



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:26 AM UTC

PDB ID : 8P8V / pdb_00008p8v
EMDB ID : EMD-17145
Title : Mycoplasma pneumoniae di-ribosome in chloramphenicol-treated cells (leading 70S)
Authors : Schacherl, M.; Xue, L.; Spahn, C.M.T.; Mahamid, J.
Deposited on : 2023-06-02
Resolution : 8.70 Å (reported)
Based on initial models : 7OOD, 7OOC

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:

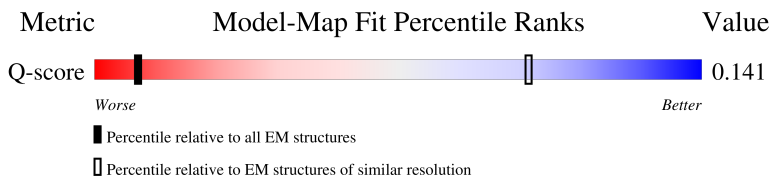
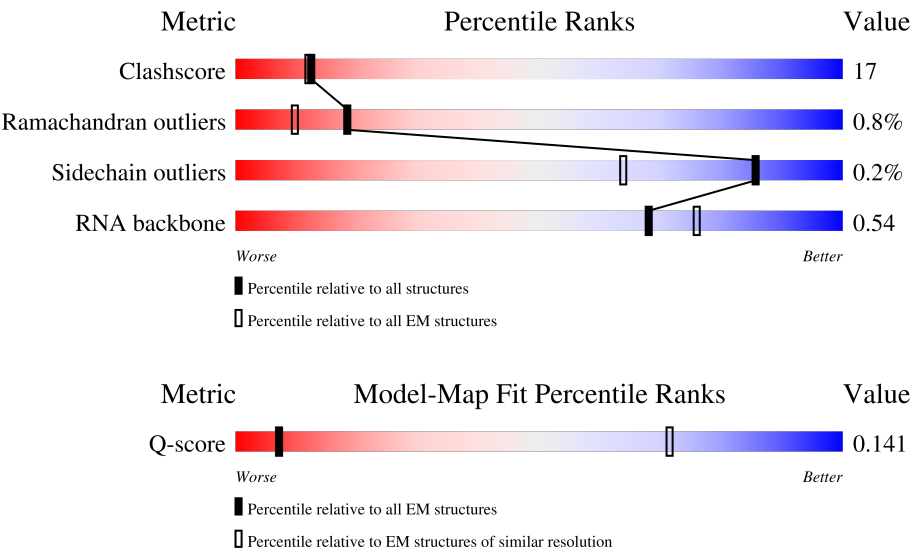
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 8.70 Å.

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



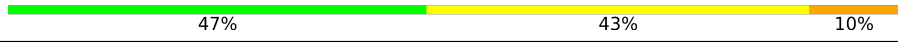
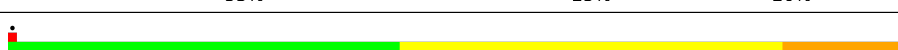
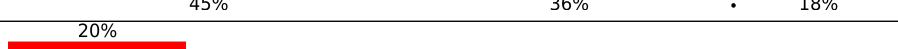
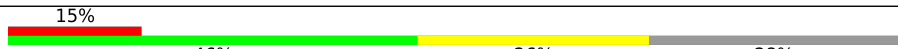
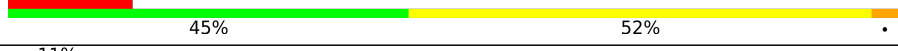
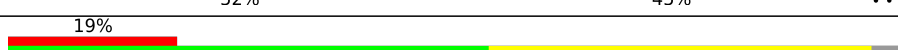
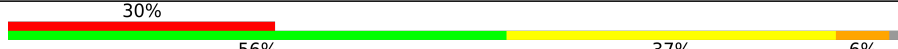
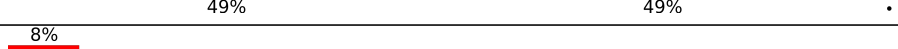
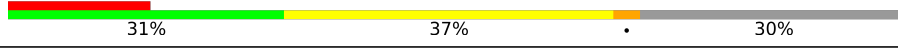
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	282 (8.20 - 9.20)

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

Mol	Chain	Length	Quality of chain
1	0	48	63% 35%
2	1	59	63% 37%
3	2	37	5% 65% 35%

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Mol	Chain	Length	Quality of chain
4	3	2907	
5	4	108	
6	5	1520	
7	6	76	
8	7	75	
9	8	76	
10	9	226	
11	A	294	
12	B	273	
13	C	205	
14	D	219	
15	E	215	
16	F	155	
17	G	142	
18	H	132	
19	I	108	
20	J	121	
21	K	139	
22	L	124	
23	M	61	
24	N	86	
25	O	94	
26	P	85	
27	Q	104	
28	R	87	

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Mol	Chain	Length	Quality of chain
29	S	87	
30	T	60	
31	X	444	
32	Y	40	
33	Z	36	
34	a	287	
35	b	287	
36	c	212	
37	d	180	
38	e	184	
39	f	149	
40	g	161	
41	h	137	
42	i	146	
43	j	122	
44	k	151	
45	l	139	
46	m	124	
47	n	116	
48	o	119	
49	p	127	
50	q	100	
51	r	159	
52	s	237	
53	t	111	

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Mol	Chain	Length	Quality of chain
54	u	104	12% 51% 34% 15%
55	v	65	12% 52% 46%
56	w	111	17% 56% 43%
57	x	97	38% 54% 38% 8%
58	y	57	9% 47% 49%
59	z	53	6% 62% 32% 6%

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 153622 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	2893	Total	C	N	O	P	0	0
			61995	27704	11293	20105	2893		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	108	Total	C	N	O	P	0	0
			2305	1030	415	752	108		

- Molecule 6 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	1506	Total	C	N	O	P	0	0
			32238	14411	5844	10477	1506		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	1003	A	G	conflict	GB 26117688

- Molecule 7 is a RNA chain called tRNA-Ala (E-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	76	Total	C	N	O	P	0	0
			1620	723	287	534	76		

- Molecule 8 is a RNA chain called tRNA-Asp (P-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	75	Total	C	N	O	P	0	0
			1599	712	279	533	75		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	17	G	-	insertion	GB 26117688
7	55	C	U	conflict	GB 26117688

- Molecule 9 is a RNA chain called tRNA-Lys (A-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	76	Total	C	N	O	P	0	0
			1615	722	284	533	76		

- Molecule 10 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	226	Total	C	N	O	S	0	0
			1711	1095	292	318	6		

- Molecule 11 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	268	Total	C	N	O	S	0	0
			2152	1368	379	396	9		

- Molecule 12 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	B	224	Total	C	N	O	S	0	0
			1764	1116	326	317	5		

- Molecule 13 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	C	204	Total	C	N	O	S	0	0
			1669	1057	316	292	4		

- Molecule 14 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D	158	Total	C	N	O	S	0	0
			1217	771	232	211	3		

- Molecule 15 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	215	Total	C	N	O	S	0	0
			1793	1111	341	339	2		

- Molecule 16 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	F	155	Total	C	N	O	S	0	0
			1254	790	240	217	7		

- Molecule 17 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	G	142	Total	C	N	O	S	0	0
			1118	728	194	193	3		

- Molecule 18 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	H	129	Total	C	N	O	S	0	0
			1040	661	195	183	1		

- Molecule 19 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	I	104	Total	C	N	O	S	0	0
			832	536	147	148	1		

- Molecule 20 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	J	120	Total	C	N	O	S	0	0
			878	547	163	162	6		

- Molecule 21 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	K	135	Total	C	N	O	S	0	0
			1071	677	212	180	2		

- Molecule 22 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L	121	Total	C	N	O		0	0
			975	609	197	169			

- Molecule 23 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 24 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	86	Total	C	N	O	S	0	0
			697	441	131	124	1		

- Molecule 25 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	O	87	Total	C	N	O	S	0	0
			705	453	130	118	4		

- Molecule 26 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P	85	Total	C	N	O	S	0	0
			693	436	138	118	1		

- Molecule 27 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Q	73	Total	C	N	O	S	0	0
			605	389	117	95	4		

- Molecule 28 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	86	Total	C	N	O	S	0	0
			700	444	132	122	2		

- Molecule 29 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	S	79	Total	C	N	O		0	0
			643	391	138	114			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	59	Total	C	N	O	S	0	0
			519	326	111	80	2		

- Molecule 31 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	30	Total	C	N	O	S	0	0
			242	155	43	43	1		

- Molecule 32 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	40	Total	C	N	O	P	0	0
			862	388	170	264	40		

- Molecule 33 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Z	36	Total	C	N	O	0	0
			187	112	37	38		

- Molecule 34 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 35 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 36 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	211	Total	C	N	O	S	0	0
			1654	1053	299	299	3		

- Molecule 37 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	179	Total	C	N	O	S	0	0
			1416	910	251	251	4		

- Molecule 38 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	e	176	Total	C	N	O	0	0
			1396	899	247	250		

- Molecule 39 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	149	Total	C	N	O	S	0	0
			1210	780	212	215	3		

- Molecule 40 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g	125	Total	C	N	O	S	0	0
			951	606	165	177	3		

- Molecule 41 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 42 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 43 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 44 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	150	Total	C	N	O	S	0	0
			1170	741	228	200	1		

- Molecule 45 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 46 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 47 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	116	Total	C	N	O	S	0	0
			918	573	181	162	2		

- Molecule 48 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	118	Total	C	N	O	S	0	0
			966	609	186	170	1		

- Molecule 49 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p	118	Total	C	N	O	S	0	0
			981	624	194	161	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 51 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	142	Total	C	N	O	S	0	0
			1091	677	212	195	7		

- Molecule 52 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	95	Total	C	N	O	S	0	0
			740	486	125	128	1		

- Molecule 53 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	t	111	Total	C	N	O	S	0	0
			871	550	166	152	3		

- Molecule 54 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	88	Total	C	N	O	S	0	0
			670	416	132	121	1		

- Molecule 55 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v	64	Total	C	N	O	S	0	0
			520	320	109	90	1		

- Molecule 56 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	w	110	Total	C	N	O		0	0
			906	576	168	162			

- Molecule 57 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	89	Total	C	N	O	S	0	0
			708	449	124	131	4		

- Molecule 58 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 59 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

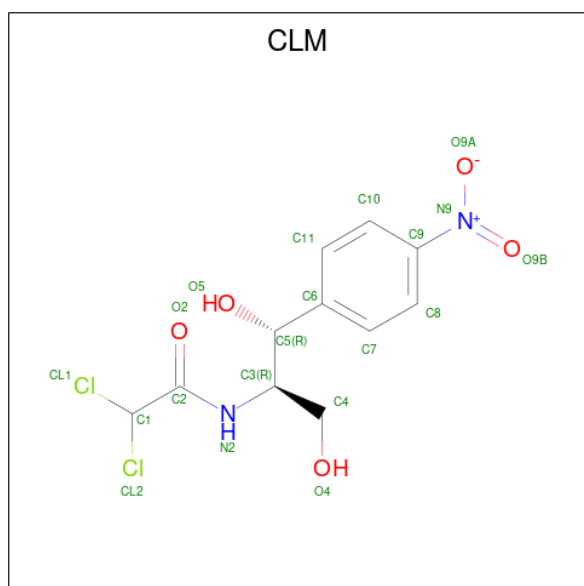
Mol	Chain	Residues	Atoms		AltConf
60	2	1	Total	Zn	0
			1	1	
60	M	1	Total	Zn	0
			1	1	
60	Q	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
60	x	1	Total	Zn	0
			1	1	
60	y	1	Total	Zn	0
			1	1	
60	z	1	Total	Zn	0
			1	1	

- Molecule 61 is CHLORAMPHENICOL (CCD ID: CLM) (formula: $C_{11}H_{12}Cl_2N_2O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
61	3	1	Total	C	Cl	N	O	0
			20	11	2	2	5	

- Molecule 62 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
62	3	1	Total	K	0
			1	1	

- Molecule 63 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

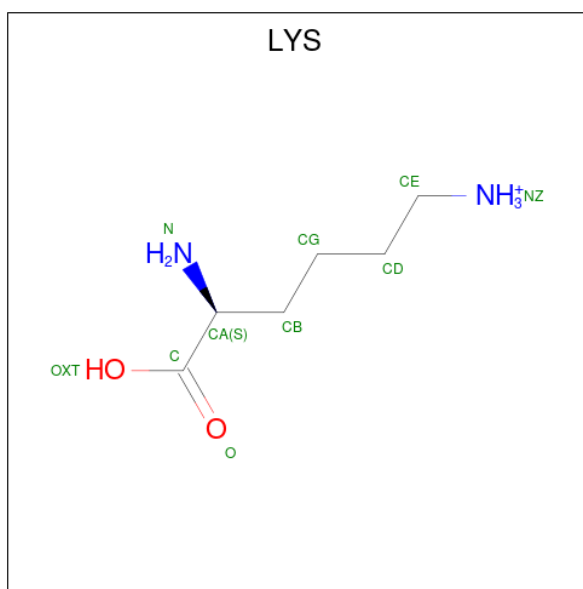
Mol	Chain	Residues	Atoms		AltConf
63	3	209	Total	Mg	0
			209	209	

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Mol	Chain	Residues	Atoms		AltConf
63	4	1	Total 1	Mg 1	0
63	5	87	Total 87	Mg 87	0
63	6	1	Total 1	Mg 1	0
63	8	1	Total 1	Mg 1	0
63	E	1	Total 1	Mg 1	0
63	K	1	Total 1	Mg 1	0
63	L	1	Total 1	Mg 1	0
63	P	1	Total 1	Mg 1	0
63	Y	2	Total 2	Mg 2	0
63	a	1	Total 1	Mg 1	0
63	b	1	Total 1	Mg 1	0
63	f	12	Total 12	Mg 12	0
63	i	1	Total 1	Mg 1	0
63	y	2	Total 2	Mg 2	0

- Molecule 64 is LYSINE (CCD ID: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
64	8	1	9	6	2	1	0

3 Residue-property plots [i](#)

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

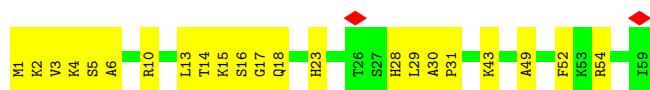
• Molecule 1: 50S ribosomal protein L34

Chain 0: 



• Molecule 2: 50S ribosomal protein L35

Chain 1: 



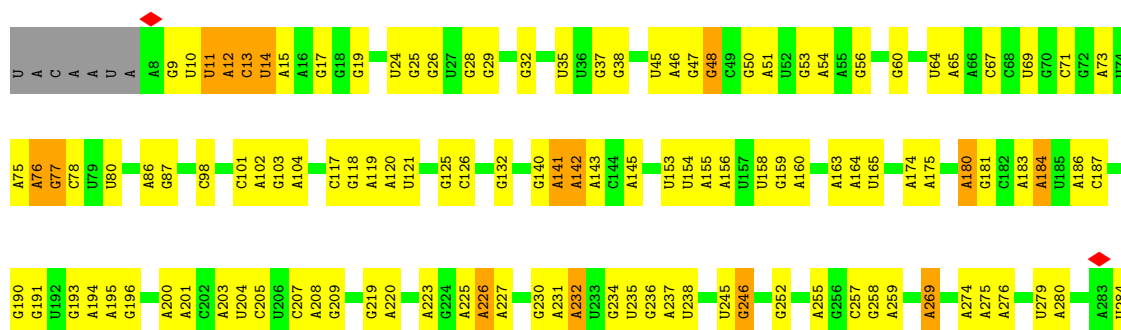
• Molecule 3: 50S ribosomal protein L36

Chain 2: 



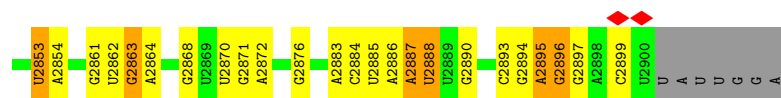
• Molecule 4: 23S ribosomal RNA

Chain 3: 

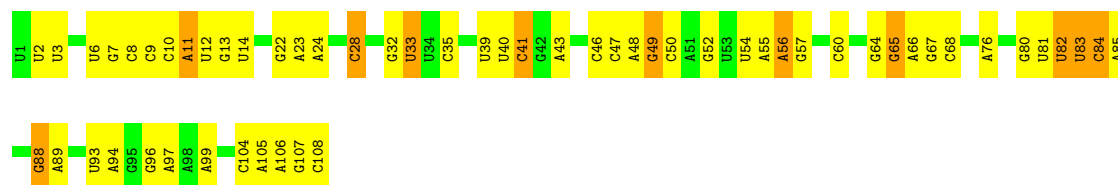




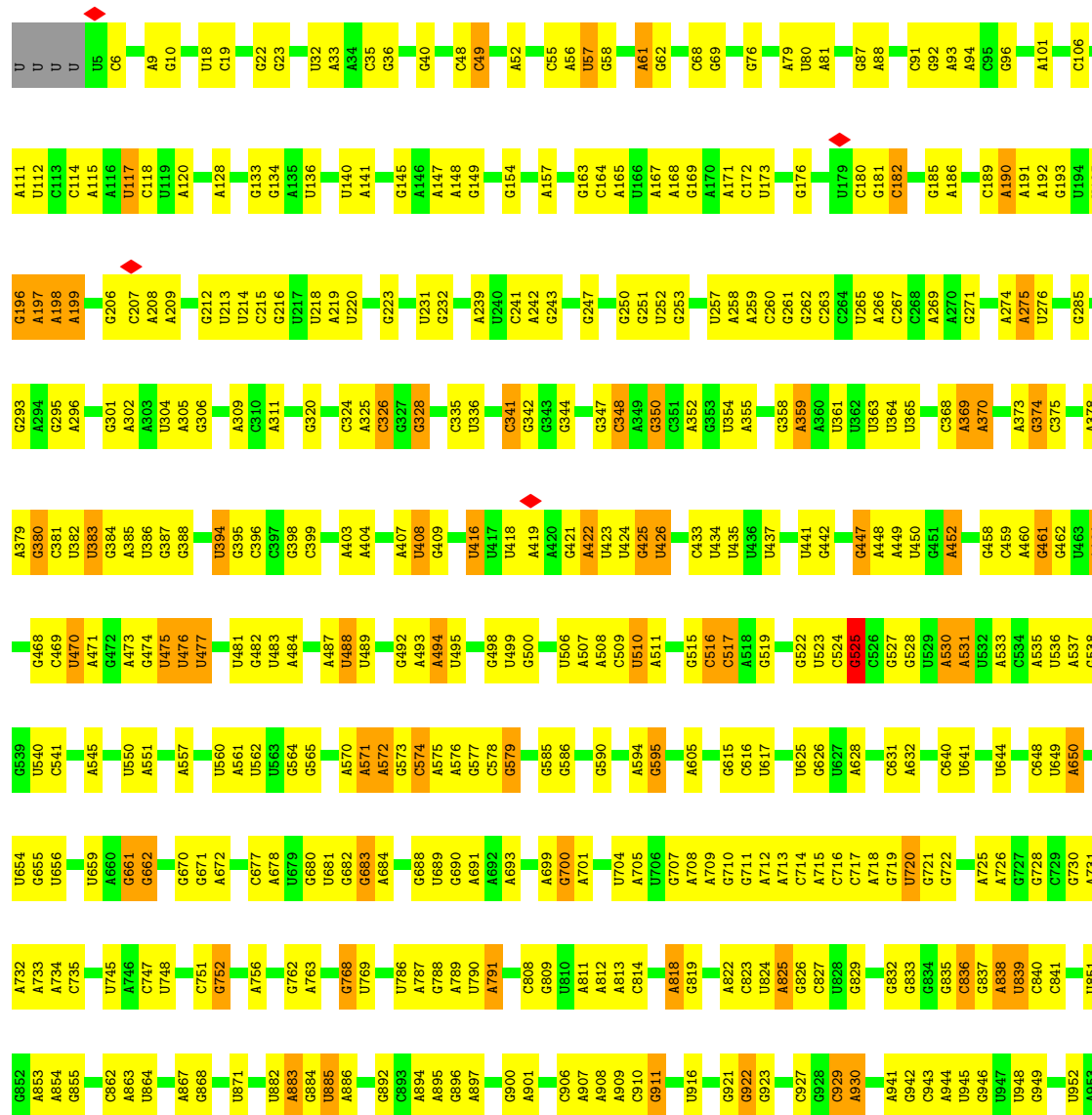
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A2773	C2666	G2581	U2482	C2305	A2220	U2153	A2089	A2012	G1909	C1802	C1697	C1599
C2779	A2668	G2582	C2483	G2308	U2221	A2154	U2092	G2019	C1910	A1804	A1698	A1600
C2780	G2669	U2485	A2484	U2308	C2223	C2222	U2093	C2024	G1913	U1805	G1701	A1601
U2781	G2670	G2486	A2485	A2309	A2224	A2156	A2094	C2025	G1913	G1806	A1702	G1602
A2782	G2671	U2487	U2487	C2310	G2225	A2157	A2095	A2026	G1913	C1807	A1703	A1603
G2785	C2675	C2393	C2488	G2311	U2226	C2158	U2098	G2027	A1920	C1808	G1708	A1604
A2786	U2587	A2394	G2489	G2312	U2227	U2159	U2099	G2028	A1926	A1809	C1709	A1606
U2787	U2588	G2397	A2490	U2313	U2228	U2160	U2099	U2029	G1926	A1810	A1710	
U2788	G2589	G2397	C2491	G2316	C2229	G2162	A2101	U2030	G1931	G1814	C1611	
U2793	U2592	G2398	G2492	A2319	A2233	U2163	A2102	A2031	C1932	U1815	A1715	
U2794	C2593	G2399	G2493	A2320	C2234	G2164	C2103	C2032	G1933	A1816	U1612	
C2795	C2594	U2401	C2402	C2321	A2235	A2165	A2104	G2033	A1934	A1817	A1613	
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A2798	C2604	G2404	G2503	U2324	U2238	C2169	G2107	G2036	G1937	A1822	U1618	
U2799	U2605	G2408	C2504	A2324	U2239	A2170	C2108	A2037	U1938	U1823	G1729	
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A2805	G2612	U2414	G2512	G2329	G2246	G2174	A2112	A2041	A1945	A1828	G1737	
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A2808	U2617	G2422	A2526	U2335	A2255	A2177	U2116	G2051	A1951	A1831	A1643	
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A2810	U2621	U2430	G2530	U2340	G2259	A2181	G2120	G2054	G1956	A1836	G1757	
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A2841	G2653	U2465	C2566	G2372	C2293	U2204	G2143	A2078	G1999	U1889	C1789	
G2842	U2654	G2474	C2567	G2373	A2294	U2205	C2144	G2079	U2000	U1890	A1791	
U2843	U2655	C2475	G2568	C2376	A2295	A2206	A2145	C2080	G2004	C1893	A1796	
A2844	G2656	A2476	A2572	A2377	G2297	A2207	U2148	U2082	U2009	G1894	A1797	
U2845	C2657	A2477	A2573	A2382	G2298	G2211	C2150	U2083	A2010	G1895	A1798	
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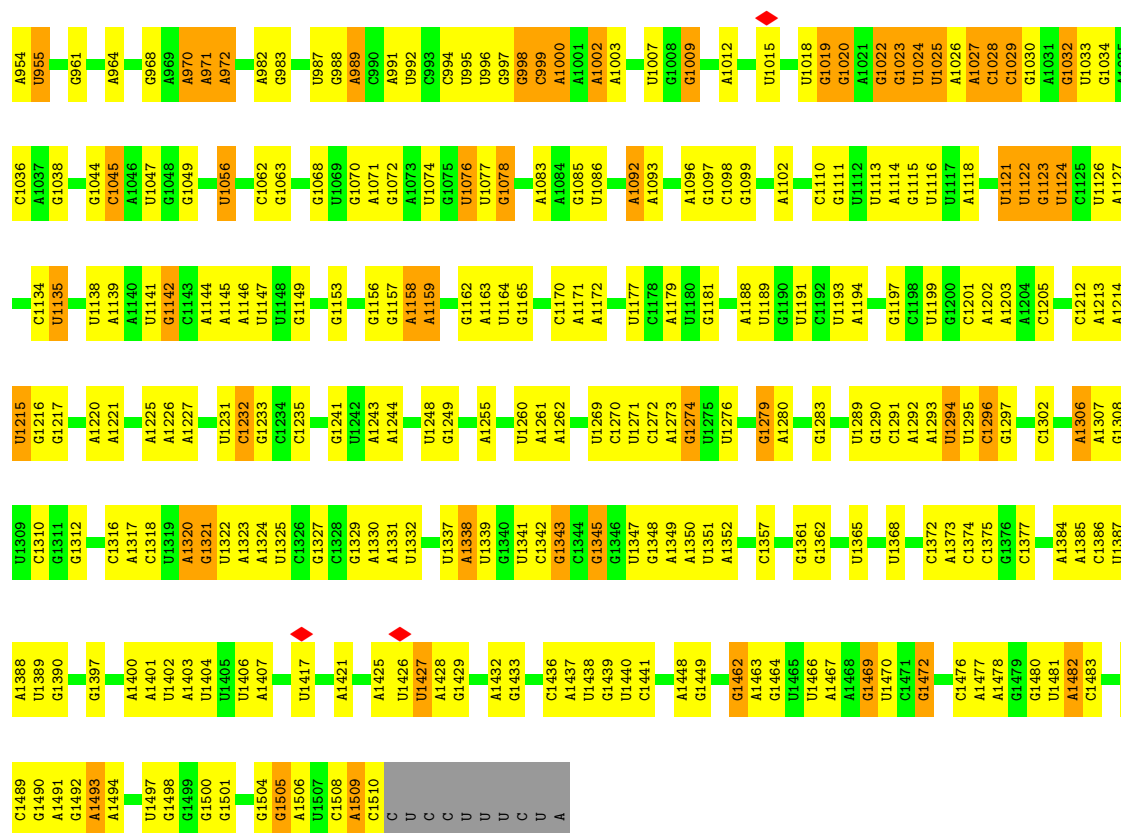


• Molecule 5: 5S ribosomal RNA



• Molecule 6: 16S ribosomal RNA





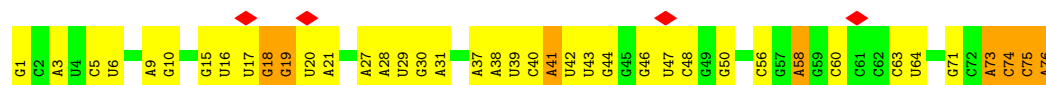
• Molecule 7: tRNA-Ala (E-site)



• Molecule 8: tRNA-Asp (P-site)

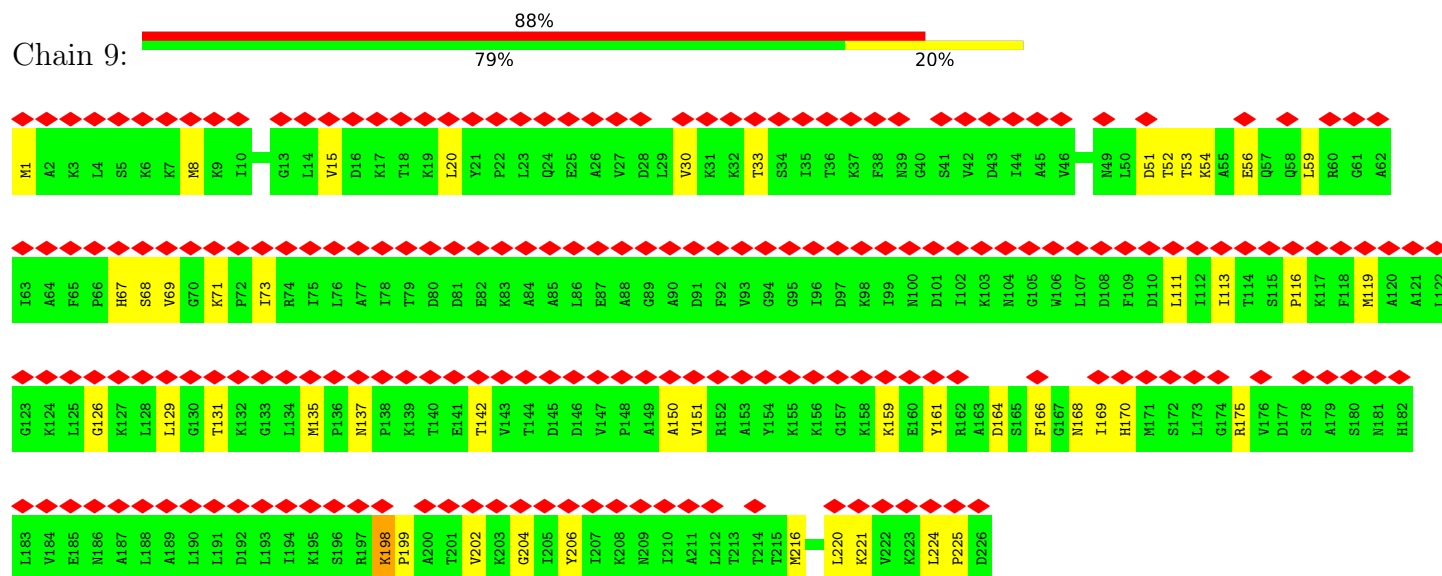


• Molecule 9: tRNA-Lys (A-site)



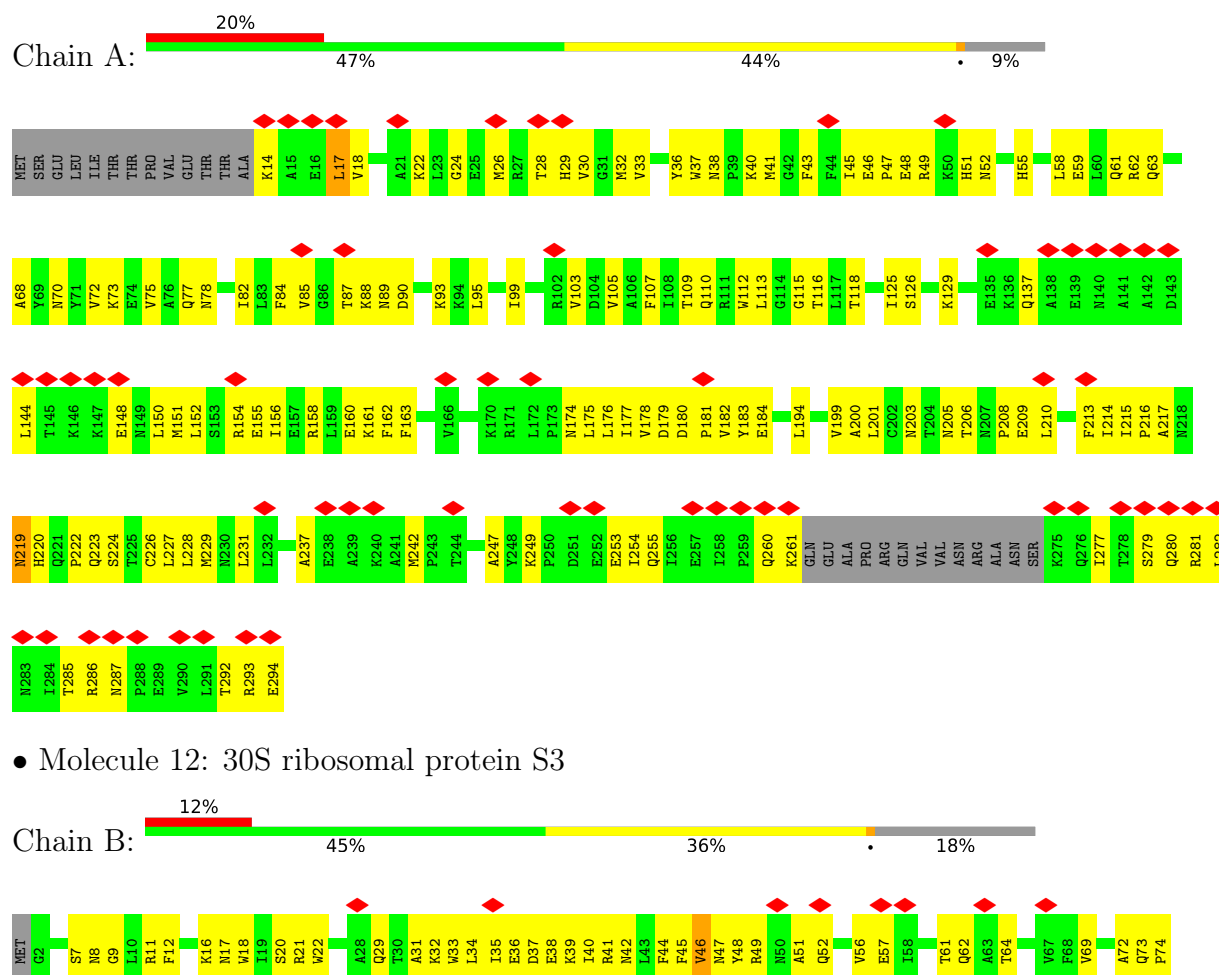
- Molecule 10: 50S ribosomal protein L1

Chain 9:



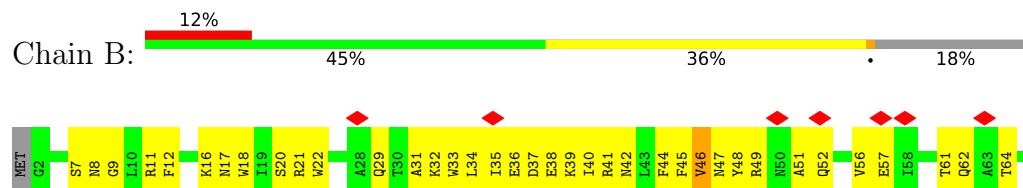
- Molecule 11: 30S ribosomal protein S2

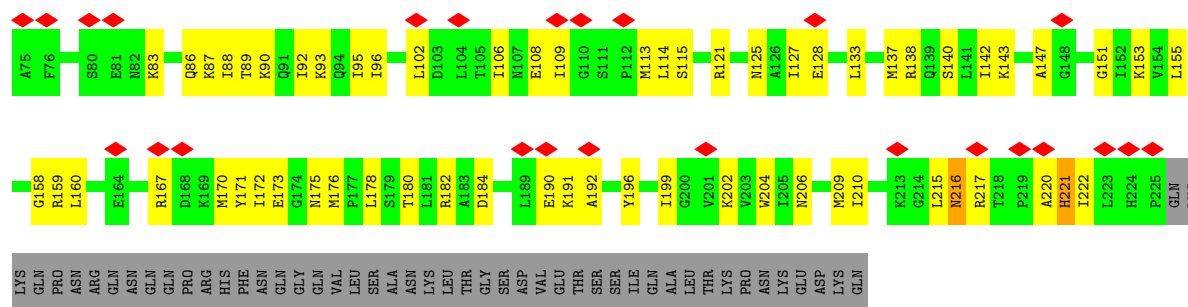
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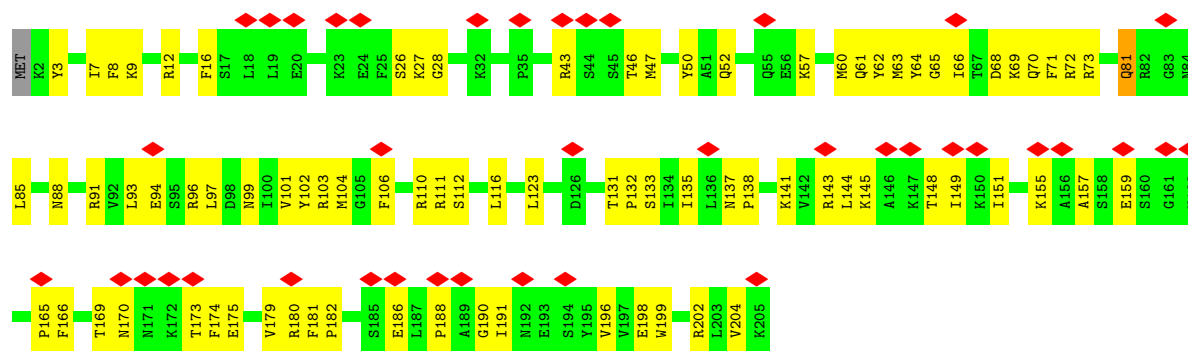
- Molecule 12: 30S ribosomal protein S3

Chain B:

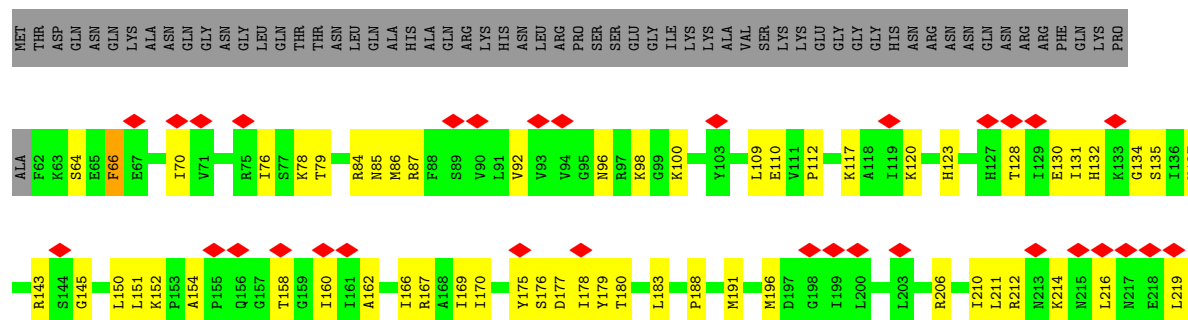




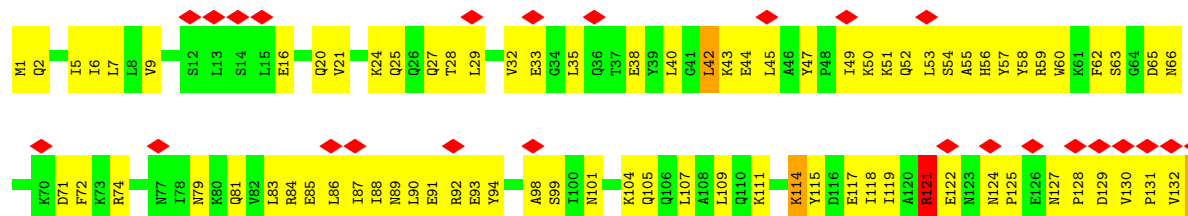
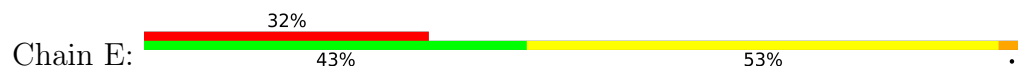
• Molecule 13: 30S ribosomal protein S4

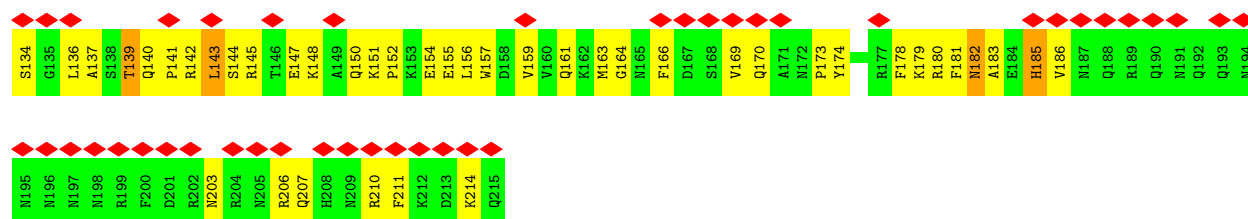


• Molecule 14: 30S ribosomal protein S5

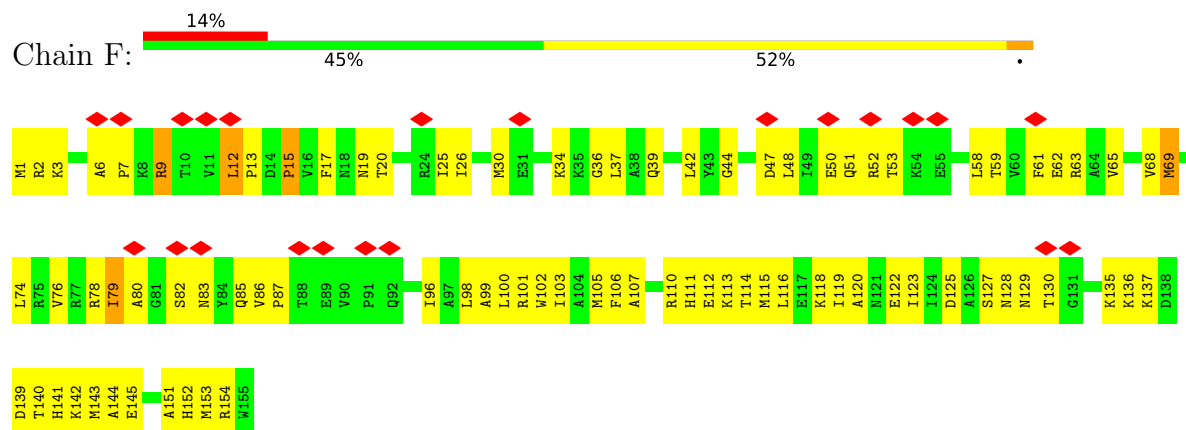


• Molecule 15: 30S ribosomal protein S6

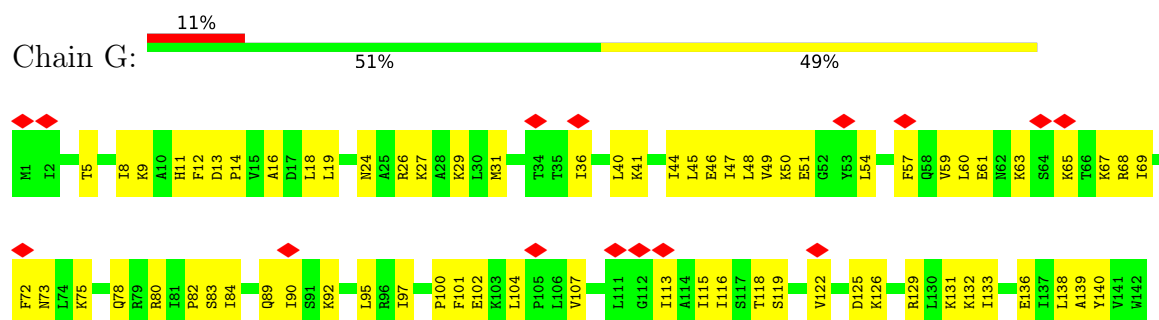




• Molecule 16: 30S ribosomal protein S7



• Molecule 17: 30S ribosomal protein S8

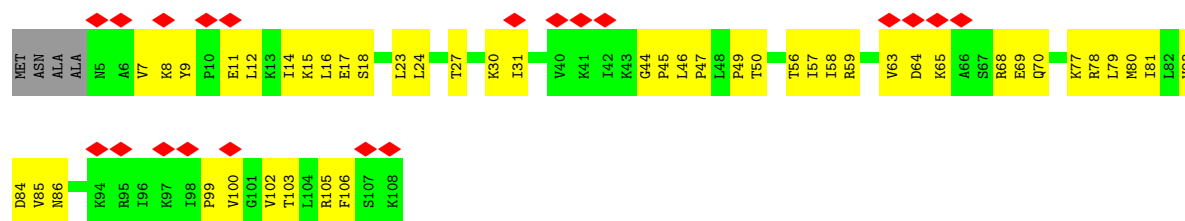


• Molecule 18: 30S ribosomal protein S9

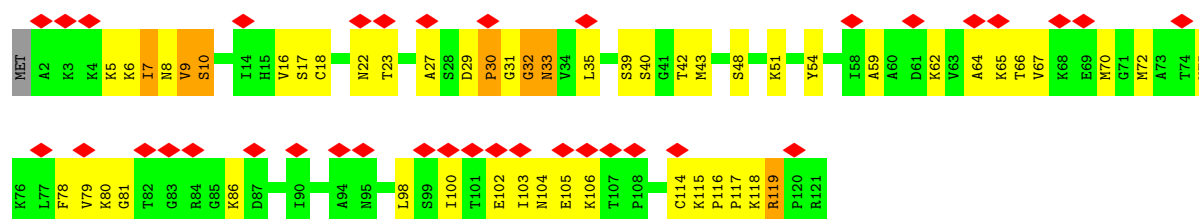


• Molecule 19: 30S ribosomal protein S10

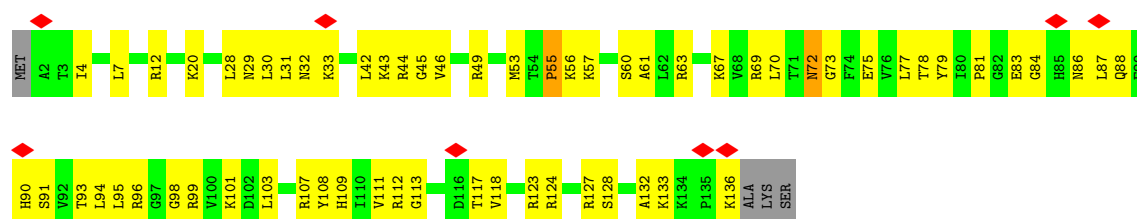




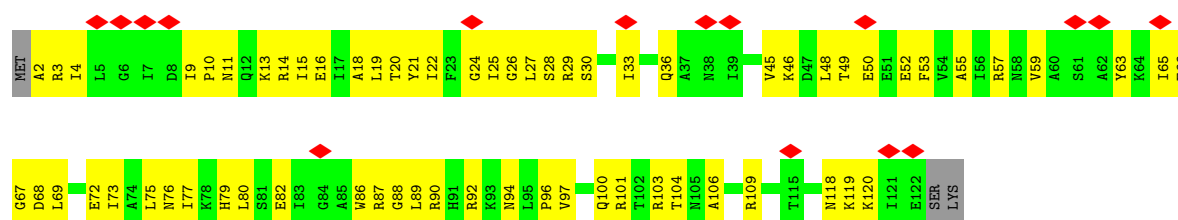
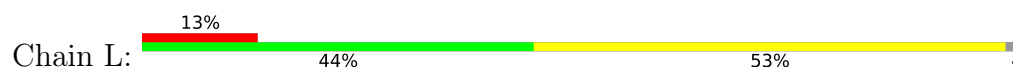
- Molecule 20: 30S ribosomal protein S11



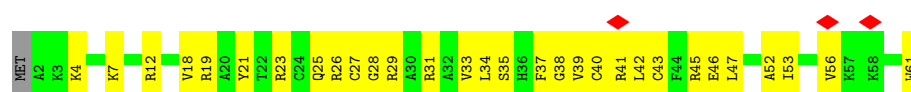
- Molecule 21: 30S ribosomal protein S12



- Molecule 22: 30S ribosomal protein S13



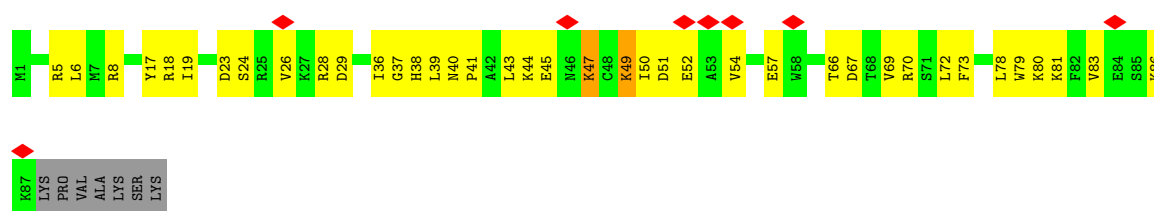
- Molecule 23: 30S ribosomal protein S14 type Z



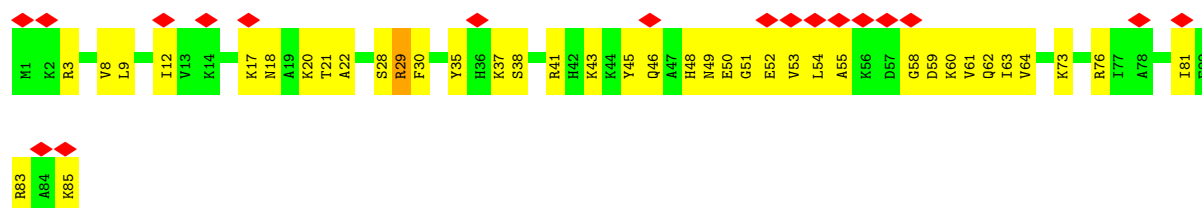
- Molecule 24: 30S ribosomal protein S15



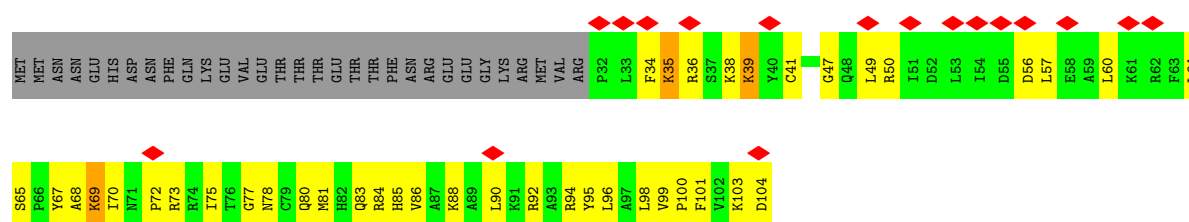
• Molecule 25: 30S ribosomal protein S16



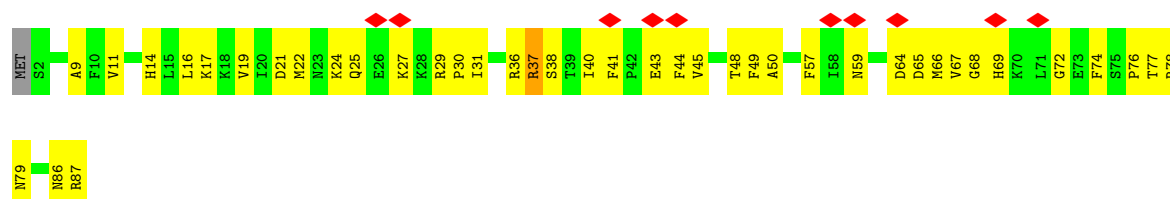
• Molecule 26: 30S ribosomal protein S17

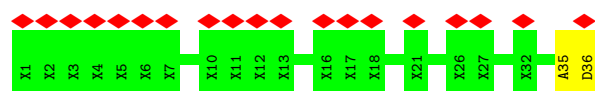


• Molecule 27: 30S ribosomal protein S18

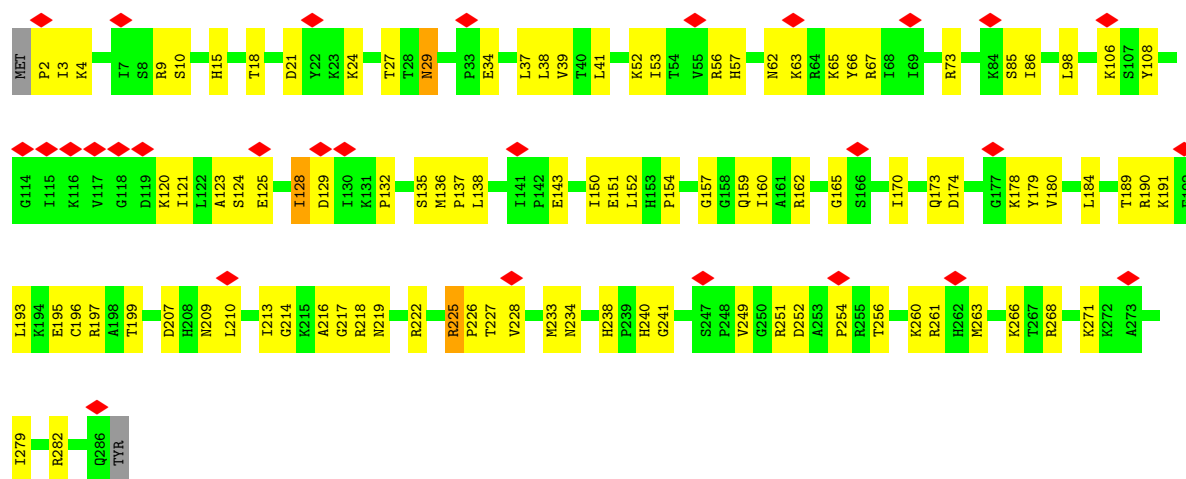


• Molecule 28: 30S ribosomal protein S19

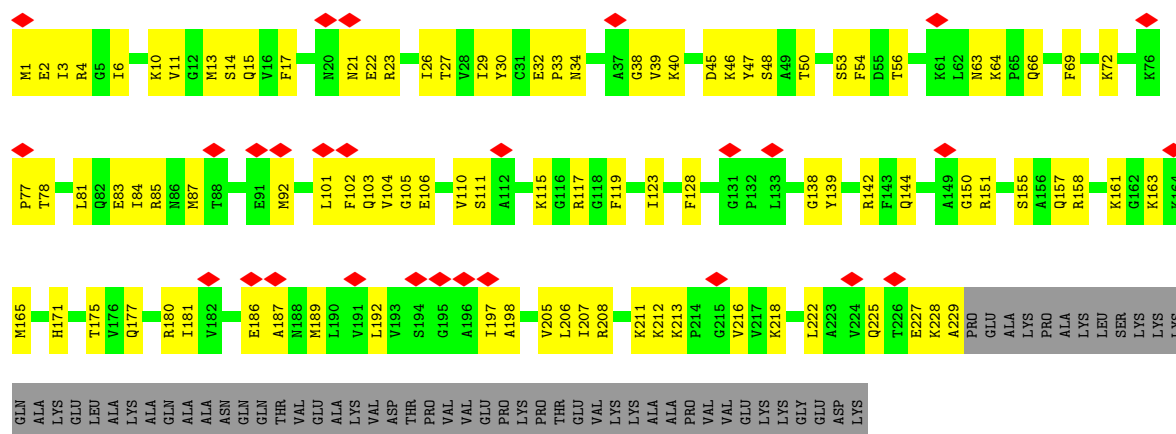




• Molecule 34: 50S ribosomal protein L2

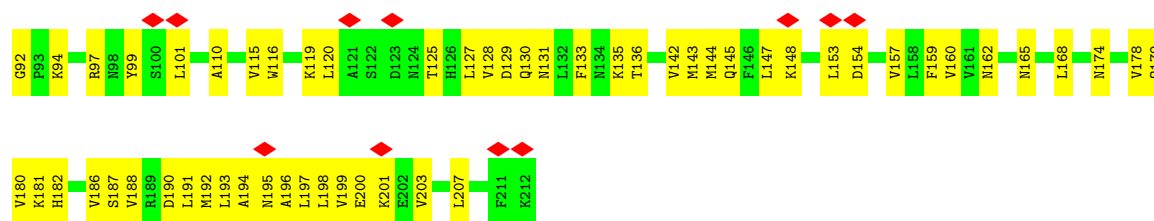


• Molecule 35: 50S ribosomal protein L3

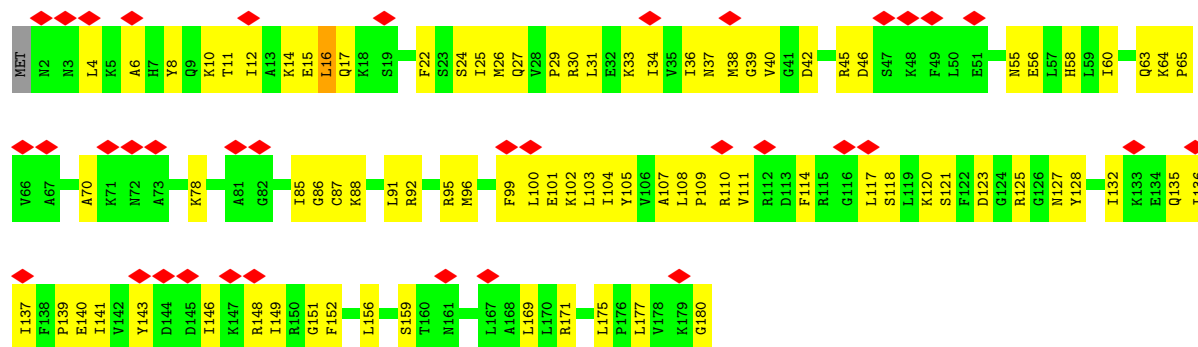


• Molecule 36: 50S ribosomal protein L4

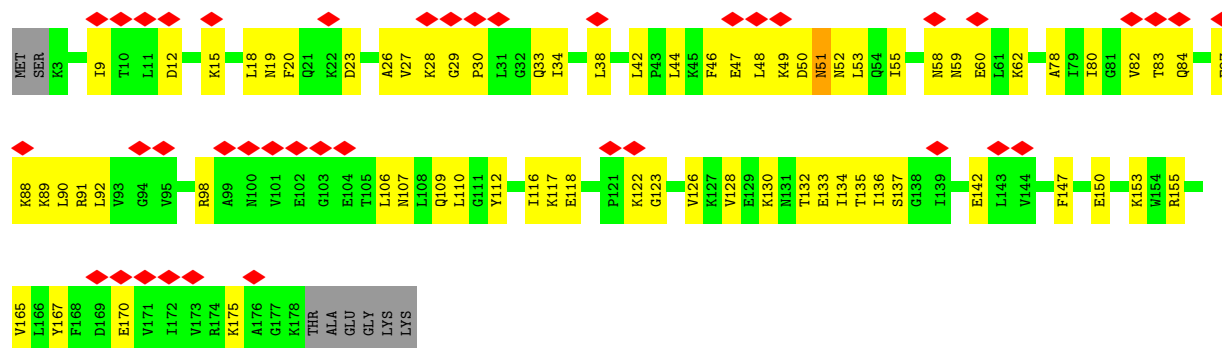




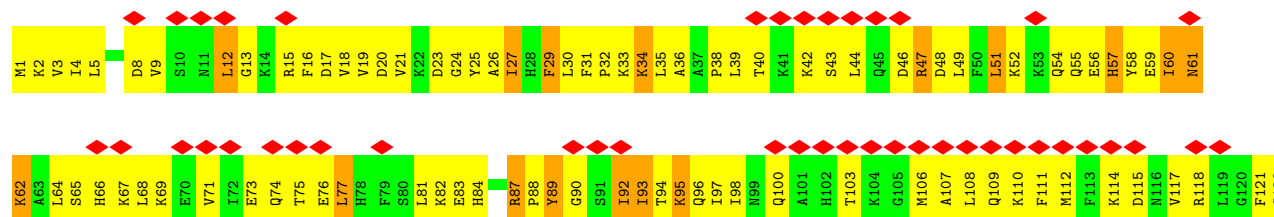
• Molecule 37: 50S ribosomal protein L5

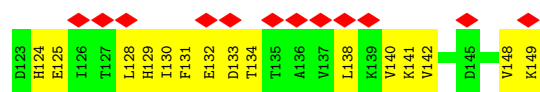


• Molecule 38: 50S ribosomal protein L6

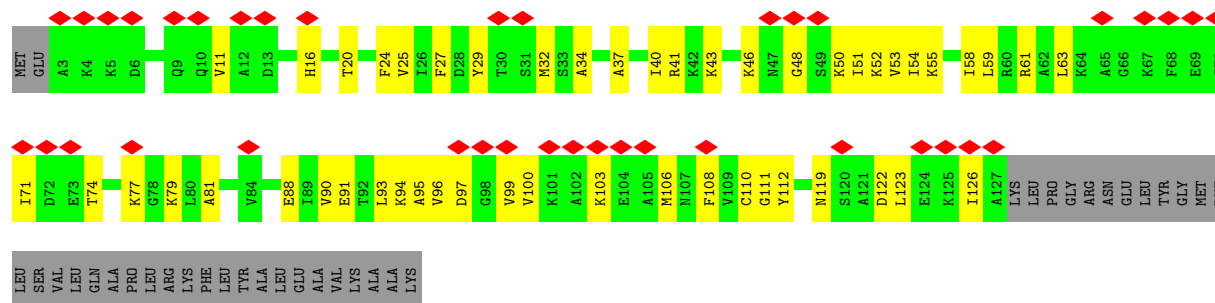


• Molecule 39: 50S ribosomal protein L9

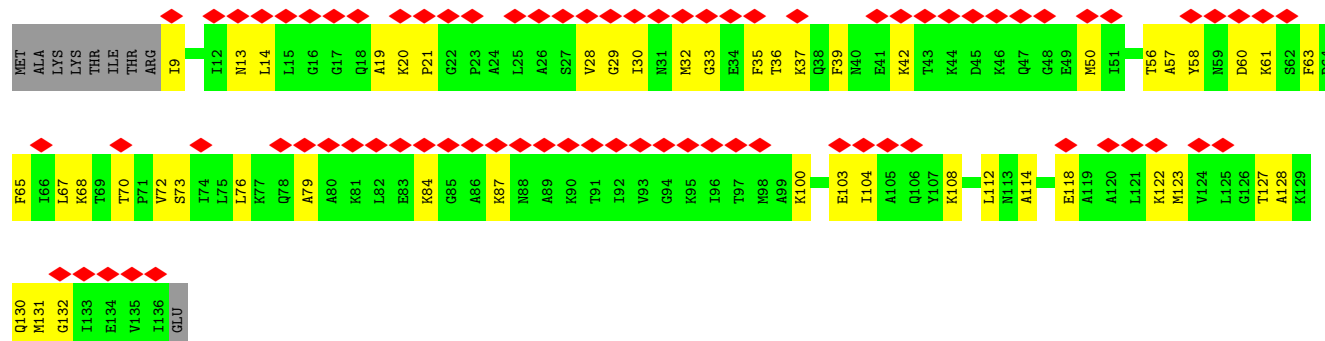




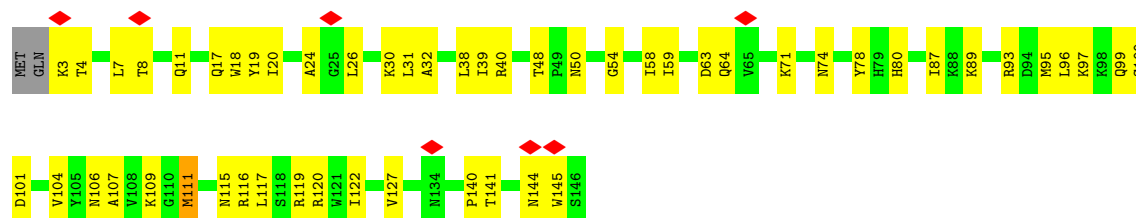
• Molecule 40: 50S ribosomal protein L10



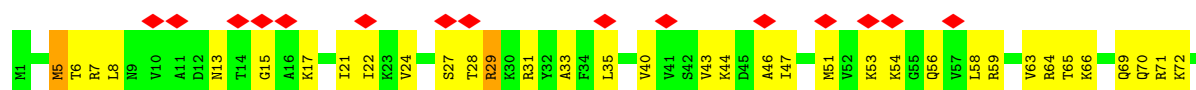
• Molecule 41: 50S ribosomal protein L11



• Molecule 42: 50S ribosomal protein L13

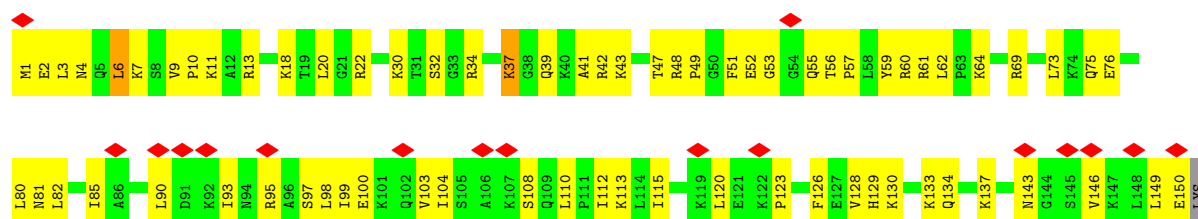


• Molecule 43: 50S ribosomal protein L14

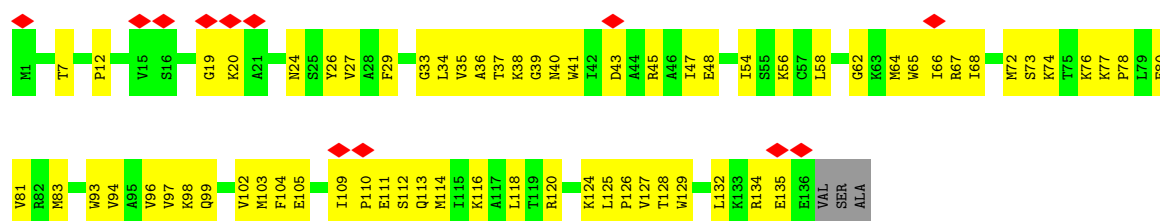




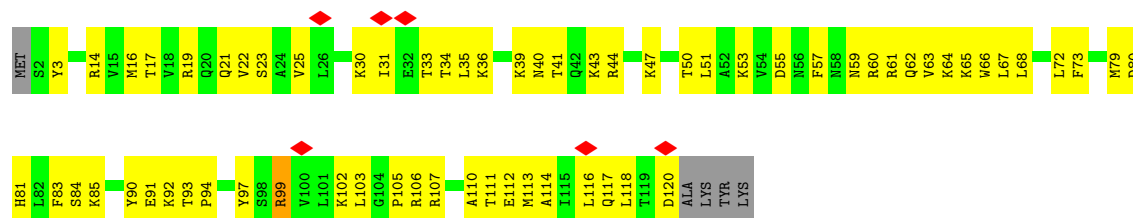
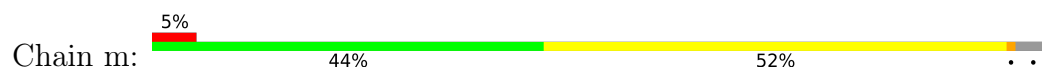
- Molecule 44: 50S ribosomal protein L15



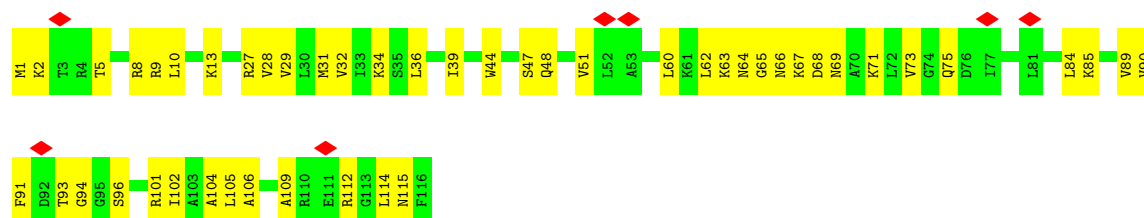
- Molecule 45: 50S ribosomal protein L16



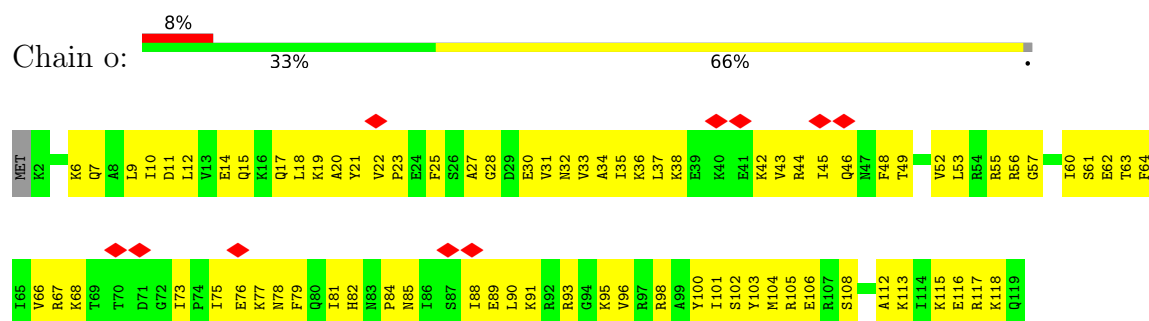
- Molecule 46: 50S ribosomal protein L17



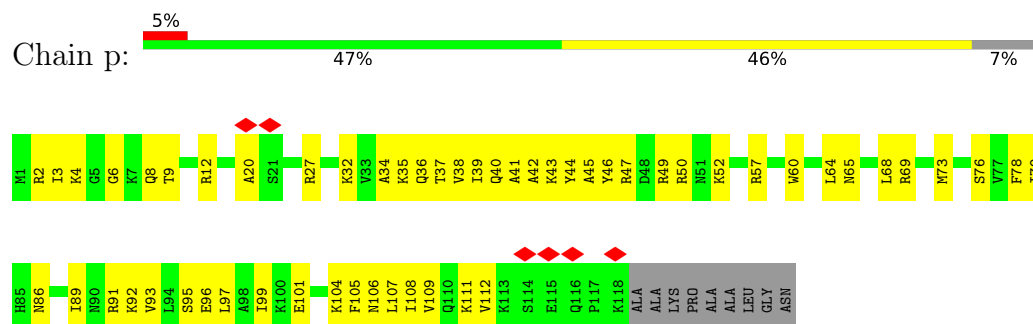
- Molecule 47: 50S ribosomal protein L18



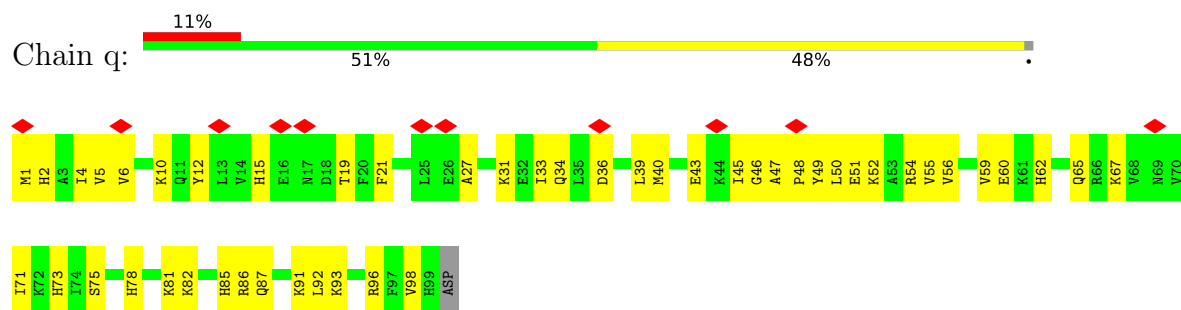
- Molecule 48: 50S ribosomal protein L19



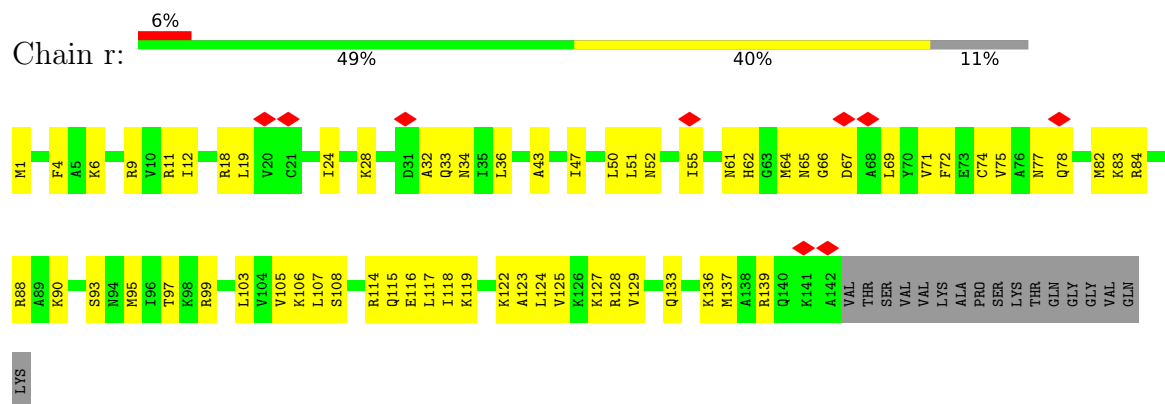
- Molecule 49: 50S ribosomal protein L20



- Molecule 50: 50S ribosomal protein L21

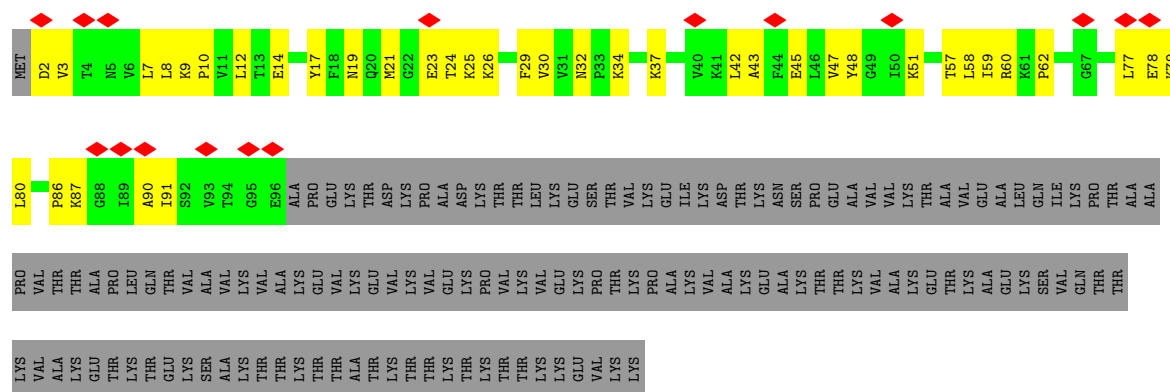


- Molecule 51: 50S ribosomal protein L22

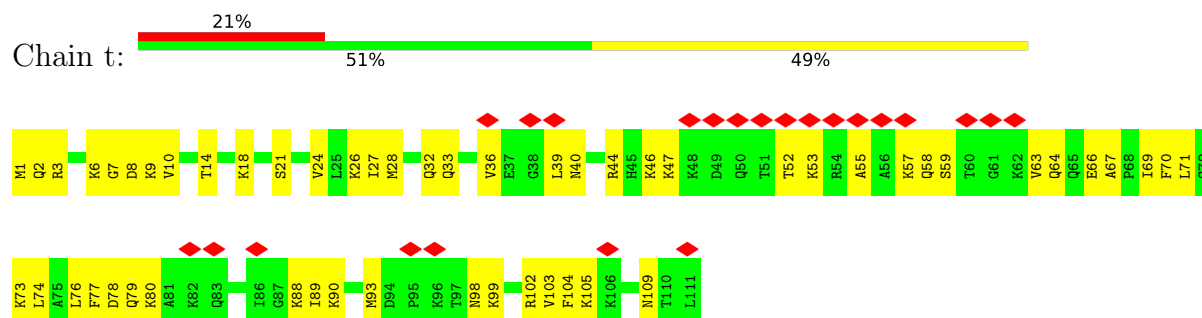


- Molecule 52: 50S ribosomal protein L23

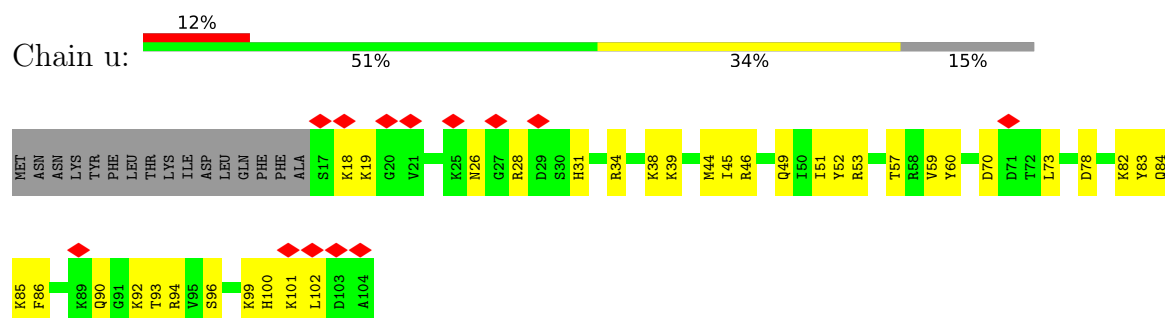




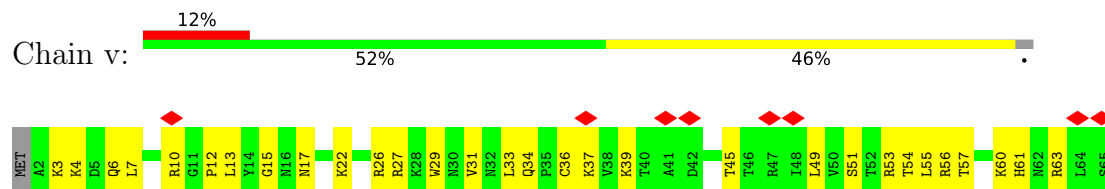
- Molecule 53: 50S ribosomal protein L24



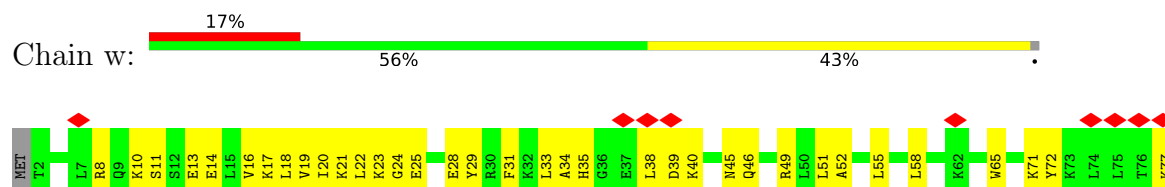
- Molecule 54: 50S ribosomal protein L27

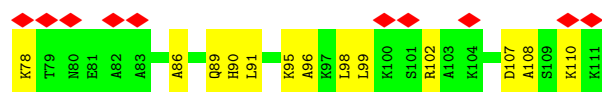


- Molecule 55: 50S ribosomal protein L28

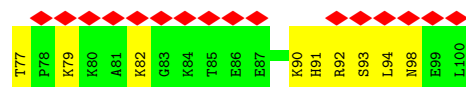
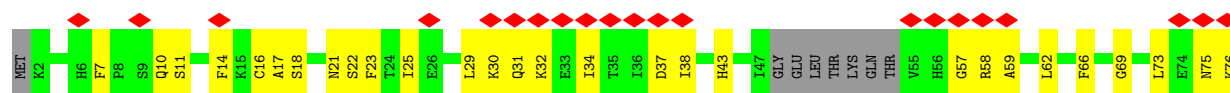
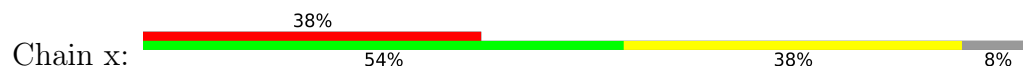


- Molecule 56: 50S ribosomal protein L29

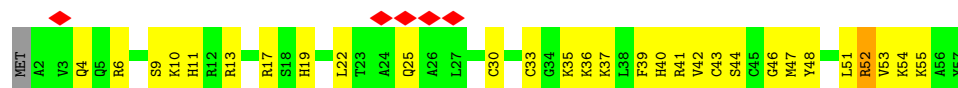




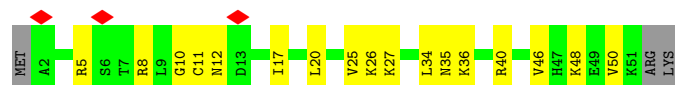
- Molecule 57: 50S ribosomal protein L31



- Molecule 58: 50S ribosomal protein L32



- Molecule 59: 50S ribosomal protein L33 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	963	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF estimation and 3D CTF correction are done in Warp	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	137	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3250	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	5.477	Depositor
Minimum map value	-2.425	Depositor
Average map value	0.022	Depositor
Map value standard deviation	0.237	Depositor
Recommended contour level	1.2	Depositor
Map size ($\text{\AA}$)	793.6, 793.6, 793.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	3.1, 3.1, 3.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, B8T, MA6, K, CLM, 7MG, 1MG, ZN, 2MA, MG, 5MC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.15	0/383	0.53	0/504
2	1	0.18	0/484	0.52	0/637
3	2	0.18	0/306	0.56	0/401
4	3	0.12	1/69363 (0.0%)	0.25	1/108161 (0.0%)
5	4	0.09	0/2578	0.21	0/4016
6	5	0.11	0/35970	0.24	0/56077
7	6	0.16	0/1810	0.48	2/2817 (0.1%)
8	7	0.19	0/1785	0.35	0/2779
9	8	0.22	1/1804 (0.1%)	0.30	0/2807
10	9	0.19	0/1735	0.56	1/2337 (0.0%)
11	A	0.24	0/2186	0.64	0/2952
12	B	0.23	0/1791	0.55	0/2421
13	C	0.22	0/1700	0.58	0/2278
14	D	0.18	0/1233	0.55	0/1651
15	E	0.34	0/1824	0.80	2/2454 (0.1%)
16	F	0.28	0/1274	0.74	1/1710 (0.1%)
17	G	0.24	0/1134	0.67	1/1527 (0.1%)
18	H	0.27	0/1056	0.72	2/1409 (0.1%)
19	I	0.19	0/843	0.57	0/1132
20	J	0.24	0/893	0.70	1/1198 (0.1%)
21	K	0.21	0/1089	0.58	0/1461
22	L	0.22	0/986	0.54	0/1321
23	M	0.18	0/483	0.52	0/643
24	N	0.18	0/703	0.53	0/936
25	O	0.21	0/718	0.67	1/962 (0.1%)
26	P	0.23	0/702	0.66	1/934 (0.1%)
27	Q	0.28	0/617	0.79	1/823 (0.1%)
28	R	0.24	0/716	0.72	2/958 (0.2%)
29	S	0.18	0/645	0.58	1/857 (0.1%)
30	T	0.29	0/524	0.74	1/685 (0.1%)
31	X	0.23	0/245	0.63	0/325
32	Y	0.21	0/969	0.50	0/1508

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Z	0.90	0/26	1.70	0/33
34	a	0.21	0/2267	0.57	2/3044 (0.1%)
35	b	0.22	0/1795	0.64	0/2412
36	c	0.19	0/1681	0.57	2/2257 (0.1%)
37	d	0.21	0/1437	0.56	1/1931 (0.1%)
38	e	0.18	0/1420	0.52	0/1912
39	f	0.60	0/1233	0.96	5/1653 (0.3%)
40	g	0.16	0/960	0.46	0/1284
41	h	0.17	0/968	0.47	0/1298
42	i	0.20	0/1186	0.51	1/1592 (0.1%)
43	j	0.68	2/953 (0.2%)	1.26	8/1275 (0.6%)
44	k	0.20	0/1187	0.65	2/1581 (0.1%)
45	l	0.20	0/1104	0.57	0/1481
46	m	0.24	0/973	0.68	2/1309 (0.2%)
47	n	0.21	0/927	0.57	0/1239
48	o	0.27	0/976	0.70	0/1296
49	p	0.23	0/996	0.64	0/1325
50	q	0.22	0/828	0.62	0/1111
51	r	0.18	0/1100	0.59	0/1471
52	s	0.20	0/752	0.52	0/1015
53	t	0.24	0/878	0.51	0/1165
54	u	0.21	0/678	0.64	0/902
55	v	0.19	0/526	0.60	0/703
56	w	0.20	0/916	0.64	0/1222
57	x	0.17	0/722	0.60	0/959
58	y	0.20	0/457	0.72	1/601 (0.2%)
59	z	0.15	0/412	0.48	0/547
All	All	0.17	4/165907 (0.0%)	0.40	42/247299 (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
34	a	0	1
39	f	0	1
55	v	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	j	93	PRO	CB-CG	14.87	2.23	1.49
43	j	93	PRO	CG-CD	-11.04	1.13	1.50
9	8	76	A	C6-N6	6.00	1.46	1.33
4	3	783	1MG	O3'-P	5.21	1.61	1.56

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	j	93	PRO	CB-CG-CD	-23.42	31.15	106.10
43	j	93	PRO	CA-N-CD	-22.36	80.69	112.00
43	j	93	PRO	N-CD-CG	13.17	122.96	103.20
10	9	198	LYS	CB-CG-CD	8.51	130.87	111.30
43	j	93	PRO	N-CA-CB	-7.70	96.46	103.31

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	a	225	ARG	Sidechain
39	f	118	ARG	Sidechain
55	v	63	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	380	0	429	18	0
2	1	477	0	530	35	0
3	2	304	0	348	14	0
4	3	61995	0	31114	1030	0
5	4	2305	0	1164	32	0
6	5	32238	0	16195	535	0
7	6	1620	0	818	25	0
8	7	1599	0	805	26	0
9	8	1615	0	816	20	0
10	9	1711	0	1829	34	0
11	A	2152	0	2222	126	0
12	B	1764	0	1833	103	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	C	1669	0	1729	94	0
14	D	1217	0	1311	47	0
15	E	1793	0	1781	161	0
16	F	1254	0	1320	85	0
17	G	1118	0	1238	86	0
18	H	1040	0	1107	70	0
19	I	832	0	918	55	0
20	J	878	0	923	56	0
21	K	1071	0	1165	65	0
22	L	975	0	1043	72	0
23	M	474	0	505	36	0
24	N	697	0	758	34	0
25	O	705	0	755	39	0
26	P	693	0	753	42	0
27	Q	605	0	644	61	0
28	R	700	0	709	43	0
29	S	643	0	694	40	0
30	T	519	0	578	57	0
31	X	242	0	263	17	0
32	Y	862	0	435	40	0
33	Z	187	0	68	3	0
34	a	2225	0	2301	99	0
35	b	1762	0	1808	108	0
36	c	1654	0	1744	79	0
37	d	1416	0	1500	80	0
38	e	1396	0	1481	56	0
39	f	1210	0	1259	117	0
40	g	951	0	1001	46	0
41	h	959	0	1039	39	0
42	i	1164	0	1192	48	0
43	j	944	0	1019	72	0
44	k	1170	0	1274	80	0
45	l	1079	0	1134	71	0
46	m	958	0	1011	71	0
47	n	918	0	979	43	0
48	o	966	0	1042	92	0
49	p	981	0	1062	71	0
50	q	811	0	858	53	0
51	r	1091	0	1178	53	0
52	s	740	0	819	43	0
53	t	871	0	972	47	0
54	u	670	0	704	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	v	520	0	565	33	0
56	w	906	0	981	46	0
57	x	708	0	710	31	0
58	y	452	0	471	51	0
59	z	408	0	436	17	0
60	2	1	0	0	0	0
60	M	1	0	0	0	0
60	Q	1	0	0	0	0
60	x	1	0	0	0	0
60	y	1	0	0	0	0
60	z	1	0	0	0	0
61	3	20	0	11	1	0
62	3	1	0	0	0	0
63	3	209	0	0	0	0
63	4	1	0	0	0	0
63	5	87	0	0	0	0
63	6	1	0	0	0	0
63	8	1	0	0	0	0
63	E	1	0	0	0	0
63	K	1	0	0	0	0
63	L	1	0	0	0	0
63	P	1	0	0	0	0
63	Y	2	0	0	0	0
63	a	1	0	0	0	0
63	b	1	0	0	0	0
63	f	12	0	0	0	0
63	i	1	0	0	0	0
63	y	2	0	0	0	0
64	8	9	0	12	0	0
All	All	153622	0	105363	4084	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 17.

The worst 5 of 4084 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)
39:f:132:GLU:O	39:f:140:VAL:HB	1.52	1.10
6:5:839:U:OP2	15:E:142:ARG:NH1	1.85	1.08
39:f:4:ILE:HG21	39:f:47:ARG:HG3	1.41	1.01
58:y:42:VAL:HG22	58:y:48:TYR:HB2	1.45	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:1322:U:O3'	18:H:125:ARG:NH2	1.98	0.96

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	45 (100%)	0	0	100	100
2	1	57/59 (97%)	57 (100%)	0	0	100	100
3	2	35/37 (95%)	35 (100%)	0	0	100	100
10	9	224/226 (99%)	218 (97%)	5 (2%)	1 (0%)	30	67
11	A	264/294 (90%)	233 (88%)	28 (11%)	3 (1%)	11	46
12	B	222/273 (81%)	198 (89%)	21 (10%)	3 (1%)	9	40
13	C	202/205 (98%)	168 (83%)	33 (16%)	1 (0%)	24	63
14	D	156/219 (71%)	147 (94%)	7 (4%)	2 (1%)	9	42
15	E	213/215 (99%)	171 (80%)	33 (16%)	9 (4%)	2	17
16	F	153/155 (99%)	132 (86%)	17 (11%)	4 (3%)	4	25
17	G	140/142 (99%)	131 (94%)	9 (6%)	0	100	100
18	H	127/132 (96%)	115 (91%)	10 (8%)	2 (2%)	7	38
19	I	102/108 (94%)	89 (87%)	12 (12%)	1 (1%)	12	49
20	J	118/121 (98%)	103 (87%)	9 (8%)	6 (5%)	1	15
21	K	133/139 (96%)	113 (85%)	16 (12%)	4 (3%)	3	23
22	L	119/124 (96%)	109 (92%)	10 (8%)	0	100	100
23	M	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
24	N	84/86 (98%)	78 (93%)	6 (7%)	0	100	100
25	O	85/94 (90%)	78 (92%)	5 (6%)	2 (2%)	4	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	P	83/85 (98%)	71 (86%)	11 (13%)	1 (1%)	10	44
27	Q	71/104 (68%)	63 (89%)	6 (8%)	2 (3%)	4	24
28	R	84/87 (97%)	79 (94%)	5 (6%)	0	100	100
29	S	77/87 (88%)	74 (96%)	2 (3%)	1 (1%)	9	42
30	T	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
31	X	28/444 (6%)	24 (86%)	4 (14%)	0	100	100
33	Z	3/36 (8%)	3 (100%)	0	0	100	100
34	a	283/287 (99%)	268 (95%)	14 (5%)	1 (0%)	30	67
35	b	227/287 (79%)	220 (97%)	7 (3%)	0	100	100
36	c	209/212 (99%)	199 (95%)	10 (5%)	0	100	100
37	d	177/180 (98%)	168 (95%)	9 (5%)	0	100	100
38	e	174/184 (95%)	162 (93%)	12 (7%)	0	100	100
39	f	147/149 (99%)	113 (77%)	29 (20%)	5 (3%)	3	21
40	g	123/161 (76%)	115 (94%)	8 (6%)	0	100	100
41	h	126/137 (92%)	121 (96%)	5 (4%)	0	100	100
42	i	142/146 (97%)	133 (94%)	9 (6%)	0	100	100
43	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
44	k	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
45	l	134/139 (96%)	130 (97%)	4 (3%)	0	100	100
46	m	117/124 (94%)	111 (95%)	6 (5%)	0	100	100
47	n	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
48	o	116/119 (98%)	107 (92%)	9 (8%)	0	100	100
49	p	116/127 (91%)	114 (98%)	2 (2%)	0	100	100
50	q	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
51	r	140/159 (88%)	137 (98%)	3 (2%)	0	100	100
52	s	93/237 (39%)	89 (96%)	4 (4%)	0	100	100
53	t	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
54	u	86/104 (83%)	82 (95%)	4 (5%)	0	100	100
55	v	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
56	w	108/111 (97%)	103 (95%)	5 (5%)	0	100	100
57	x	85/97 (88%)	63 (74%)	21 (25%)	1 (1%)	10	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	y	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
59	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	6295/7376 (85%)	5799 (92%)	447 (7%)	49 (1%)	18	54

5 of 49 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	D	216	LEU
15	E	121	ARG
15	E	143	LEU
18	H	102	SER
20	J	32	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
10	9	186/186 (100%)	186 (100%)	0	100	100
11	A	239/262 (91%)	239 (100%)	0	100	100
12	B	187/232 (81%)	187 (100%)	0	100	100
13	C	182/183 (100%)	182 (100%)	0	100	100
14	D	128/178 (72%)	128 (100%)	0	100	100
15	E	196/196 (100%)	195 (100%)	1 (0%)	81	83
16	F	132/132 (100%)	132 (100%)	0	100	100
17	G	124/124 (100%)	124 (100%)	0	100	100
18	H	112/115 (97%)	112 (100%)	0	100	100
19	I	97/99 (98%)	97 (100%)	0	100	100
20	J	96/97 (99%)	96 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	K	117/120 (98%)	117 (100%)	0	100	100
22	L	102/105 (97%)	102 (100%)	0	100	100
23	M	47/48 (98%)	47 (100%)	0	100	100
24	N	78/78 (100%)	78 (100%)	0	100	100
25	O	76/82 (93%)	76 (100%)	0	100	100
26	P	75/75 (100%)	75 (100%)	0	100	100
27	Q	64/94 (68%)	64 (100%)	0	100	100
28	R	76/77 (99%)	76 (100%)	0	100	100
29	S	71/77 (92%)	71 (100%)	0	100	100
30	T	55/56 (98%)	55 (100%)	0	100	100
31	X	27/406 (7%)	27 (100%)	0	100	100
33	Z	2/2 (100%)	2 (100%)	0	100	100
34	a	241/243 (99%)	240 (100%)	1 (0%)	84	84
35	b	186/233 (80%)	186 (100%)	0	100	100
36	c	183/184 (100%)	183 (100%)	0	100	100
37	d	153/154 (99%)	153 (100%)	0	100	100
38	e	153/159 (96%)	152 (99%)	1 (1%)	76	81
39	f	134/134 (100%)	128 (96%)	6 (4%)	24	46
40	g	100/129 (78%)	100 (100%)	0	100	100
41	h	102/110 (93%)	102 (100%)	0	100	100
42	i	126/128 (98%)	126 (100%)	0	100	100
43	j	103/103 (100%)	103 (100%)	0	100	100
44	k	125/126 (99%)	125 (100%)	0	100	100
45	l	113/115 (98%)	113 (100%)	0	100	100
46	m	105/109 (96%)	105 (100%)	0	100	100
47	n	99/99 (100%)	99 (100%)	0	100	100
48	o	104/105 (99%)	104 (100%)	0	100	100
49	p	104/108 (96%)	103 (99%)	1 (1%)	68	78
50	q	90/91 (99%)	90 (100%)	0	100	100
51	r	118/132 (89%)	118 (100%)	0	100	100
52	s	84/208 (40%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	t	96/96 (100%)	96 (100%)	0	100	100
54	u	70/85 (82%)	70 (100%)	0	100	100
55	v	59/60 (98%)	59 (100%)	0	100	100
56	w	97/98 (99%)	97 (100%)	0	100	100
57	x	79/86 (92%)	79 (100%)	0	100	100
58	y	48/49 (98%)	48 (100%)	0	100	100
59	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5514/6345 (87%)	5504 (100%)	10 (0%)	85	87

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	f	89	TYR
39	f	92	ILE
49	p	2	ARG
39	f	47	ARG
39	f	51	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
44	k	39	GLN
53	t	33	GLN
44	k	81	ASN
47	n	69	ASN
57	x	31	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	Y	39/40 (97%)	25 (64%)	6 (15%)
4	3	2892/2907 (99%)	532 (18%)	20 (0%)
5	4	107/108 (99%)	29 (27%)	0
6	5	1505/1520 (99%)	252 (16%)	8 (0%)
7	6	76/76 (100%)	22 (28%)	6 (7%)
8	7	74/75 (98%)	20 (27%)	2 (2%)
9	8	75/76 (98%)	23 (30%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4768/4802 (99%)	903 (18%)	42 (0%)

5 of 903 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	3	11	U
4	3	12	A
4	3	13	C
4	3	14	U
4	3	28	G

5 of 42 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	6	1	G
8	7	46	U
7	6	15	A
7	6	46	G
32	Y	65	C

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

8 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
6	B8T	5	1377	6	19,22,23	3.32	8 (42%)	25,31,34	0.85	1 (4%)
6	MA6	5	1493	6	23,26,27	1.41	3 (13%)	33,38,41	3.17	14 (42%)
6	7MG	5	525	6	23,26,27	3.64	11 (47%)	27,39,42	2.16	9 (33%)
4	2MA	3	2511	4,63	22,25,26	4.13	10 (45%)	32,37,40	3.53	12 (37%)
4	OMG	3	2259	4,8	23,26,27	2.60	7 (30%)	32,38,41	2.44	10 (31%)
6	5MC	5	1375	6	19,22,23	4.56	8 (42%)	26,32,35	1.02	2 (7%)
6	MA6	5	1494	6	23,26,27	1.40	3 (13%)	33,38,41	3.23	14 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	1MG	3	783	4	23,26,27	0.61	0	33,39,42	0.74	1 (3%)

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
6	B8T	5	1377	6	-	2/7/27/28	0/2/2/2
6	MA6	5	1493	6	-	0/11/29/30	0/3/3/3
6	7MG	5	525	6	-	2/7/37/38	0/3/3/3
4	2MA	3	2511	4,63	-	1/7/25/26	0/3/3/3
4	OMG	3	2259	4,8	-	3/9/27/28	0/3/3/3
6	5MC	5	1375	6	-	0/7/25/26	0/2/2/2
6	MA6	5	1494	6	-	2/11/29/30	0/3/3/3
4	1MG	3	783	4	-	0/7/25/26	0/3/3/3

The worst 5 of 50 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	3	2511	2MA	C4-N3	11.95	1.49	1.34
6	5	1375	5MC	C6-C5	10.01	1.50	1.34
6	5	1375	5MC	C5-C4	9.26	1.51	1.44
6	5	525	7MG	C8-N9	8.71	1.51	1.45
4	3	2511	2MA	C2-N3	8.09	1.47	1.34

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	3	2511	2MA	C1'-N9-C8	-12.43	99.51	127.09
4	3	2511	2MA	C4-N9-C1'	10.80	151.88	126.63
6	5	1494	MA6	N1-C6-N6	-10.43	104.15	116.86
6	5	1493	MA6	N1-C6-N6	-9.77	104.95	116.86
4	3	2259	OMG	C1'-N9-C8	-6.83	107.32	126.73

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	3	2259	OMG	O4'-C4'-C5'-O5'

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	3	2259	OMG	C1'-C2'-O2'-CM2
6	5	525	7MG	O4'-C4'-C5'-O5'
6	5	1494	MA6	O4'-C4'-C5'-O5'
4	3	2259	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	5	1493	MA6	1	0
6	5	525	7MG	1	0
4	3	2511	2MA	2	0
4	3	783	1MG	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 331 ligands modelled in this entry, 329 are monoatomic - leaving 2 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	$\# Z > 2$
61	CLM	3	3001	-	20,20,20	2.09	2 (10%)	23,27,27	0.87	0
64	LYS	8	102	9	7,8,9	0.88	0	3,8,10	0.29	0

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
61	CLM	3	3001	-	-	2/20/22/22	0/1/1/1
64	LYS	8	102	9	-	3/6/7/9	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	3	3001	CLM	C2-N2	7.41	1.49	1.34
61	3	3001	CLM	O9B-N9	-2.66	1.18	1.22

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

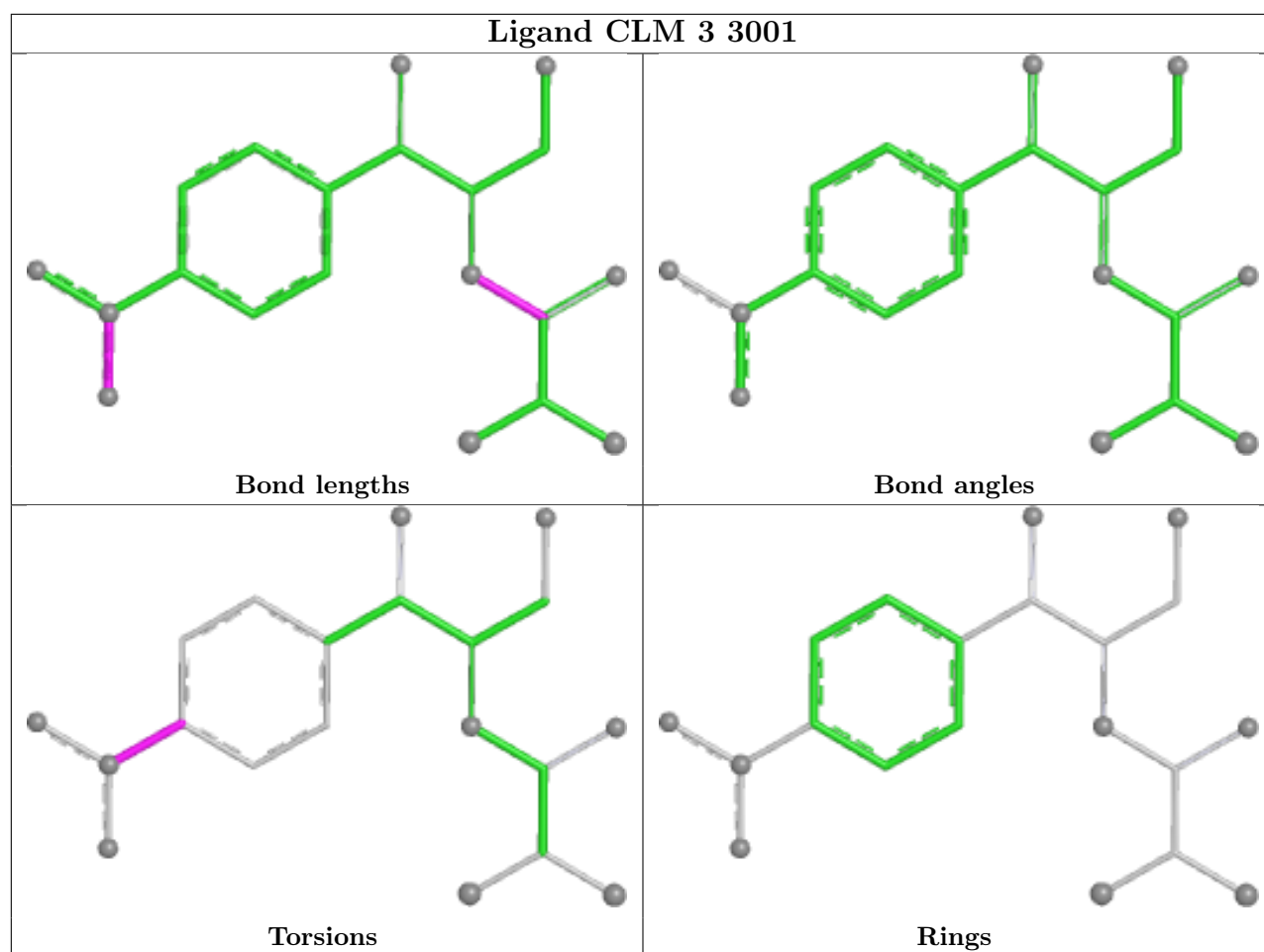
Mol	Chain	Res	Type	Atoms
64	8	102	LYS	O-C-CA-CB
64	8	102	LYS	N-CA-CB-CG
64	8	102	LYS	C-CA-CB-CG
61	3	3001	CLM	C8-C9-N9-O9B
61	3	3001	CLM	C10-C9-N9-O9B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	3	3001	CLM	1	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.

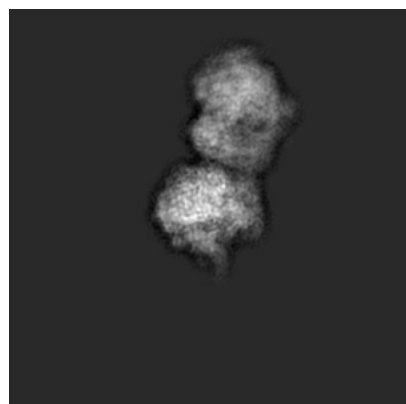
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17145. These allow visual inspection of the internal detail of the map and identification of artifacts.

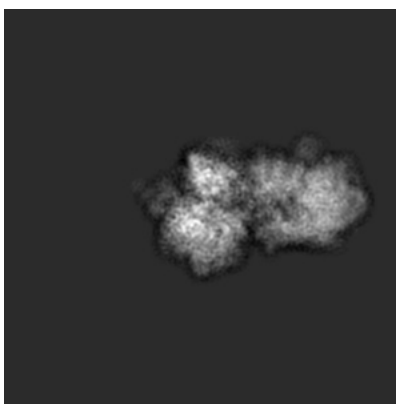
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

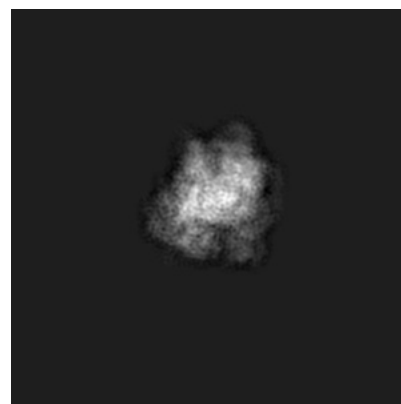
6.1.1 Primary map



X

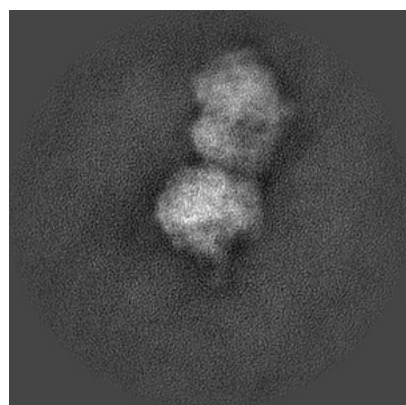


Y

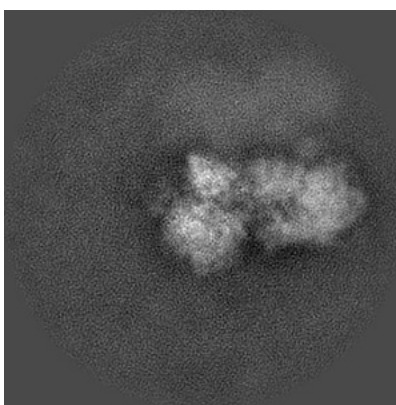


Z

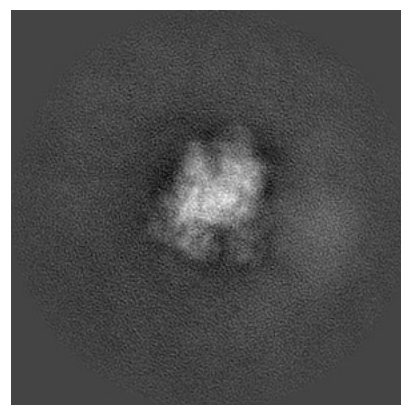
6.1.2 Raw map



X



Y

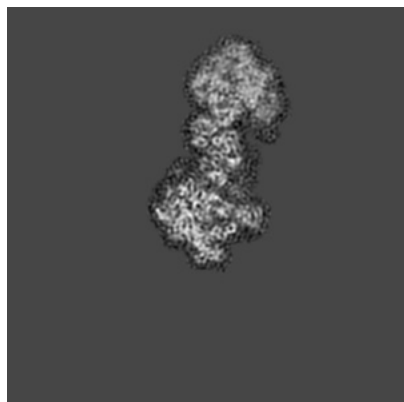


Z

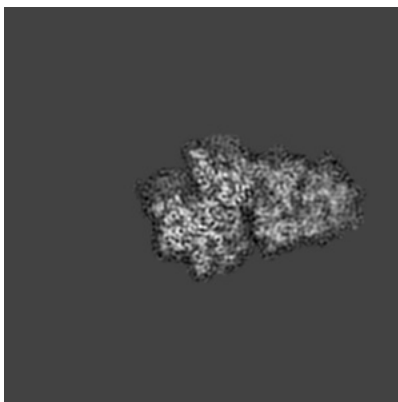
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

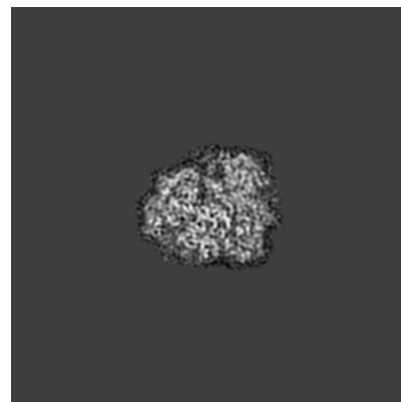
6.2.1 Primary map



X Index: 128

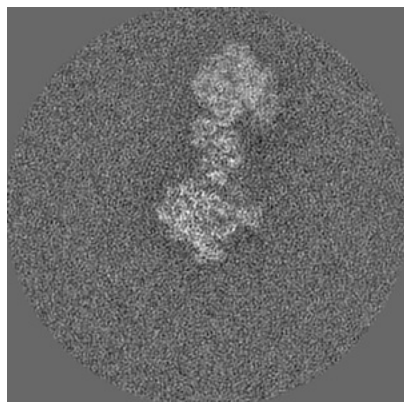


Y Index: 128

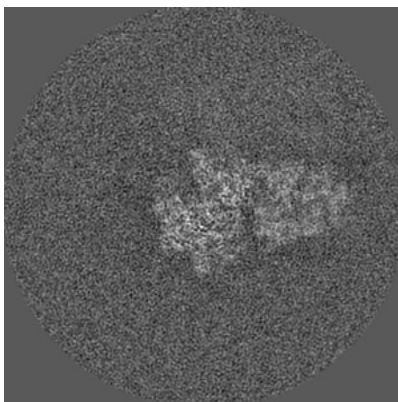


Z Index: 128

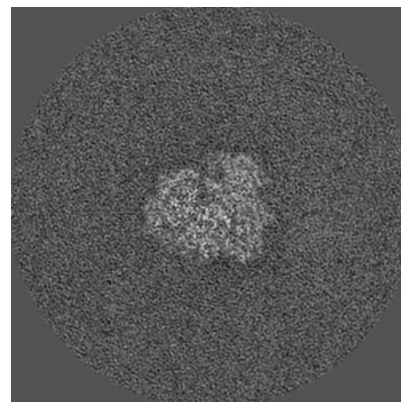
6.2.2 Raw map



X Index: 128



Y Index: 128

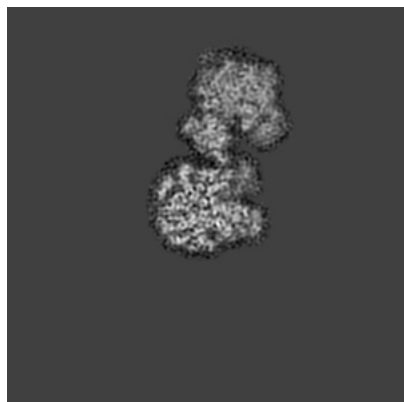


Z Index: 128

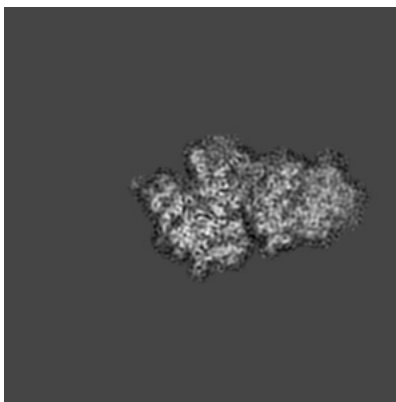
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

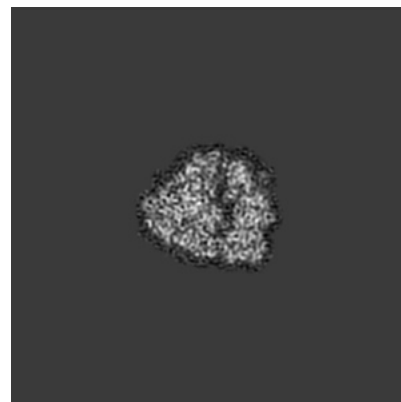
6.3.1 Primary map



X Index: 117

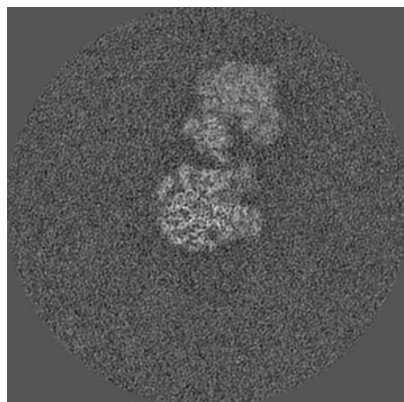


Y Index: 131

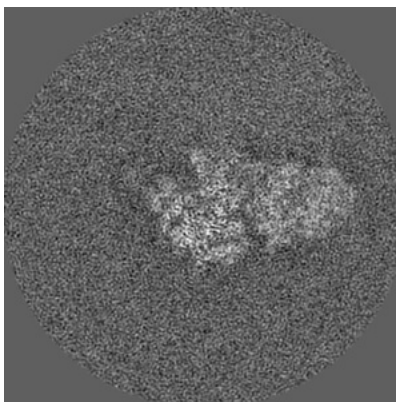


Z Index: 124

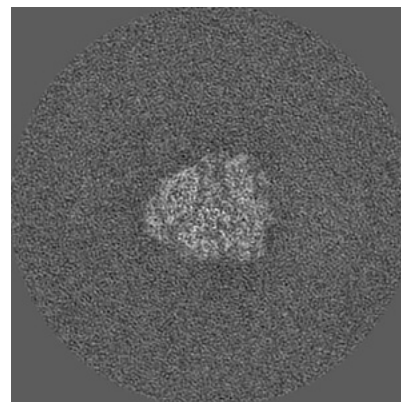
6.3.2 Raw map



X Index: 117



Y Index: 131

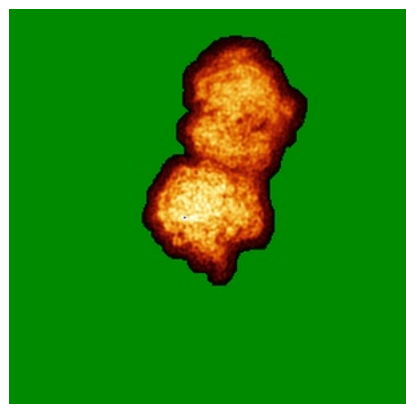


Z Index: 127

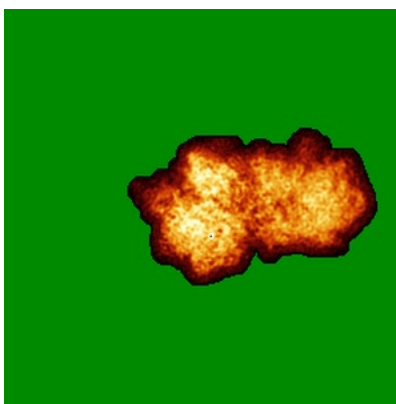
The images above show the largest variance slices of the map in three orthogonal directions.

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

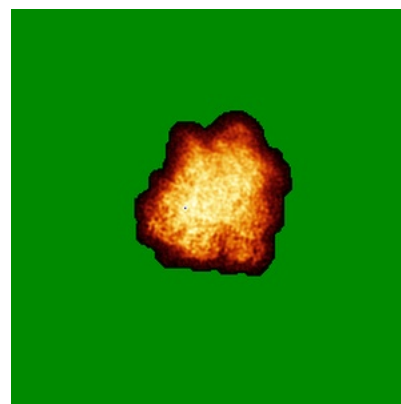
6.4.1 Primary map



X

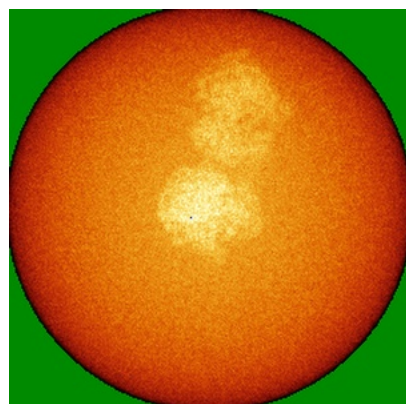


Y

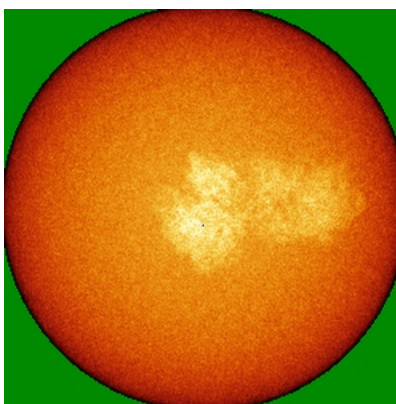


Z

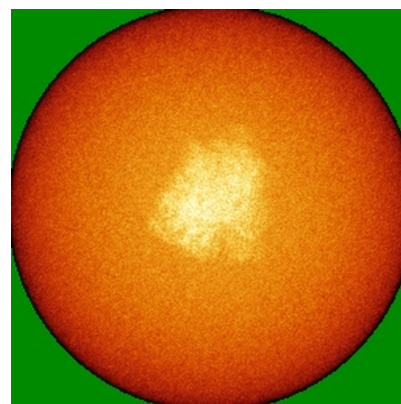
6.4.2 Raw map



X



Y

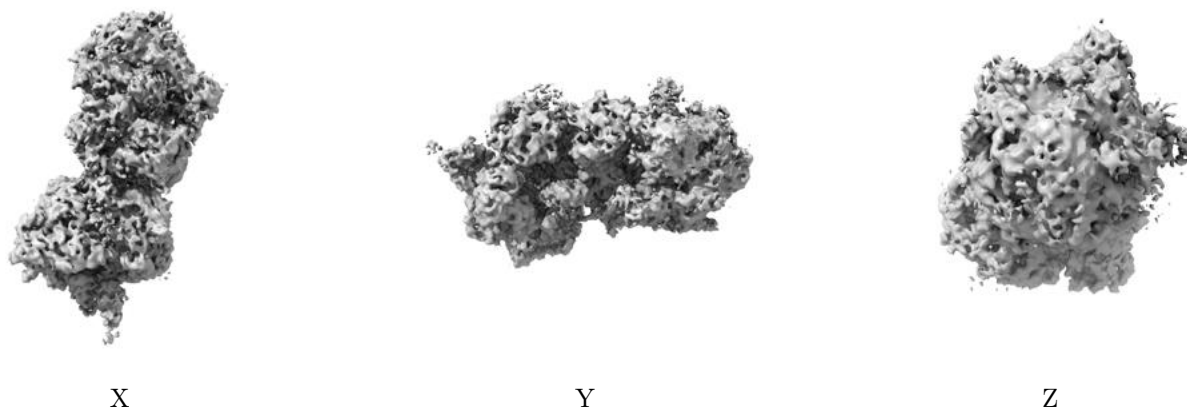


Z

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.

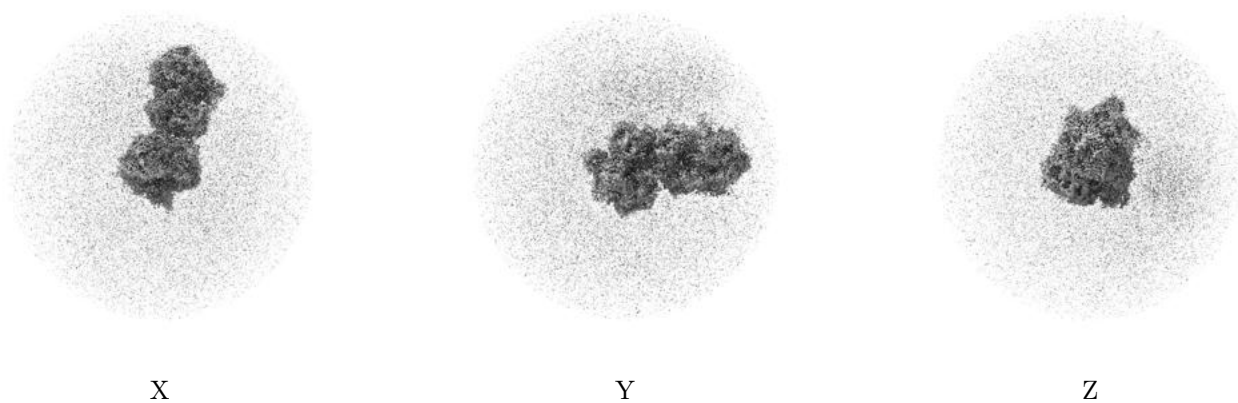
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.2. 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



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.

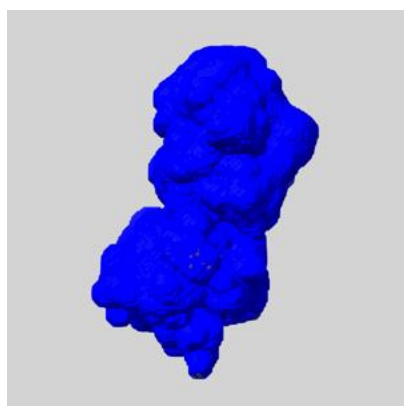
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

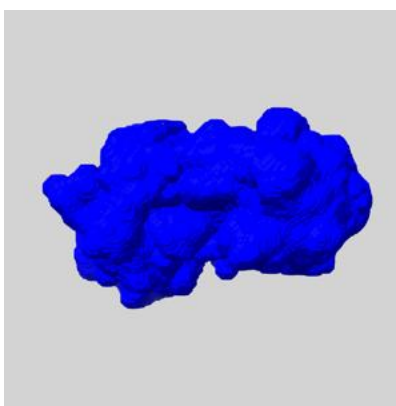
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

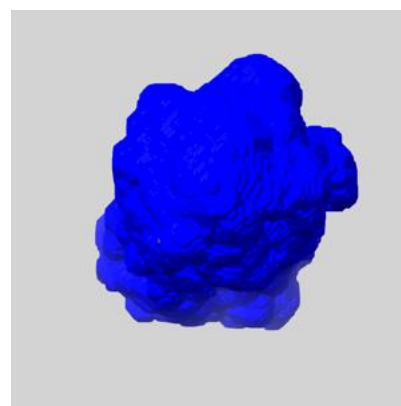
6.6.1 emd_17145_msk_1.map [i](#)



X



Y

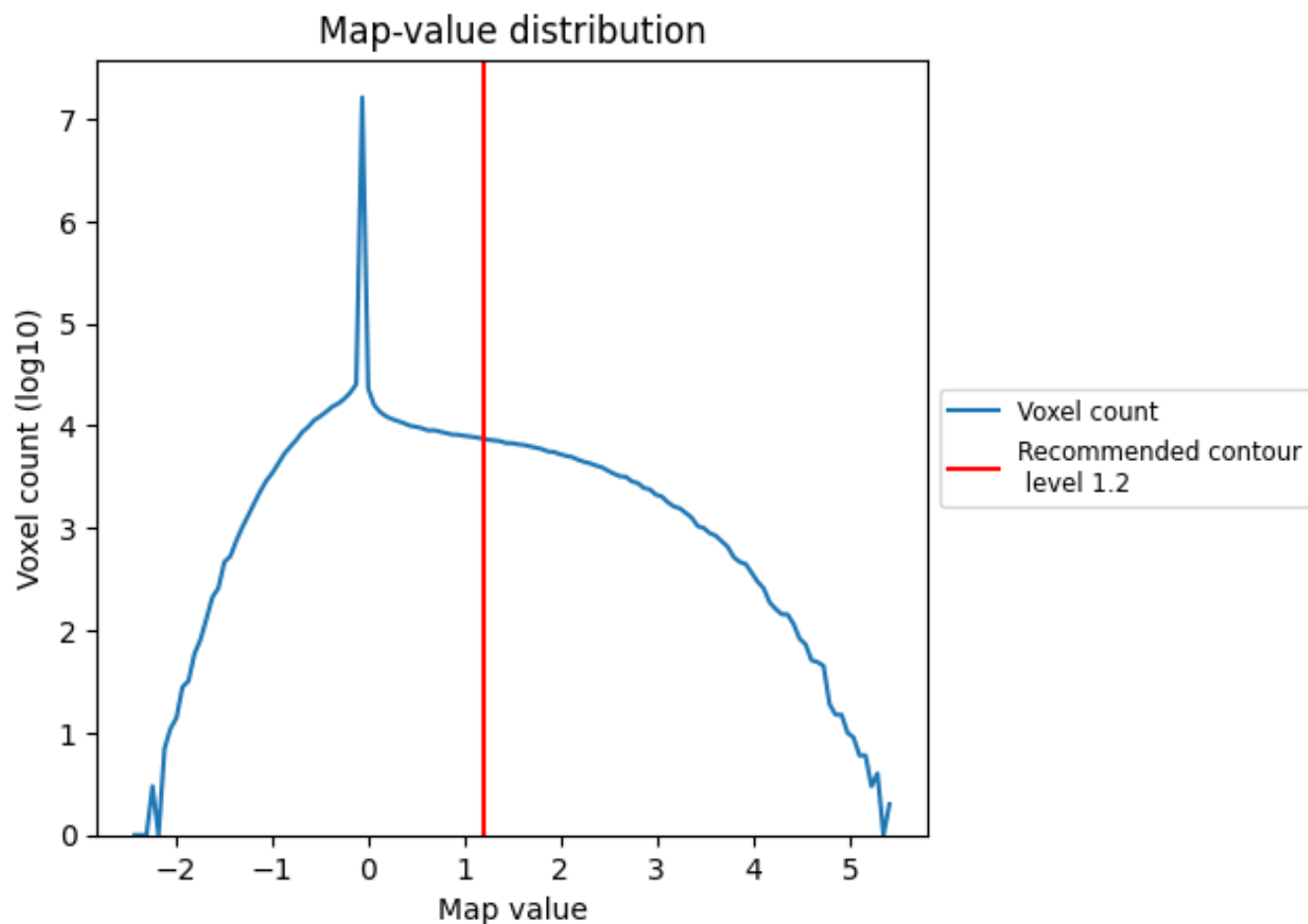


Z

7 Map analysis [i](#)

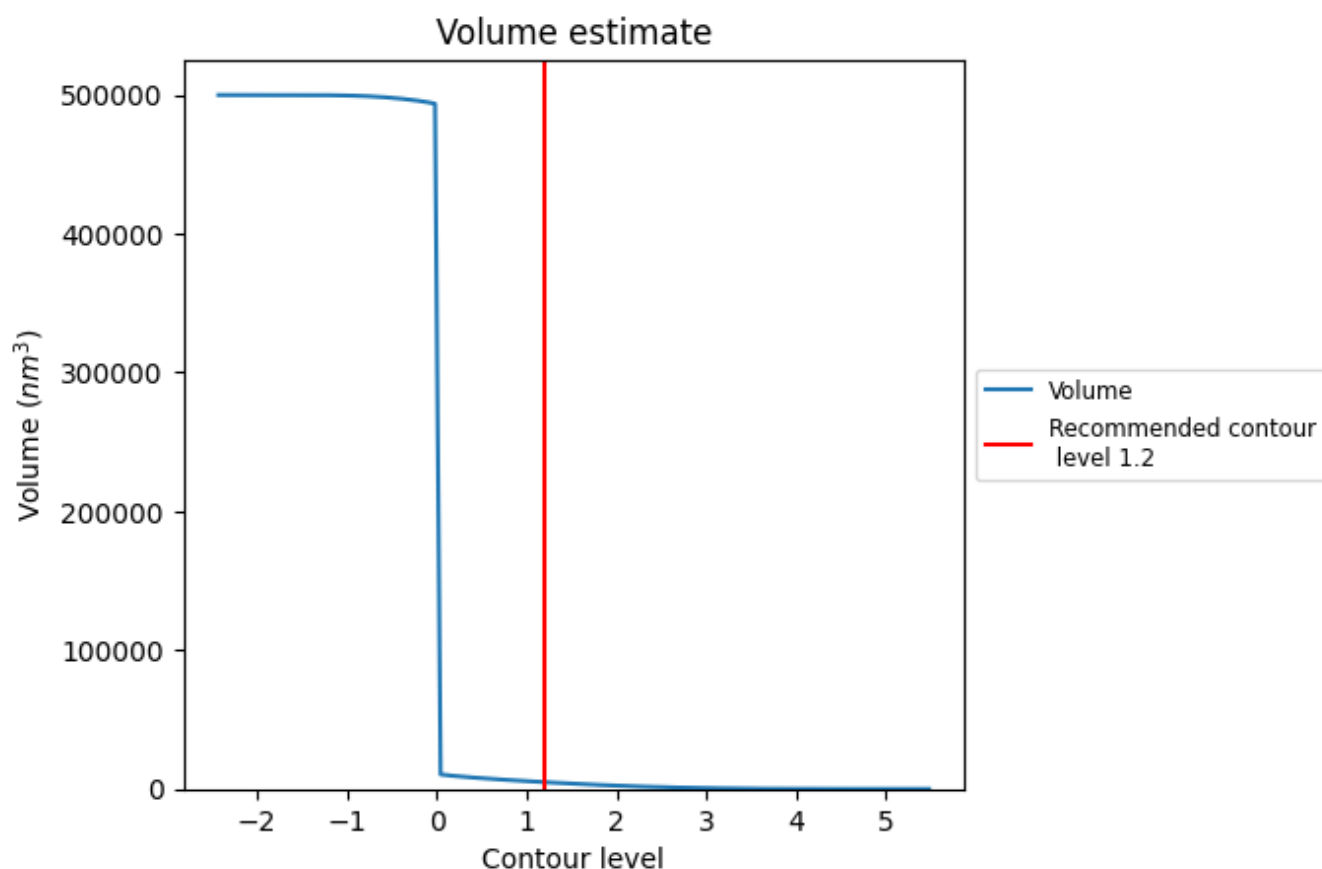
This section contains the results of statistical analysis of the map.

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.

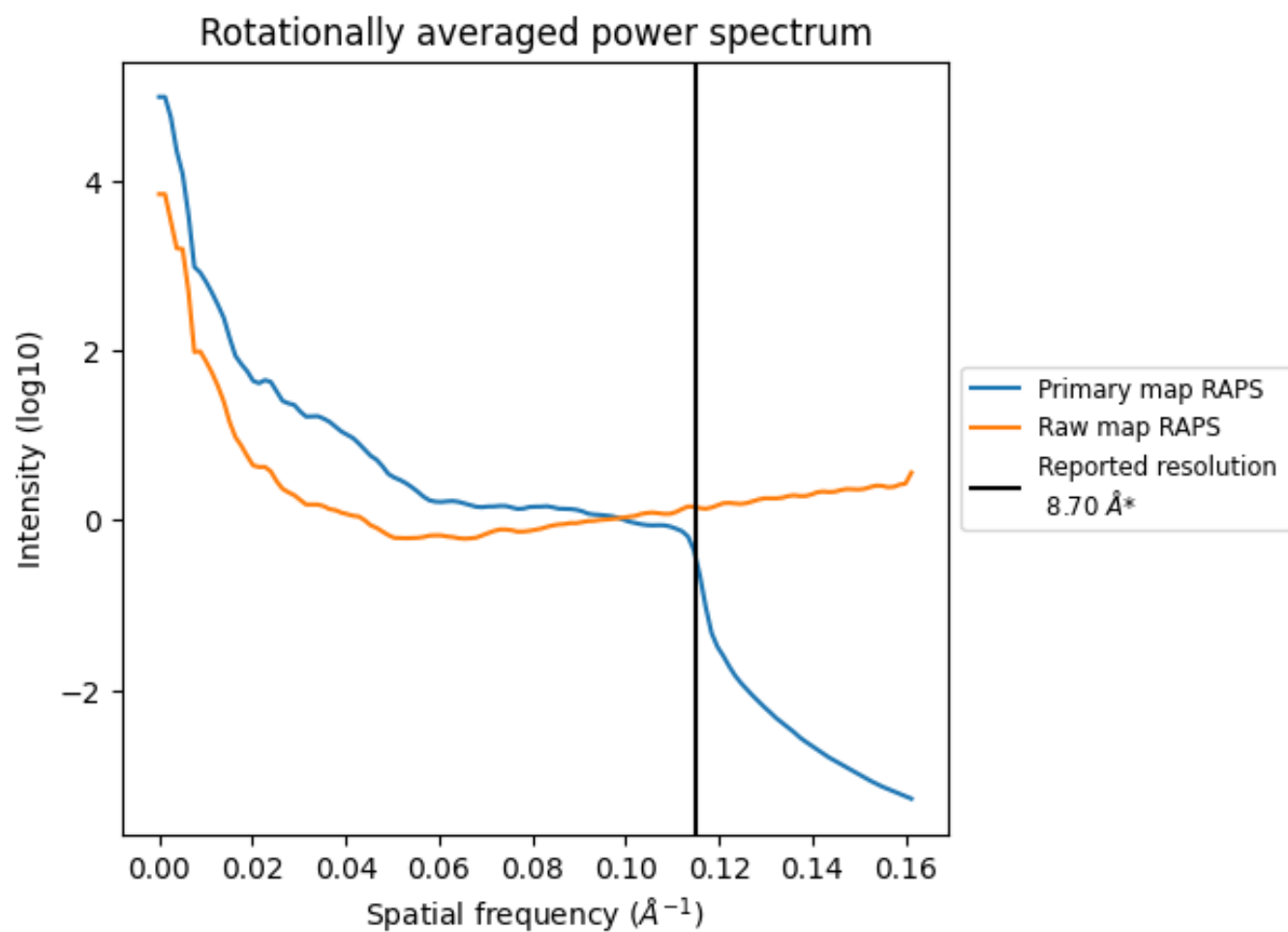
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4893 nm^3 ; this corresponds to an approximate mass of 4420 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 ⓘ

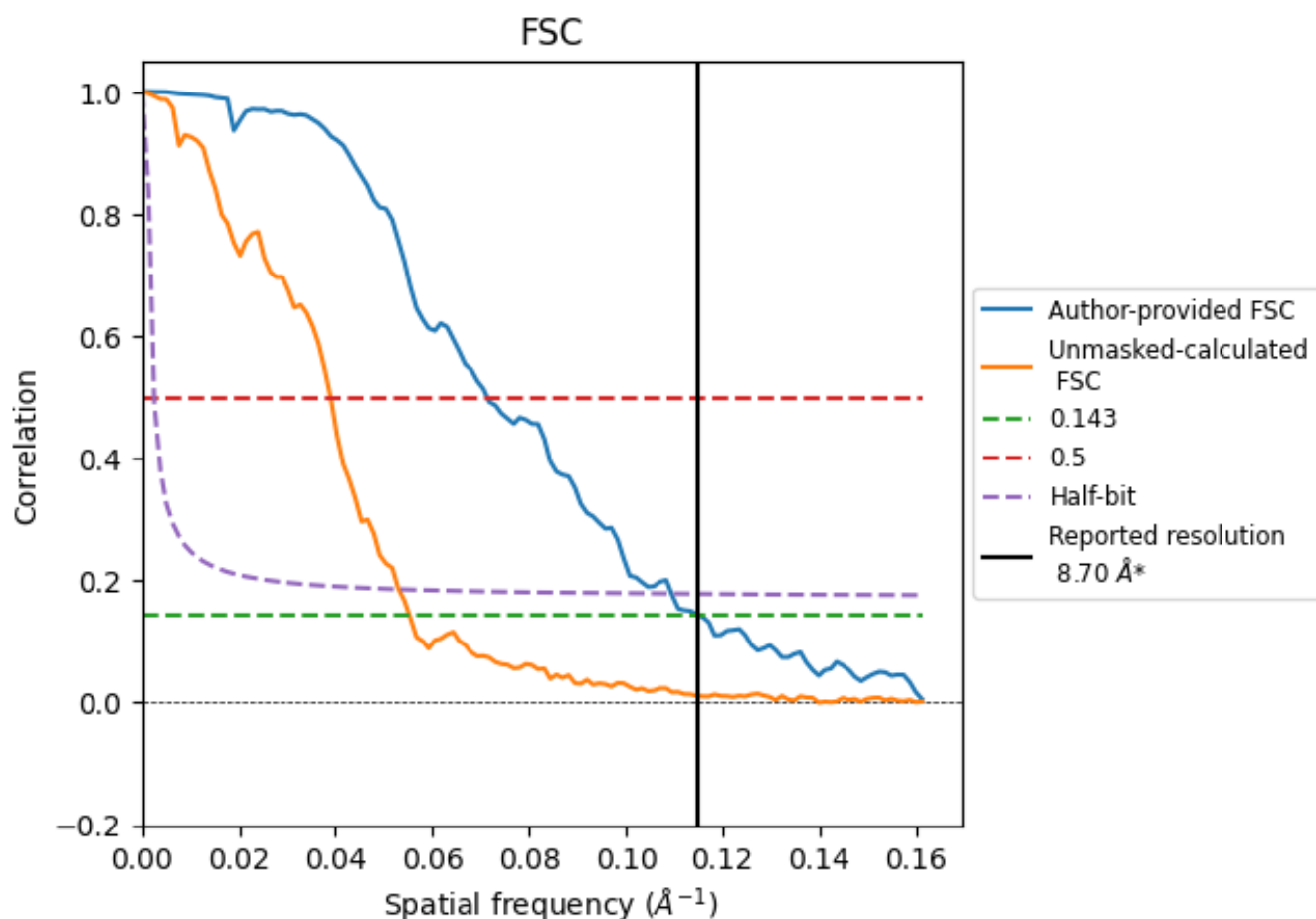


*Reported resolution corresponds to spatial frequency of 0.115 $\text{\AA}^{-1}$

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 0.115 Å⁻¹

8.2 Resolution estimates [i](#)

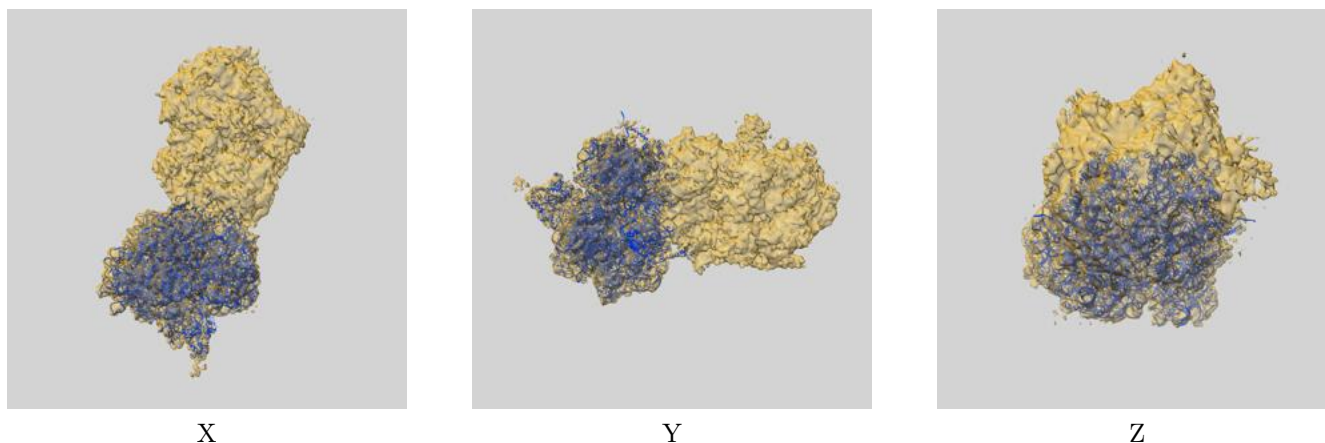
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.70	-	-
Author-provided FSC curve	8.68	14.01	9.13
Unmasked-calculated*	18.08	25.71	18.83

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 18.08 differs from the reported value 8.7 by more than 10 %

9 Map-model fit [i](#)

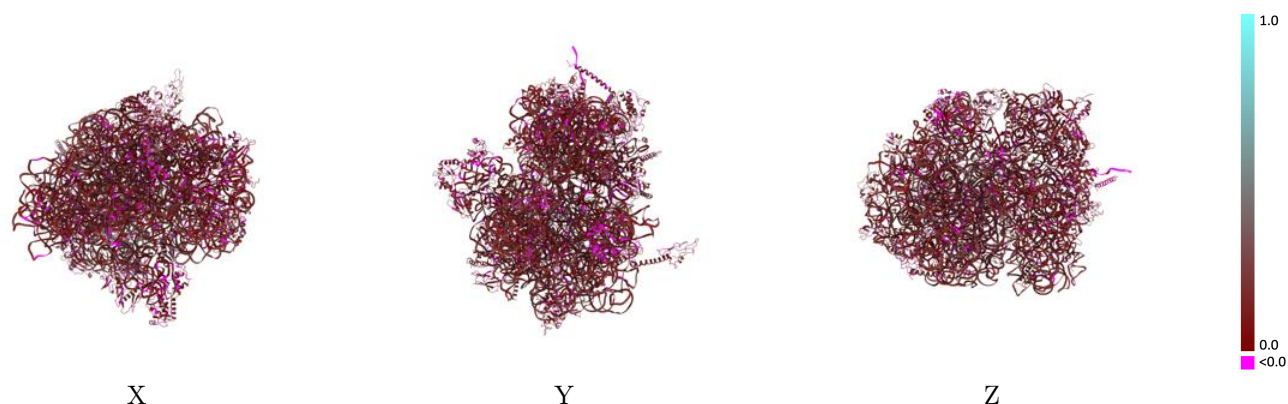
This section contains information regarding the fit between EMDB map EMD-17145 and PDB model 8P8V. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



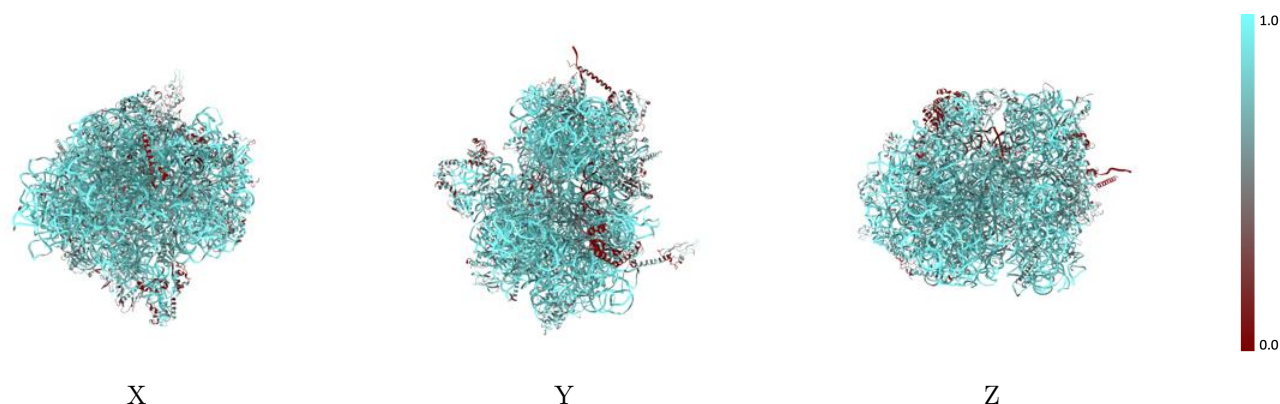
The images above show the 3D surface view of the map at the recommended contour level 1.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



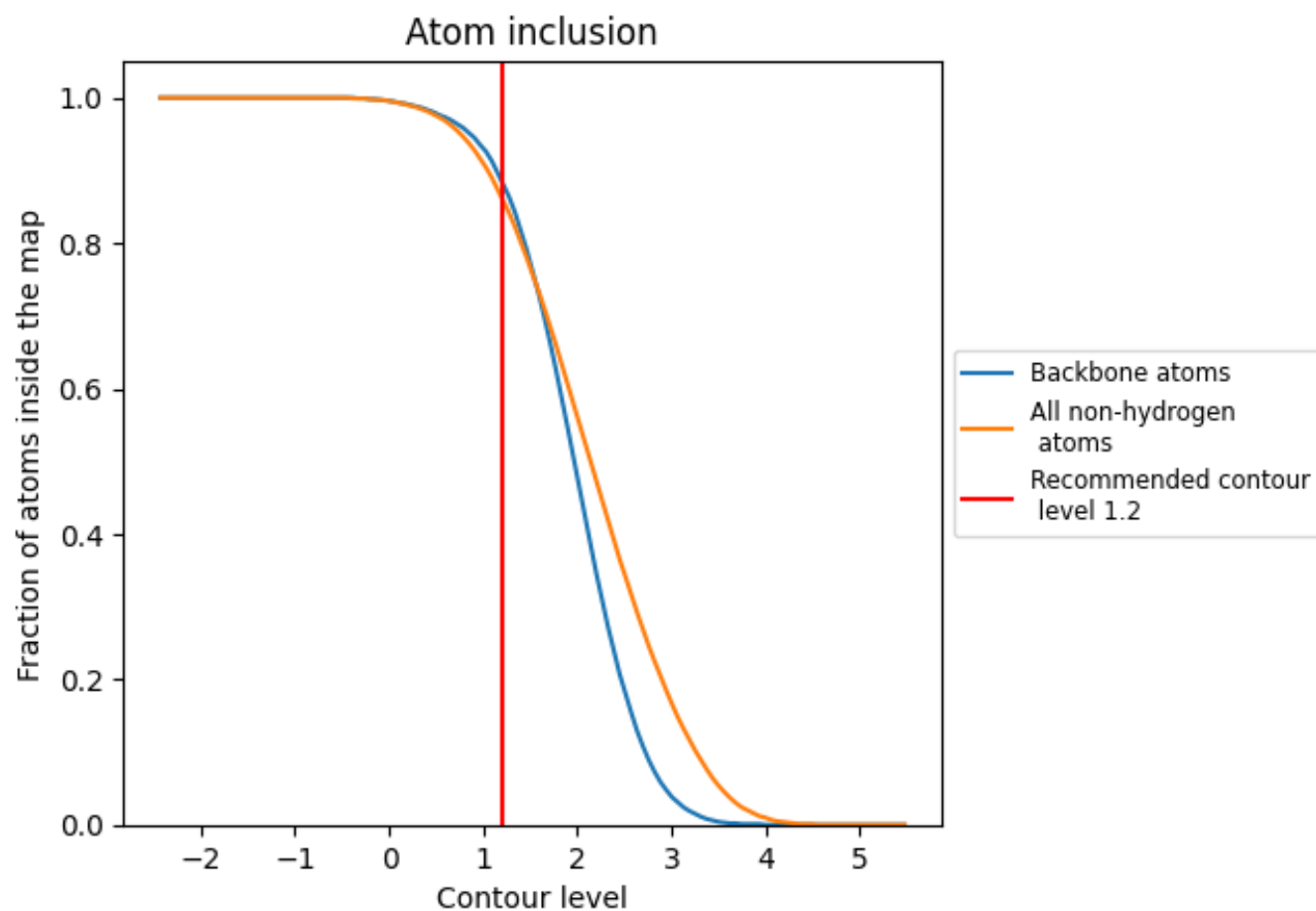
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (1.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8620	 0.1410
0	 0.8790	 0.1210
1	 0.8050	 0.1100
2	 0.8250	 0.0770
3	 0.9670	 0.1560
4	 0.9660	 0.1580
5	 0.9610	 0.1540
6	 0.4120	 0.0900
7	 0.9360	 0.1530
8	 0.7940	 0.1540
9	 0.1110	 0.0370
A	 0.6140	 0.1390
B	 0.7110	 0.1250
C	 0.6850	 0.1130
D	 0.6690	 0.1170
E	 0.5570	 0.1310
F	 0.7200	 0.1370
G	 0.7170	 0.1230
H	 0.7390	 0.0960
I	 0.6440	 0.0920
J	 0.5920	 0.0980
K	 0.7840	 0.1280
L	 0.7260	 0.1310
M	 0.8000	 0.1130
N	 0.7850	 0.1540
O	 0.7800	 0.1100
P	 0.6880	 0.1210
Q	 0.6090	 0.1400
R	 0.7520	 0.1000
S	 0.7930	 0.1330
T	 0.6920	 0.1580
X	 0.4890	 0.1050
Y	 0.5720	 0.0990
Z	 0.4330	 0.0540
a	 0.7790	 0.1030



Continued on next page...

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Chain	Atom inclusion	Q-score
b	 0.7210	 0.0960
c	 0.7490	 0.1230
d	 0.6910	 0.1180
e	 0.6440	 0.1270
f	 0.5230	 0.1390
g	 0.6170	 0.0990
h	 0.3690	 0.0540
i	 0.7920	 0.1160
j	 0.6980	 0.1170
k	 0.7500	 0.1210
l	 0.7860	 0.1190
m	 0.8060	 0.1090
n	 0.8000	 0.1200
o	 0.7350	 0.1280
p	 0.8070	 0.1270
q	 0.7550	 0.1180
r	 0.8050	 0.1380
s	 0.7240	 0.1220
t	 0.6840	 0.1210
u	 0.7410	 0.0790
v	 0.7970	 0.1030
w	 0.6800	 0.1620
x	 0.4950	 0.1020
y	 0.8050	 0.0930
z	 0.8440	 0.1260