



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 12:27 AM UTC

PDB ID : 8OJ5 / pdb_00008oj5
EMDB ID : EMD-16905
Title : 60S ribosomal subunit bound to the E3-UFM1 complex - state 3 (in-vitro reconstitution)
Authors : Penchev, I.; DaRosa, P.A.; Peter, J.J.; Kulathu, Y.; Becker, T.; Beckmann, R.; Kopito, R.
Deposited on : 2023-03-23
Resolution : 2.90 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

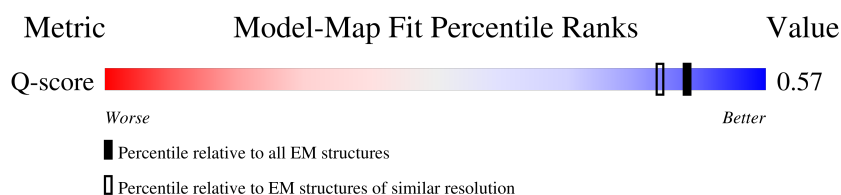
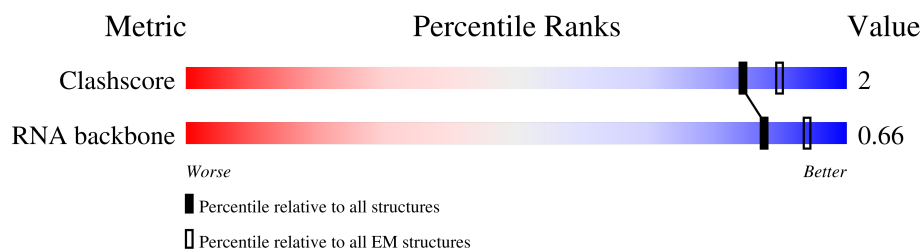
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	5	5070	 56% 12% 31%
2	7	121	 85% 12% ..
3	8	157	 78% 16% 6%
4	A	794	 12% 77% 10% 13%
5	B	506	 23% 74% 6% 20%

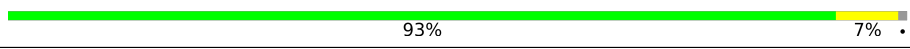
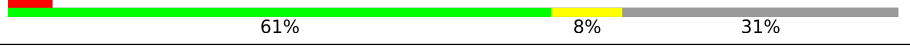
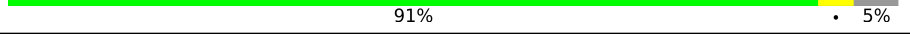
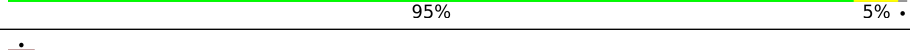
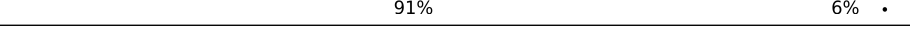
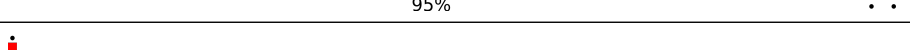
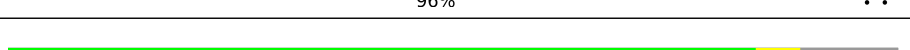
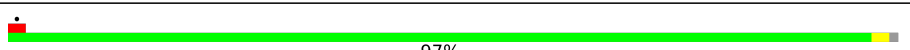
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Mol	Chain	Length	Quality of chain
6	C	314	
7	D	85	
8	LA	257	
9	LB	403	
10	LC	427	
11	LD	297	
12	LE	288	
13	LF	248	
14	LG	266	
15	LH	192	
16	LI	214	
17	LJ	178	
18	LL	211	
19	LM	215	
20	LN	204	
21	LO	203	
22	LP	184	
23	LQ	188	
24	LR	196	
25	LS	176	
26	LT	160	
27	LU	128	
28	LV	140	
29	LW	157	
30	LX	156	

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Mol	Chain	Length	Quality of chain
31	LY	145	
32	LZ	136	
33	La	148	
34	Lb	159	
35	Lc	115	
36	Ld	125	
37	Le	135	
38	Lf	110	
39	Lg	117	
40	Lh	123	
41	Li	105	
42	Lj	97	
43	Lk	70	
44	Ll	51	
45	Lm	128	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	Lz	217	

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 145041 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3474	Total	C	N	O	P	0	0
			74502	33181	13653	24195	3473		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	148	Total	C	N	O	P	0	0
			3152	1407	563	1035	147		

- Molecule 4 is a protein called E3 UFM1-protein ligase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	692	Total	C	N	O	S	0	0
			5479	3453	957	1050	19		

- Molecule 5 is a protein called CDK5 regulatory subunit-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	403	Total	C	N	O	S	0	0
			3234	2049	545	624	16		

- Molecule 6 is a protein called DDRGK domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	188	Total	C	N	O	S	0	0
			1547	954	279	313	1		

- Molecule 7 is a protein called Ubiquitin-fold modifier 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	78	Total	C	N	O	S	0	0
			588	382	96	109	1		

- Molecule 8 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LB	402	Total	C	N	O	S	0	0
			3239	2060	608	557	14		

- Molecule 10 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 11 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 12 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LE	220	Total	C	N	O	S	0	0
			1765	1136	334	291	4		

- Molecule 13 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 14 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 15 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 16 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LI	202	Total	C	N	O	S	0	0
			1634	1038	314	269	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	87	ILE	MET	conflict	UNP Q96L21

- Molecule 17 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LJ	175	Total	C	N	O	S	0	0
			1401	882	261	252	6		

- Molecule 18 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LL	194	Total	C	N	O	S	0	0
			1573	987	327	255	4		

- Molecule 19 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LM	136	Total	C	N	O	S	0	0
			1120	719	215	179	7		

- Molecule 20 is a protein called 60S ribosomal protein L15.

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

- Molecule 21 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 22 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 23 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 24 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LR	155	Total	C	N	O	S	0	0
			1294	808	278	199	9		

- Molecule 25 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 26 is a protein called 60S ribosomal protein L21.

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

- Molecule 27 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 28 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 29 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 30 is a protein called 60S ribosomal protein L23a.

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

- Molecule 31 is a protein called 60S ribosomal protein L26.

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

- Molecule 32 is a protein called 60S ribosomal protein L27.

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

- Molecule 33 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 34 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 35 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 36 is a protein called 60S ribosomal protein L31.

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

- Molecule 37 is a protein called 60S ribosomal protein L32.

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

- Molecule 38 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 39 is a protein called 60S ribosomal protein L34.

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

- Molecule 40 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 41 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 42 is a protein called 60S ribosomal protein L37.

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

- Molecule 43 is a protein called 60S ribosomal protein L38.

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

- Molecule 44 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 45 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 46 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lo	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 47 is a protein called 60S ribosomal protein L37a.

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

- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 49 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lz	217	Total	C	N	O	S	0	0
			1744	1114	314	307	9		

- Molecule 50 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
50	5	207	Total	Mg	0
			207	207	
50	7	2	Total	Mg	0
			2	2	
50	8	5	Total	Mg	0
			5	5	
50	LP	1	Total	Mg	0
			1	1	
50	LV	1	Total	Mg	0
			1	1	
50	Le	2	Total	Mg	0
			2	2	
50	Lf	1	Total	Mg	0
			1	1	
50	Lj	1	Total	Mg	0
			1	1	

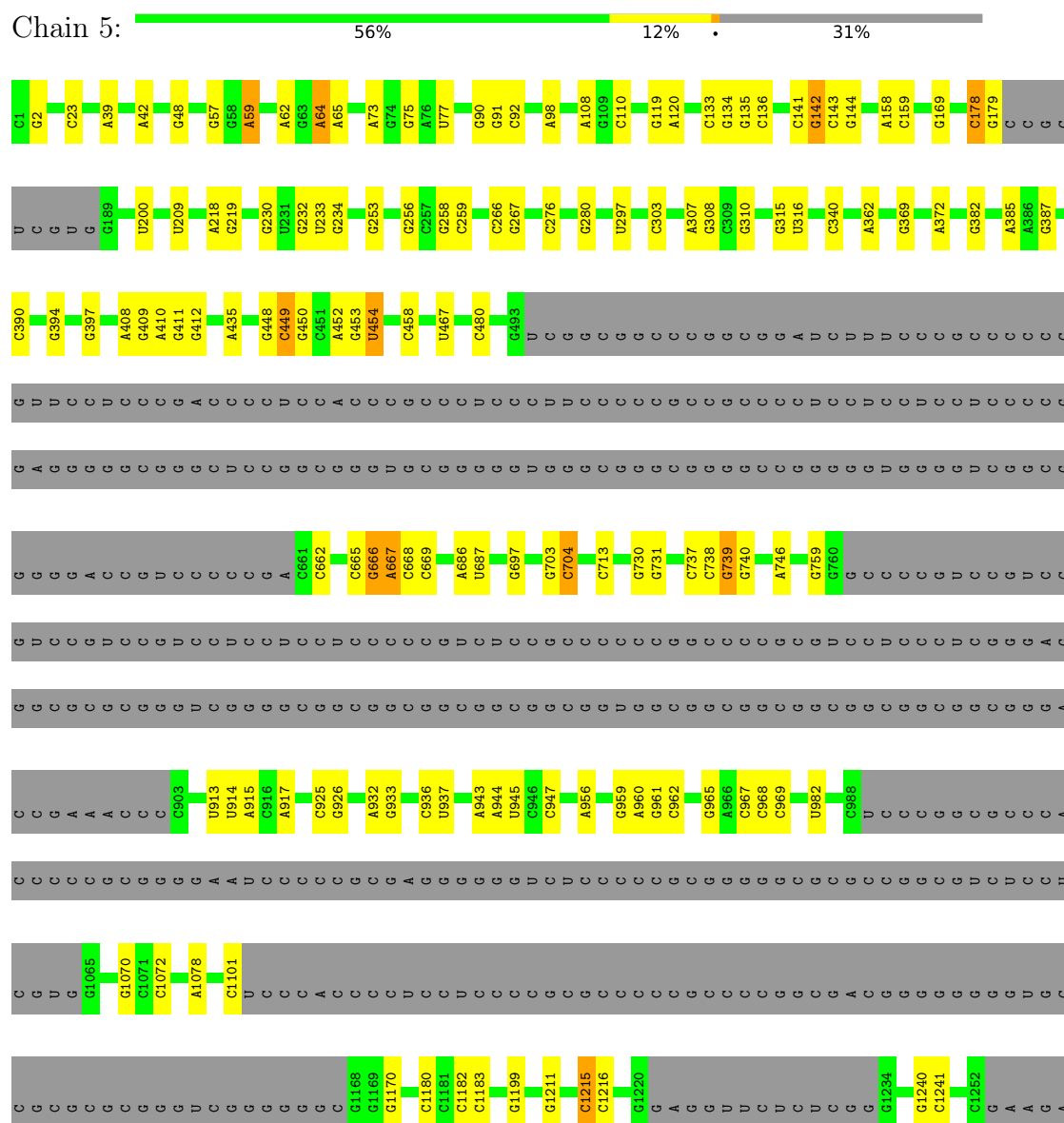
- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
51	Lg	1	Total	Zn	0
			1	1	
51	Lj	1	Total	Zn	0
			1	1	
51	Lm	1	Total	Zn	0
			1	1	
51	Lo	1	Total	Zn	0
			1	1	
51	Lp	1	Total	Zn	0
			1	1	

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: 28S rRNA

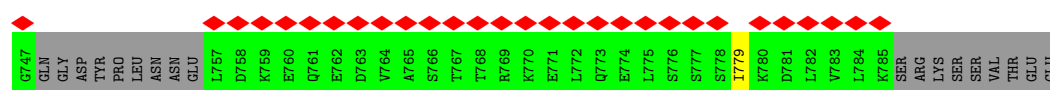
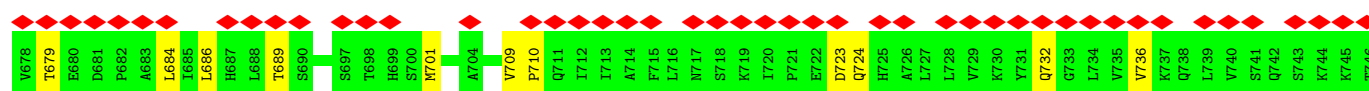
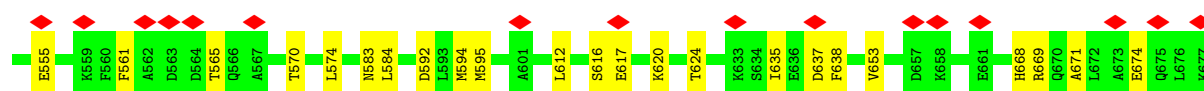
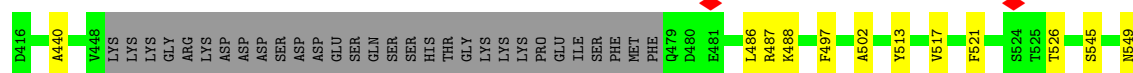




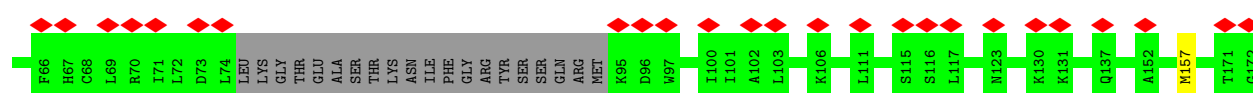
- Molecule 2: 5S rRNA

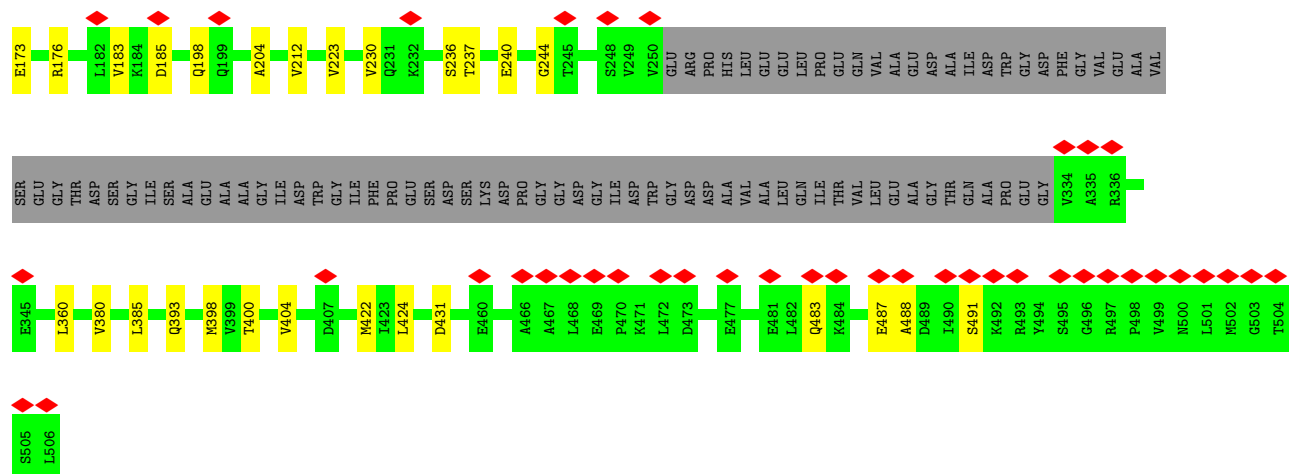
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Met	ASP	TRP	GLU	ILE	ARG	ARG	LEU	ALA	ASP	PHE	GLN	ARG	ALA	GLN	PHE	ALA	GLU	THR	GLN	ARG	LEU	SER
E29	C32	V36	Q44	L45	E46	V47	Y56	I57	T58	Q83	L90	E133	C143	D147	L161	D172	I190	I207				

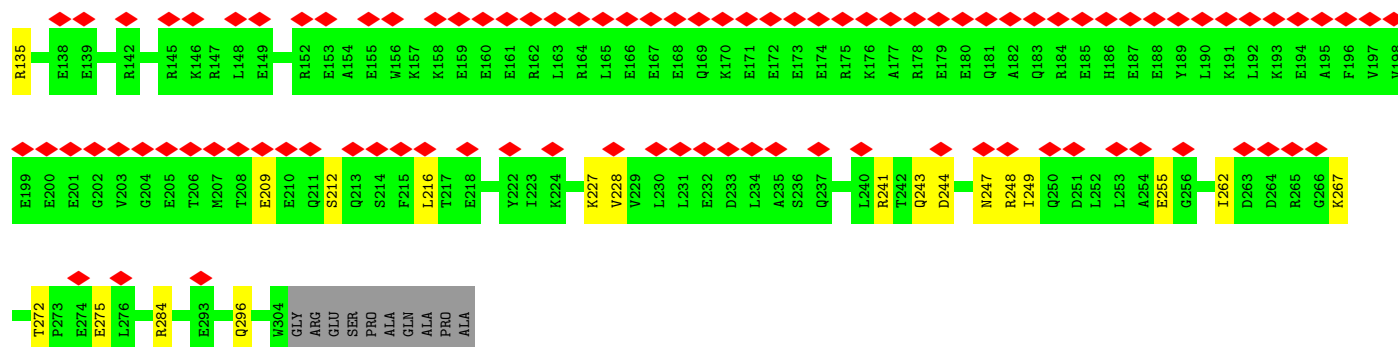
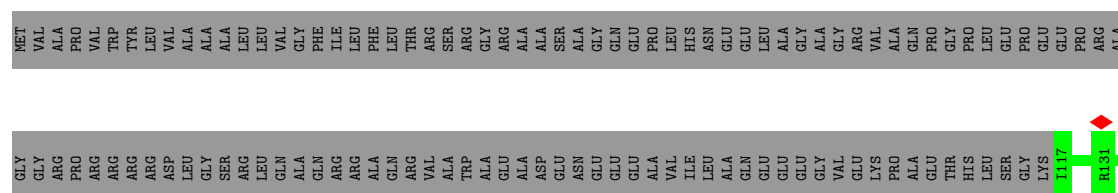


M1	E2	D3	H4	Q5	H6	V7	P8	I9	D10	I11	Q12	T13	S14	K15	L16	L17	L18	W19	D22	R23	R24	H25	C26	S27	L28	K29	W30	L33	T36	I37	R38	E39	K40	I41	N42	A43	A44	I45	Q46	D47	M48	P49	E50	S51	E52	E53	I54	A55	A56	Q56	L57	L58	S59	G60	S61	Y62	L63	S64	L65	L66	L67	L68	L69	L70	L71	L72	L73	L74	L75	L76	L77	L78	L79	L80	L81	L82	L83	L84	L85	L86	L87	L88	L89	L90	L91	L92	L93	L94	L95	L96	L97	L98	L99	L100	L101	L102	L103	L104	L105	L106	L107	L108	L109	L110	L111	L112	L113	L114	L115	L116	L117	L118	L119	L120	L121	L122	L123	L124	L125	L126	L127	L128	L129	L130	L131	L132	L133	L134	L135	L136	L137	L138	L139	L140	L141	L142	L143	L144	L145	L146	L147	L148	L149	L150	L151	L152	L153	L154	L155	L156	L157	L158	L159	L160	L161	L162	L163	L164	L165	L166	L167	L168	L169	L170	L171	L172	L173	L174	L175	L176	L177	L178	L179	L180	L181	L182	L183	L184	L185	L186	L187	L188	L189	L190	L191	L192	L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528
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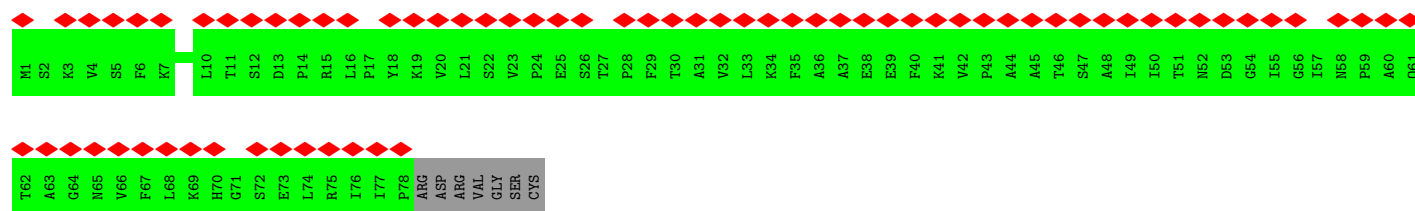
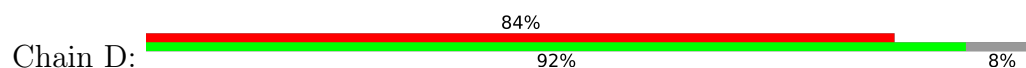




• Molecule 6: DDRGK domain-containing protein 1

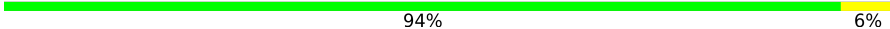


• Molecule 7: Ubiquitin-fold modifier 1



• Molecule 8: 60S ribosomal protein L8



Chain LN:  94% 6%



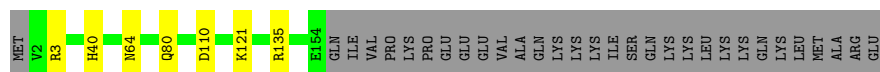
- Molecule 21: 60S ribosomal protein L13a

Chain LO:  90% 9%

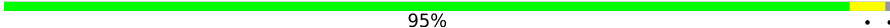


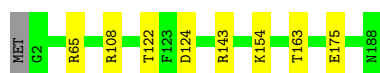
- Molecule 22: 60S ribosomal protein L17

Chain LP:  79% 17%



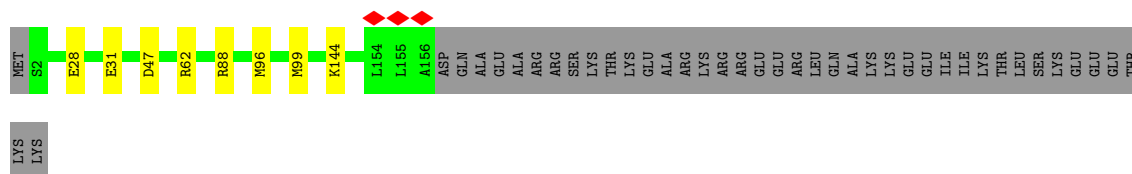
- Molecule 23: 60S ribosomal protein L18

Chain LQ:  95%

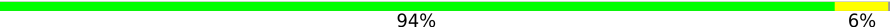


- Molecule 24: 60S ribosomal protein L19

Chain LR:  75% 21%

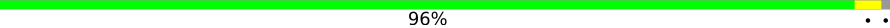


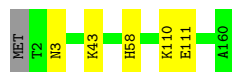
- Molecule 25: 60S ribosomal protein L18a

Chain LS:  94% 6%



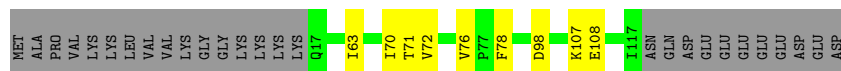
- Molecule 26: 60S ribosomal protein L21

Chain LT:  96%



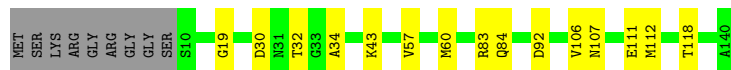
- Molecule 27: 60S ribosomal protein L22

Chain LU:  72% 7% 21%



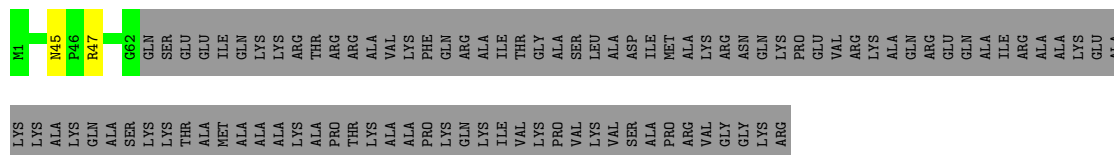
- Molecule 28: 60S ribosomal protein L23

Chain LV:  83% 11% 6%



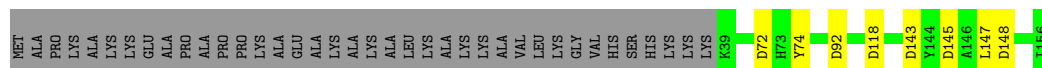
- Molecule 29: 60S ribosomal protein L24

Chain LW:  38% 61%



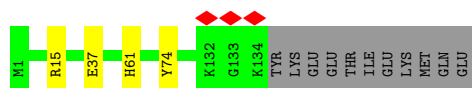
- Molecule 30: 60S ribosomal protein L23a

Chain LX:  71% 5% 24%



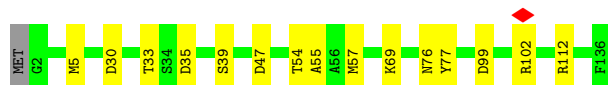
- Molecule 31: 60S ribosomal protein L26

Chain LY:  90% 8%



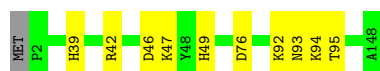
- Molecule 32: 60S ribosomal protein L27

Chain LZ:  88% 11%

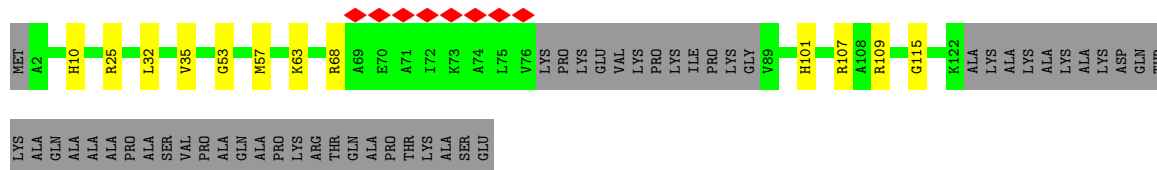


- Molecule 33: 60S ribosomal protein L27a

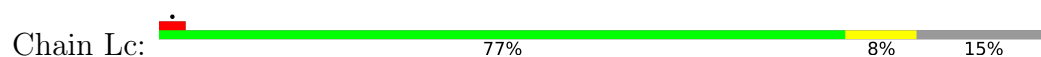
Chain La:  93% 7%



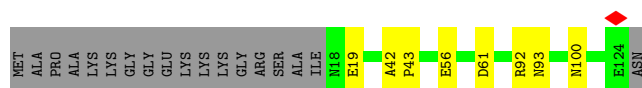
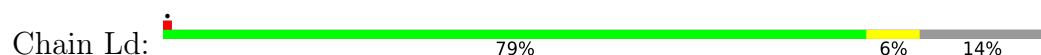
- Molecule 34: 60S ribosomal protein L29



- Molecule 35: 60S ribosomal protein L30



- Molecule 36: 60S ribosomal protein L31



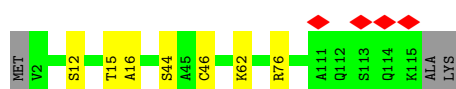
- Molecule 37: 60S ribosomal protein L32



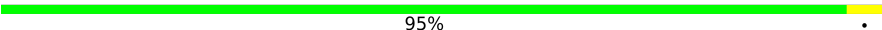
- Molecule 38: 60S ribosomal protein L35a

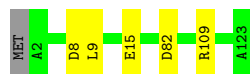


- Molecule 39: 60S ribosomal protein L34

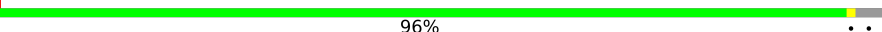


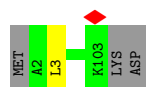
- Molecule 40: 60S ribosomal protein L35

Chain Lh:  95%



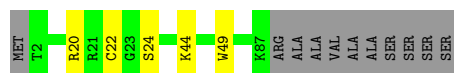
- Molecule 41: 60S ribosomal protein L36

Chain Li:  96%

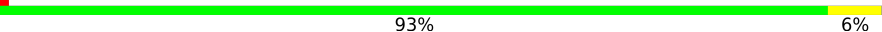


- Molecule 42: 60S ribosomal protein L37

Chain Lj:  84% 5% 11%



- Molecule 43: 60S ribosomal protein L38

Chain Lk:  93% 6%



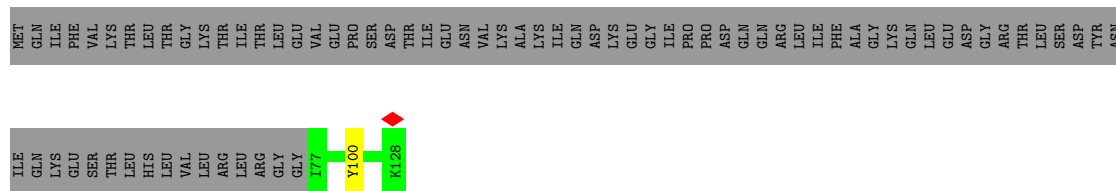
- Molecule 44: 60S ribosomal protein L39

Chain Ll:  82% 16%

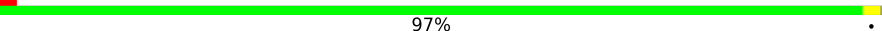


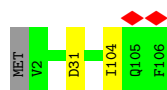
- Molecule 45: Ubiquitin-60S ribosomal protein L40

Chain Lm:  40% 59%

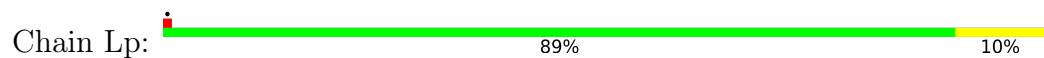


- Molecule 46: 60S ribosomal protein L36a

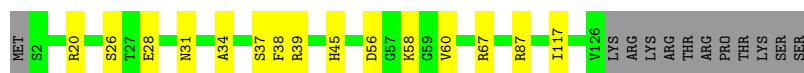
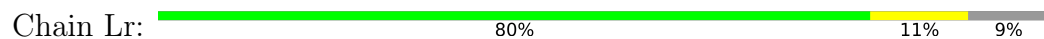
Chain Lo:  97%



- Molecule 47: 60S ribosomal protein L37a



- Molecule 48: 60S ribosomal protein L28



- Molecule 49: 60S ribosomal protein L10a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35935	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.100	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	377.1, 377.1, 377.1	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.838, 0.838, 0.838	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	5	0.07	0/83342	0.15	0/129985
2	7	0.06	0/2861	0.14	0/4459
3	8	0.06	0/3520	0.15	0/5481
4	A	0.14	0/5549	0.25	0/7469
5	B	0.08	0/3280	0.19	0/4426
6	C	0.07	0/1560	0.16	0/2085
7	D	0.10	0/601	0.21	0/818
8	LA	0.09	0/1936	0.20	0/2596
9	LB	0.08	0/3307	0.20	0/4424
10	LC	0.08	0/2981	0.20	0/4002
11	LD	0.09	0/2428	0.20	0/3252
12	LE	0.08	0/1799	0.23	0/2414
13	LF	0.07	0/1905	0.19	0/2539
14	LG	0.09	0/1960	0.21	0/2637
15	LH	0.09	0/1537	0.22	0/2066
16	LI	0.10	0/1673	0.22	0/2234
17	LJ	0.08	0/1424	0.19	0/1904
18	LL	0.08	0/1604	0.20	0/2149
19	LM	0.08	0/1142	0.19	0/1527
20	LN	0.09	0/1746	0.19	0/2338
21	LO	0.08	0/1682	0.21	0/2250
22	LP	0.08	0/1268	0.20	0/1701
23	LQ	0.10	0/1537	0.21	0/2052
24	LR	0.10	0/1310	0.23	0/1734
25	LS	0.09	0/1493	0.22	0/2003
26	LT	0.09	0/1326	0.22	0/1770
27	LU	0.09	0/839	0.21	0/1126
28	LV	0.09	0/993	0.22	0/1332
29	LW	0.09	0/532	0.16	0/708
30	LX	0.07	0/984	0.20	0/1323
31	LY	0.09	0/1132	0.21	0/1504
32	LZ	0.10	0/1130	0.19	0/1507

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	La	0.07	0/1191	0.20	0/1591
34	Lb	0.10	0/889	0.23	0/1175
35	Lc	0.10	0/774	0.19	0/1038
36	Ld	0.11	0/903	0.25	0/1216
37	Le	0.09	0/1071	0.20	0/1429
38	Lf	0.10	0/895	0.23	0/1198
39	Lg	0.09	0/916	0.22	0/1220
40	Lh	0.08	0/1023	0.18	0/1351
41	Li	0.09	0/843	0.18	0/1115
42	Lj	0.09	0/720	0.20	0/952
43	Lk	0.08	0/575	0.20	0/761
44	Ll	0.11	0/454	0.20	0/599
45	Lm	0.10	0/435	0.21	0/575
46	Lo	0.09	0/877	0.21	0/1156
47	Lp	0.10	0/718	0.20	0/953
48	Lr	0.09	0/1017	0.21	0/1364
49	Lz	0.09	0/1772	0.23	0/2375
All	All	0.08	0/155454	0.18	0/227883

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	5	74502	0	37637	233	0
2	7	2561	0	1295	12	0
3	8	3152	0	1601	9	0
4	A	5479	0	5608	57	0
5	B	3234	0	3287	20	0
6	C	1547	0	1543	12	0
7	D	588	0	616	0	0
8	LA	1898	0	1993	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	LB	3239	0	3376	31	0
10	LC	2927	0	3104	13	0
11	LD	2382	0	2410	17	0
12	LE	1765	0	1917	14	0
13	LF	1870	0	1996	8	0
14	LG	1927	0	2074	6	0
15	LH	1518	0	1601	13	0
16	LI	1634	0	1673	12	0
17	LJ	1401	0	1428	10	0
18	LL	1573	0	1681	7	0
19	LM	1120	0	1187	8	0
20	LN	1701	0	1749	8	0
21	LO	1650	0	1794	15	0
22	LP	1242	0	1269	5	0
23	LQ	1513	0	1628	6	0
24	LR	1294	0	1434	9	0
25	LS	1453	0	1490	7	0
26	LT	1298	0	1366	4	0
27	LU	825	0	850	8	0
28	LV	979	0	1039	10	0
29	LW	519	0	533	1	0
30	LX	967	0	1040	7	0
31	LY	1115	0	1205	5	0
32	LZ	1107	0	1182	9	0
33	La	1162	0	1213	8	0
34	Lb	876	0	948	10	0
35	Lc	764	0	804	5	0
36	Ld	888	0	930	5	0
37	Le	1053	0	1147	4	0
38	Lf	876	0	912	4	0
39	Lg	906	0	998	7	0
40	Lh	1015	0	1148	4	0
41	Li	832	0	917	1	0
42	Lj	705	0	737	4	0
43	Lk	569	0	637	3	0
44	Ll	444	0	483	5	0
45	Lm	429	0	465	1	0
46	Lo	863	0	929	3	0
47	Lp	708	0	756	7	0
48	Lr	1002	0	1068	10	0
49	Lz	1744	0	1859	21	0
50	5	207	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	7	2	0	0	0	0
50	8	5	0	0	0	0
50	LP	1	0	0	0	0
50	LV	1	0	0	0	0
50	Le	2	0	0	0	0
50	Lf	1	0	0	0	0
50	Lj	1	0	0	0	0
51	Lg	1	0	0	0	0
51	Lj	1	0	0	0	0
51	Lm	1	0	0	0	0
51	Lo	1	0	0	0	0
51	Lp	1	0	0	0	0
All	All	145041	0	108557	564	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 2.

The worst 5 of 564 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)
1:5:3641:U:OP2	1:5:3646:A:N6	2.07	0.88
1:5:4620:U:OP2	1:5:4670:C:N4	2.07	0.86
1:5:1591:U:OP2	1:5:2856:C:O2'	1.94	0.85
47:Lp:32:SER:OG	47:Lp:69:TRP:O	1.97	0.83
1:5:4522:G:O2'	1:5:4525:C:OP2	1.97	0.81

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3451/5070 (68%)	365 (10%)	5 (0%)
2	7	119/121 (98%)	6 (5%)	0
3	8	145/157 (92%)	15 (10%)	0
All	All	3715/5348 (69%)	386 (10%)	5 (0%)

5 of 386 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	39	A
1	5	42	A
1	5	48	G
1	5	59	A

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	1590	C
1	5	1633	G
1	5	1757	U
1	5	4095	G
1	5	4699	U

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 225 ligands modelled in this entry, 225 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.

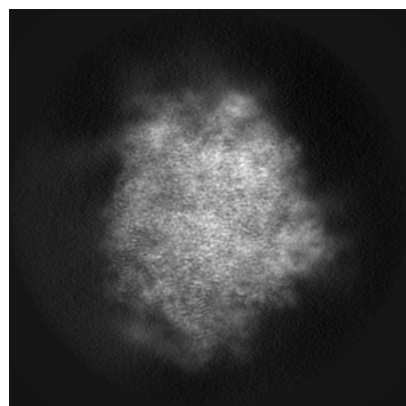
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16905. These allow visual inspection of the internal detail of the map and identification of artifacts.

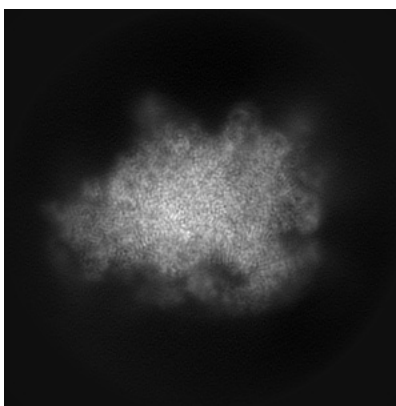
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

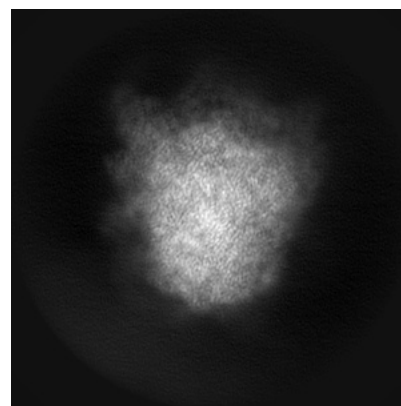
6.1.1 Primary map



X

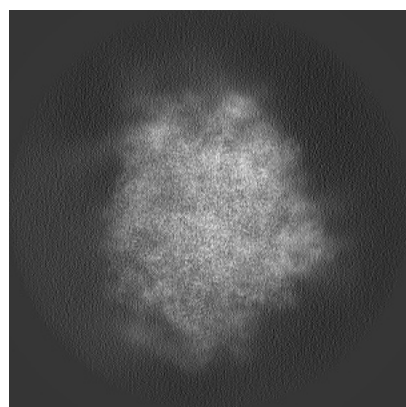


Y

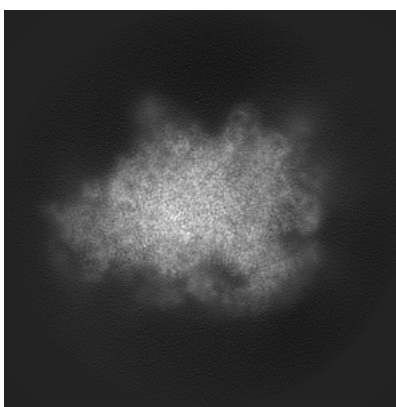


Z

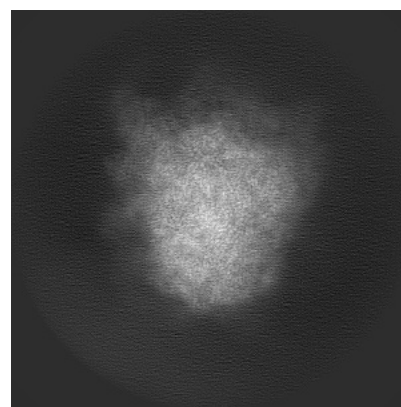
6.1.2 Raw map



X



Y

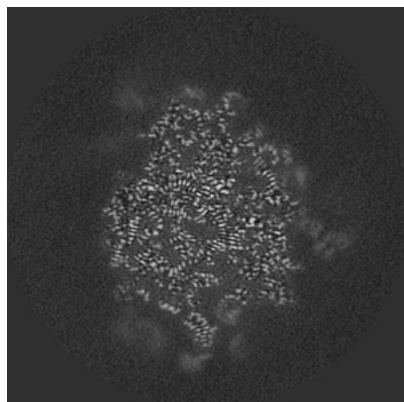


Z

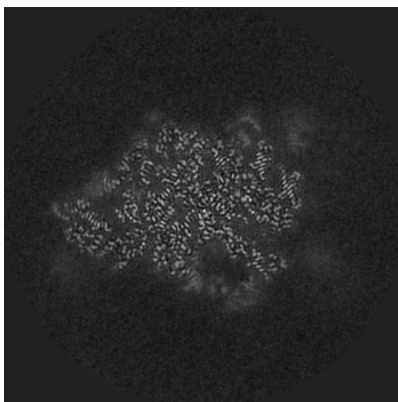
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

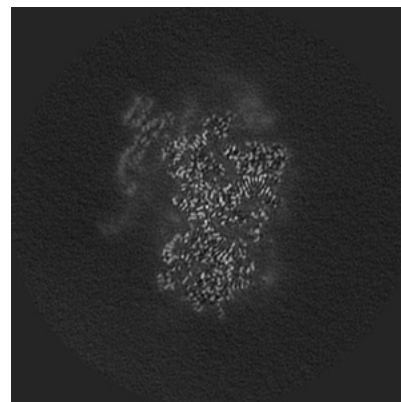
6.2.1 Primary map



X Index: 225

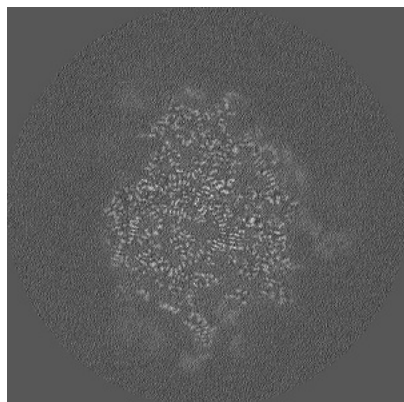


Y Index: 225

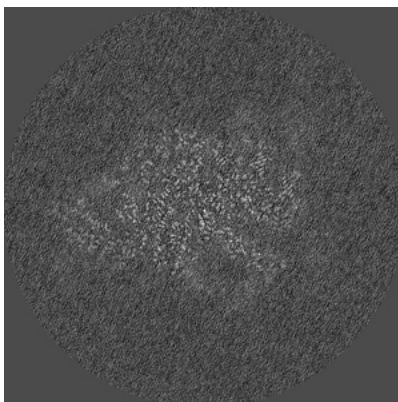


Z Index: 225

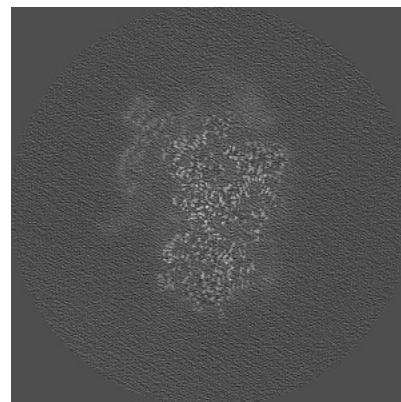
6.2.2 Raw map



X Index: 225



Y Index: 225

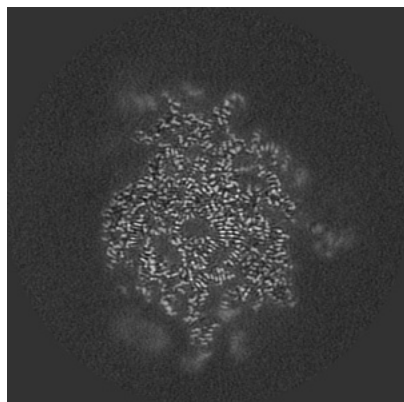


Z Index: 225

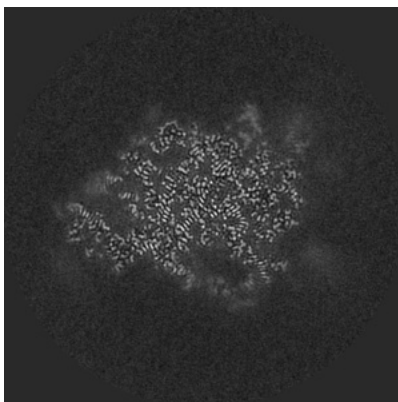
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

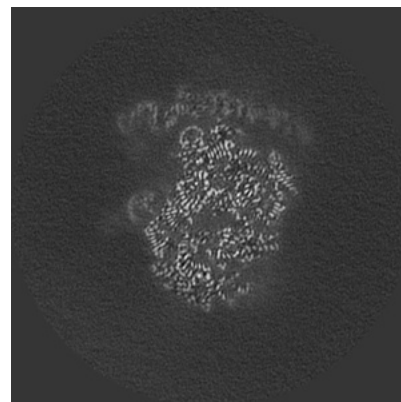
6.3.1 Primary map



X Index: 221

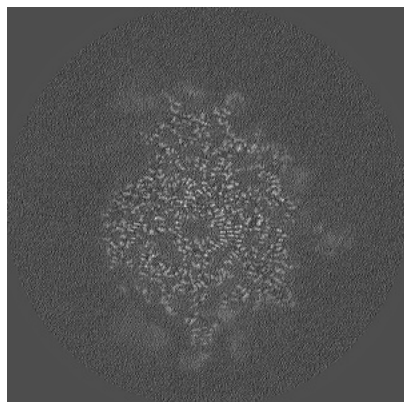


Y Index: 230

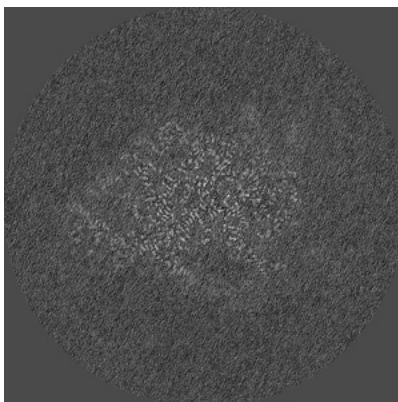


Z Index: 205

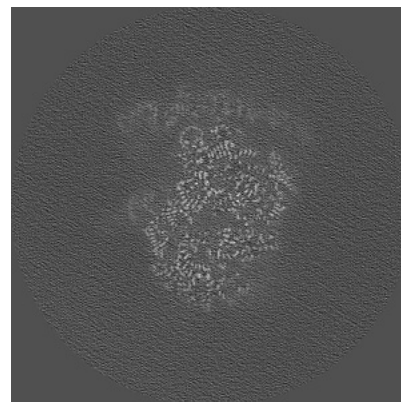
6.3.2 Raw map



X Index: 222



Y Index: 229

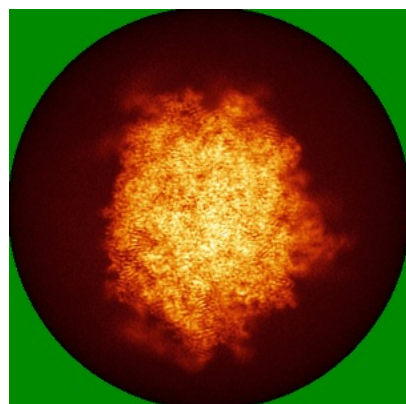


Z Index: 205

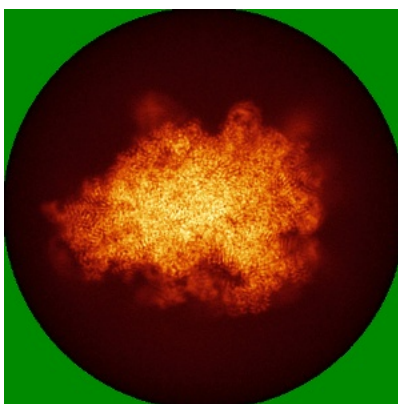
The images above show the largest variance slices of the map in three orthogonal directions.

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

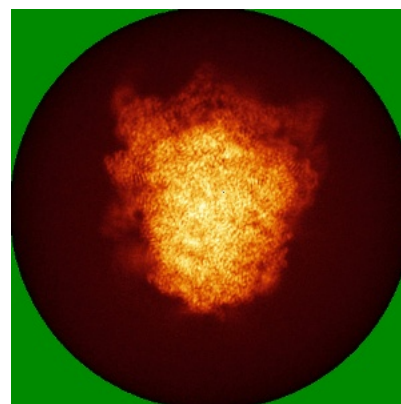
6.4.1 Primary map



X

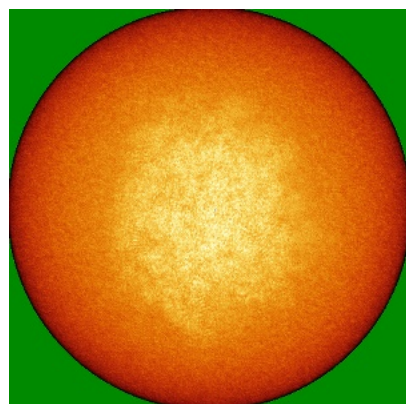


Y

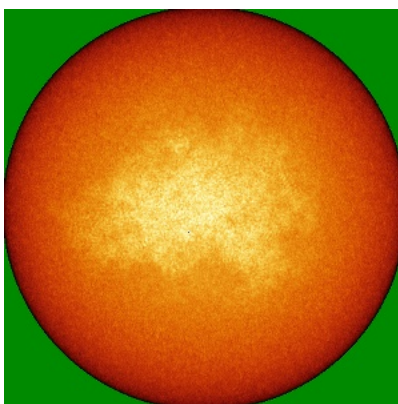


Z

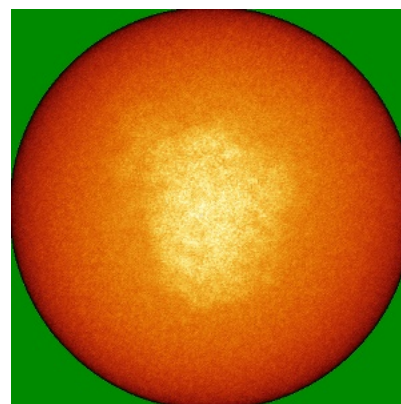
6.4.2 Raw map



X



Y

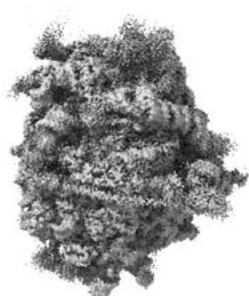


Z

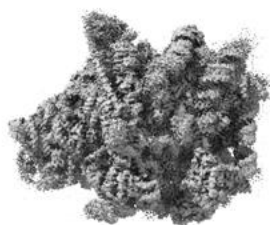
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



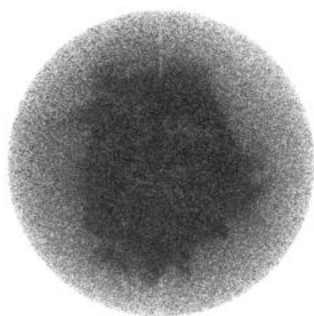
Y



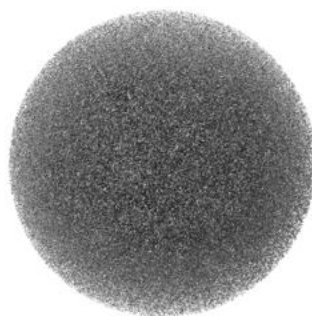
Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

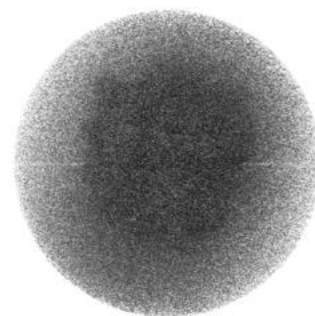
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

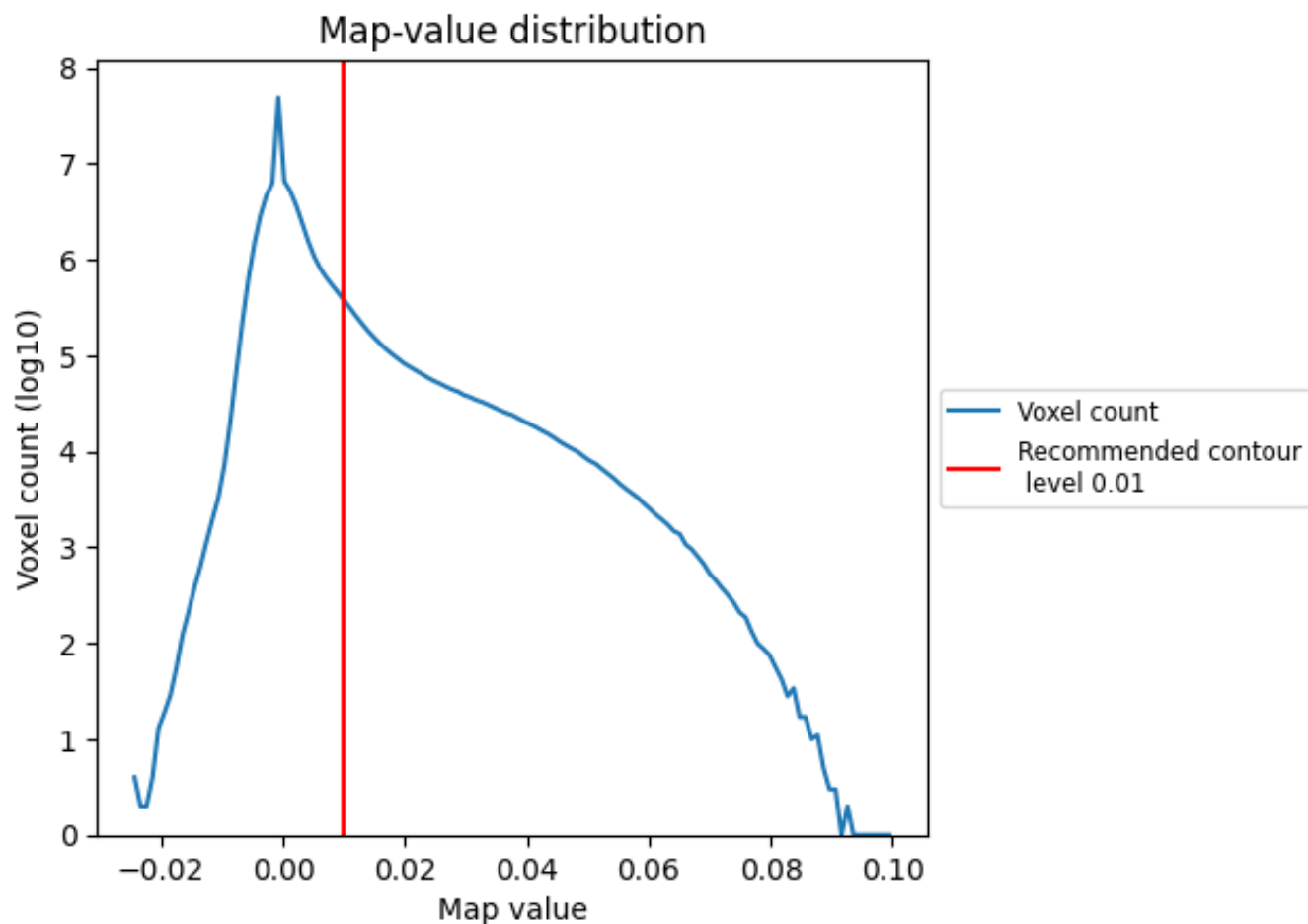
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

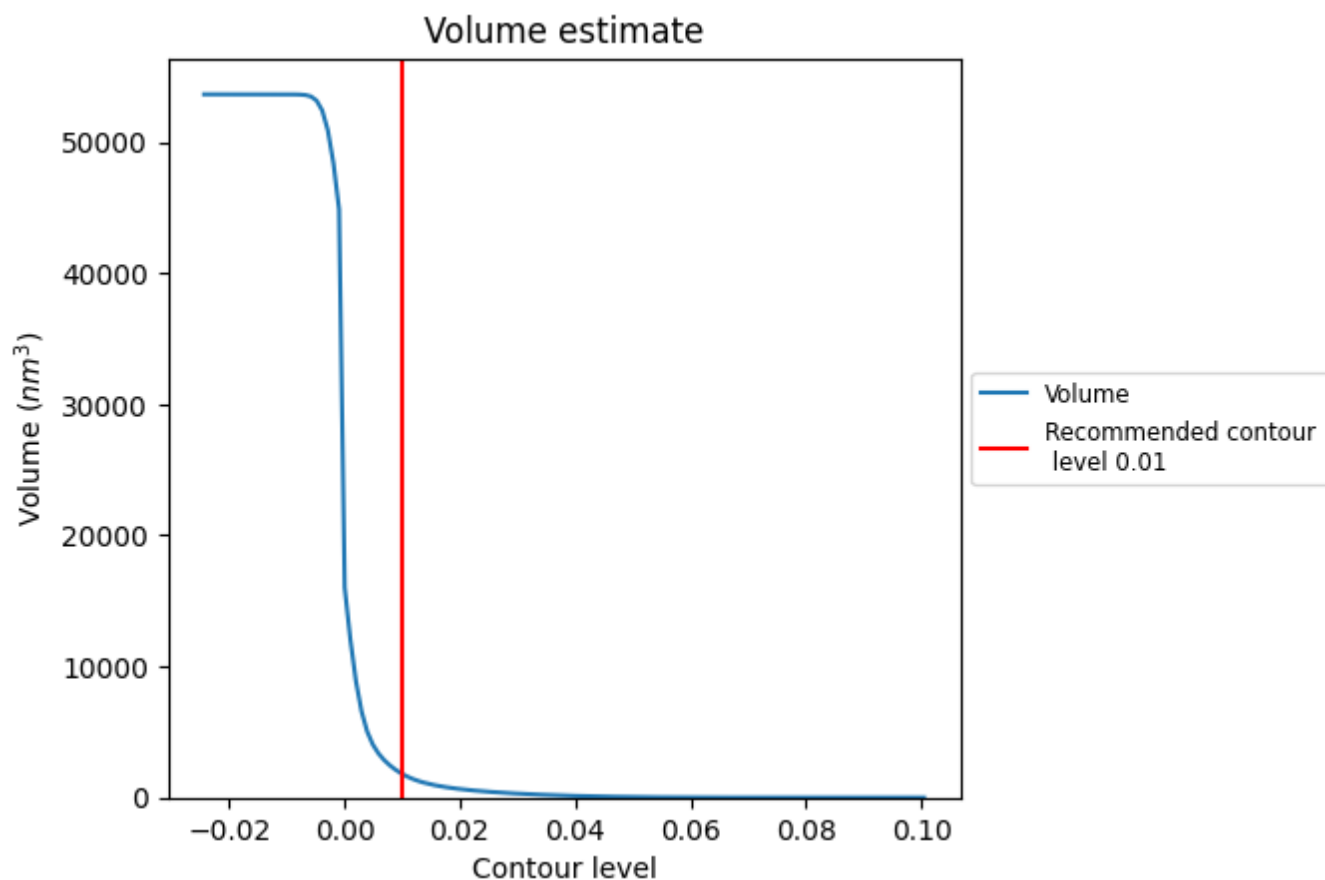
This section contains the results of statistical analysis of the map.

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.

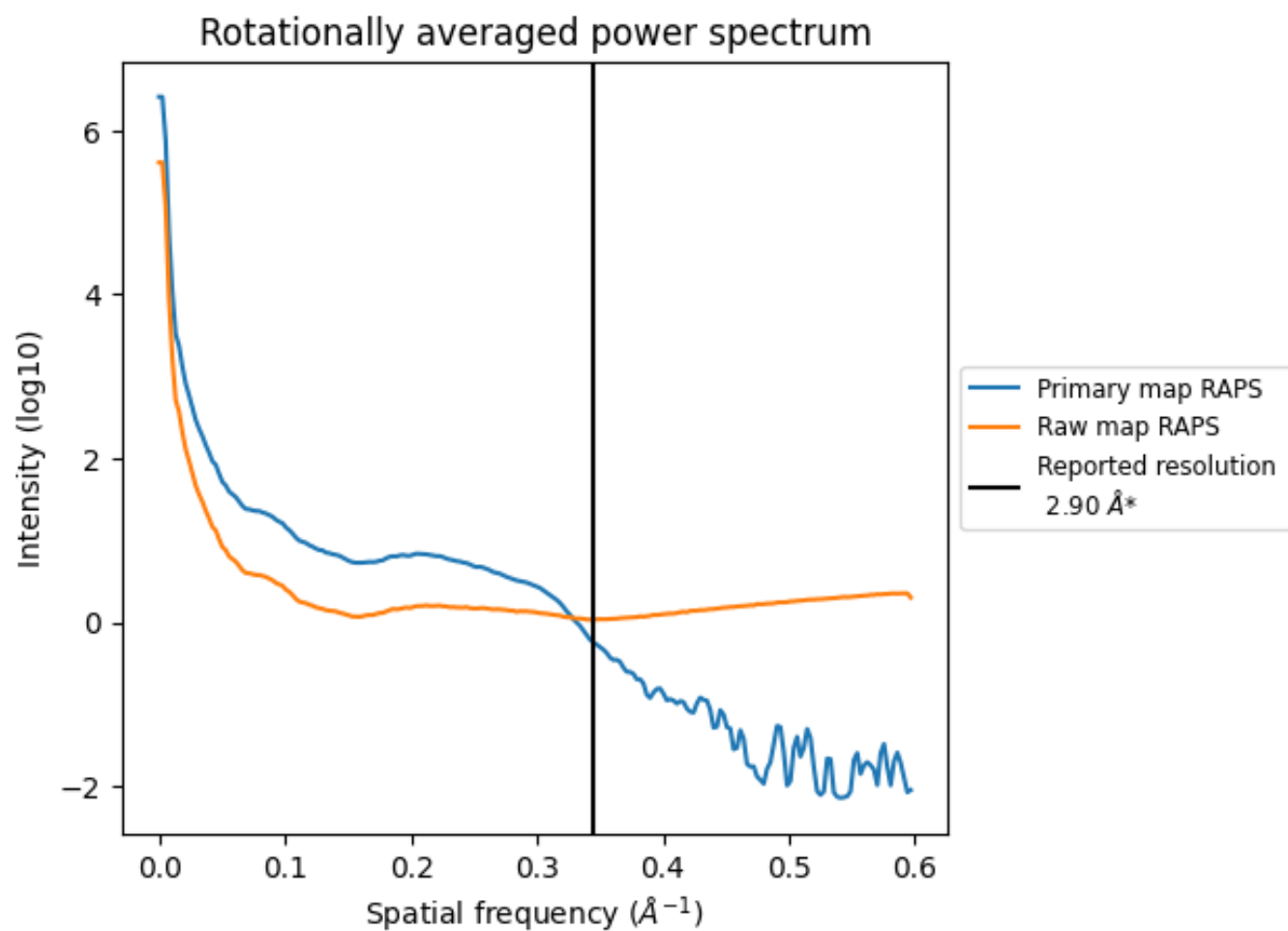
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1811 nm³; this corresponds to an approximate mass of 1636 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 ⓘ

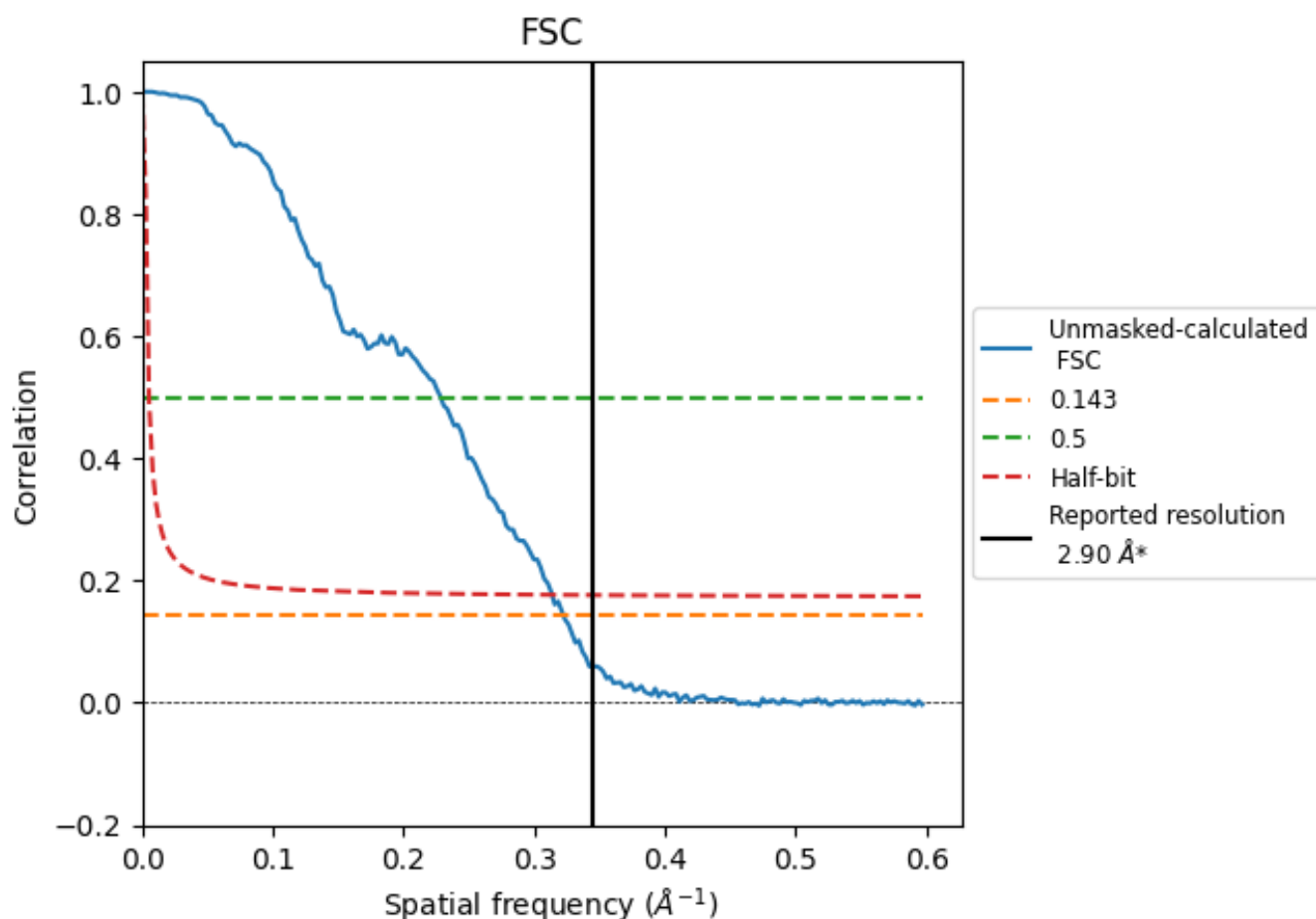


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

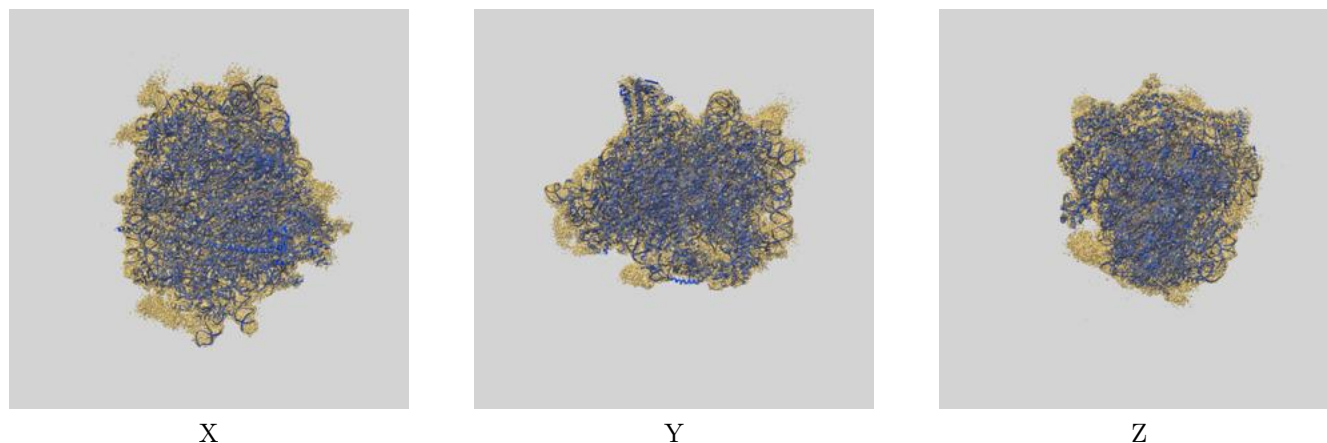
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.10	4.38	3.19

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

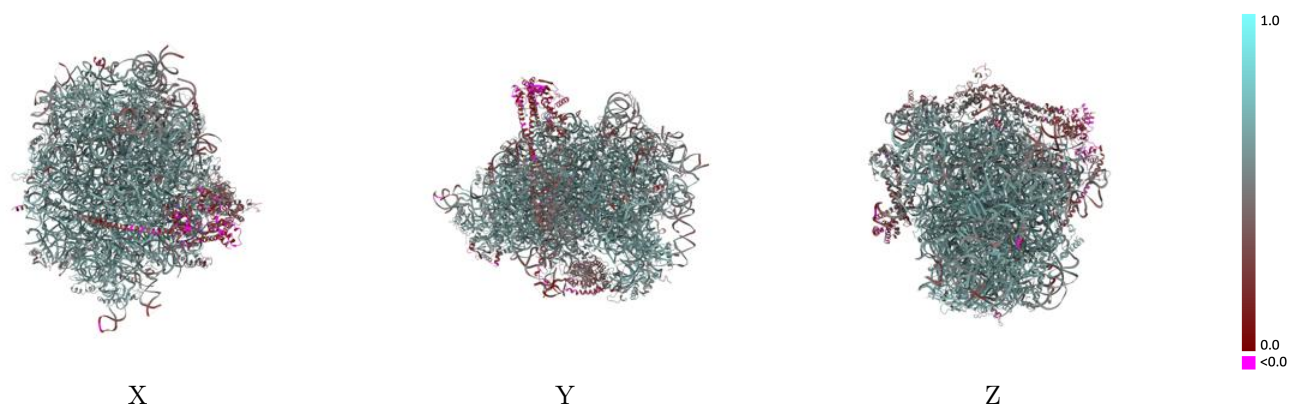
This section contains information regarding the fit between EMDB map EMD-16905 and PDB model 8OJ5. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



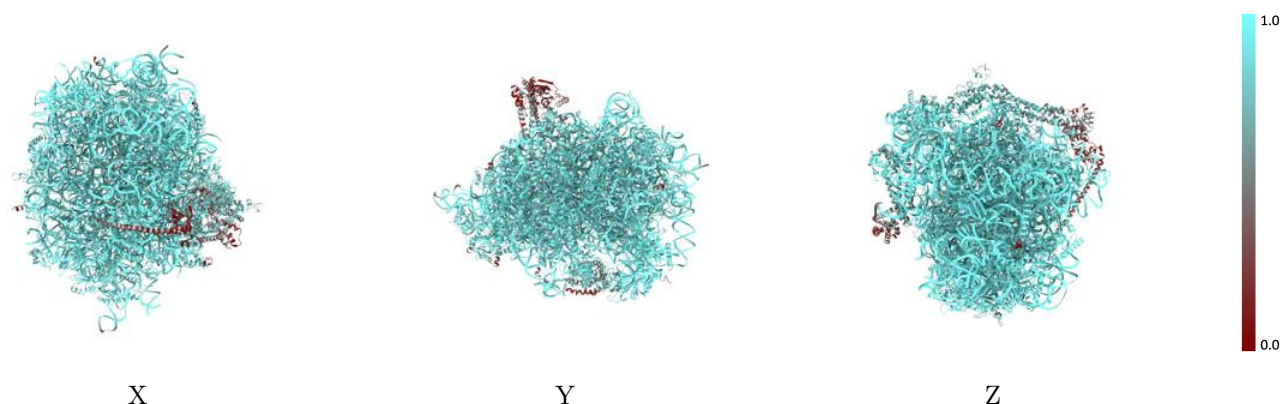
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



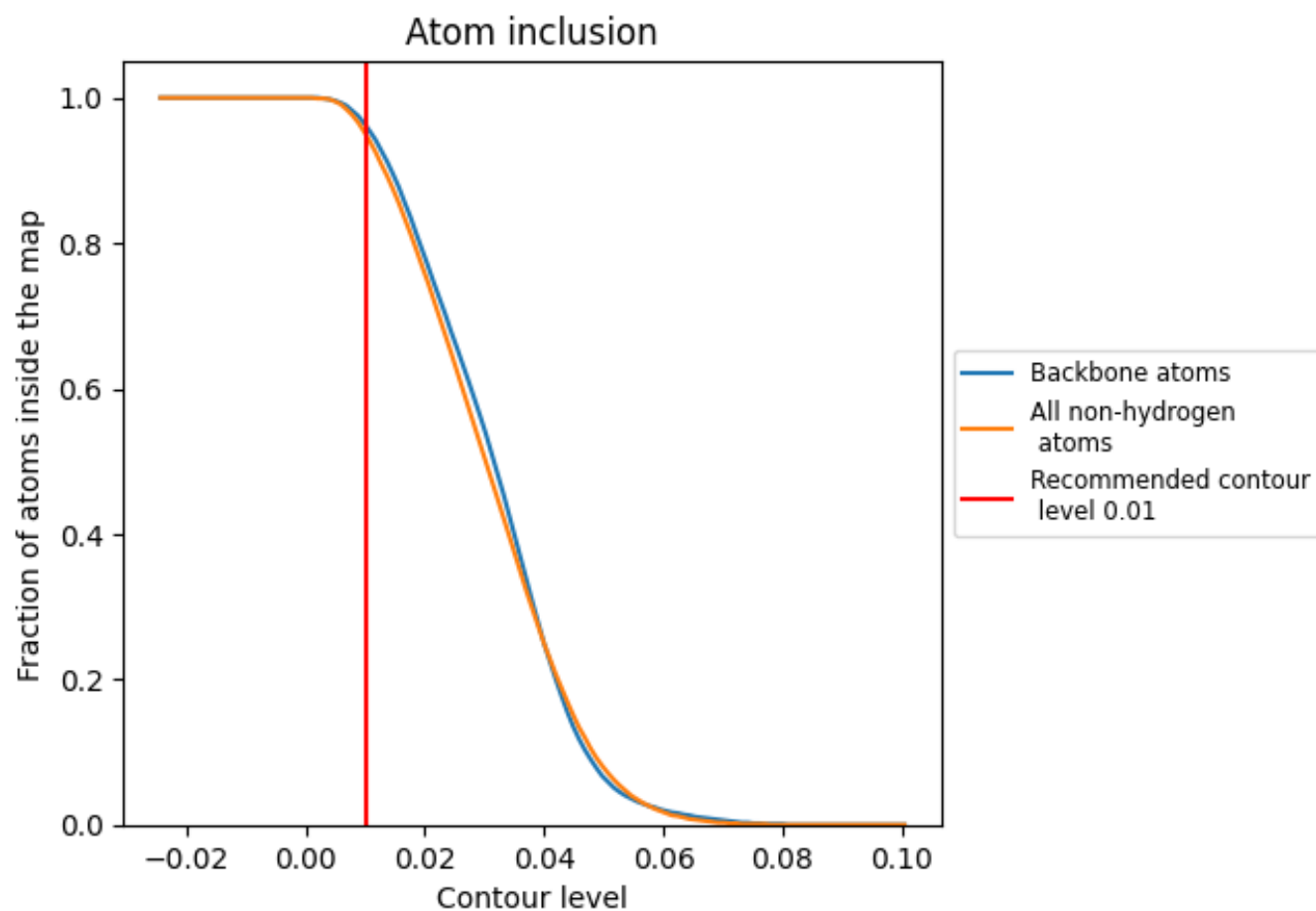
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9510	 0.5700
5	 0.9870	 0.5890
7	 0.9950	 0.6310
8	 0.9970	 0.6240
A	 0.7360	 0.3690
B	 0.5800	 0.2310
C	 0.4020	 0.2010
D	 0.1360	 0.0880
LA	 0.9910	 0.6390
LB	 0.9580	 0.6120
LC	 0.9690	 0.6030
LD	 0.9620	 0.5810
LE	 0.9730	 0.5660
LF	 0.9910	 0.6230
LG	 0.8990	 0.5490
LH	 0.9680	 0.6000
LI	 0.9870	 0.6210
LJ	 0.9050	 0.5320
LL	 0.9660	 0.5840
LM	 0.9830	 0.6100
LN	 0.9980	 0.6460
LO	 0.9810	 0.6220
LP	 0.9900	 0.6290
LQ	 0.9930	 0.6280
LR	 0.9560	 0.5870
LS	 0.9910	 0.6320
LT	 0.9910	 0.6100
LU	 0.8870	 0.5050
LV	 0.9770	 0.6040
LW	 0.9800	 0.6040
LX	 0.9810	 0.6130
LY	 0.9640	 0.6030
LZ	 0.9640	 0.5830
La	 0.9900	 0.6300
Lb	 0.9090	 0.5250



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Chain	Atom inclusion	Q-score
Lc	 0.9290	 0.5590
Ld	 0.9700	 0.5880
Le	 0.9940	 0.6350
Lf	 0.9950	 0.6440
Lg	 0.9430	 0.5890
Lh	 0.9690	 0.5970
Li	 0.9640	 0.5790
Lj	 0.9970	 0.6500
Lk	 0.8830	 0.5560
Ll	 0.9950	 0.6000
Lm	 0.9660	 0.6070
Lo	 0.9760	 0.6120
Lp	 0.9740	 0.6070
Lr	 0.9830	 0.6070
Lz	 0.8450	 0.4080