



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 10:16 PM UTC

PDB ID : 8UU8 / pdb_00008uu8
EMDB ID : EMD-42571
Title : Cryo-EM structure of the *Listeria innocua* 70S ribosome (head-swiveled) in complex with HflXr and pe/E-tRNA (structure II-C)
Authors : Seely, S.M.; Basu, R.S.; Gagnon, M.G.
Deposited on : 2023-10-31
Resolution : 3.10 Å(reported)
Based on initial model : 7NHN

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:

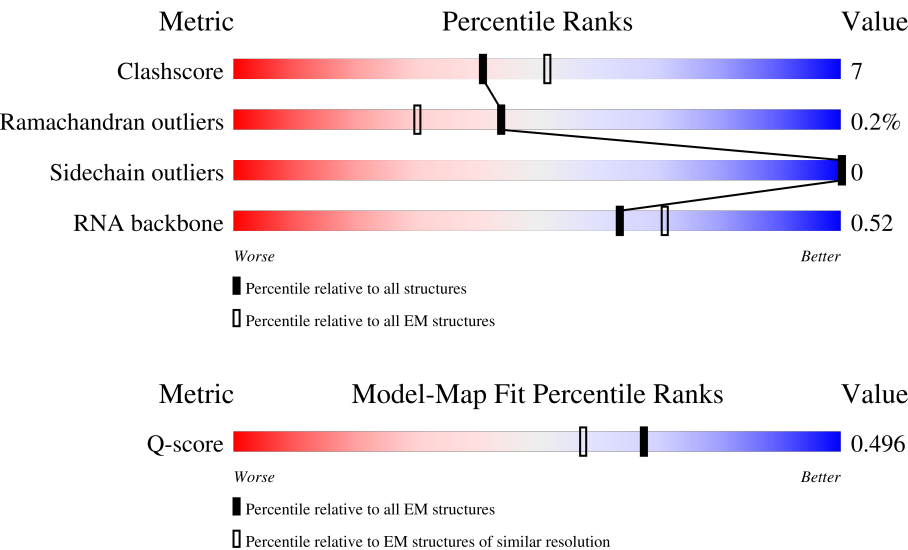
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 3.10 Å.

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



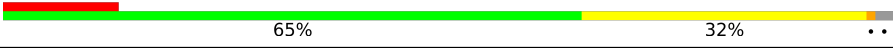
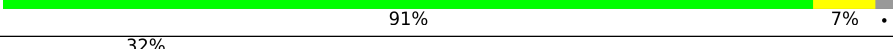
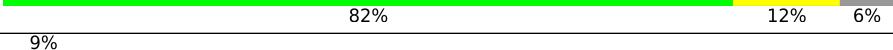
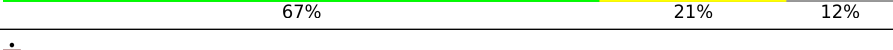
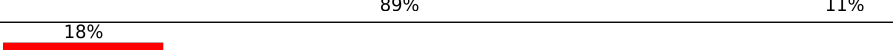
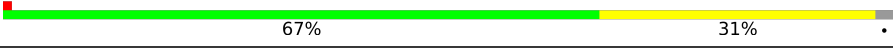
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	a	1550	
2	b	249	
3	c	218	

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Mol	Chain	Length	Quality of chain
4	d	200	
5	e	167	
6	f	97	
7	g	156	
8	h	132	
9	i	130	
10	j	102	
11	k	129	
12	l	137	
13	m	121	
14	n	61	
15	o	89	
16	p	90	
17	q	87	
18	r	79	
19	s	92	
20	t	84	
21	x	76	
22	w	21	
23	v	418	
24	A	2932	
25	B	116	
26	C	277	
27	D	209	
28	E	207	

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Mol	Chain	Length	Quality of chain
29	F	179	
30	G	178	
31	I	166	
32	H	141	
33	L	145	
34	M	122	
35	N	146	
36	O	144	
37	P	135	
38	Q	119	
39	R	114	
40	S	119	
41	T	102	
42	U	118	
43	V	94	
44	W	103	
45	Y	96	
46	Z	62	
47	1	63	
48	2	59	
49	3	81	
50	4	57	
51	5	49	
52	6	44	
53	7	66	

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Mol	Chain	Length	Quality of chain
54	8	37	78% 19%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 142031 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 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1516	Total	C	N	O	P	0	0
			32515	14504	5960	10535	1516		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	209	Total	C	N	O	S	0	0
			1396	888	249	255	4		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	c	204	Total	C	N	O	0	0
			1003	595	204	204		

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	199	Total	C	N	O	S	0	0
			1562	978	289	293	2		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	152	Total	C	N	O	S	0	0
			1057	666	197	192	2		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	95	Total	C	N	O	S	0	0
			785	496	138	149	2		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	130	Total	C	N	O	S	0	0
			650	387	130	132	1		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			1022	651	180	189	2		

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	i	127	Total	C	N	O	0	0
			635	377	128	130		

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	j	96	Total	C	N	O	0	0
			477	285	96	96		

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	114	Total	C	N	O	S	0	0
			748	455	149	141	3		

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	135	Total	C	N	O	S	0	0
			993	615	198	179	1		

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	m	108	Total	C	N	O	0	0
			529	313	108	108		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	50	Total	C	N	O	S	0	0
			260	154	53	50	3		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	87	Total	C	N	O	S	0	0
			695	431	137	125	2		

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	88	Total	C	N	O	S	0	0
			661	418	126	114	3		

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	80	Total	C	N	O	S	0	0
			650	410	120	119	1		

- Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	64	Total	C	N	O	S	0	0
			494	319	93	81	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	s	74	Total	C	N	O	0	0
			365	217	74	74		

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	81	Total	C	N	O	S	0	0
			583	353	117	112	1		

- Molecule 21 is a RNA chain called pe/E Hybrid State Phenylalanine tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	x	74	Total	C	N	O	P	S	0	0
			1591	713	285	517	74	2		

- Molecule 22 is a RNA chain called F-Stop mRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	w	9	Total	C	N	O	P		0	0
			190	86	34	61	9			

- Molecule 23 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	v	417	Total	C	N	O	S		0	0
			3282	2067	566	639	10			

- Molecule 24 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	A	2901	Total	C	N	O	P		0	0
			62318	27812	11528	20077	2901			

- Molecule 25 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	B	114	Total	C	N	O	P		0	0
			2428	1082	428	804	114			

- Molecule 26 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	C	274	Total	C	N	O	S		0	0
			2084	1293	408	376	7			

- Molecule 27 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	D	206	Total	C	N	O	S		0	0
			1544	975	288	277	4			

- Molecule 28 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	E	205	Total	C	N	O	0	0
			1536	976	286	274		

- Molecule 29 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	F	175	Total	C	N	O	S	0	0
			1173	732	215	222	4		

- Molecule 30 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	G	171	Total	C	N	O	S	0	0
			1305	822	241	241	1		

- Molecule 31 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	I	129	Total	C	N	O	0	0
			636	378	129	129		

- Molecule 32 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	H	135	Total	C	N	O	0	0
			673	403	135	135		

- Molecule 33 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L	143	Total	C	N	O	S	0	0
			1112	707	205	197	3		

- Molecule 34 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	M	122	Total	C	N	O	S	0	0
			893	554	170	165	4		

- Molecule 35 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	N	146	Total	C	N	O	S	0	0
			1071	662	209	199	1		

- Molecule 36 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	O	135	Total	C	N	O	S	0	0
			1062	679	203	174	6		

- Molecule 37 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	P	122	Total	C	N	O	S	0	0
			982	616	193	172	1		

- Molecule 38 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Q	119	Total	C	N	O	S	0	0
			884	545	172	166	1		

- Molecule 39 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R	113	Total	C	N	O	S	0	0
			885	560	171	153	1		

- Molecule 40 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S	118	Total	C	N	O	S	0	0
			949	602	187	156	4		

- Molecule 41 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	T	101	Total	C	N	O	S	0	0
			774	502	134	137	1		

- Molecule 42 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	U	112	Total	C	N	O	0	0
			850	537	159	154		

- Molecule 43 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	V	92	Total	C	N	O	S	0
			726	463	126	134	3	0

- Molecule 44 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	W	102	Total	C	N	O	S	0
			760	482	140	135	3	0

- Molecule 45 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	Y	76	Total	C	N	O	S	0
			567	347	110	109	1	0

- Molecule 46 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	Z	59	Total	C	N	O	S	0
			444	274	92	76	2	0

- Molecule 47 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	1	60	Total	C	N	O	S	0
			477	295	94	87	1	0

- Molecule 48 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	2	56	Total	C	N	O	S	0
			433	272	82	78	1	0

- Molecule 49 is a protein called Large ribosomal subunit protein bL31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	3	73	Total	C	N	O	S	0	0
			523	328	90	104	1		

- Molecule 50 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	4	53	Total	C	N	O	S	0	0
			417	256	86	70	5		

- Molecule 51 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	5	48	Total	C	N	O	S	0	0
			394	241	79	70	4		

- Molecule 52 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	6	43	Total	C	N	O	S	0	0
			365	222	88	53	2		

- Molecule 53 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	64	Total	C	N	O	S	0	0
			520	322	114	79	5		

- Molecule 54 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	8	36	Total	C	N	O	S	0	0
			280	174	56	44	6		

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	a	151	Total	Mg	0
			151	151	
55	b	1	Total	Mg	0
			1	1	
55	c	1	Total	Mg	0
			1	1	

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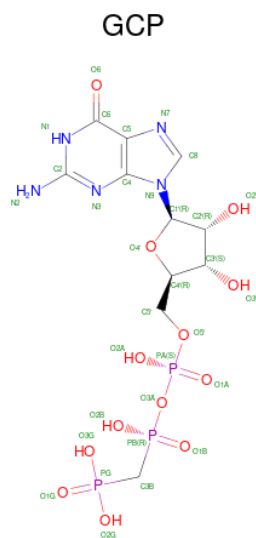
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Mol	Chain	Residues	Atoms		AltConf
55	g	1	Total 1	Mg 1	0
55	i	2	Total 2	Mg 2	0
55	m	1	Total 1	Mg 1	0
55	n	2	Total 2	Mg 2	0
55	o	1	Total 1	Mg 1	0
55	v	2	Total 2	Mg 2	0
55	A	249	Total 249	Mg 249	0
55	B	5	Total 5	Mg 5	0
55	C	1	Total 1	Mg 1	0
55	D	2	Total 2	Mg 2	0
55	M	1	Total 1	Mg 1	0
55	N	1	Total 1	Mg 1	0
55	S	1	Total 1	Mg 1	0
55	W	1	Total 1	Mg 1	0

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	n	1	Total 1	Zn 1	0
56	4	1	Total 1	Zn 1	0
56	5	1	Total 1	Zn 1	0
56	8	1	Total 1	Zn 1	0

- Molecule 57 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
57	v	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 58 is water.

Mol	Chain	Residues	Atoms	AltConf
58	a	94	Total O 94 94	0
58	d	1	Total O 1 1	0
58	e	1	Total O 1 1	0
58	f	1	Total O 1 1	0
58	i	1	Total O 1 1	0
58	p	3	Total O 3 3	0
58	t	1	Total O 1 1	0
58	v	2	Total O 2 2	0
58	A	235	Total O 235 235	0
58	B	6	Total O 6 6	0
58	C	2	Total O 2 2	0

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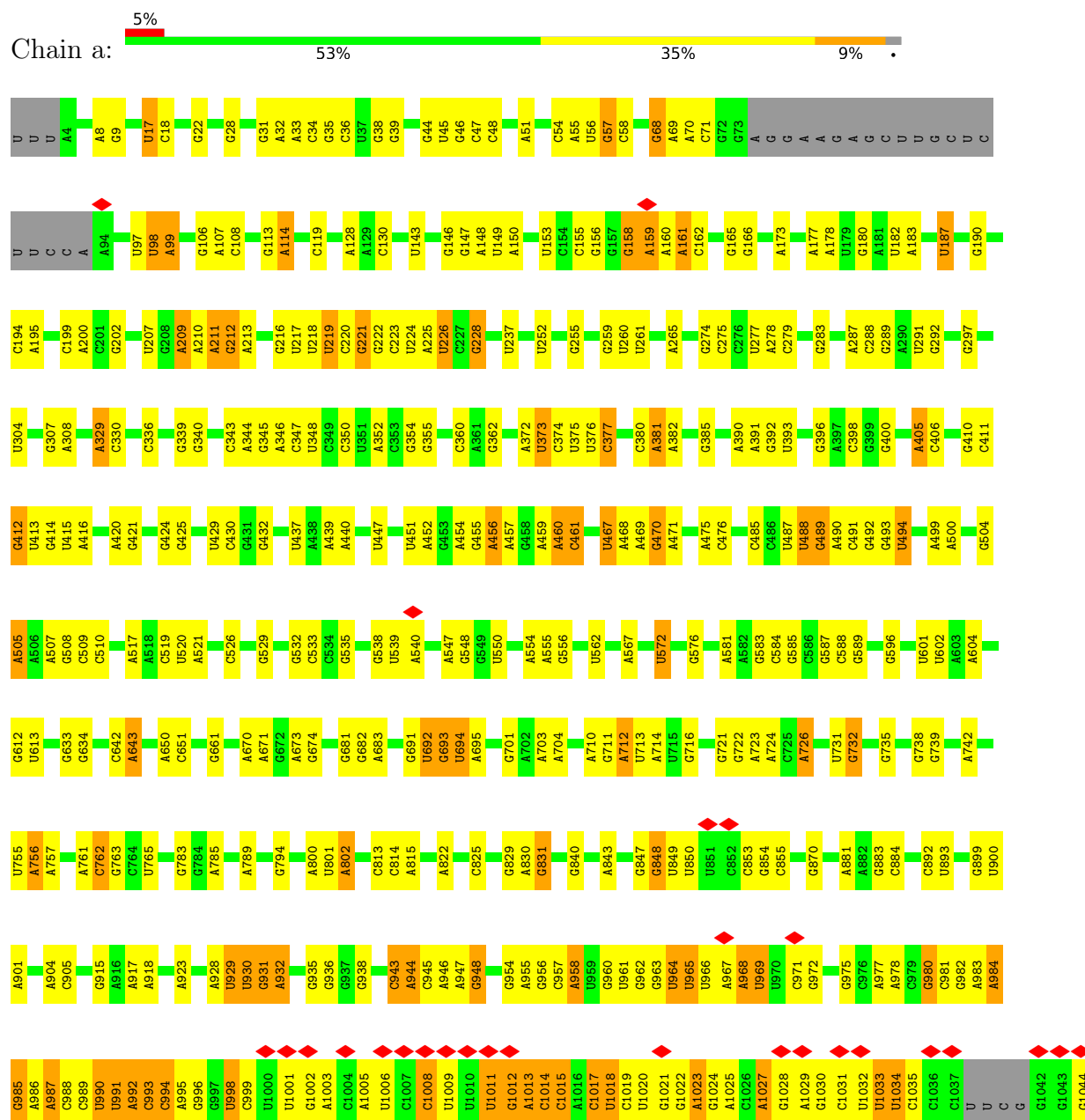
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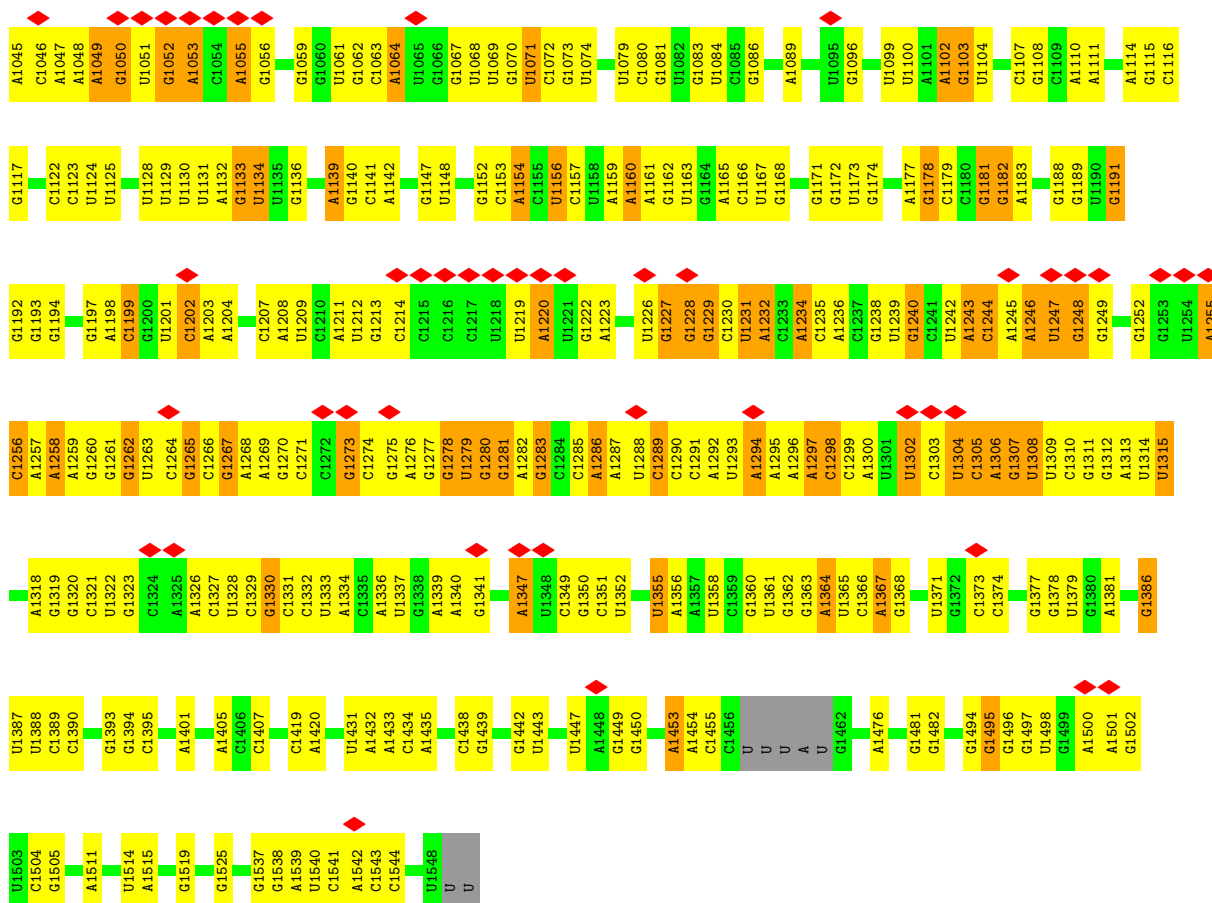
Mol	Chain	Residues	Atoms		AltConf
58	D	1	Total 1	O 1	0
58	N	5	Total 5	O 5	0
58	O	1	Total 1	O 1	0
58	P	1	Total 1	O 1	0
58	S	2	Total 2	O 2	0
58	T	1	Total 1	O 1	0
58	U	2	Total 2	O 2	0
58	V	1	Total 1	O 1	0
58	Z	2	Total 2	O 2	0
58	2	1	Total 1	O 1	0

3 Residue-property plots

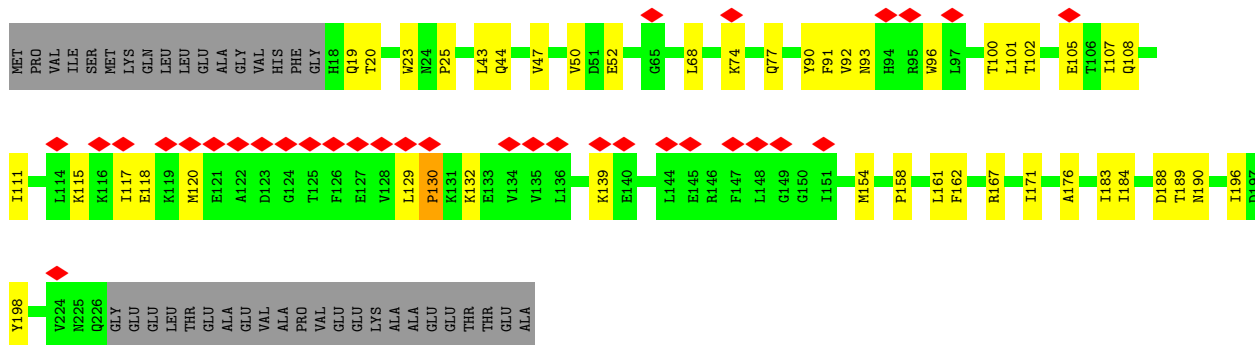
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S Ribosomal RNA

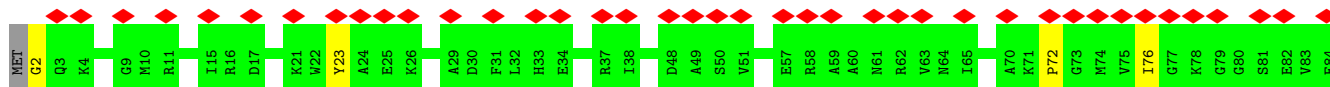
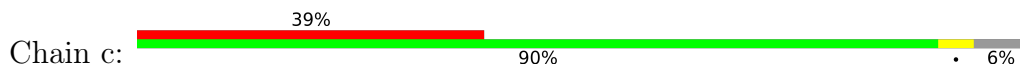


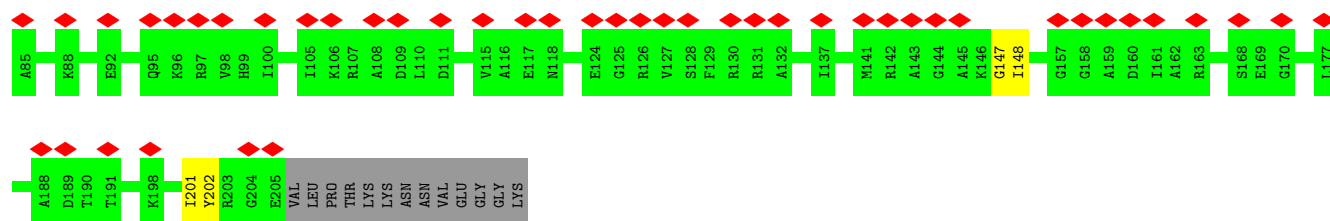


• Molecule 2: Small ribosomal subunit protein uS2

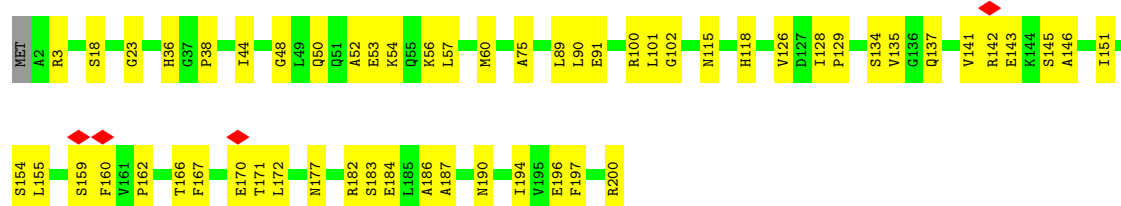


• Molecule 3: Small ribosomal subunit protein uS3

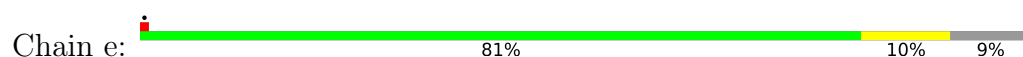




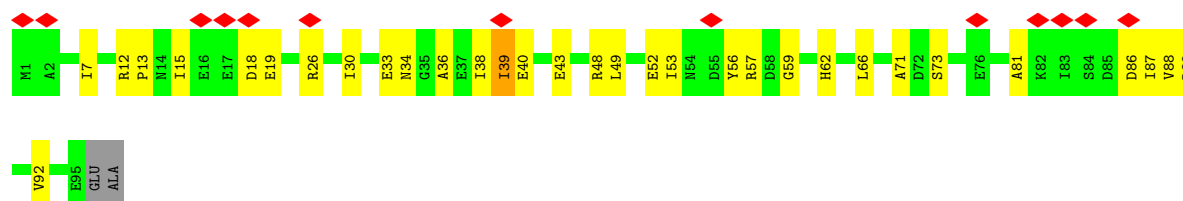
• Molecule 4: Small ribosomal subunit protein uS4



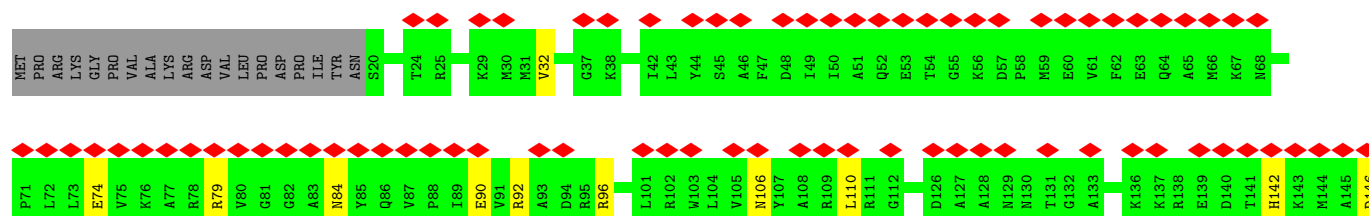
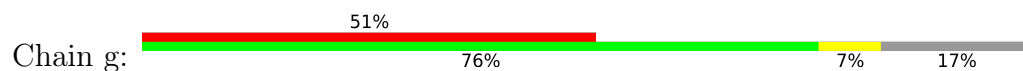
• Molecule 5: Small ribosomal subunit protein uS5

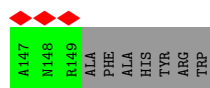


• Molecule 6: Small ribosomal subunit protein bS6



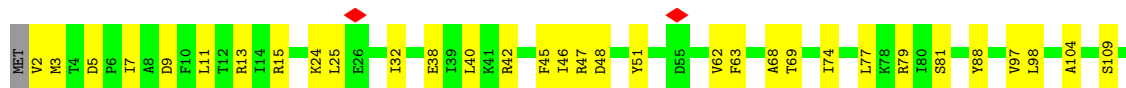
• Molecule 7: Small ribosomal subunit protein uS7





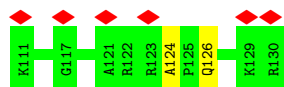
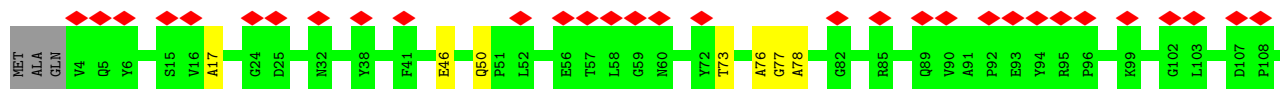
- Molecule 8: Small ribosomal subunit protein uS8

Chain h: 72% 27%



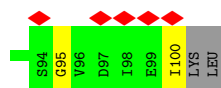
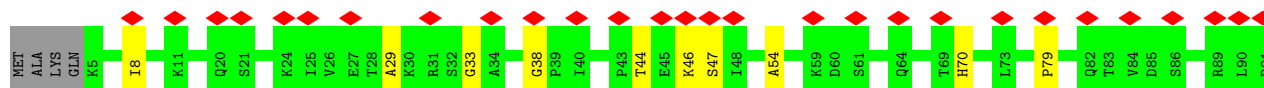
- Molecule 9: Small ribosomal subunit protein uS9

Chain i: 28% 91% 7%



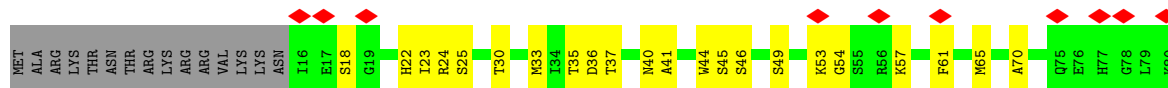
- Molecule 10: Small ribosomal subunit protein uS10

Chain j: 32% 82% 12% 6%



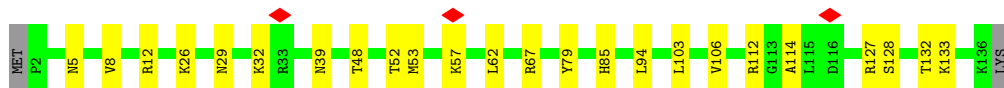
- Molecule 11: Small ribosomal subunit protein uS11

Chain k: 9% 67% 21% 12%

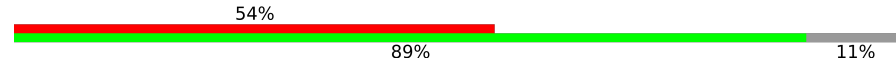


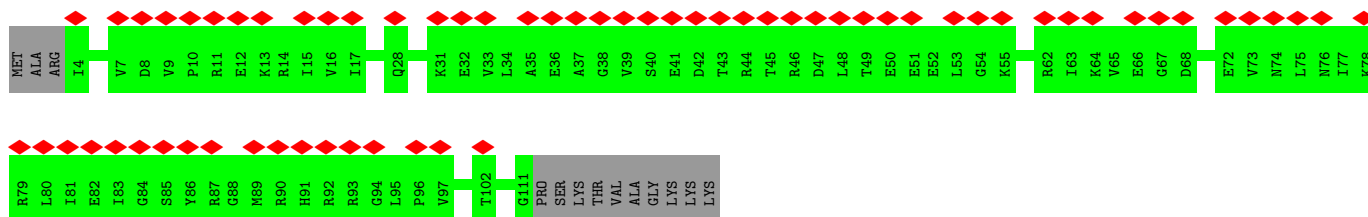
- Molecule 12: Small ribosomal subunit protein uS12

Chain l: 



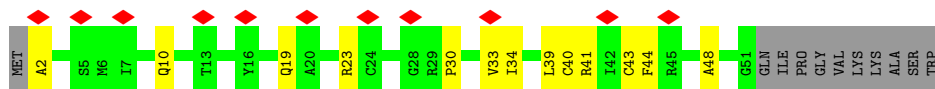
- Molecule 13: Small ribosomal subunit protein uS13

Chain m: 



- Molecule 14: Small ribosomal subunit protein uS14

Chain n: 



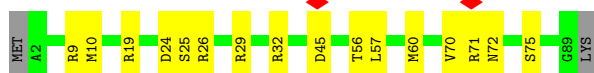
- Molecule 15: Small ribosomal subunit protein uS15

Chain o: 



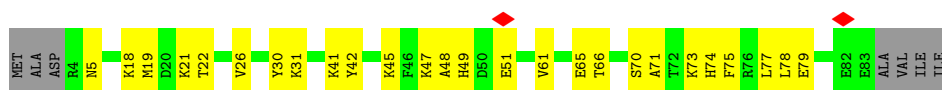
- Molecule 16: Small ribosomal subunit protein bS16

Chain p: 



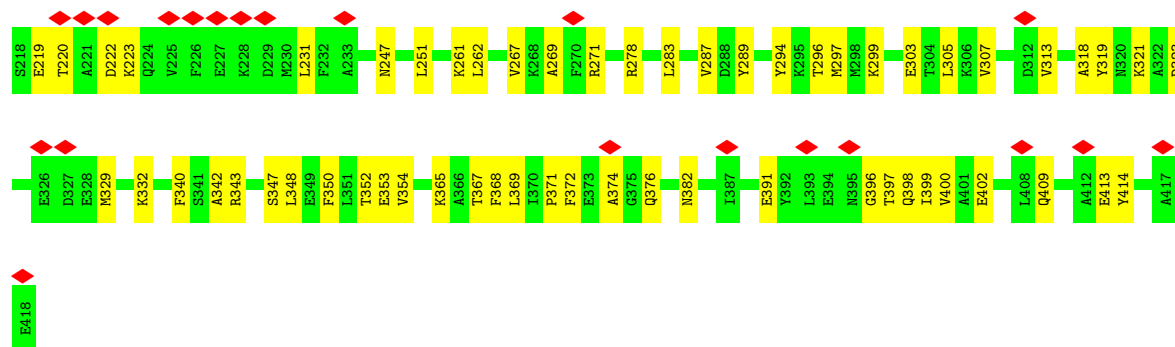
- Molecule 17: Small ribosomal subunit protein uS17

Chain q: 



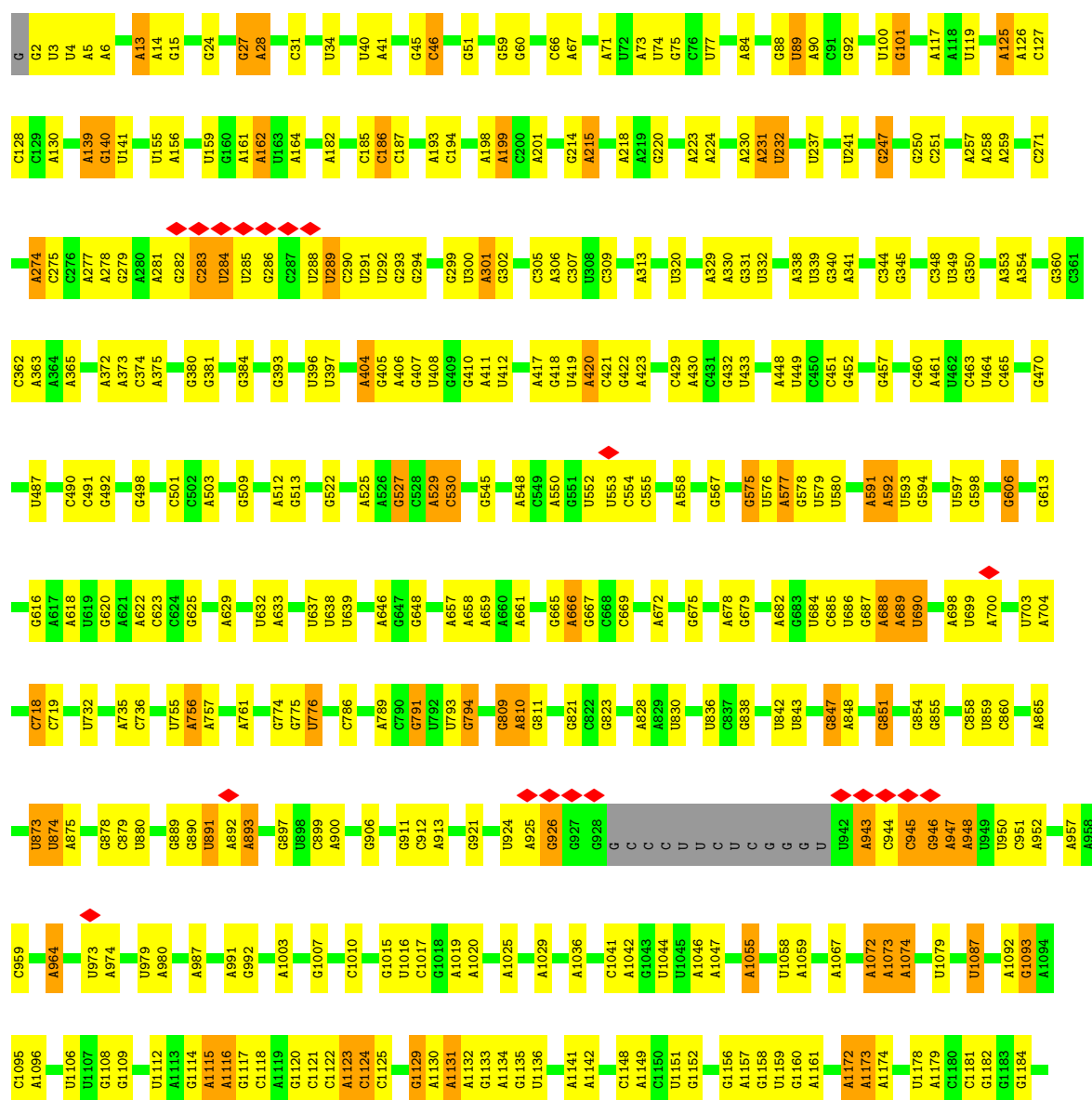
- Molecule 18: Small ribosomal subunit protein bS18

Chain r: 



• Molecule 24: 23S Ribosomal RNA

Chain A: 66% 27% 6%



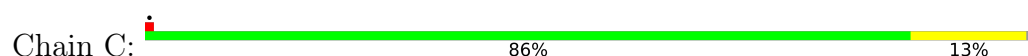
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U2339	G2340	G2341	A2344	U2345	U2346	U2347	U2348	U2349	U2350	U2351	U2352	U2353	U2354	U2355	U2356	U2357	U2358	U2359	U2360	U2361	U2362	U2363	U2364	U2365	U2366	U2367	U2368	U2369	U2370	U2371	U2372	U2373	U2374	U2375	U2376	U2377	U2378	U2379	U2380	U2381	U2382	U2383	U2384	U2385	U2386	U2387	U2388	U2389	U2390	U2391	U2392	U2393	U2394	U2395	U2396	U2397	U2398	U2399	U2400	U2401	U2402	U2403	U2404	U2405	U2406	U2407	U2408	U2409	U2410	U2411	U2412	U2413	U2414	U2415	U2416	U2417	U2418	U2419	U2420	U2421	U2422	U2423	U2424	U2425	U2426	U2427	U2428	U2429	U2430	U2431	U2432	U2433	U2434	U2435	U2436	U2437	U2438	U2439	U2440	U2441	U2442	U2443	U2444	U2445	U2446	U2447	U2448	U2449	U2450	U2451	U2452	U2453	U2454	U2455	U2456	U2457	U2458	U2459	U2460	U2461	U2462	U2463	U2464	U2465	U2466	U2467	U2468	U2469	U2470	U2471	U2472	U2473	U2474	U2475	U2476	U2477	U2478	U2479	U2480	U2481	U2482	U2483	U2484	U2485	U2486	U2487	U2488	U2489	U2490	U2491	U2492	U2493	U2494	U2495	U2496	U2497	U2498	U2499	U2500	U2501	U2502	U2503	U2504	U2505	U2506	U2507	U2508	U2509	U2510	U2511	U2512	U2513	U2514	U2515	U2516	U2517	U2518	U2519	U2520	U2521	U2522	U2523	U2524	U2525	U2526	U2527	U2528	U2529	U2530	U2531	U2532	U2533	U2534	U2535	U2536	U2537	U2538	U2539	U2540	U2541	U2542	U2543	U2544	U2545	U2546	U2547	U2548	U2549	U2550	U2551	U2552	U2553	U2554	U2555	U2556	U2557	U2558	U2559	U2560	U2561	U2562	U2563	U2564	U2565	U2566	U2567	U2568	U2569	U2570	U2571	U2572	U2573	U2574	U2575	U2576	U2577	U2578	U2579	U2580	U2581	U2582	U2583	U2584	U2585	U2586	U2587	U2588	U2589	U2590	U2591	U2592	U2593	U2594	U2595	U2596	U2597	U2598	U2599	U2600	U2601	U2602	U2603	U2604	U2605	U2606	U2607	U2608	U2609	U2610	U2611	U2612	U2613	U2614	U2615	U2616	U2617	U2618	U2619	U2620	U2621	U2622	U2623	U2624	U2625	U2626	U2627	U2628	U2629	U2630	U2631	U2632	U2633	U2634	U2635	U2636	U2637	U2638	U2639	U2640	U2641	U2642	U2643	U2644	U2645	U2646	U2647	U2648	U2649	U2650	U2651	U2652	U2653	U2654	U2655	U2656	U2657	U2658	U2659	U2660	U2661	U2662	U2663	U2664	U2665	U2666	U2667	U2668	U2669	U2670	U2671	U2672	U2673	U2674	U2675	U2676	U2677	U2678	U2679	U2680	U2681	U2682	U2683	U2684	U2685	U2686	U2687	U2688	U2689	U2690	U2691	U2692	U2693	U2694	U2695	U2696	U2697	U2698	U2699	U2700	U2701	U2702	U2703	U2704	U2705	U2706	U2707	U2708	U2709	U2710	U2711	U2712	U2713	U2714	U2715	U2716	U2717	U2718	U2719	U2720	U2721	U2722	U2723	U2724	U2725	U2726	U2727	U2728	U2729	U2730	U2731	U2732	U2733	U2734	U2735	U2736	U2737	U2738	U2739	U2740	U2741	U2742	U2743	U2744	U2745	U2746	U2747	U2748	U2749	U2750	U2751	U2752	U2753	U2754	U2755	U2756	U2757	U2758	U2759	U2760	U2761	U2762	U2763	U2764	U2765	U2766	U2767	U2768	U2769	U2770	U2771	U2772	U2773	U2774	U2775	U2776	U2777	U2778	U2779	U2780	U2781	U2782	U2783	U2784	U2785	U2786	U2787	U2788	U2789	U2790	U2791	U2792	U2793	U2794	U2795	U2796	U2797	U2798	U2799	U2800	U2801	U2802	U2803	U2804	U2805	U2806	U2807	U2808	U2809	U2810	U2811	U2812	U2813	U2814	U2815	U2816	U2817	U2818	U2819	U2820	U2821	U2822	U2823	U2824	U2825	U2826	U2827	U2828	U2829	U2830	U2831	U2832	U2833	U2834	U2835	U2836	U2837	U2838	U2839	U2840	U2841	U2842	U2843	U2844	U2845	U2846	U2847	U2848	U2849	U2850	U2851	U2852	U2853	U2854	U2855	U2856	U2857	U2858	U2859	U2860	U2861																																																																																																																																																										
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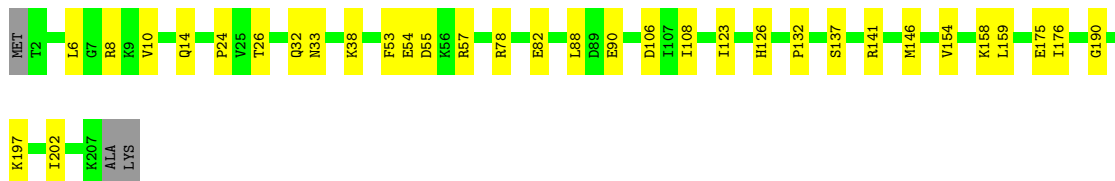
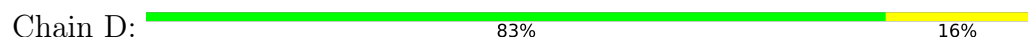
- Molecule 25: 5S Ribosomal RNA



- Molecule 26: Large ribosomal subunit protein uL2



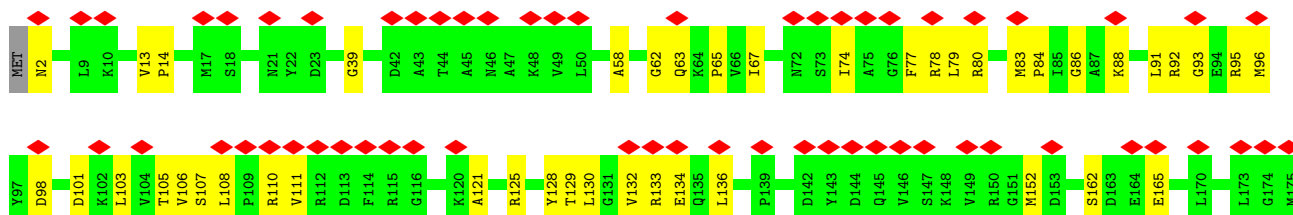
- Molecule 27: Large ribosomal subunit protein uL3



- Molecule 28: Large ribosomal subunit protein uL4



- Molecule 29: Large ribosomal subunit protein uL5

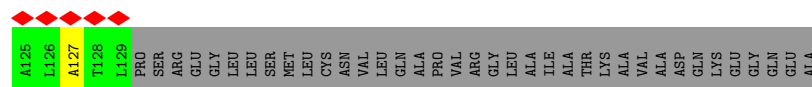
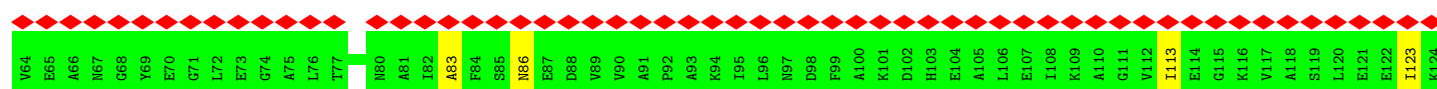
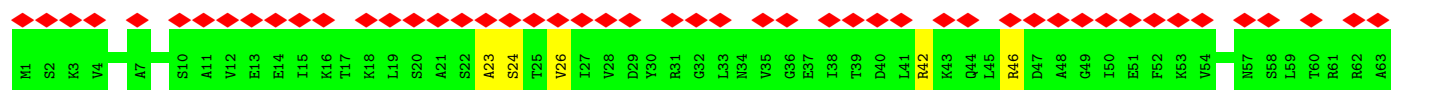




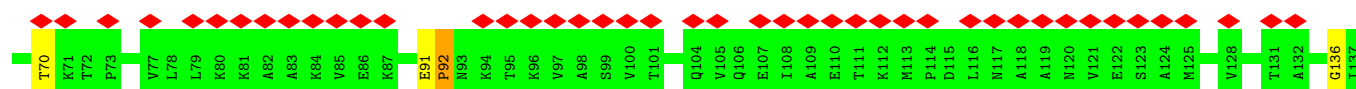
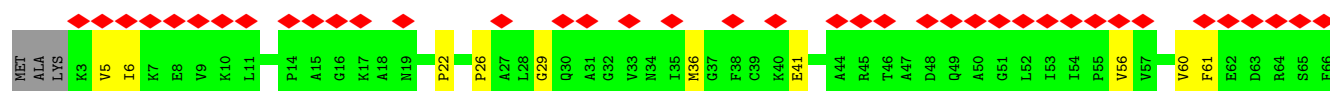
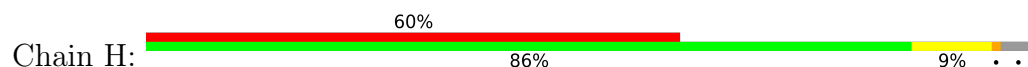
- Molecule 30: Large ribosomal subunit protein uL6



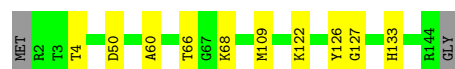
- Molecule 31: Large ribosomal subunit protein uL10



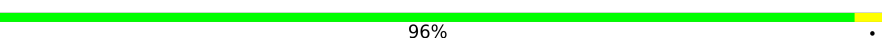
- Molecule 32: Large ribosomal subunit protein uL11



- Molecule 33: Large ribosomal subunit protein uL13



- Molecule 34: Large ribosomal subunit protein uL14

Chain M:  96%



- Molecule 35: Large ribosomal subunit protein uL15

Chain N:  83%



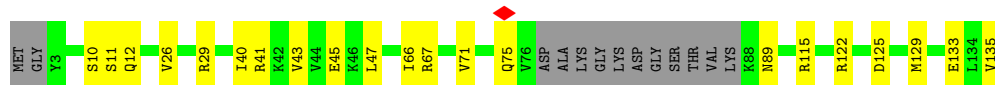
- Molecule 36: Large ribosomal subunit protein uL16

Chain O:  86%



- Molecule 37: Large ribosomal subunit protein bL17

Chain P:  75%



- Molecule 38: Large ribosomal subunit protein uL18

Chain Q:  8%



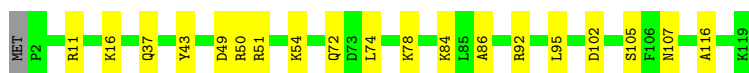
- Molecule 39: Large ribosomal subunit protein bL19

Chain R:  89%

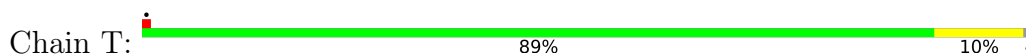


- Molecule 40: Large ribosomal subunit protein bL20

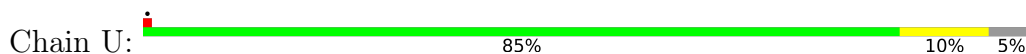
Chain S:  83%



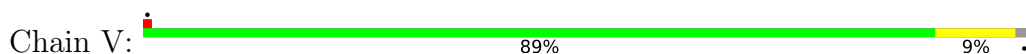
- Molecule 41: Large ribosomal subunit protein bL21



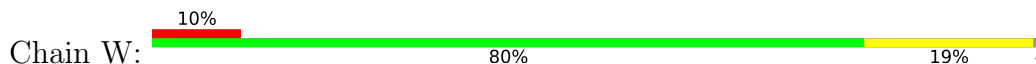
- Molecule 42: Large ribosomal subunit protein uL22



- Molecule 43: Large ribosomal subunit protein uL23



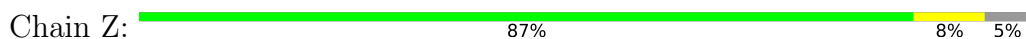
- Molecule 44: Large ribosomal subunit protein uL24



- Molecule 45: Large ribosomal subunit protein bL27



- Molecule 46: Large ribosomal subunit protein bL28



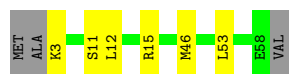
- Molecule 47: Large ribosomal subunit protein uL29

Chain 1:  79% 16% 5%



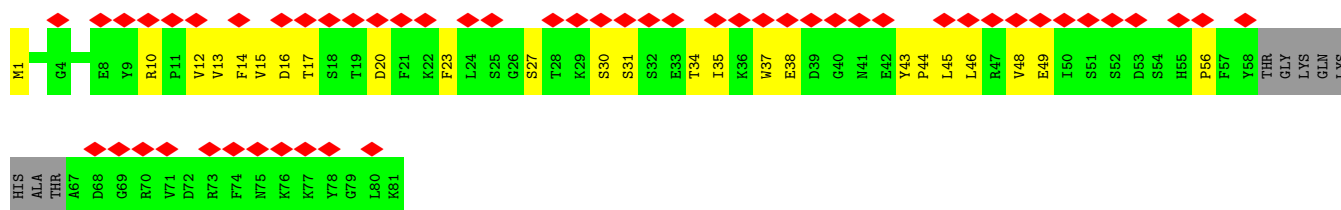
- Molecule 48: Large ribosomal subunit protein uL30

Chain 2:  85% 10% 5%



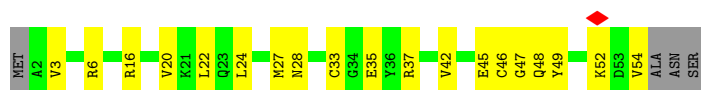
- Molecule 49: Large ribosomal subunit protein bL31B

Chain 3:  65% 60% 30% 10%



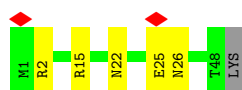
- Molecule 50: Large ribosomal subunit protein bL32

Chain 4:  60% 33% 7%



- Molecule 51: Large ribosomal subunit protein bL33

Chain 5:  88% 10%



- Molecule 52: Large ribosomal subunit protein bL34

Chain 6:  89% 9%

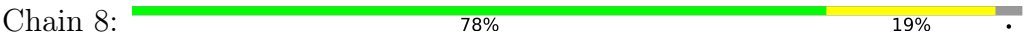


- Molecule 53: Large ribosomal subunit protein bL35

Chain 7:  83% 14%



- Molecule 54: Large ribosomal subunit protein bL36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	55099	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	34.334	Depositor
Minimum map value	-17.982	Depositor
Average map value	0.002	Depositor
Map value standard deviation	1.124	Depositor
Recommended contour level	3.5	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: G7M, GCP, 5MU, MIA, ZN, PSU, MG, 4SU

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	a	0.26	0/36403	0.35	1/56778 (0.0%)
2	b	0.19	0/1419	0.42	1/1945 (0.1%)
3	c	0.15	0/1002	0.32	0/1391
4	d	0.23	0/1590	0.37	0/2142
5	e	0.25	0/1069	0.41	0/1451
6	f	0.20	0/797	0.48	0/1068
7	g	0.15	0/649	0.37	0/901
8	h	0.29	0/1035	0.45	0/1392
9	i	0.18	0/636	0.37	0/878
10	j	0.18	0/476	0.41	0/663
11	k	0.18	0/760	0.36	0/1031
12	l	0.25	0/1009	0.43	0/1365
13	m	0.15	0/528	0.32	0/731
14	n	0.25	0/259	0.56	0/357
15	o	0.23	0/705	0.53	0/949
16	p	0.24	0/674	0.47	0/909
17	q	0.23	0/659	0.40	0/882
18	r	0.27	0/502	0.46	0/673
19	s	0.13	0/364	0.30	0/505
20	t	0.23	0/586	0.44	0/788
21	x	0.23	0/1605	0.30	0/2497
22	w	0.15	0/212	0.30	0/327
23	v	0.20	0/3324	0.40	0/4483
24	A	0.24	0/69819	0.30	0/108917
25	B	0.15	0/2711	0.21	0/4224
26	C	0.24	0/2120	0.31	0/2848
27	D	0.25	0/1566	0.36	0/2108
28	E	0.22	0/1557	0.34	0/2103
29	F	0.13	0/1186	0.38	0/1615
30	G	0.16	0/1327	0.30	0/1793
31	I	0.07	0/635	0.19	0/882
32	H	0.12	0/676	0.32	0/942

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	L	0.23	0/1135	0.28	0/1526
34	M	0.22	0/900	0.29	0/1212
35	N	0.22	0/1082	0.31	0/1446
36	O	0.21	0/1084	0.29	0/1450
37	P	0.24	0/993	0.31	0/1328
38	Q	0.13	0/893	0.27	0/1201
39	R	0.22	0/897	0.31	0/1206
40	S	0.25	0/962	0.28	0/1280
41	T	0.25	0/787	0.32	0/1057
42	U	0.24	0/860	0.29	0/1165
43	V	0.21	0/735	0.28	0/988
44	W	0.18	0/770	0.33	0/1032
45	Y	0.23	0/574	0.37	0/766
46	Z	0.22	0/449	0.33	0/597
47	1	0.16	0/478	0.25	0/640
48	2	0.22	0/436	0.28	0/585
49	3	0.13	0/532	0.36	0/720
50	4	0.34	0/425	0.49	0/567
51	5	0.17	0/398	0.26	0/534
52	6	0.27	0/368	0.28	0/479
53	7	0.25	0/527	0.41	0/685
54	8	0.24	0/283	0.27	0/375
All	All	0.24	0/153428	0.33	2/230377 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
12	l	0	1
16	p	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	b	130	PRO	CA-N-CD	-8.04	100.75	112.00
1	a	756	A	C2'-C3'-O3'	7.94	121.41	109.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	l	57	LYS	Peptide
16	p	45	ASP	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	a	32515	0	16372	462	0
2	b	1396	0	1188	30	0
3	c	1003	0	487	5	0
4	d	1562	0	1543	38	0
5	e	1057	0	1082	11	0
6	f	785	0	774	21	0
7	g	650	0	328	6	0
8	h	1022	0	1078	26	0
9	i	635	0	321	7	0
10	j	477	0	203	9	0
11	k	748	0	658	20	0
12	l	993	0	995	16	0
13	m	529	0	239	0	0
14	n	260	0	140	9	0
15	o	695	0	684	13	0
16	p	661	0	638	10	0
17	q	650	0	676	15	0
18	r	494	0	502	10	0
19	s	365	0	163	3	0
20	t	583	0	578	7	0
21	x	1591	0	818	26	0
22	w	190	0	97	6	0
23	v	3282	0	3294	88	0
24	A	62318	0	31333	496	0
25	B	2428	0	1229	20	0
26	C	2084	0	2133	23	0
27	D	1544	0	1591	21	0
28	E	1536	0	1617	18	0
29	F	1173	0	1020	30	0
30	G	1305	0	1347	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	I	636	0	321	5	0
32	H	673	0	350	8	0
33	L	1112	0	1142	7	0
34	M	893	0	919	3	0
35	N	1071	0	1084	16	0
36	O	1062	0	1121	6	0
37	P	982	0	1043	16	0
38	Q	884	0	880	18	0
39	R	885	0	933	10	0
40	S	949	0	1018	16	0
41	T	774	0	812	6	0
42	U	850	0	901	11	0
43	V	726	0	743	5	0
44	W	760	0	818	14	0
45	Y	567	0	559	6	0
46	Z	444	0	465	3	0
47	1	477	0	492	7	0
48	2	433	0	479	5	0
49	3	523	0	454	18	0
50	4	417	0	412	16	0
51	5	394	0	403	4	0
52	6	365	0	417	3	0
53	7	520	0	571	8	0
54	8	280	0	301	5	0
55	A	249	0	0	0	0
55	B	5	0	0	0	0
55	C	1	0	0	0	0
55	D	2	0	0	0	0
55	M	1	0	0	0	0
55	N	1	0	0	0	0
55	S	1	0	0	0	0
55	W	1	0	0	0	0
55	a	151	0	0	0	0
55	b	1	0	0	0	0
55	c	1	0	0	0	0
55	g	1	0	0	0	0
55	i	2	0	0	0	0
55	m	1	0	0	0	0
55	n	2	0	0	0	0
55	o	1	0	0	0	0
55	v	2	0	0	0	0
56	4	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	5	1	0	0	0	0
56	8	1	0	0	0	0
56	n	1	0	0	0	0
57	v	32	0	14	3	0
58	2	1	0	0	1	0
58	A	235	0	0	4	0
58	B	6	0	0	0	0
58	C	2	0	0	0	0
58	D	1	0	0	0	0
58	N	5	0	0	0	0
58	O	1	0	0	0	0
58	P	1	0	0	0	0
58	S	2	0	0	1	0
58	T	1	0	0	0	0
58	U	2	0	0	1	0
58	V	1	0	0	0	0
58	Z	2	0	0	0	0
58	a	94	0	0	1	0
58	d	1	0	0	0	0
58	e	1	0	0	0	0
58	f	1	0	0	0	0
58	i	1	0	0	0	0
58	p	3	0	0	1	0
58	t	1	0	0	0	0
58	v	2	0	0	1	0
All	All	142031	0	89780	1545	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 7.

The worst 5 of 1545 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)
24:A:419:U:HO2'	24:A:420:A:H8	1.00	0.97
1:a:68:G:H1	1:a:99:A:N6	1.62	0.96
1:a:693:G:H21	1:a:714:A:H61	1.14	0.95
1:a:1270:G:H1	1:a:1279:U:H3	1.11	0.94
1:a:1173:U:H3	1:a:1178:G:H1	1.09	0.94

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	207/249 (83%)	180 (87%)	26 (13%)	1 (0%)	24	57
3	c	202/218 (93%)	176 (87%)	26 (13%)	0	100	100
4	d	197/200 (98%)	181 (92%)	16 (8%)	0	100	100
5	e	150/167 (90%)	137 (91%)	13 (9%)	0	100	100
6	f	93/97 (96%)	72 (77%)	20 (22%)	1 (1%)	11	39
7	g	128/156 (82%)	118 (92%)	10 (8%)	0	100	100
8	h	129/132 (98%)	115 (89%)	14 (11%)	0	100	100
9	i	125/130 (96%)	105 (84%)	20 (16%)	0	100	100
10	j	94/102 (92%)	71 (76%)	22 (23%)	1 (1%)	11	39
11	k	112/129 (87%)	100 (89%)	12 (11%)	0	100	100
12	l	133/137 (97%)	120 (90%)	13 (10%)	0	100	100
13	m	106/121 (88%)	92 (87%)	14 (13%)	0	100	100
14	n	48/61 (79%)	33 (69%)	15 (31%)	0	100	100
15	o	85/89 (96%)	78 (92%)	7 (8%)	0	100	100
16	p	86/90 (96%)	74 (86%)	11 (13%)	1 (1%)	10	37
17	q	78/87 (90%)	71 (91%)	7 (9%)	0	100	100
18	r	62/79 (78%)	56 (90%)	6 (10%)	0	100	100
19	s	72/92 (78%)	65 (90%)	7 (10%)	0	100	100
20	t	79/84 (94%)	77 (98%)	2 (2%)	0	100	100
23	v	415/418 (99%)	382 (92%)	33 (8%)	0	100	100
26	C	272/277 (98%)	261 (96%)	10 (4%)	1 (0%)	30	61
27	D	204/209 (98%)	194 (95%)	10 (5%)	0	100	100
28	E	203/207 (98%)	189 (93%)	14 (7%)	0	100	100
29	F	173/179 (97%)	161 (93%)	12 (7%)	0	100	100
30	G	169/178 (95%)	156 (92%)	13 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	I	127/166 (76%)	122 (96%)	5 (4%)	0	100	100
32	H	133/141 (94%)	122 (92%)	9 (7%)	2 (2%)	8	32
33	L	141/145 (97%)	135 (96%)	6 (4%)	0	100	100
34	M	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
35	N	144/146 (99%)	133 (92%)	11 (8%)	0	100	100
36	O	133/144 (92%)	129 (97%)	4 (3%)	0	100	100
37	P	118/135 (87%)	113 (96%)	5 (4%)	0	100	100
38	Q	117/119 (98%)	107 (92%)	10 (8%)	0	100	100
39	R	111/114 (97%)	104 (94%)	7 (6%)	0	100	100
40	S	116/119 (98%)	113 (97%)	3 (3%)	0	100	100
41	T	99/102 (97%)	96 (97%)	3 (3%)	0	100	100
42	U	110/118 (93%)	107 (97%)	3 (3%)	0	100	100
43	V	90/94 (96%)	84 (93%)	5 (6%)	1 (1%)	11	39
44	W	100/103 (97%)	98 (98%)	2 (2%)	0	100	100
45	Y	74/96 (77%)	68 (92%)	6 (8%)	0	100	100
46	Z	57/62 (92%)	53 (93%)	4 (7%)	0	100	100
47	1	58/63 (92%)	56 (97%)	2 (3%)	0	100	100
48	2	54/59 (92%)	51 (94%)	3 (6%)	0	100	100
49	3	69/81 (85%)	61 (88%)	7 (10%)	1 (1%)	9	34
50	4	51/57 (90%)	44 (86%)	7 (14%)	0	100	100
51	5	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
52	6	41/44 (93%)	41 (100%)	0	0	100	100
53	7	62/66 (94%)	57 (92%)	5 (8%)	0	100	100
54	8	34/37 (92%)	32 (94%)	2 (6%)	0	100	100
All	All	5827/6270 (93%)	5350 (92%)	468 (8%)	9 (0%)	44	73

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	j	79	PRO
16	p	25	SER
32	H	92	PRO
49	3	56	PRO
2	b	129	LEU

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	
2	b	104/214 (49%)	104 (100%)	0	100	100
4	d	162/170 (95%)	162 (100%)	0	100	100
5	e	104/131 (79%)	104 (100%)	0	100	100
6	f	81/85 (95%)	81 (100%)	0	100	100
7	g	4/130 (3%)	4 (100%)	0	100	100
8	h	109/110 (99%)	109 (100%)	0	100	100
9	i	4/102 (4%)	4 (100%)	0	100	100
11	k	58/100 (58%)	58 (100%)	0	100	100
12	l	101/118 (86%)	101 (100%)	0	100	100
14	n	5/52 (10%)	5 (100%)	0	100	100
15	o	71/81 (88%)	71 (100%)	0	100	100
16	p	63/80 (79%)	63 (100%)	0	100	100
17	q	72/78 (92%)	72 (100%)	0	100	100
18	r	47/67 (70%)	47 (100%)	0	100	100
20	t	55/66 (83%)	55 (100%)	0	100	100
23	v	351/365 (96%)	351 (100%)	0	100	100
26	C	215/225 (96%)	215 (100%)	0	100	100
27	D	158/171 (92%)	158 (100%)	0	100	100
28	E	161/174 (92%)	161 (100%)	0	100	100
29	F	93/155 (60%)	93 (100%)	0	100	100
30	G	139/147 (95%)	139 (100%)	0	100	100
32	H	4/111 (4%)	4 (100%)	0	100	100
33	L	116/121 (96%)	116 (100%)	0	100	100
34	M	92/101 (91%)	92 (100%)	0	100	100
35	N	105/115 (91%)	105 (100%)	0	100	100
36	O	105/113 (93%)	105 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	P	102/111 (92%)	102 (100%)	0	100	100
38	Q	88/97 (91%)	88 (100%)	0	100	100
39	R	93/99 (94%)	93 (100%)	0	100	100
40	S	95/97 (98%)	95 (100%)	0	100	100
41	T	78/82 (95%)	78 (100%)	0	100	100
42	U	90/97 (93%)	90 (100%)	0	100	100
43	V	76/84 (90%)	76 (100%)	0	100	100
44	W	83/88 (94%)	83 (100%)	0	100	100
45	Y	57/76 (75%)	57 (100%)	0	100	100
46	Z	45/53 (85%)	45 (100%)	0	100	100
47	1	48/55 (87%)	48 (100%)	0	100	100
48	2	50/52 (96%)	50 (100%)	0	100	100
49	3	48/73 (66%)	48 (100%)	0	100	100
50	4	44/50 (88%)	44 (100%)	0	100	100
51	5	44/48 (92%)	44 (100%)	0	100	100
52	6	39/39 (100%)	39 (100%)	0	100	100
53	7	54/56 (96%)	54 (100%)	0	100	100
54	8	32/35 (91%)	32 (100%)	0	100	100
All	All	3745/4674 (80%)	3745 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
27	D	152	ASN
53	7	35	ASN
30	G	147	ASN
51	5	26	ASN
45	Y	48	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1512/1550 (97%)	340 (22%)	0
21	x	72/76 (94%)	18 (25%)	0
22	w	8/21 (38%)	6 (75%)	0
24	A	2897/2932 (98%)	457 (15%)	29 (1%)
25	B	113/116 (97%)	12 (10%)	0
All	All	4602/4695 (98%)	833 (18%)	29 (0%)

5 of 833 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	9	G
1	a	17	U
1	a	22	G
1	a	31	G
1	a	32	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	A	1468	G
24	A	2809	A
24	A	1530	G
24	A	2438	G
24	A	1528	G

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

7 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
21	G7M	x	46	21	23,26,27	2.38	5 (21%)	34,39,42	3.07	11 (32%)
21	5MU	x	54	21	19,22,23	1.36	5 (26%)	27,32,35	2.13	6 (22%)
21	MIA	x	37	21	28,31,32	2.29	6 (21%)	38,44,47	2.79	14 (36%)
21	PSU	x	55	21	18,21,22	1.36	2 (11%)	21,30,33	2.02	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	PSU	x	39	21	18,21,22	1.30	2 (11%)	21,30,33	2.13	4 (19%)
21	4SU	x	8	21	18,21,22	1.87	5 (27%)	25,30,33	2.45	6 (24%)
21	PSU	x	32	21	18,21,22	1.36	2 (11%)	21,30,33	2.03	3 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	G7M	x	46	21	-	4/7/25/26	0/3/3/3
21	5MU	x	54	21	-	0/7/25/26	0/2/2/2
21	MIA	x	37	21	-	1/15/33/34	0/3/3/3
21	PSU	x	55	21	-	0/7/25/26	0/2/2/2
21	PSU	x	39	21	-	0/7/25/26	0/2/2/2
21	4SU	x	8	21	-	2/7/25/26	0/2/2/2
21	PSU	x	32	21	-	0/7/25/26	0/2/2/2

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	x	46	G7M	C8-N7	7.49	1.45	1.33
21	x	37	MIA	C13-C14	6.81	1.52	1.32
21	x	37	MIA	C2-S10	-6.66	1.70	1.75
21	x	8	4SU	C4-S4	-5.03	1.59	1.68
21	x	46	G7M	C5-N7	-4.81	1.33	1.39

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	x	37	MIA	C12-C13-C14	-9.03	110.80	127.01
21	x	46	G7M	CN7-N7-C8	-8.14	112.46	124.79
21	x	37	MIA	C5-C4-N3	-8.05	118.70	127.18
21	x	8	4SU	C4-N3-C2	-7.15	120.46	127.31
21	x	46	G7M	N9-C4-N3	6.76	139.48	125.95

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
21	x	37	MIA	C12-C13-C14-C16
21	x	46	G7M	O4'-C4'-C5'-O5'
21	x	8	4SU	O4'-C4'-C5'-O5'
21	x	46	G7M	C3'-C4'-C5'-O5'
21	x	8	4SU	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	x	46	G7M	2	0
21	x	37	MIA	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 428 ligands modelled in this entry, 427 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	GCP	v	503	55	32,34,34	1.40	7 (21%)	49,54,54	1.77	8 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	GCP	v	503	55	-	5/19/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	v	503	GCP	C5-C4	2.90	1.46	1.38
57	v	503	GCP	PG-O3G	2.75	1.61	1.55
57	v	503	GCP	PG-O2G	2.70	1.61	1.55
57	v	503	GCP	C6-N1	-2.46	1.34	1.38
57	v	503	GCP	C5-N7	-2.36	1.34	1.39

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	v	503	GCP	C5-C4-N3	-5.96	118.91	128.39
57	v	503	GCP	C2-N3-C4	4.97	120.86	112.30
57	v	503	GCP	N9-C4-N3	4.45	134.85	125.95
57	v	503	GCP	C6-C5-N7	3.12	135.96	130.29
57	v	503	GCP	PB-O3A-PA	-2.87	122.99	132.37

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	v	503	GCP	C5'-O5'-PA-O3A
57	v	503	GCP	C5'-O5'-PA-O1A
57	v	503	GCP	O4'-C4'-C5'-O5'
57	v	503	GCP	C3'-C4'-C5'-O5'
57	v	503	GCP	C5'-O5'-PA-O2A

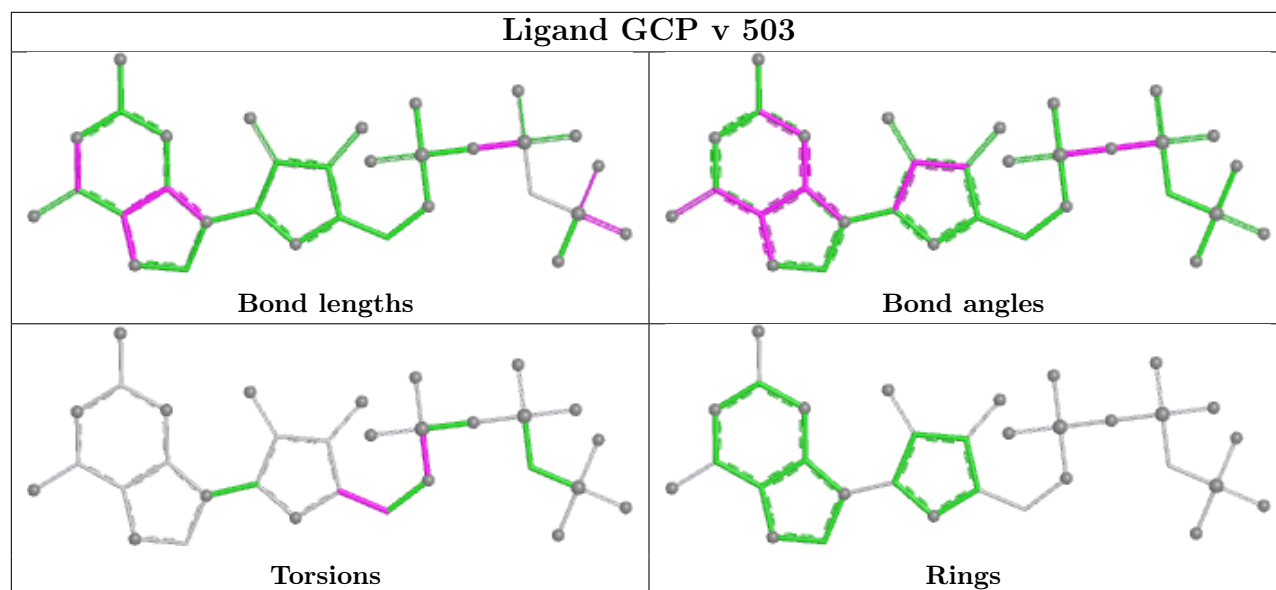
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	v	503	GCP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.



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.

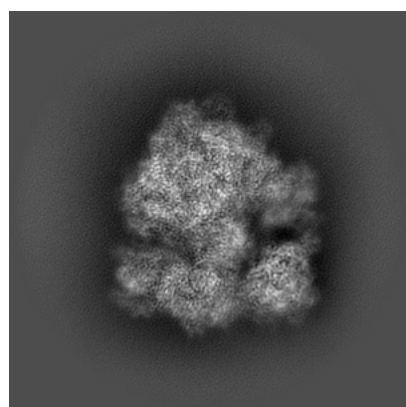
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42571. These allow visual inspection of the internal detail of the map and identification of artifacts.

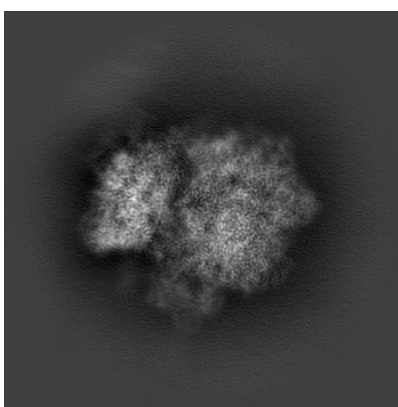
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

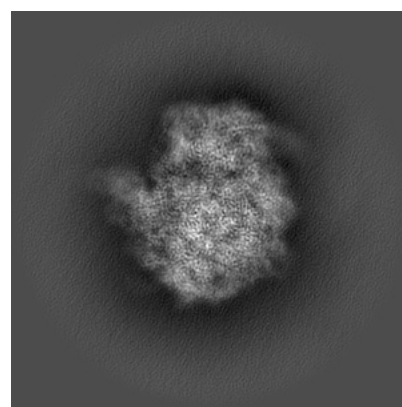
6.1.1 Primary map



X



Y

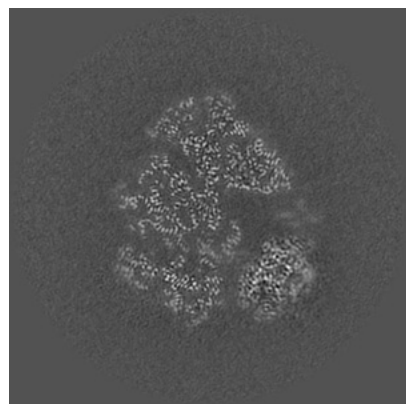


Z

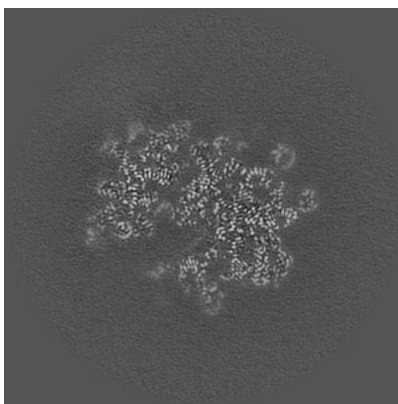
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

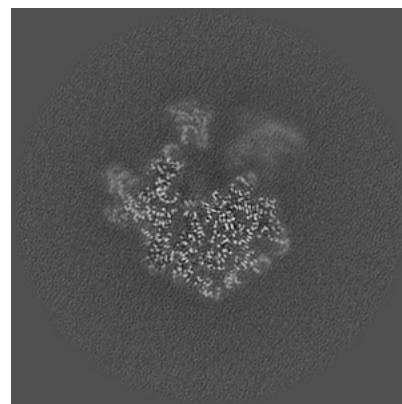
6.2.1 Primary map



X Index: 256



Y Index: 256

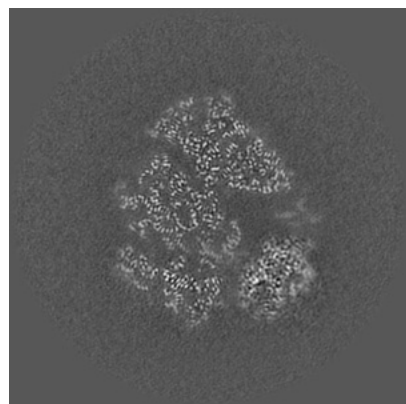


Z Index: 256

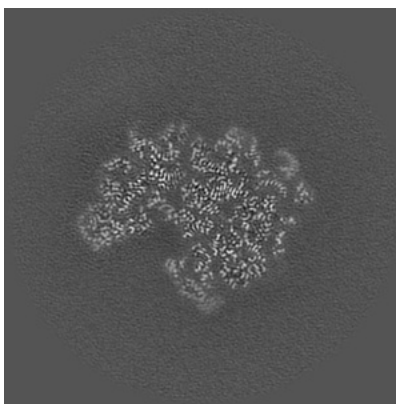
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

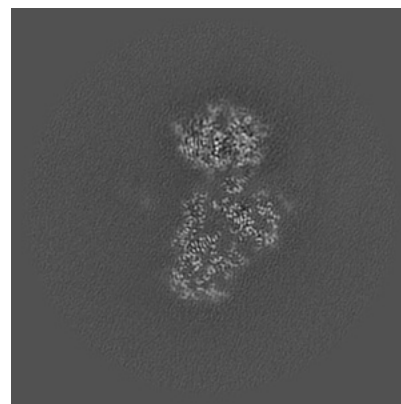
6.3.1 Primary map



X Index: 255



Y Index: 244

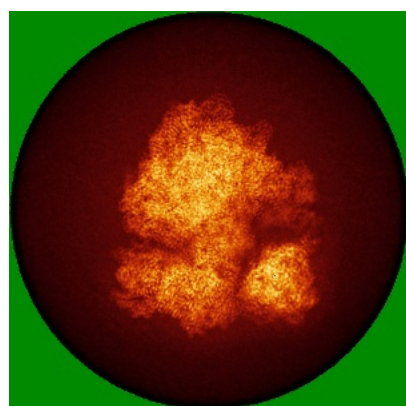


Z Index: 178

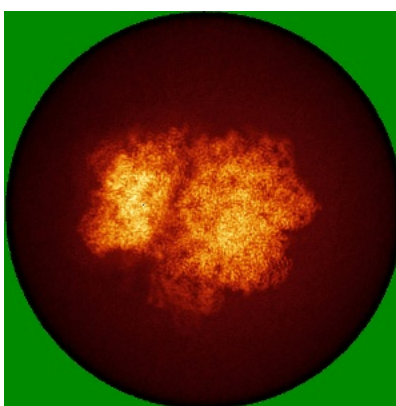
The images above show the largest variance slices of the map in three orthogonal directions.

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

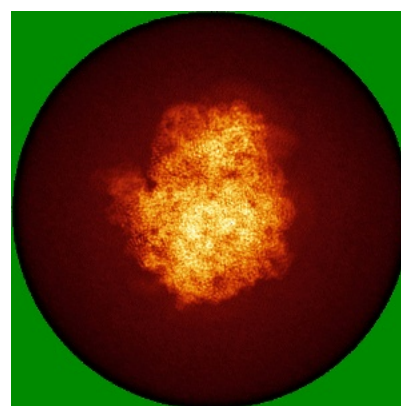
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

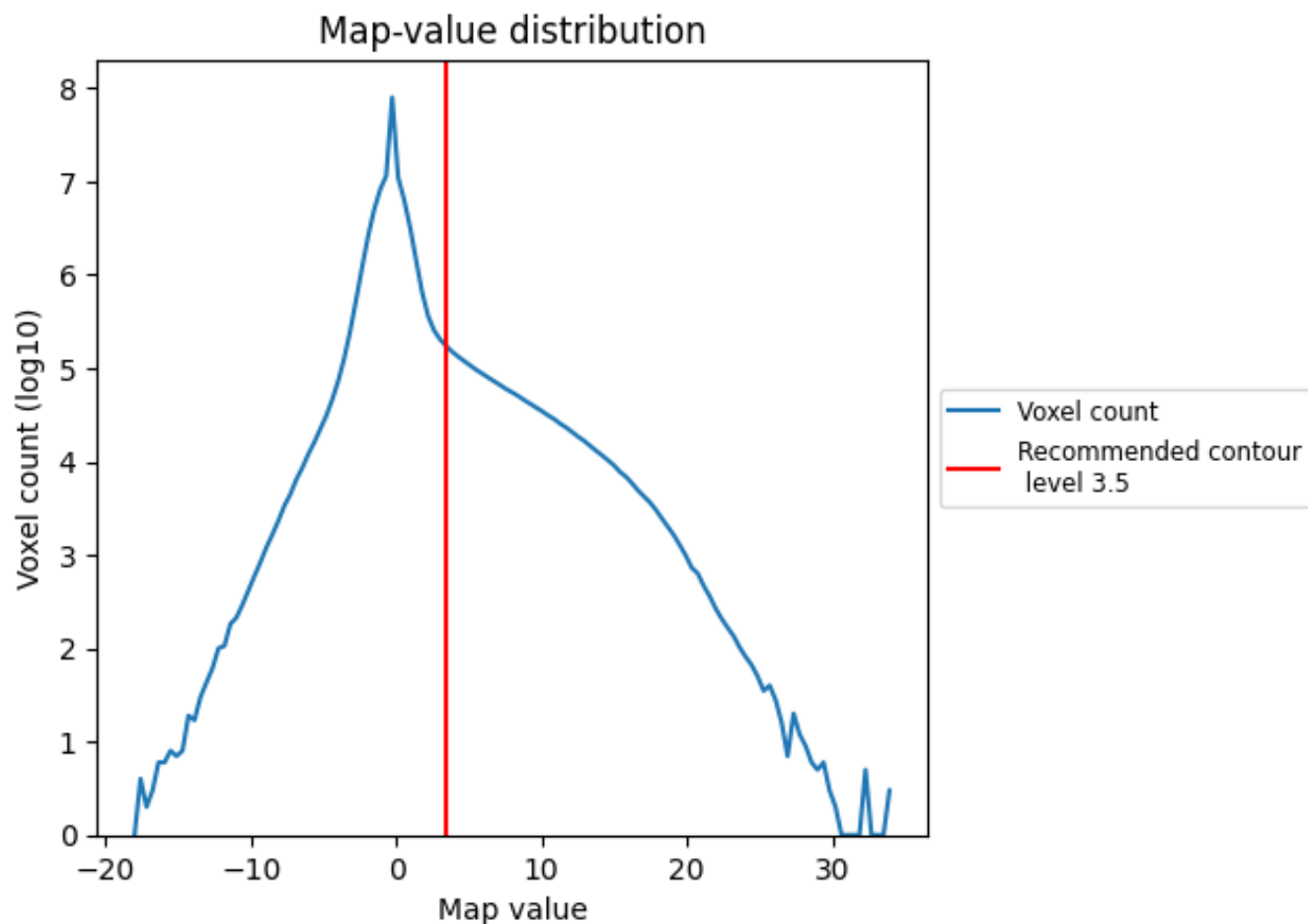
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

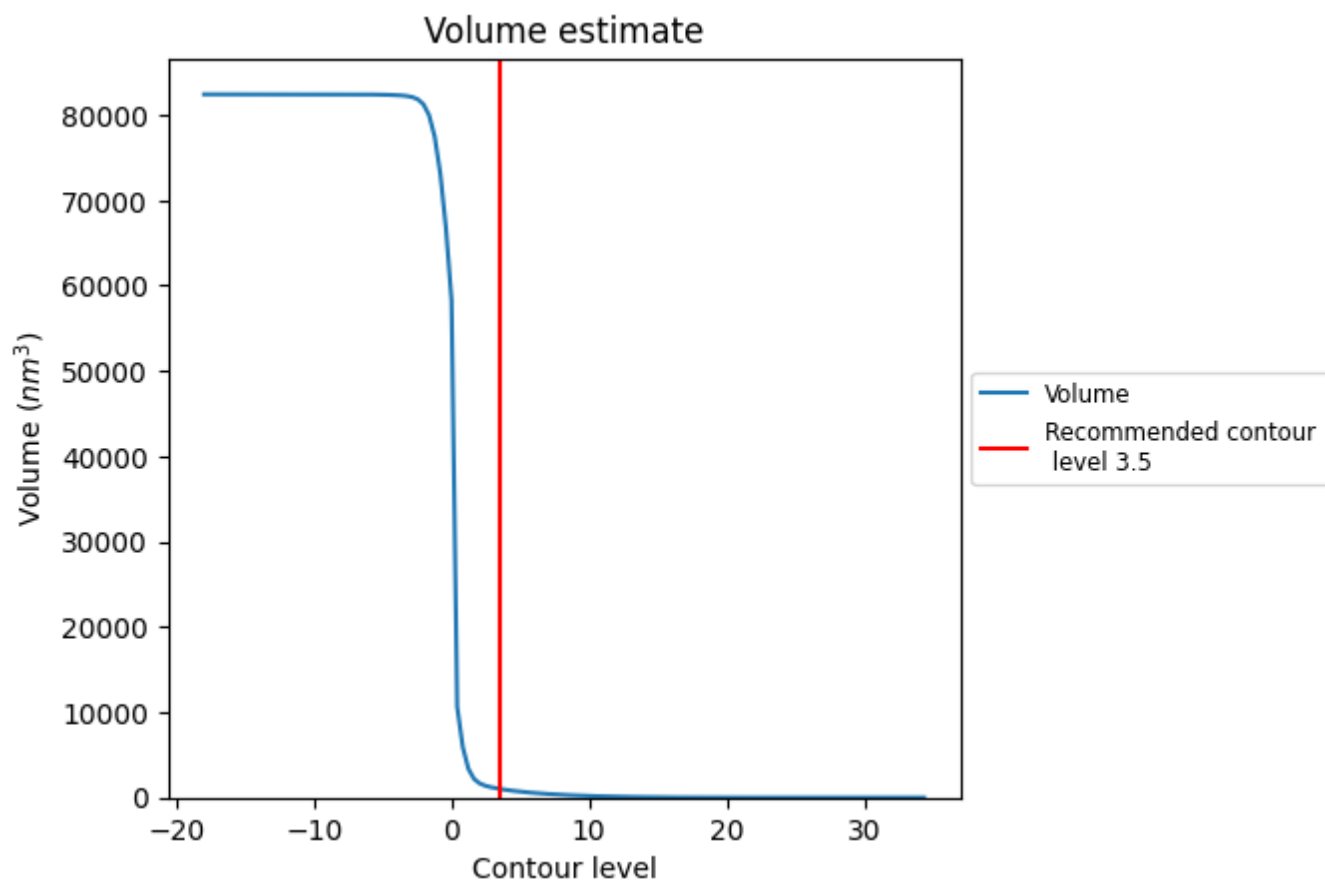
This section contains the results of statistical analysis of the map.

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.

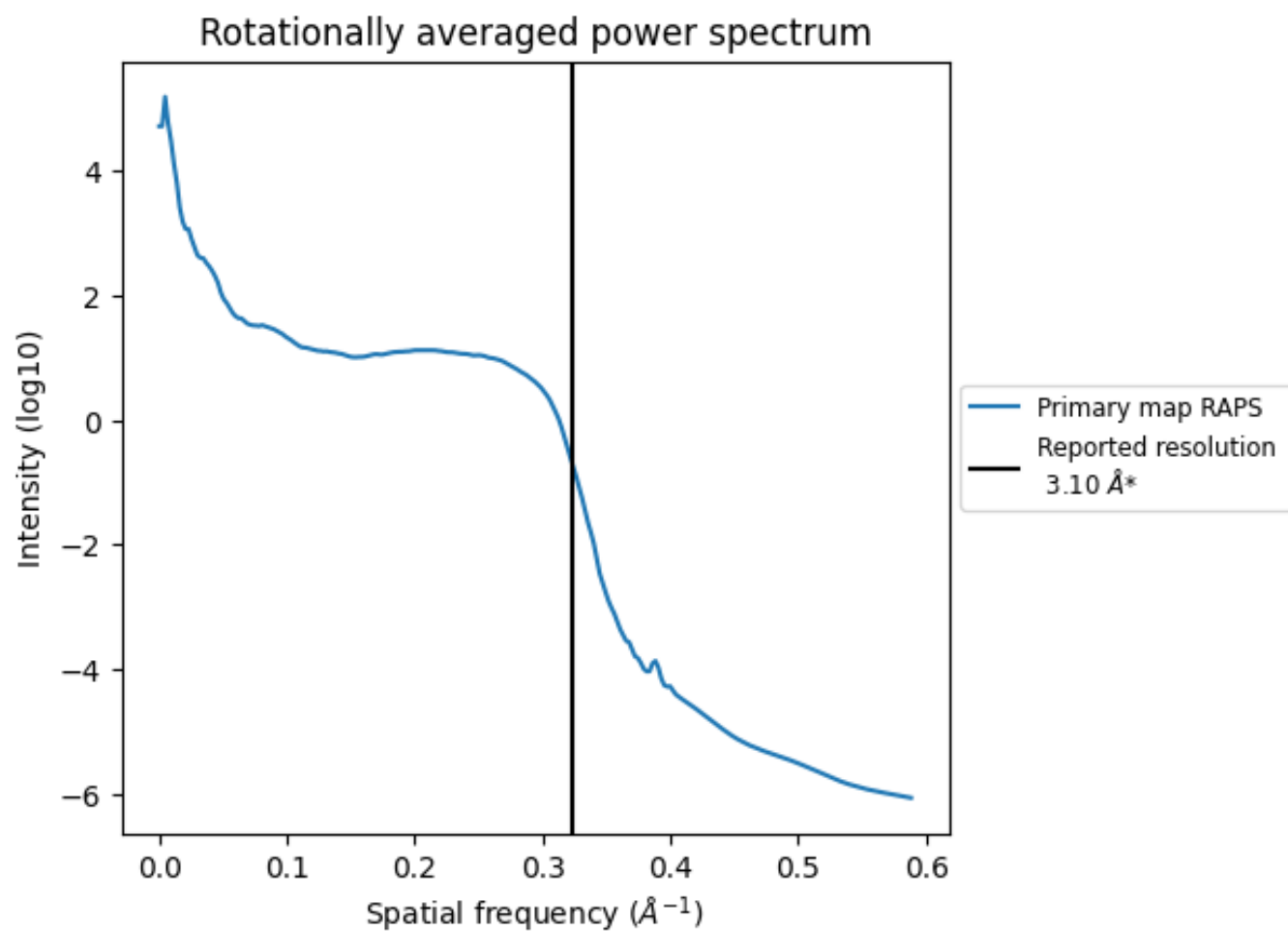
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1018 nm³; this corresponds to an approximate mass of 919 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

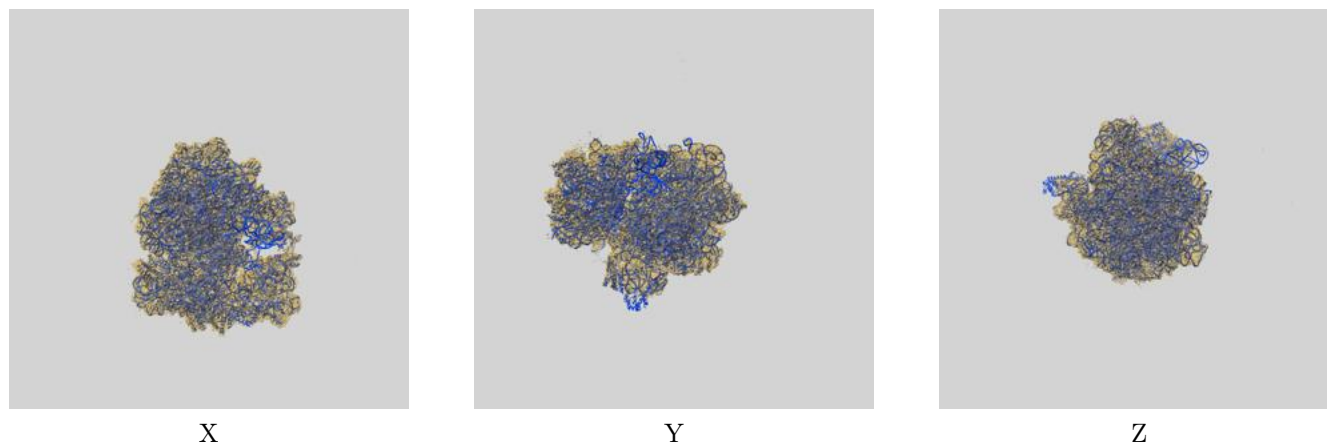
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

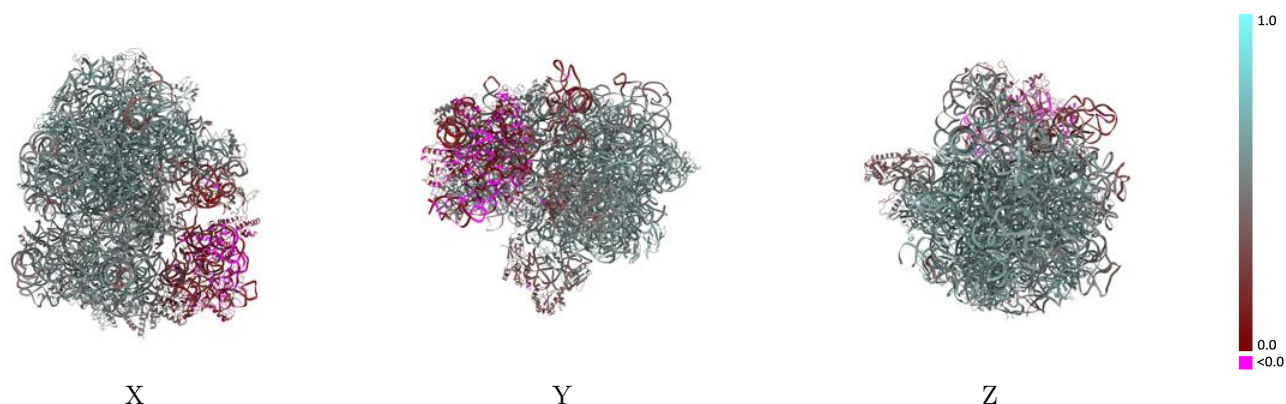
This section contains information regarding the fit between EMDB map EMD-42571 and PDB model 8UU8. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

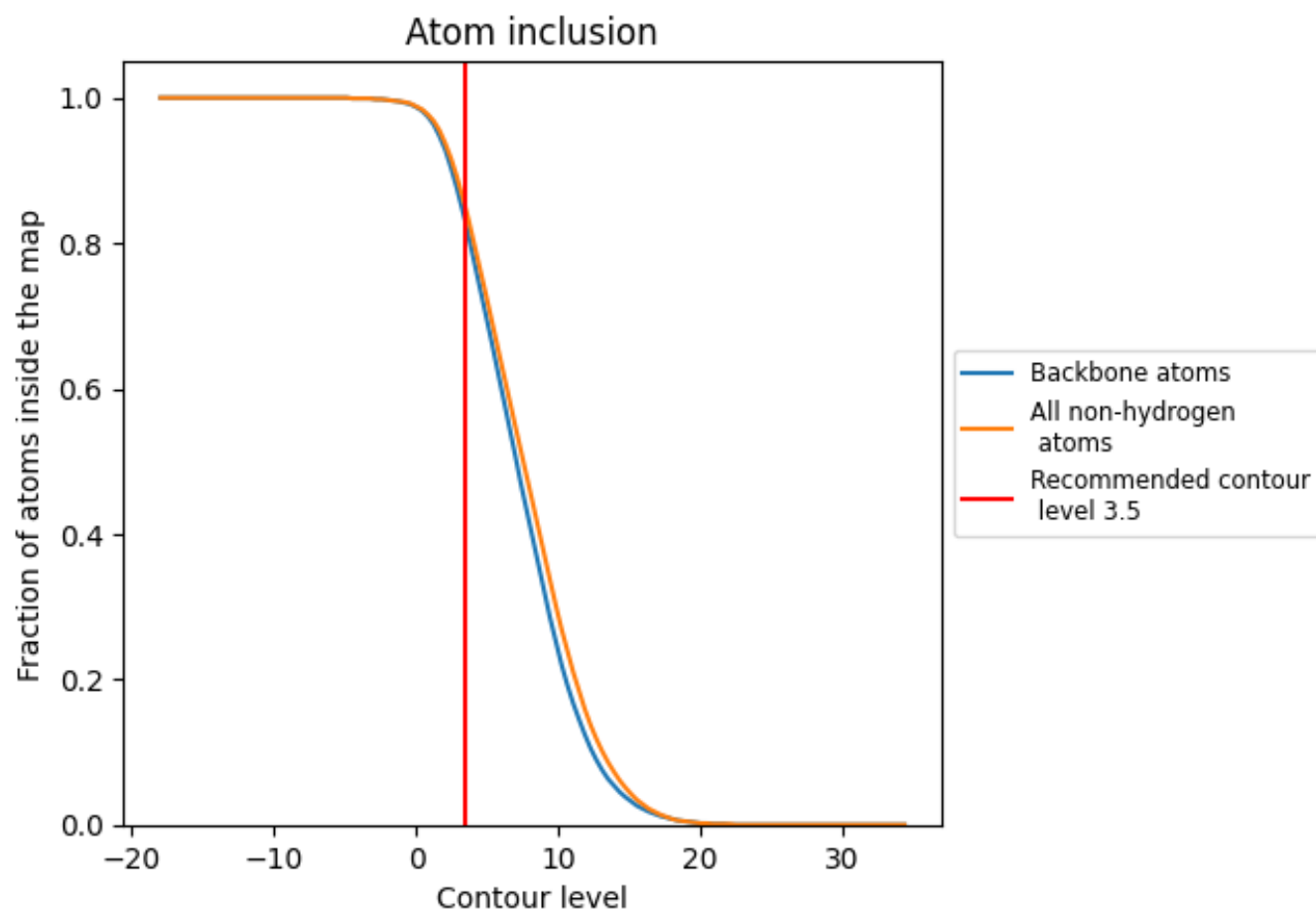


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.4960
1	 0.8590	 0.5500
2	 0.8820	 0.5800
3	 0.3020	 0.2860
4	 0.8910	 0.5710
5	 0.8390	 0.5660
6	 0.9360	 0.6050
7	 0.9240	 0.6010
8	 0.8910	 0.5920
A	 0.9200	 0.5500
B	 0.9080	 0.4850
C	 0.8710	 0.5900
D	 0.8960	 0.5870
E	 0.8740	 0.5700
F	 0.5140	 0.4000
G	 0.6820	 0.4780
H	 0.3860	 0.3430
I	 0.1510	 0.3370
L	 0.9260	 0.5950
M	 0.8450	 0.5760
N	 0.8600	 0.5600
O	 0.8680	 0.5810
P	 0.8770	 0.5780
Q	 0.7450	 0.5010
R	 0.8400	 0.5760
S	 0.9230	 0.5940
T	 0.9200	 0.5940
U	 0.8840	 0.5870
V	 0.8720	 0.5720
W	 0.7820	 0.5250
Y	 0.9120	 0.5890
Z	 0.8730	 0.5650
a	 0.8410	 0.4110
b	 0.6710	 0.4360
c	 0.5490	 0.1920



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Chain	Atom inclusion	Q-score
d	 0.8700	 0.5170
e	 0.8670	 0.5350
f	 0.7060	 0.4520
g	 0.3860	 0.0340
h	 0.8590	 0.5290
i	 0.6450	 0.1130
j	 0.6020	 0.0820
k	 0.7420	 0.4800
l	 0.8530	 0.5560
m	 0.4170	 0.1220
n	 0.6900	 0.0940
o	 0.7910	 0.5200
p	 0.8960	 0.5470
q	 0.8040	 0.5060
r	 0.8750	 0.5140
s	 0.2050	 0.0830
t	 0.8370	 0.5190
v	 0.7140	 0.4890
w	 0.3630	 0.3800
x	 0.1390	 0.3140