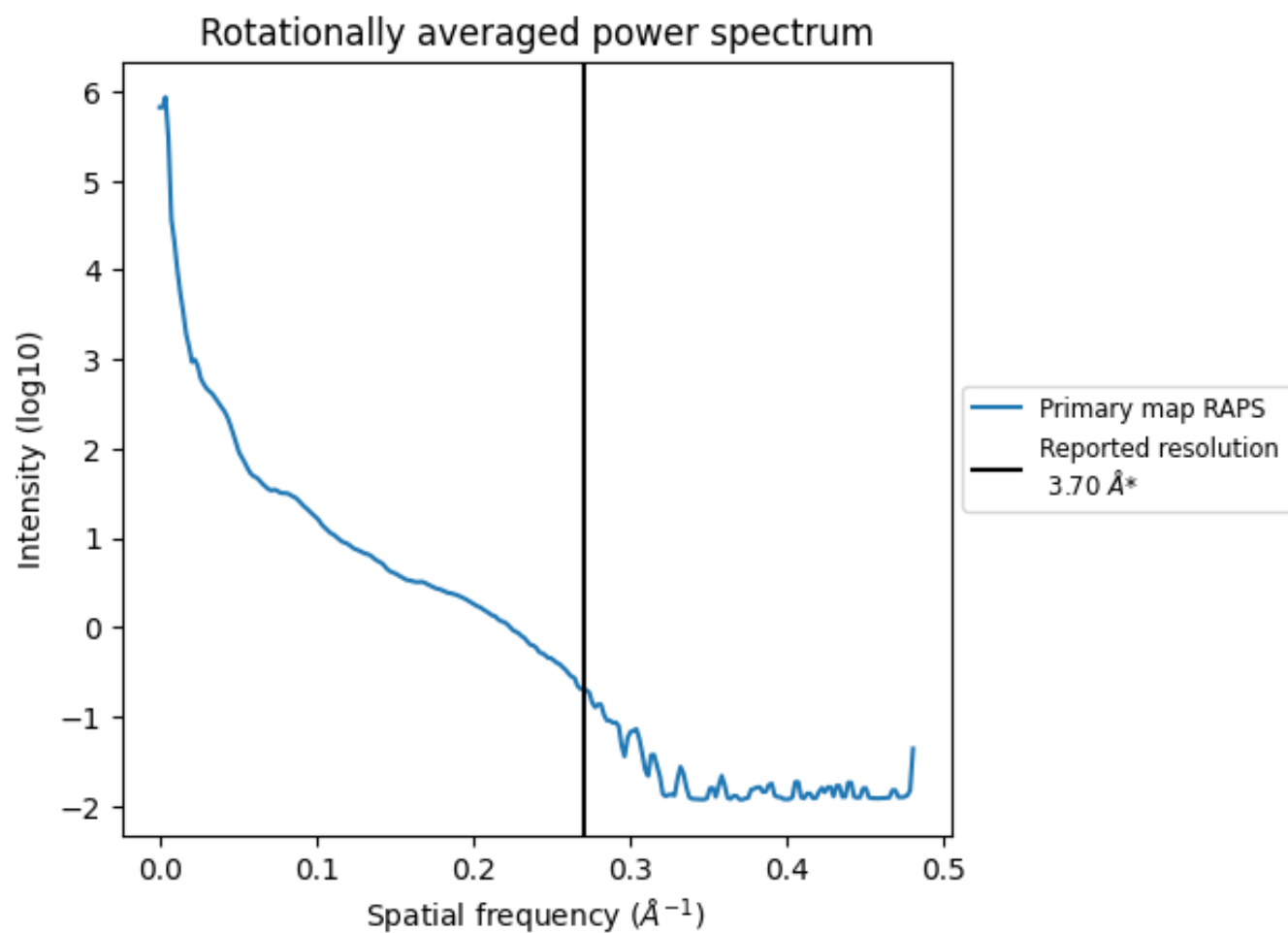
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4172 nm³; this corresponds to an approximate mass of 3769 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 0.270 Å⁻¹

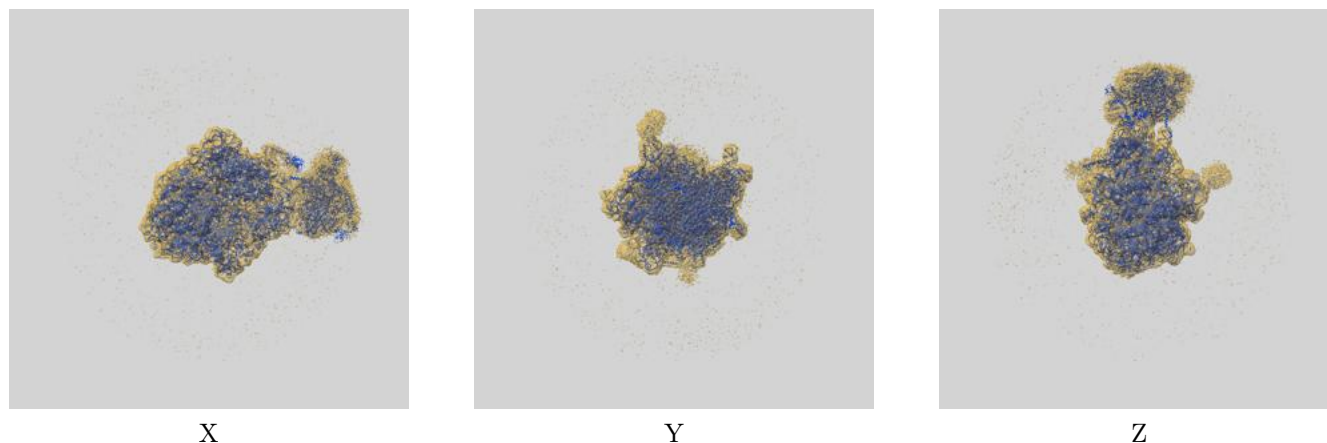
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

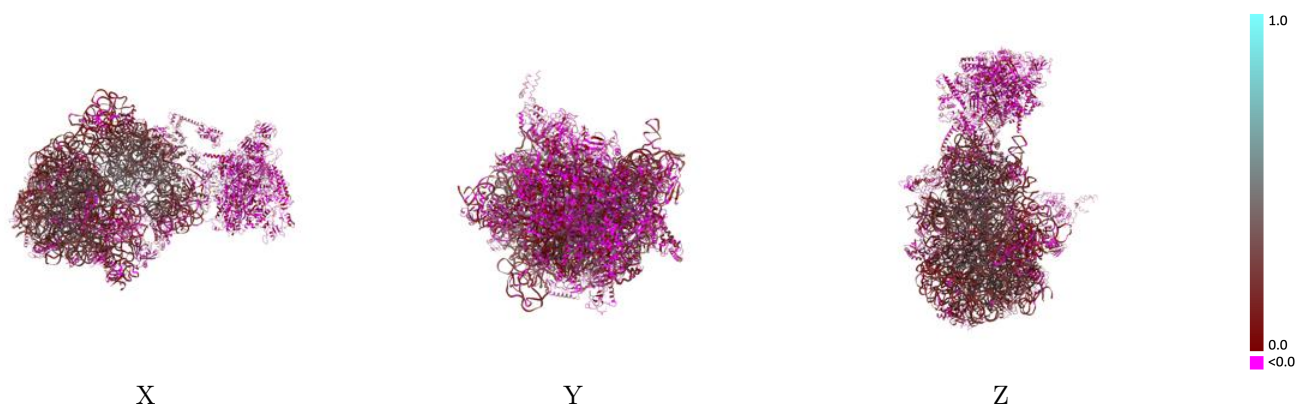
This section contains information regarding the fit between EMDB map EMD-22141 and PDB model 6XDQ. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



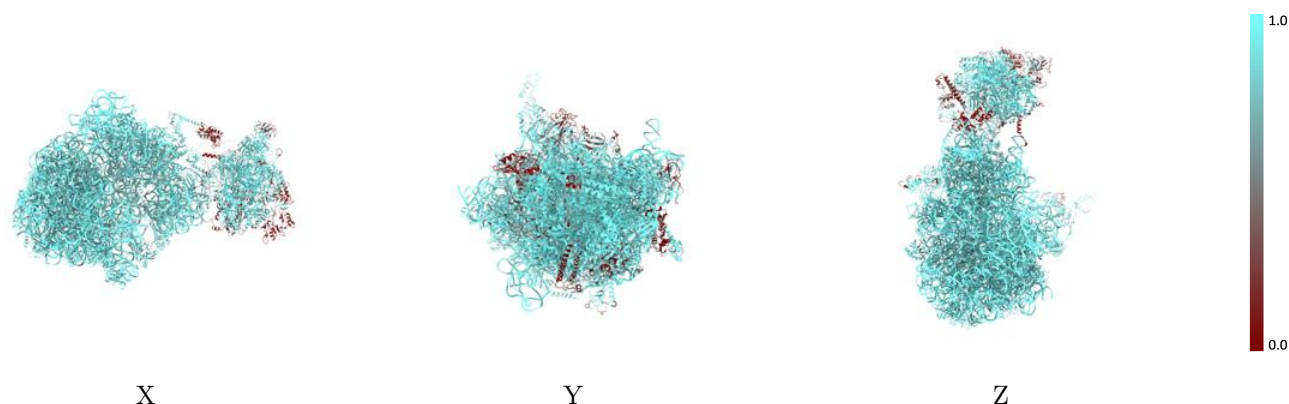
The images above show the 3D surface view of the map at the recommended contour level 0.00359 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



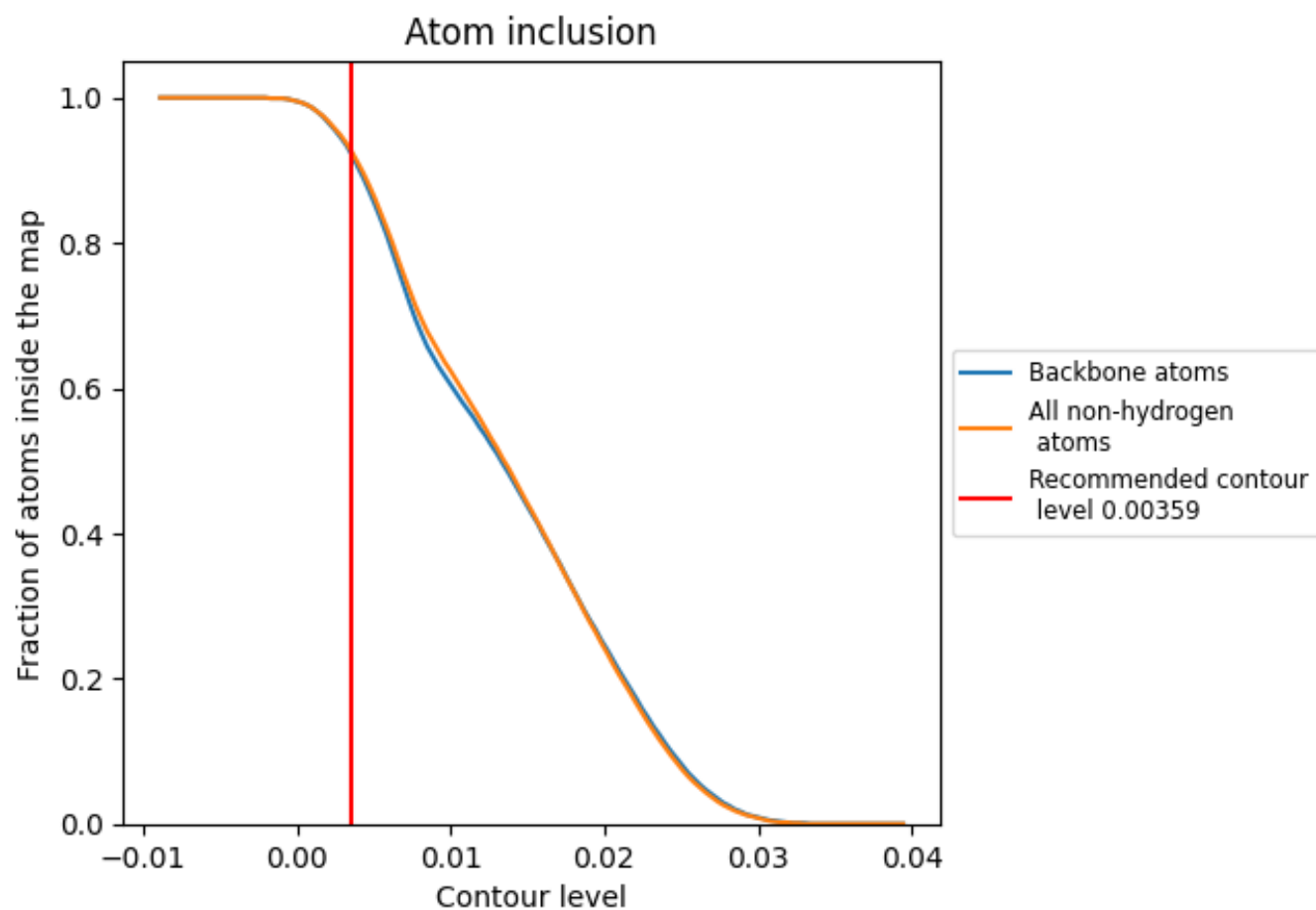
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00359).

9.4 Atom inclusion ⓘ



At the recommended contour level, 92% 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 (0.00359) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9250	 0.1750
0	 0.9360	 0.1880
1	 0.9380	 0.2750
2	 0.9140	 0.1340
3	 0.9450	 0.1200
4	 0.9400	 0.1220
5	 0.8900	 0.0180
6	 0.9610	 0.0240
7	 0.9440	 0.0680
9	 0.8770	 0.0300
A	 0.9980	 0.1920
AA	 0.7490	 0.0110
AB	 0.7330	 0.0390
AC	 0.7050	 0.0230
AD	 0.6300	 0.0140
AE	 0.8150	 0.0130
AF	 0.7080	 -0.0110
AG	 0.7700	 0.0870
B	 0.8930	 0.0740
C	 0.9560	 0.1710
D	 0.9930	 0.2500
E	 0.9620	 0.1080
F	 0.9450	 0.2240
G	 0.9230	 0.1830
H	 0.7990	 0.0360
I	 0.9400	 0.2120
J	 0.9500	 0.1860
K	 0.9660	 0.3140
L	 0.9180	 0.1040
M	 0.9340	 0.1710
N	 0.9540	 0.2430
O	 0.9480	 0.1460
P	 0.9230	 0.1430
Q	 0.9630	 0.1940
R	 0.9750	 0.3010



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Chain	Atom inclusion	Q-score
S	 0.9560	 0.1410
T	 0.9640	 0.2030
U	 0.9590	 0.1030
V	 0.9480	 0.2250
W	 0.8690	 0.0450
X	 0.9020	 0.0720
Y	 0.7380	 0.0150
Z	 0.8330	 0.0180
a	 0.9930	 0.2350
b	 0.9470	 0.1360
c	 0.9470	 0.1970
d	 0.9880	 0.1350
e	 0.9120	 0.0940
f	 0.9500	 0.1830
g	 0.9290	 0.0380
h	 0.9490	 0.1910
i	 0.9580	 0.2310
j	 0.9490	 0.1660
k	 0.9280	 0.0880
l	 0.9340	 0.1680
m	 0.9750	 0.3110
n	 0.9130	 0.0610
o	 0.9470	 0.1880
p	 0.9320	 0.0620
q	 0.9520	 0.1030
r	 0.8490	 0.0530
s	 0.9510	 0.1750
t	 0.9140	 0.1690
u	 0.9470	 0.1790
v	 0.9550	 0.1880
w	 0.9440	 0.1840
x	 0.9320	 0.0210
y	 0.9230	 0.1170
z	 0.9630	 0.2310