



wwPDB EM Validation Summary Report ⓘ

Dec 29, 2024 – 03:13 PM EST

PDB ID : 7QVP
EMDB ID : EMD-14181
Title : Human collided disome (di-ribosome) stalled on XBP1 mRNA
Authors : Denk, T.G.; Tesina, P.; Beckmann, R.
Deposited on : 2022-01-22
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

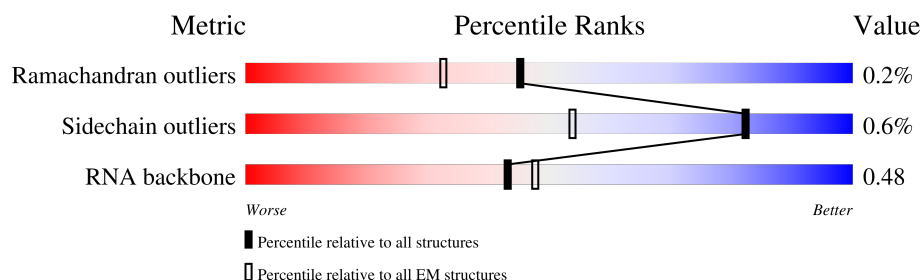
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.




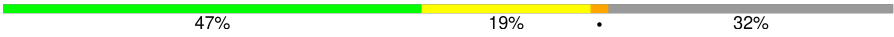


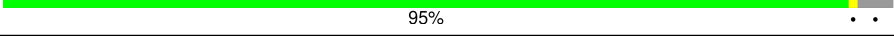
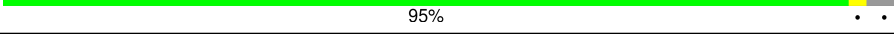
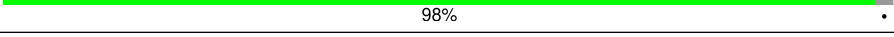
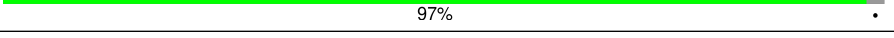
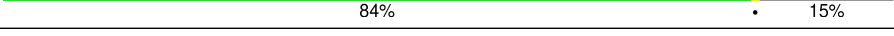

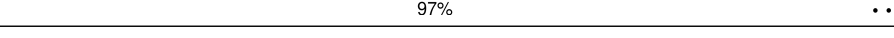
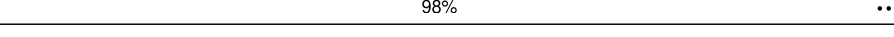

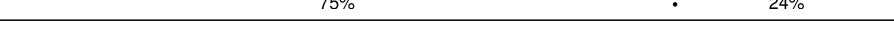


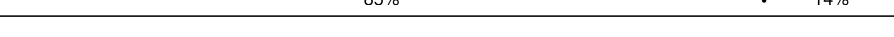

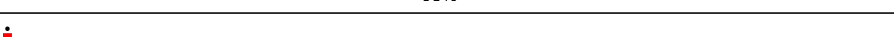






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A4	14	
2	A5	11	
3	B4	76	
3	D5	76	
4	B5	75	
5	CC	75	
6	L1	157	
6	L8	157	

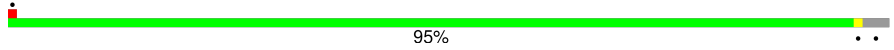

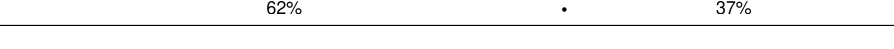
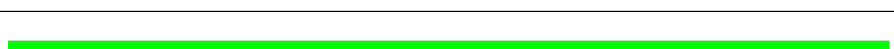
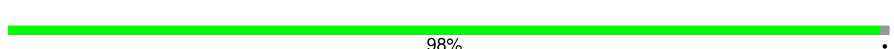
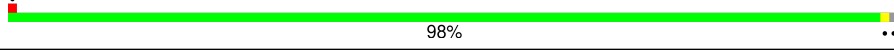
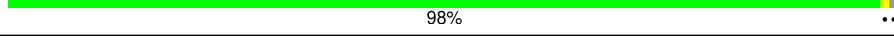
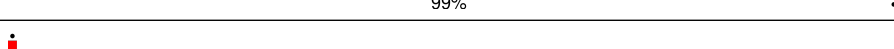


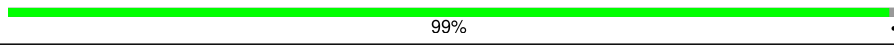
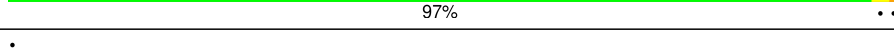
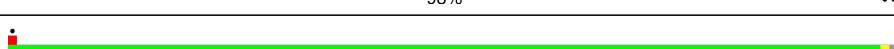
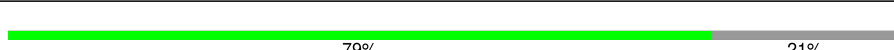

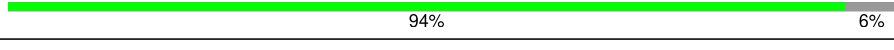
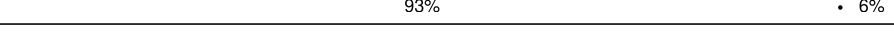



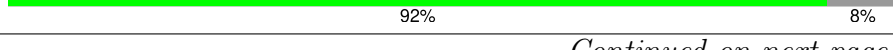



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Mol	Chain	Length	Quality of chain
7	L5	5227	
7	L6	5227	
8	L7	121	
8	L9	121	
9	LA	257	
9	MA	257	
10	LB	403	
10	MB	403	
11	LC	427	
11	MC	427	
12	LD	297	
12	MD	297	
13	LE	288	
13	ME	288	
14	LF	248	
14	MF	248	
15	LG	266	
15	MG	266	
16	LH	192	
16	MH	192	
17	LI	214	
17	MI	214	
18	LJ	178	
18	MJ	178	
19	LL	211	

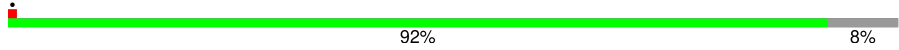
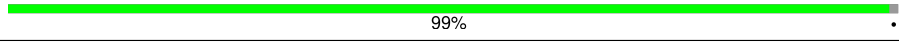
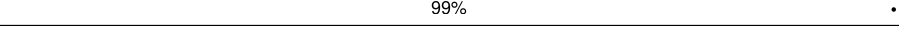
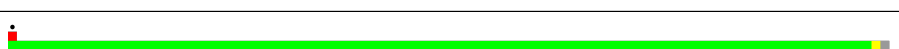



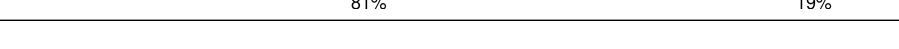

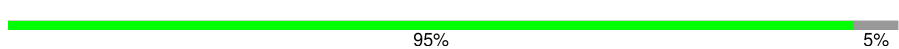
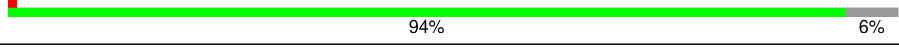
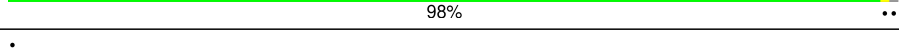
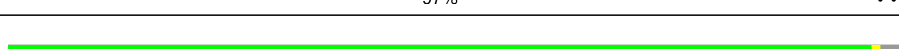
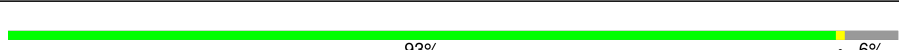
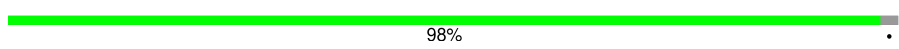
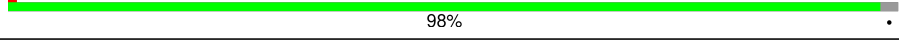
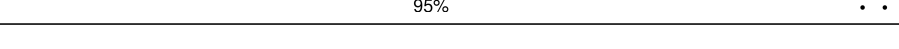


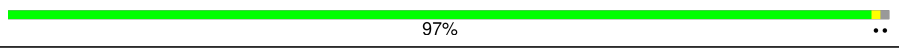
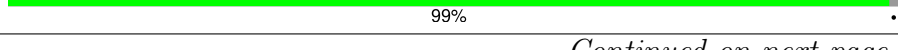



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Mol	Chain	Length	Quality of chain
19	ML	211	
20	LM	215	
20	MM	215	
21	LN	204	
21	MN	204	
22	LO	203	
22	MO	203	
23	LP	154	
24	LQ	188	
24	MQ	188	
25	LR	196	
25	MR	196	
26	LS	176	
26	MS	176	
27	LT	160	
27	MT	160	
28	LU	128	
28	MU	128	
29	LV	140	
29	MV	140	
30	LW	157	
30	MW	157	
31	LX	156	
31	MX	156	
32	LY	145	

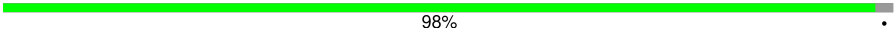
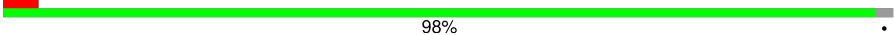




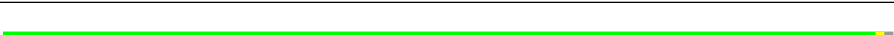
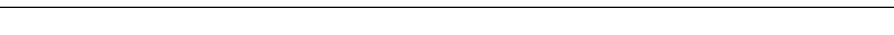
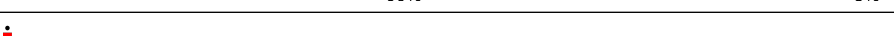
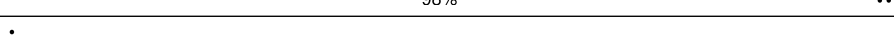
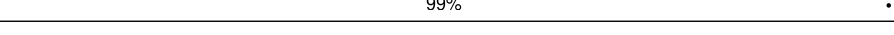
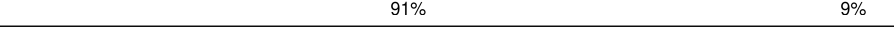











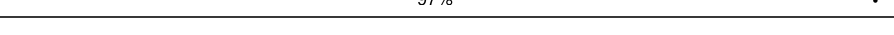
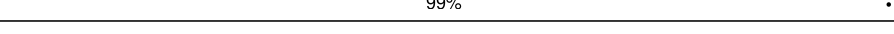
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Mol	Chain	Length	Quality of chain
32	MY	145	
33	LZ	136	
33	MZ	136	
34	La	148	
34	Ma	148	
35	Lb	159	
35	Mb	159	
36	Lc	115	
36	Mc	115	
37	Ld	125	
37	Md	125	
38	Le	135	
38	Me	135	
39	Lf	110	
39	Mf	110	
40	Lg	117	
40	Mg	117	
41	Lh	123	
41	Mh	123	
42	Li	105	
42	Mi	105	
43	Lj	88	
43	Mj	88	
44	Lk	70	
44	Mk	70	


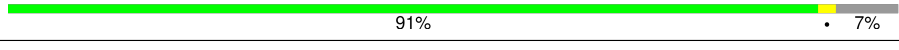
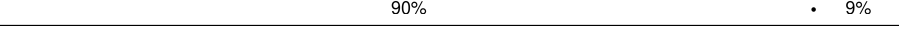
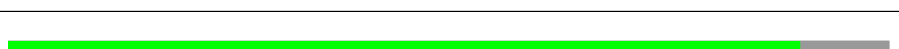
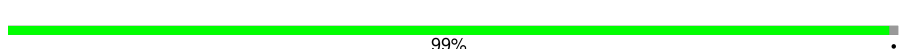

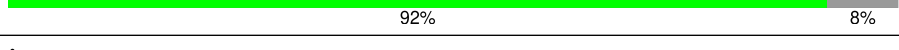
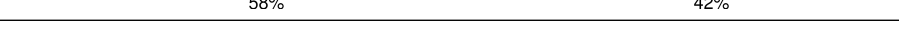


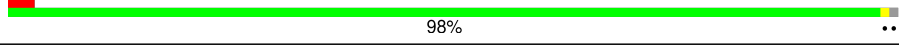
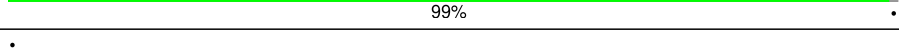

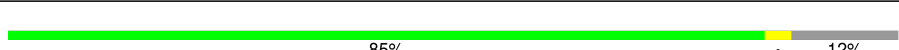

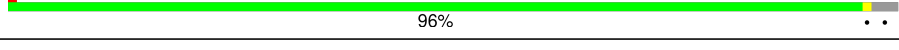
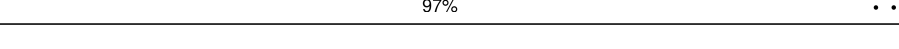


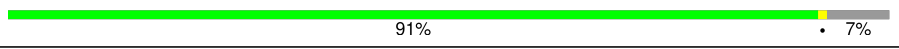
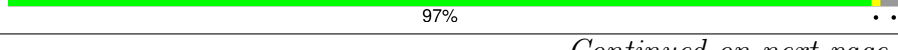



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Mol	Chain	Length	Quality of chain
45	Ll	51	
45	Ml	51	
46	Lm	128	
46	Mm	128	
47	Ln	25	
47	Mn	25	
48	Lo	106	
48	Mo	106	
49	Lp	92	
49	Mp	92	
50	Lr	137	
50	Mr	137	
51	MP	184	
52	RA	295	
52	SA	295	
53	RB	264	
53	SB	264	
54	RC	293	
54	SC	293	
55	RD	243	
55	SD	243	
56	RE	263	
56	SE	263	
57	RF	204	
57	SF	204	

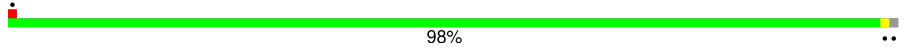


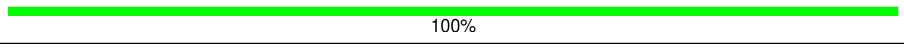
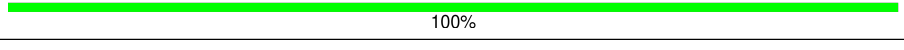
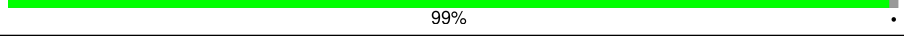
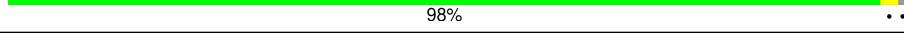
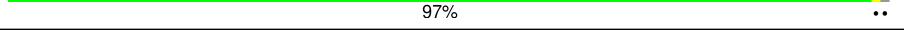
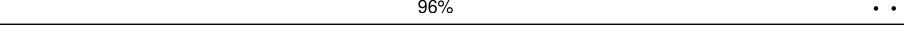
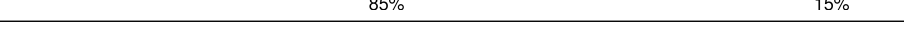


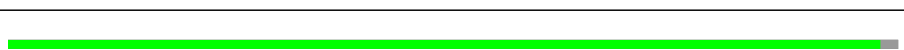
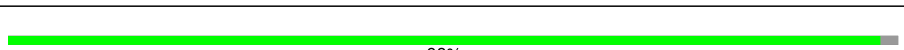
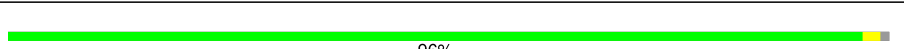
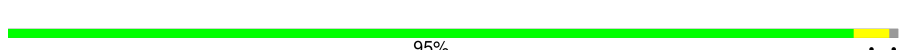


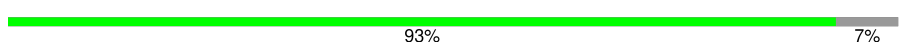
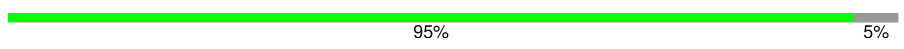
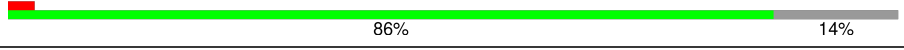
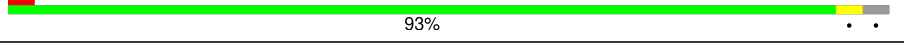



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Mol	Chain	Length	Quality of chain
58	RG	249	
58	SG	249	
59	RH	194	
59	SH	194	
60	RI	208	
60	SI	208	
61	RJ	194	
61	SJ	194	
62	RK	165	
62	SK	165	
63	RL	158	
63	SL	158	
64	RN	151	
64	SN	151	
65	RO	151	
65	SO	151	
66	RP	145	
66	SP	145	
67	RQ	146	
67	SQ	146	
68	RR	135	
68	SR	135	
69	RS	152	
69	SS	152	
70	RT	145	

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Mol	Chain	Length	Quality of chain
70	ST	145	
71	RU	119	
71	SU	119	
72	RV	83	
72	SV	83	
73	RW	130	
73	SW	130	
74	RX	143	
74	SX	143	
75	RY	133	
75	SY	133	
76	RZ	125	
76	SZ	125	
77	Ra	101	
77	Sa	101	
78	Rb	84	
78	Sb	84	
79	Rc	69	
79	Sc	69	
80	Rd	56	
80	Sd	56	
81	Re	59	
81	Se	59	
82	Rf	132	
83	Rg	317	

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Mol	Chain	Length	Quality of chain
83	Sg	317	<div><div></div><div>96%</div><div></div><div></div></div>
84	Rh	156	<div><div></div><div>26%</div><div></div><div>74%</div></div>
85	S2	1869	<div><div></div><div>57%</div><div></div><div>31%</div><div></div><div>•</div><div>8%</div></div>
85	S3	1869	<div><div></div><div>58%</div><div></div><div>29%</div><div></div><div>•</div><div>9%</div></div>

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 417512 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 mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A4	14	Total	C	N	O	P	0	0
			280	126	28	112	14		

- Molecule 2 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A5	11	Total	C	N	O	P	0	0
			220	99	22	88	11		

- Molecule 3 is a RNA chain called tRNA P/P.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B4	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		
3	D5	73	Total	C	N	O	P	0	0
			1559	696	283	508	72		

- Molecule 4 is a RNA chain called tRNA P/E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B5	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 5 is a RNA chain called tRNA E/E.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CC	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CC	11	C	U	conflict	GB 176418

- Molecule 6 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L1	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		
6	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 7 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L5	3611	Total	C	N	O	P	0	0
			77405	34468	14160	25167	3610		
7	L6	3572	Total	C	N	O	P	0	0
			76565	34095	14005	24894	3571		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		
8	L9	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 9 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		
9	MA	248	Total	C	N	O	S	0	0
			1886	1183	386	311	6		

- Molecule 10 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LB	395	Total	C	N	O	S	0	0
			3183	2027	597	545	14		
10	MB	393	Total	C	N	O	S	0	0
			3101	1979	583	525	14		

- Molecule 11 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	364	Total	C	N	O	S	0	0
			2884	1814	576	479	15		
11	MC	365	Total	C	N	O	S	0	0
			2894	1819	578	482	15		

- Molecule 12 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	293	Total	C	N	O	S	0	0
			2361	1496	430	421	14		
12	MD	293	Total	C	N	O	S	0	0
			2287	1455	426	392	14		

- Molecule 13 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	219	Total	C	N	O	S	0	0
			1754	1129	334	287	4		
13	ME	220	Total	C	N	O	S	0	0
			1713	1104	326	279	4		

- Molecule 14 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		
14	MF	225	Total	C	N	O	S	0	0
			1844	1189	355	291	9		

- Molecule 15 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	229	Total	C	N	O	S	0	0
			1818	1157	351	306	4		
15	MG	229	Total	C	N	O	S	0	0
			1733	1106	335	288	4		

- Molecule 16 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
16	MH	189	Total	C	N	O	S	0	0
			1439	910	273	250	6		

- Molecule 17 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	206	Total	C	N	O	S	0	0
			1651	1051	318	268	14		
17	MI	203	Total	C	N	O	S	0	0
			1581	1007	306	254	14		

- Molecule 18 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	169	Total	C	N	O	S	0	0
			1329	841	250	232	6		
18	MJ	167	Total	C	N	O	S	0	0
			1226	780	228	212	6		

- Molecule 19 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LL	205	Total	C	N	O	S	0	0
			1630	1020	340	266	4		
19	ML	204	Total	C	N	O	S	0	0
			1580	992	335	249	4		

- Molecule 20 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LM	139	Total	C	N	O	S	0	0
			1122	720	216	179	7		
20	MM	136	Total	C	N	O	S	0	0
			1097	705	211	174	7		

- Molecule 21 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		
21	MN	203	Total	C	N	O	S	0	0
			1693	1068	359	262	4		

- Molecule 22 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LO	200	Total	C	N	O	S	0	0
			1633	1053	318	257	5		
22	MO	201	Total	C	N	O	S	0	0
			1613	1042	318	248	5		

- Molecule 23 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LP	153	Total	C	N	O	S	0	0
			1234	771	240	214	9		

- Molecule 24 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LQ	187	Total	C	N	O	S	0	0
			1502	939	313	245	5		
24	MQ	187	Total	C	N	O	S	0	0
			1493	931	311	246	5		

- Molecule 25 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LR	176	Total	C	N	O	S	0	0
			1452	898	318	227	9		
25	MR	175	Total	C	N	O	S	0	0
			1412	874	312	218	8		

- Molecule 26 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LS	175	Total	C	N	O	S	0	0
			1452	925	283	234	10		
26	MS	175	Total	C	N	O	S	0	0
			1436	915	281	230	10		

- Molecule 27 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LT	159	Total	C	N	O	S	0	0
			1282	813	250	213	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
27	MT	159	Total	C	N	O	S	0	0
			1268	805	249	209	5		

- Molecule 28 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LU	101	Total	C	N	O	S	0	0
			799	515	140	142	2		
28	MU	101	Total	C	N	O	S	0	0
			768	497	136	133	2		

- Molecule 29 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LV	131	Total	C	N	O	S	0	0
			971	613	183	170	5		
29	MV	131	Total	C	N	O	S	0	0
			954	604	180	165	5		

- Molecule 30 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LW	115	Total	C	N	O	S	0	0
			808	506	160	139	3		
30	MW	115	Total	C	N	O	S	0	0
			784	493	154	135	2		

- Molecule 31 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LX	120	Total	C	N	O	S	0	0
			981	627	184	169	1		
31	MX	120	Total	C	N	O	S	0	0
			950	611	182	156	1		

- Molecule 32 is a protein called KOW domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LY	134	Total	C	N	O	S	0	0
			1111	697	225	186	3		
32	MY	134	Total	C	N	O	S	0	0
			1084	681	220	180	3		

- Molecule 33 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		
33	MZ	135	Total	C	N	O	S	0	0
			1082	703	207	169	3		

- Molecule 34 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	La	147	Total	C	N	O	S	0	0
			1154	731	236	184	3		
34	Ma	146	Total	C	N	O	S	0	0
			1145	726	233	183	3		

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lb	75	Total	C	N	O	S	0	0
			590	367	123	97	3		
35	Mb	63	Total	C	N	O	S	0	0
			499	310	107	80	2		

- Molecule 36 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lc	97	Total	C	N	O	S	0	0
			742	473	130	133	6		
36	Mc	93	Total	C	N	O	S	0	0
			716	456	125	129	6		

- Molecule 37 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ld	107	Total	C	N	O	S	0	0
			874	554	171	147	2		
37	Md	107	Total	C	N	O	S	0	0
			856	546	168	140	2		

- Molecule 38 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Le	128	Total	C	N	O	S	0	0
			1049	664	215	165	5		
38	Me	127	Total	C	N	O	S	0	0
			1045	661	215	164	5		

- Molecule 39 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		
39	Mf	109	Total	C	N	O	S	0	0
			864	547	173	141	3		

- Molecule 40 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lg	114	Total	C	N	O	S	0	0
			889	557	184	142	6		
40	Mg	110	Total	C	N	O	S	0	0
			851	531	175	139	6		

- Molecule 41 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lh	121	Total	C	N	O	S	0	0
			1006	635	203	167	1		
41	Mh	121	Total	C	N	O	S	0	0
			975	617	200	157	1		

- Molecule 42 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Li	102	Total	C	N	O	S	0	0
			813	510	176	123	4		
42	Mi	101	Total	C	N	O	S	0	0
			797	500	170	122	5		

- Molecule 43 is a protein called Ribosomal protein L37.

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
43	Mj	86	Total	C	N	O	S	0	0
			701	431	154	111	5		

- Molecule 44 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lk	69	Total	C	N	O	S	0	0
			542	350	100	91	1		
44	Mk	69	Total	C	N	O	S	0	0
			528	339	99	89	1		

- Molecule 45 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		
45	Ml	50	Total	C	N	O	S	0	0
			440	278	97	64	1		

- Molecule 46 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lm	52	Total	C	N	O	S	0	0
			425	264	90	65	6		
46	Mm	50	Total	C	N	O	S	0	0
			393	244	82	61	6		

- Molecule 47 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		
47	Mn	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 48 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lo	105	Total	C	N	O	S	0	0
			848	532	173	137	6		
48	Mo	98	Total	C	N	O	S	0	0
			774	488	159	121	6		

- Molecule 49 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lp	91	Total	C	N	O	S	0	0
			696	440	135	114	7		
49	Mp	91	Total	C	N	O	S	0	0
			689	436	132	114	7		

- Molecule 50 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lr	125	Total	C	N	O	S	0	0
			997	618	207	168	4		
50	Mr	125	Total	C	N	O	S	0	0
			982	609	205	164	4		

- Molecule 51 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	MP	153	Total	C	N	O	S	0	0
			1203	754	238	202	9		

- Molecule 52 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RA	212	Total	C	N	O	S	0	0
			1575	1016	285	266	8		
52	SA	216	Total	C	N	O	S	0	0
			1671	1068	297	298	8		

- Molecule 53 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RB	214	Total	C	N	O	S	0	0
			1627	1041	296	277	13		
53	SB	213	Total	C	N	O	S	0	0
			1718	1092	308	304	14		

- Molecule 54 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RC	217	Total	C	N	O	S	0	0
			1590	1039	276	266	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
54	SC	219	Total	C	N	O	S	0	0
			1661	1076	284	291	10		

- Molecule 55 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	RD	215	Total	C	N	O	S	0	0
			1475	950	267	251	7		
55	SD	223	Total	C	N	O	S	0	0
			1580	1016	286	271	7		

- Molecule 56 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RE	257	Total	C	N	O	S	0	0
			1891	1218	358	307	8		
56	SE	262	Total	C	N	O	S	0	0
			1972	1270	370	324	8		

- Molecule 57 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	RF	180	Total	C	N	O	S	0	0
			1365	861	261	237	6		
57	SF	187	Total	C	N	O	S	0	0
			1416	886	269	254	7		

- Molecule 58 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	RG	213	Total	C	N	O	S	0	0
			1551	972	313	260	6		
58	SG	231	Total	C	N	O	S	0	0
			1634	1026	332	269	7		

- Molecule 59 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	RH	176	Total	C	N	O	S	0	0
			1342	871	249	221	1		
59	SH	183	Total	C	N	O		0	0
			1274	819	242	213			

- Molecule 60 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RI	187	Total	C	N	O	S	0	0
			1450	910	286	249	5		
60	SI	206	Total	C	N	O	S	0	0
			1574	989	308	272	5		

- Molecule 61 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	RJ	176	Total	C	N	O	S	0	0
			1407	899	280	226	2		
61	SJ	179	Total	C	N	O	S	0	0
			1431	915	290	224	2		

- Molecule 62 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	RK	95	Total	C	N	O	S	0	0
			736	482	131	119	4		
62	SK	96	Total	C	N	O	S	0	0
			726	479	127	115	5		

- Molecule 63 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	RL	140	Total	C	N	O	S	0	0
			1139	725	214	194	6		
63	SL	144	Total	C	N	O	S	0	0
			1143	730	213	194	6		

- Molecule 64 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	RN	150	Total	C	N	O	S	0	0
			1199	766	229	203	1		
64	SN	150	Total	C	N	O	S	0	0
			1182	758	226	197	1		

- Molecule 65 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	RO	135	Total	C	N	O	S	0	0
			1003	615	198	184	6		
65	SO	134	Total	C	N	O	S	0	0
			969	596	194	173	6		

- Molecule 66 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	RP	127	Total	C	N	O	S	0	0
			1001	636	188	170	7		
66	SP	128	Total	C	N	O	S	0	0
			975	617	185	167	6		

- Molecule 67 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	RQ	141	Total	C	N	O	S	0	0
			1078	690	207	178	3		
67	SQ	142	Total	C	N	O	S	0	0
			1071	687	204	177	3		

- Molecule 68 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	RR	125	Total	C	N	O	S	0	0
			879	551	166	159	3		
68	SR	131	Total	C	N	O	S	0	0
			942	600	179	159	4		

- Molecule 69 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	RS	138	Total	C	N	O	S	0	0
			1080	684	220	175	1		
69	SS	141	Total	C	N	O	S	0	0
			1118	706	226	185	1		

- Molecule 70 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	RT	141	Total	C	N	O	S	0	0
			993	624	195	172	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
70	ST	143	Total	C	N	O	S	0	0
			1081	679	210	189	3		

- Molecule 71 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	RU	100	Total	C	N	O	S	0	0
			749	470	143	134	2		
71	SU	101	Total	C	N	O	S	0	0
			713	447	137	125	4		

- Molecule 72 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	RV	83	Total	C	N	O	S	0	0
			589	369	111	104	5		
72	SV	83	Total	C	N	O	S	0	0
			618	385	115	113	5		

- Molecule 73 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	RW	129	Total	C	N	O	S	0	0
			1027	655	192	174	6		
73	SW	129	Total	C	N	O	S	0	0
			1026	655	193	172	6		

- Molecule 74 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	RX	141	Total	C	N	O	S	0	0
			1048	663	206	176	3		
74	SX	141	Total	C	N	O	S	0	0
			1078	682	212	181	3		

- Molecule 75 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	RY	113	Total	C	N	O	S	0	0
			855	544	164	143	4		
75	SY	123	Total	C	N	O	S	0	0
			927	588	183	152	4		

- Molecule 76 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	RZ	70	Total	C	N	O	S	0	0
			487	311	90	85	1		
76	SZ	75	Total	C	N	O	S	0	0
			559	361	105	92	1		

- Molecule 77 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ra	99	Total	C	N	O	S	0	0
			762	478	157	122	5		
77	Sa	99	Total	C	N	O	S	0	0
			781	487	165	124	5		

- Molecule 78 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Rb	83	Total	C	N	O	S	0	0
			617	390	114	109	4		
78	Sb	83	Total	C	N	O	S	0	0
			618	386	118	107	7		

- Molecule 79 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Rc	61	Total	C	N	O	S	0	0
			430	267	83	78	2		
79	Sc	63	Total	C	N	O	S	0	0
			472	289	92	89	2		

- Molecule 80 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Rd	52	Total	C	N	O	S	0	0
			420	264	83	69	4		
80	Sd	53	Total	C	N	O	S	0	0
			433	271	87	70	5		

- Molecule 81 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Re	51	Total	C	N	O	S	0	0
			386	240	83	62	1		
81	Se	57	Total	C	N	O	S	0	0
			426	259	96	70	1		

- Molecule 82 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Rf	78	Total	C	N	O	S	0	0
			483	307	90	82	4		

- Molecule 83 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Rg	283	Total	C	N	O	S	0	0
			1952	1243	341	359	9		
83	Sg	308	Total	C	N	O	S	0	0
			2172	1388	379	394	11		

- Molecule 84 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Rh	41	Total	C	N	O	S	0	0
			269	168	54	44	3		

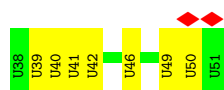
- Molecule 85 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	S2	1714	Total	C	N	O	P	0	0
			36582	16329	6568	11972	1713		
85	S3	1705	Total	C	N	O	P	0	0
			36401	16247	6542	11908	1704		

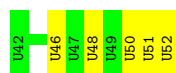
3 Residue-property plots

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: mRNA



- Molecule 2: mRNA



- Molecule 3: tRNA P/P



- Molecule 3: tRNA P/P



- Molecule 4: tRNA P/E



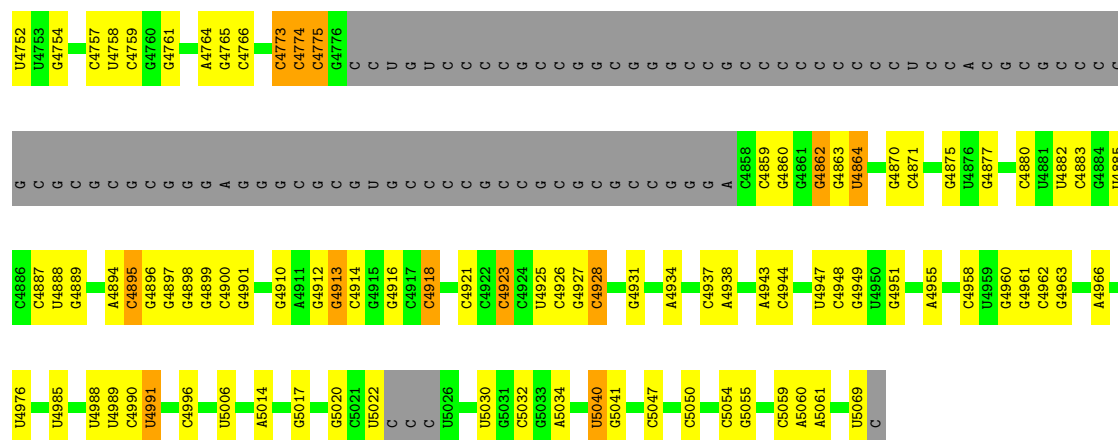
U1959	A1805	C1703	A1554	C1409	G1275	U1209	G	U	C	A915	G	C	U	C896	C	G	G
A1960	G1806	C1704	C1566	U1410	G1280	G1210	G	G1064	C	C916	C	C	C	G897	G	G	C
G1961	C1809	A1706	G1705	C1411	G1284	C1211	G	G1068	G	A917	G	G	G	G700	G	G	C
A1962	G1810	C1707	U1577	C1414	U1285	C1214	G	G1069	C	C923	G	C	C	G703	C	C	C
G1963	G1815	G	U1578	C1415	C1286	C1215	G	G1070	C	C924	G	G	G	C704	C	C	C
A1964	C1816	C	C1585	G1416	C1287	C1216	U	C1071	C	C925	C	G	U	G705	G	G	C
G1965	A	C	C1417	C1417	G	U	G	G1075	C	C926	G	G	C	G706	G	U	U
C1966	C	C	A1420	A1420	G1293	G1219	C	C1076	C	A929	G	A	C	G707	G	C	C
A1970	U1821	C	U1591	A1425	A1294	G1220	C	G1079	C	G	G	U	C	G708	G	C	C
U1974	U1822	C	U1596	G1425	C1295	G1221	C	C1082	C	A932	G	C	C	G730	U	U	C
G1975	G1832	C1715	U1597	G1435	C1301	A	G	U1083	C	G933	C	C	C	G731	G	G	C
G1976	G1833	G1716	C1598	C1436	U1302	G	C	C1089	C	C934	G	C	C	C738	G	G	C
C	U1834	C1717	C1607	U1437	A1303	U	C	U1092	C	A935	G	C	C	G739	G	G	U
C	G1835	C1718	C1607	U1437	C1304	C	C	G1093	C	C936	G	C	C	G740	G	U	U
A	G1836	A1719	U1438	C1439	C	U	C	G1094	C	U937	C	C	C	C741	C	C	C
U	A1837	C1720	U1440	U1440	C1309	U	C	A1095	C	C941	G	C	C	G742	C	C	C
G	G1842	G1724	C1441	C1441	C	U	C	U1100	C	G	G	A	G	C	G	C	C
G	U1725	U1725	C1442	C1442	A1324	U	U	C	C	A944	G	C	C	A746	C	C	C
A	G1853	U1726	A1443	C1443	C1325	C	C	U	C	U945	G	C	C	C753	C	C	C
G	G1854	A1443	G1444	G1444	C	G	G	C	C	G	G	G	C	G757	C	C	C
U	G1855	U1735	C1447	C1447	C1327	G1234	G	U1100	C	G959	G	C	C	G758	C	C	C
C	G1869	G1741	G1454	G1454	A1337	G1235	G	C	C	A960	G	C	C	C760	C	C	C
G	U1882	A1742	G1458	C1458	C1340	A1238	G	C	C	C961	G	C	C	C	C	C	C
A	A1891	G1750	C1458	C1458	C1344	C1241	G	C	C	C962	G	C	C	C	C	C	C
A	A1892	G1753	C1467	C1467	C1348	G1242	G	C	C	A964	G	C	C	C	C	C	C
C	U1893	U1754	C1468	C1468	U1348	C1243	G	C	C	A965	G	C	C	C	C	C	C
G1994	A1897	C1755	C1469	C1469	A1354	C1244	G	C	C	A966	G	C	C	C	C	C	C
G1995	U1756	U1756	C1472	C1472	C1354	C1245	G	C	C	C967	C	C	C	C	C	C	C
C1996	U1757	G1758	C1477	C1477	G1358	C1248	G	C	C	G970	G	C	C	C	C	C	C
U1997	G1760	G1760	C1477	C1477	G1359	C1249	G	C	C	U971	G	C	C	C	C	C	C
A1998	G1761	G1761	C1483	C1483	G1360	C1250	G	C	C	C972	C	C	C	C	C	C	C
U1918	C1762	C1762	C1483	C1483	C1365	C1251	G	C	C	C977	G	C	C	C	C	C	C
G1919	G1763	G1763	C1493	C1493	C1366	C1252	G	C	C	U982	G	C	C	C	C	C	C
C1920	G1764	G1764	A1497	A1497	G1377	A	G	C	C	C983	A	C	C	C	C	C	C
G1921	A1765	A1765	G1498	G1498	C1378	G	C	C	C	C984	C	C	C	C	C	C	C
A1923	A1766	A1766	C1501	C1501	C1379	A1257	G	C	C	C985	C	C	C	C	C	C	C
C1924	C	C	G1502	G1502	G1380	G1258	G	C	C	C988	A	C	C	C	C	C	C
U1929	G1769	G1769	C1501	C1501	U1381	G1259	G	C	C	U989	A	C	C	C	C	C	C
G1930	A1770	A1770	C1502	C1502	G1381	G1260	G	C	C	C990	A	C	C	C	C	C	C
C1931	U1771	U1771	U1514	U1514	A1387	G1261	G	C	C	C991	A	C	C	C	C	C	C
A1932	U1781	U1781	A1515	A1515	G1393	G1262	G	C	C	C992	A	C	C	C	C	C	C
C1935	A	A	G1516	G1516	U1395	A1263	G	C	C	G993	C	C	C	C	C	C	C
A1936	C1937	C1937	A1525	A1525	G1394	G1266	G	C	C	C	C	C	C	C	C	C	C
C1937	U1787	U1787	A1525	A1525	U1395	G1266	G	C	C	C	C	C	C	C	C	C	C
U1938	A1792	U1792	A1534	A1534	C1402	G1269	G	C	C	C	C	C	C	C	C	C	C
C1940	U1792	U1792	U1538	U1538	G1403	A1270	G	C	C	C	C	C	C	C	C	C	C
A	G1797	G1797	U1538	U1538	G1404	G1271	G	C	C	C	C	C	C	C	C	C	C
A	U1700	U1700	A1547	A1547	C1405	C1272	G	C	C	C	C	C	C	C	C	C	C
G1948	G1803	A1804	C1702	C1702	G1408	G1273	G	C	C	C	C	C	C	C	C	C	C
U1949	C2017	C2017	C1698	C1698	C1402	G1274	G	C	C	C	C	C	C	C	C	C	C
C2018	C2018	C2018	A1699	A1699	G1403	G1271	G	C	C	C	C	C	C	C	C	C	C
U2020	U1949	U1949	G1700	G1700	G1404	G1272	G	C	C	C	C	C	C	C	C	C	C
G2021	C2019	C2019	A1701	A1701	C1405	G1273	G	C	C	C	C	C	C	C	C	C	C
			C1702	C1702	G1408	A1274	G	C	C	C	C	C	C	C	C	C	C





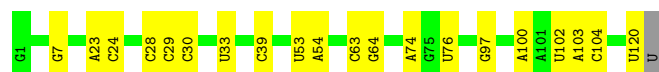






- Molecule 8: 5S ribosomal RNA

Chain L7: 83% 17%



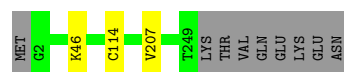
- Molecule 8: 5S ribosomal RNA

Chain L9: 80% 19%



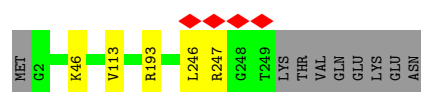
- Molecule 9: 60S ribosomal protein L8

Chain LA: 95%



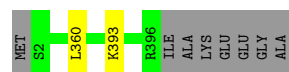
- Molecule 9: 60S ribosomal protein L8

Chain MA: 95%



- Molecule 10: 60S ribosomal protein L3

Chain LB: 98%



- Molecule 10: 60S ribosomal protein L3

MET
 S2
 L292
 ILE
 LYS
 ASP
 GLY
 LYS
 L298
 L360
 K399
 GLU
 GLU
 GLY
 ALA

-
- Sequence logo for the 10th position. The y-axis represents information content in bits, ranging from 0 to 0.4. The x-axis shows amino acids: PRO, ALA, GLU, LYS, THR, GLU, LYS, PRO, ALA. The logo shows a strong preference for LYS at this position, with a peak of approximately 0.35 bits. Other amino acids have very low information content at this position.


- [illegible]

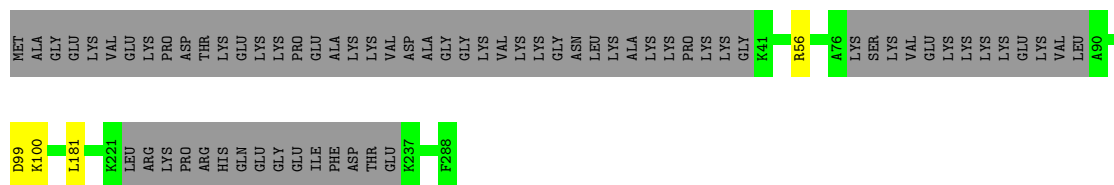
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- MET G2 K5 V231 T232 A294 ALA GLU SER

- [illegible]

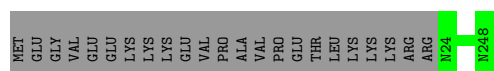
- 
- WORLDWIDE
PDB
PROTEIN DATA BANK

Chain ME:  75% 24%



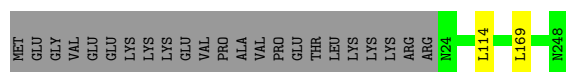
- Molecule 14: 60S ribosomal protein L7

Chain LF:  91% 9%




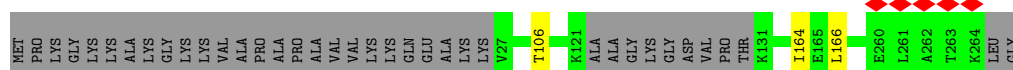
- Molecule 14: 60S ribosomal protein L7

Chain MF:  90% 9%




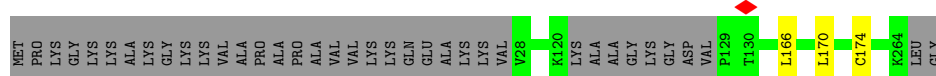
- Molecule 15: 60S ribosomal protein L7a

Chain LG:  85% 14%



- Molecule 15: 60S ribosomal protein L7a

Chain MG:  85% 14%



- Molecule 16: 60S ribosomal protein L9

Chain LH:  98%



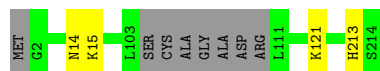
- Molecule 16: 60S ribosomal protein L9

Chain MH:  97%



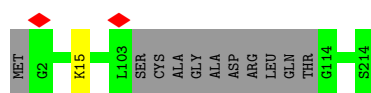
- Molecule 17: 60S ribosomal protein L10-like

Chain LI: 94%



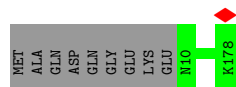
- Molecule 17: 60S ribosomal protein L10-like

Chain MI: 94%



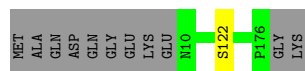
- Molecule 18: 60S ribosomal protein L11

Chain LJ: 95%



- Molecule 18: 60S ribosomal protein L11

Chain MJ: 93%



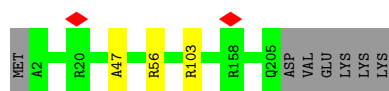
- Molecule 19: 60S ribosomal protein L13

Chain LL: 95%



- Molecule 19: 60S ribosomal protein L13

Chain ML: 95%



- Molecule 20: 60S ribosomal protein L14



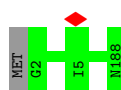
- Molecule 24: 60S ribosomal protein L18

Chain LQ: 99% ..



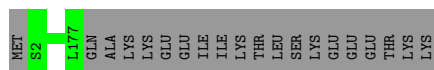
- Molecule 24: 60S ribosomal protein L18

Chain MQ: 99% .



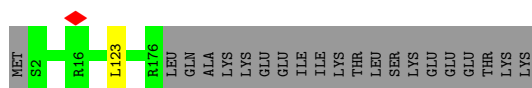
- Molecule 25: 60S ribosomal protein L19

Chain LR: 90% 10%



- Molecule 25: 60S ribosomal protein L19

Chain MR: 89% 11%



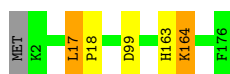
- Molecule 26: 60S ribosomal protein L18a

Chain LS: 99% .



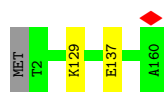
- Molecule 26: 60S ribosomal protein L18a

Chain MS: 97% ...

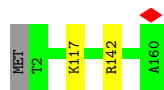


- Molecule 27: 60S ribosomal protein L21

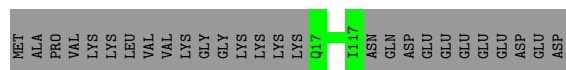
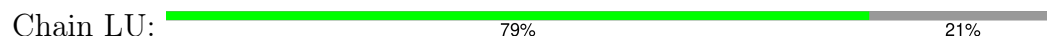
Chain LT: 98% ..



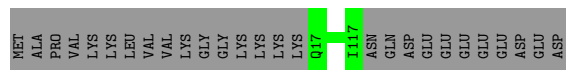
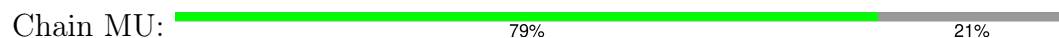
- Molecule 27: 60S ribosomal protein L21



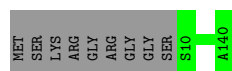
- Molecule 28: 60S ribosomal protein L22



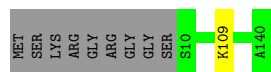
- Molecule 28: 60S ribosomal protein L22



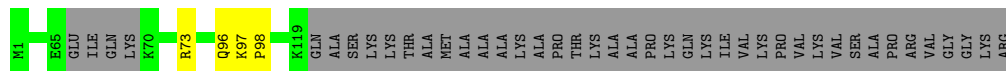
- Molecule 29: 60S ribosomal protein L23



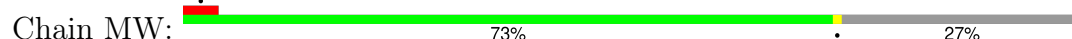
- Molecule 29: 60S ribosomal protein L23

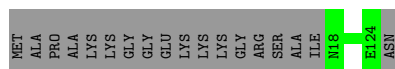


- Molecule 30: 60S ribosomal protein L24



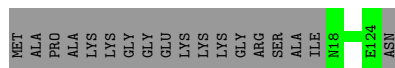
- Molecule 30: 60S ribosomal protein L24





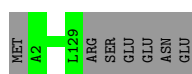
- Molecule 37: 60S ribosomal protein L31

Chain Md: 86% 14%



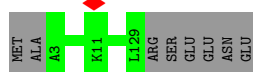
- Molecule 38: 60S ribosomal protein L32

Chain Le: 95% 5%



- Molecule 38: 60S ribosomal protein L32

Chain Me: 94% 6%



- Molecule 39: 60S ribosomal protein L35a

Chain Lf: 98% ..



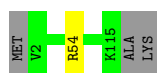
- Molecule 39: 60S ribosomal protein L35a

Chain Mf: 97% ..



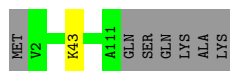
- Molecule 40: 60S ribosomal protein L34

Chain Lg: 97% ..



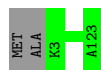
- Molecule 40: 60S ribosomal protein L34

Chain Mg: 93% • 6%



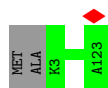
- Molecule 41: 60S ribosomal protein L35

Chain Lh: 98%



- Molecule 41: 60S ribosomal protein L35

Chain Mh: 98%



- Molecule 42: 60S ribosomal protein L36

Chain Li: 95%



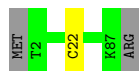
- Molecule 42: 60S ribosomal protein L36

Chain Mi: 93%



- Molecule 43: Ribosomal protein L37

Chain Lj: 97%



- Molecule 43: Ribosomal protein L37

Chain Mj: 97%



- Molecule 44: 60S ribosomal protein L38

Chain Lk: 97%



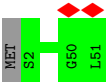
• Molecule 44: 60S ribosomal protein L38



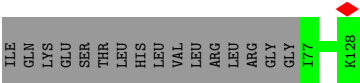
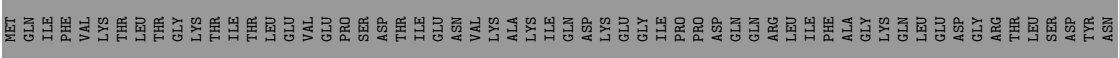
• Molecule 45: 60S ribosomal protein L39



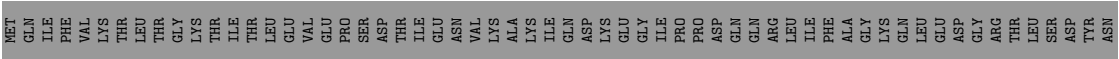
• Molecule 45: 60S ribosomal protein L39



• Molecule 46: Ubiquitin-60S ribosomal protein L40



• Molecule 46: Ubiquitin-60S ribosomal protein L40



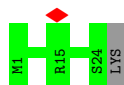
• Molecule 47: 60S ribosomal protein L41





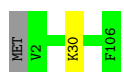
- Molecule 47: 60S ribosomal protein L41

Chain Mn: 96%



- Molecule 48: 60S ribosomal protein L36a

Chain Lo: 98%



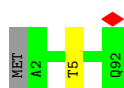
- Molecule 48: 60S ribosomal protein L36a

Chain Mo: 90% 8%



- Molecule 49: 60S ribosomal protein L37a

Chain Lp: 98%



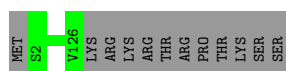
- Molecule 49: 60S ribosomal protein L37a

Chain Mp: 99%



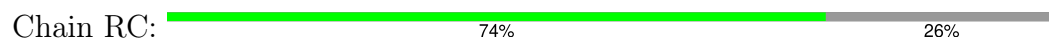
- Molecule 50: 60S ribosomal protein L28

Chain Lr: 91% 9%



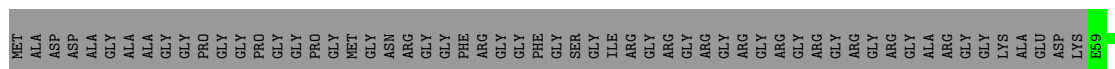
- Molecule 50: 60S ribosomal protein L28

Chain Mr: 89% 9%



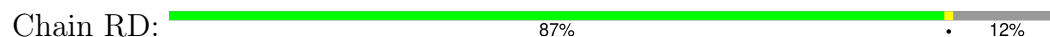
K275 THR HIS THR ARG VAL SER VAL GLN ARG THR GLN ALA PRO ALA VAL ALA THR THR

- Molecule 54: 40S ribosomal protein S2



V209
R227
Y248
H277
THR
ARG
VAL
SER
VAL
GLN
ARG
THR
GLN
ALA
PRO
ALA
VAL
ALA
THR
THR

- Molecule 55: 40S ribosomal protein S3



MET	ALA	VAL	GLN	IS	V41	THR	PRO	T44	R76	L86	P191	K214	ASP	GLU	ILE	L218	P219	T220	THR	P222	E225	GLN	LYS	GLY	GLY	LYS	PRO	PRO	GLU	PRO	PRO	ALA	MET	PRO	GLN	PRO	VAL	PRO	THR	ALA
-----	-----	-----	-----	----	-----	-----	-----	-----	-----	-----	------	------	-----	-----	-----	------	------	------	-----	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 55: 40S ribosomal protein S3



MET
 ALA
 V3
 R76
 L177
 D215
 GLU
 ILE
 L218
 K227
 GLY
 GLY
 LYS
 PRO
 PRO
 GLU
 PRO
 PRO
 PRO
 ALA
 MET
 PRO
 GLN
 PRO
 VAL
 PRO
 THR
 ALA

- Molecule 56: 40S ribosomal protein S4, X isoform

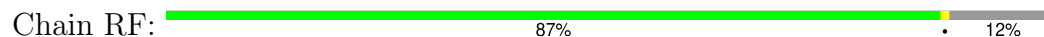


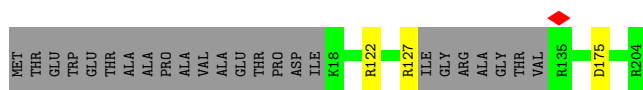
Sequence logo for the R39 position. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis shows amino acids: MET, A2, R39, V208, A258, LYS, GLN, SER, SER, GLY. R39 is the most conserved position, with a peak of approximately 1.4 bits. A red diamond is placed above the R39 position.

- Molecule 56: 40S ribosomal protein S4, X isoform

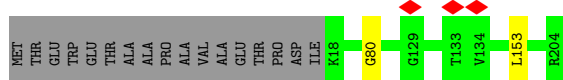


- Molecule 57: 40S ribosomal protein S5

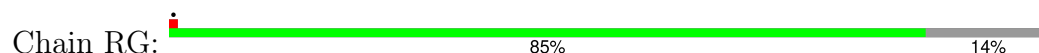




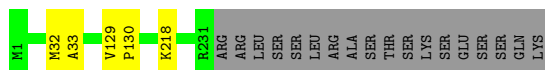
- Molecule 57: 40S ribosomal protein S5



- Molecule 58: 40S ribosomal protein S6



- Molecule 58: 40S ribosomal protein S6



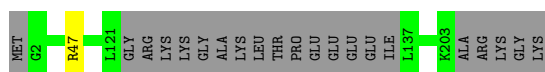
- Molecule 59: 40S ribosomal protein S7



- Molecule 59: 40S ribosomal protein S7

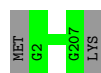


- Molecule 60: 40S ribosomal protein S8



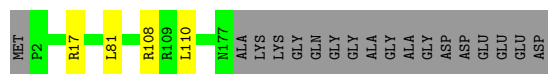
- Molecule 60: 40S ribosomal protein S8

Chain SI:  99%



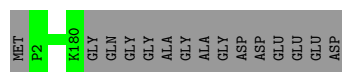
- Molecule 61: 40S ribosomal protein S9

Chain RJ:  89%



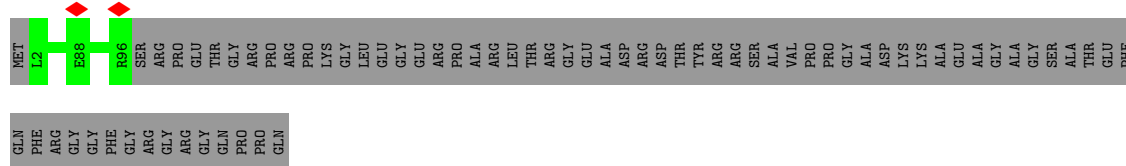
- Molecule 61: 40S ribosomal protein S9

Chain SJ:  92%



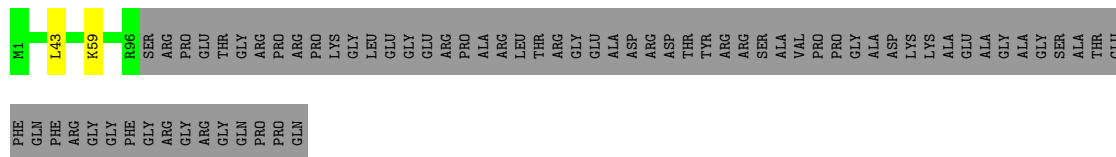
- Molecule 62: 40S ribosomal protein S10

Chain RK:  58%




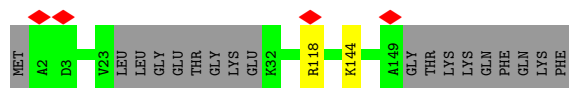
- Molecule 62: 40S ribosomal protein S10

Chain SK:  57%



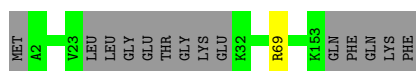
- Molecule 63: 40S ribosomal protein S11

Chain RL:  87%



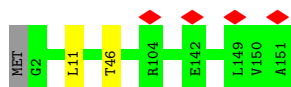
- Molecule 63: 40S ribosomal protein S11

Chain SL:  91%



- Molecule 64: 40S ribosomal protein S13

Chain RN: 98%



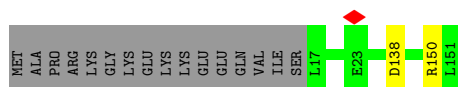
- Molecule 64: 40S ribosomal protein S13

Chain SN: 99%



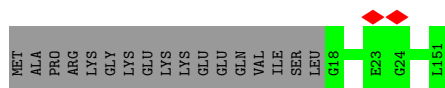
- Molecule 65: 40S ribosomal protein S14

Chain RO: 88% 11%



- Molecule 65: 40S ribosomal protein S14

Chain SO: 89% 11%



- Molecule 66: 40S ribosomal protein S15

Chain RP: 85% 12%

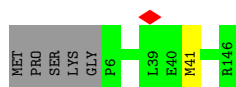


- Molecule 66: 40S ribosomal protein S15

Chain SP: 88% 12%



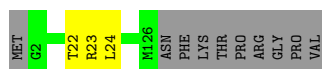
- Molecule 67: 40S ribosomal protein S16



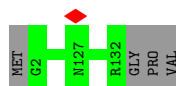
- Molecule 67: 40S ribosomal protein S16



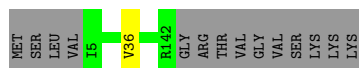
- Molecule 68: 40S ribosomal protein S17



- Molecule 68: 40S ribosomal protein S17



- Molecule 69: 40S ribosomal protein S18



- Molecule 69: 40S ribosomal protein S18

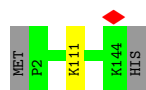


- Molecule 70: 40S ribosomal protein S19




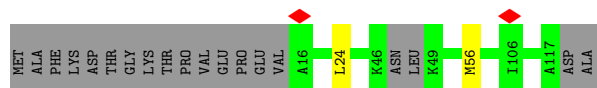
- Molecule 70: 40S ribosomal protein S19

Chain ST:  98%




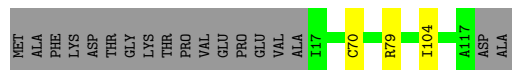
- Molecule 71: 40S ribosomal protein S20

Chain RU:  82% 16%



- Molecule 71: 40S ribosomal protein S20

Chain SU:  82% 15%



- Molecule 72: 40S ribosomal protein S21

Chain RV:  100%

There are no outlier residues recorded for this chain.

- Molecule 72: 40S ribosomal protein S21

Chain SV:  100%

There are no outlier residues recorded for this chain.

- Molecule 73: 40S ribosomal protein S15a

Chain RW:  99%



- Molecule 73: 40S ribosomal protein S15a

Chain SW:  98%



- Molecule 74: 40S ribosomal protein S23

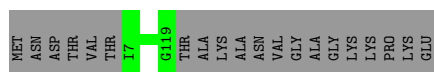
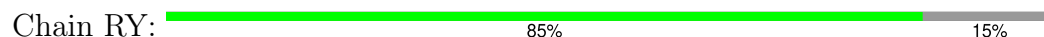
Chain RX:  97%



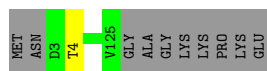
- Molecule 74: 40S ribosomal protein S23



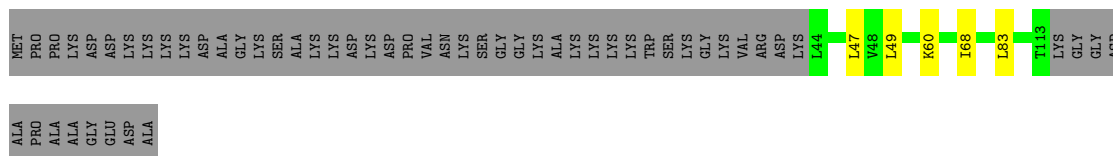
- Molecule 75: 40S ribosomal protein S24



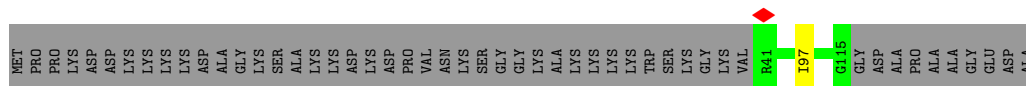
- Molecule 75: 40S ribosomal protein S24



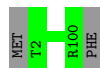
- Molecule 76: 40S ribosomal protein S25



- Molecule 76: 40S ribosomal protein S25



- Molecule 77: 40S ribosomal protein S26



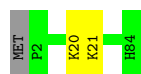
- Molecule 77: 40S ribosomal protein S26

Chain Sa:  98% .



- Molecule 78: 40S ribosomal protein S27

Chain Rb:  96% ..




- Molecule 78: 40S ribosomal protein S27

Chain Sb:  95% ..



- Molecule 79: 40S ribosomal protein S28

Chain Rc:  86% . 12%



- Molecule 79: 40S ribosomal protein S28

Chain Sc:  90% . 9%



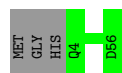
- Molecule 80: 40S ribosomal protein S29

Chain Rd:  93% 7%

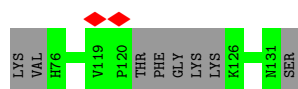
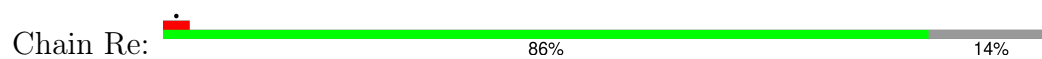


- Molecule 80: 40S ribosomal protein S29

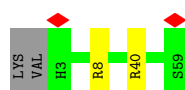
Chain Sd:  95% 5%



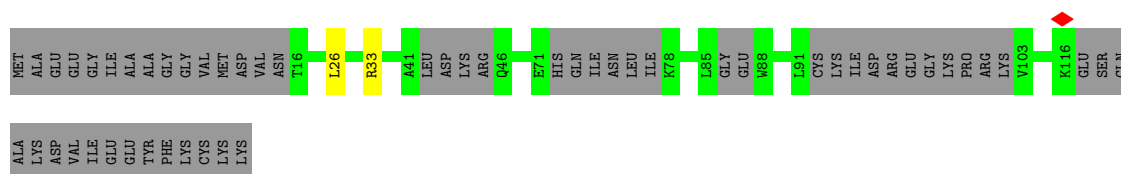
- Molecule 81: 40S ribosomal protein S30



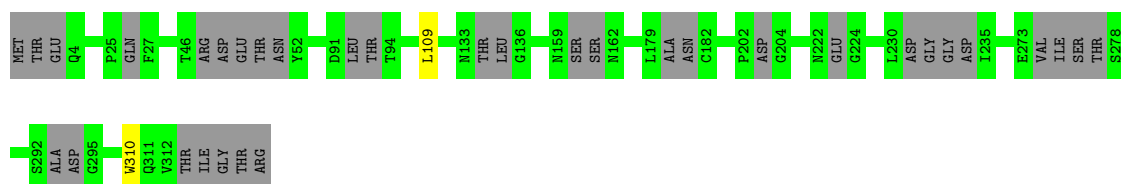
- Molecule 81: 40S ribosomal protein S30



- Molecule 82: 40S ribosomal protein S12



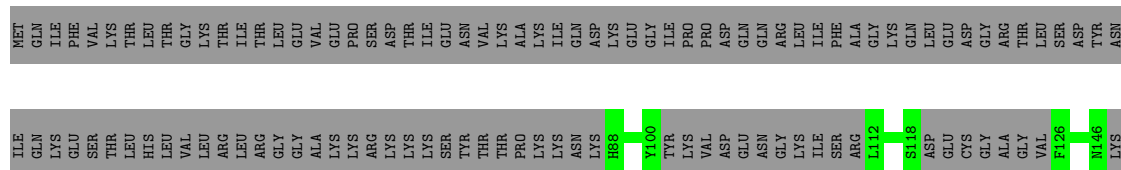
- Molecule 83: Receptor of activated protein C kinase 1



- Molecule 83: Receptor of activated protein C kinase 1



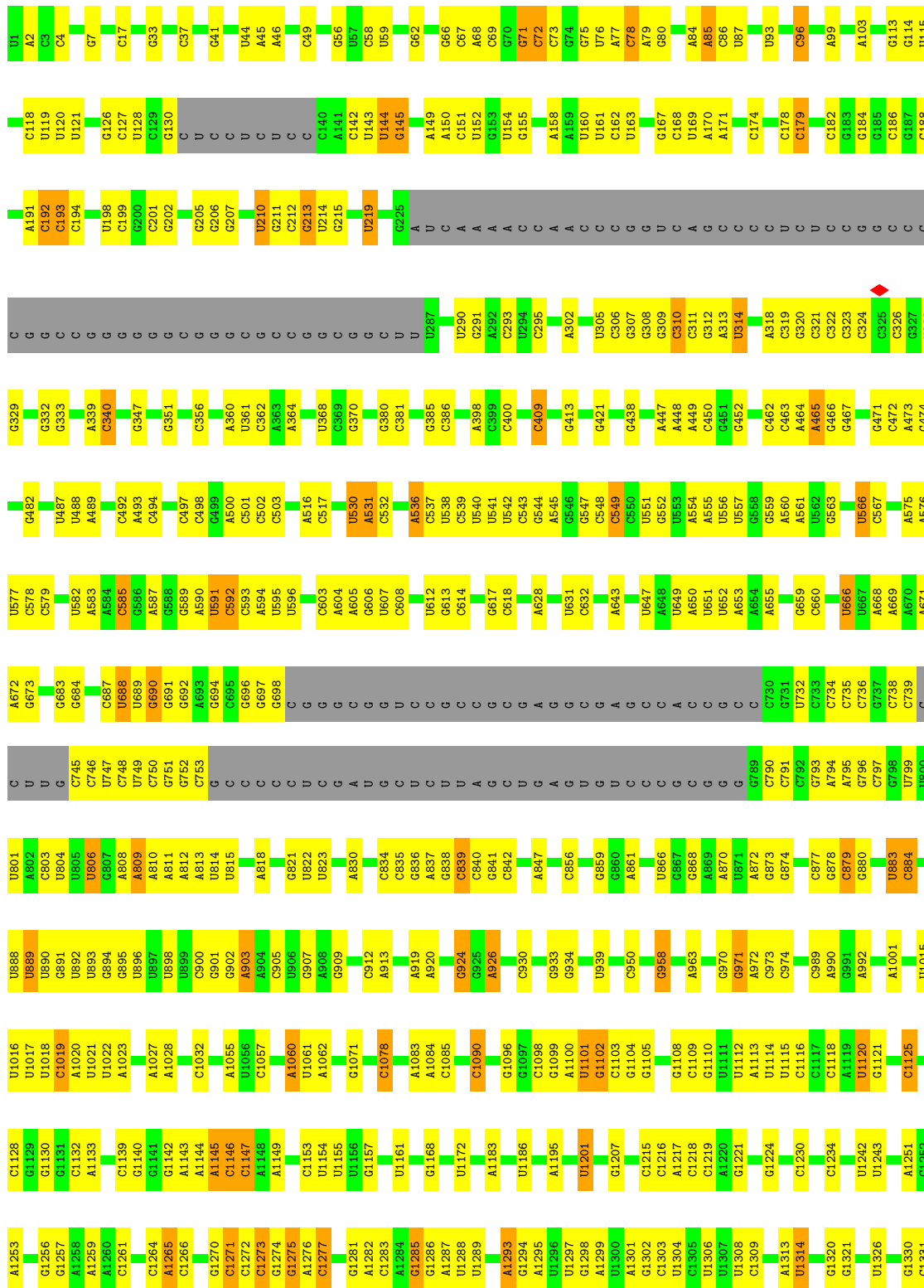
- Molecule 84: Ubiquitin-40S ribosomal protein S27a

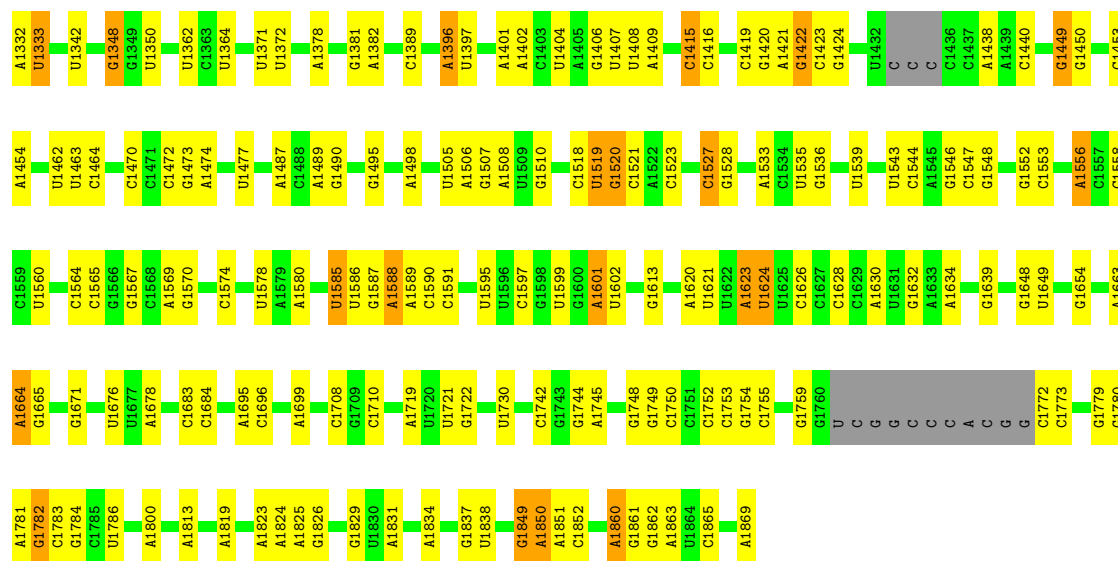


PRO
GLU
ASP
LYS

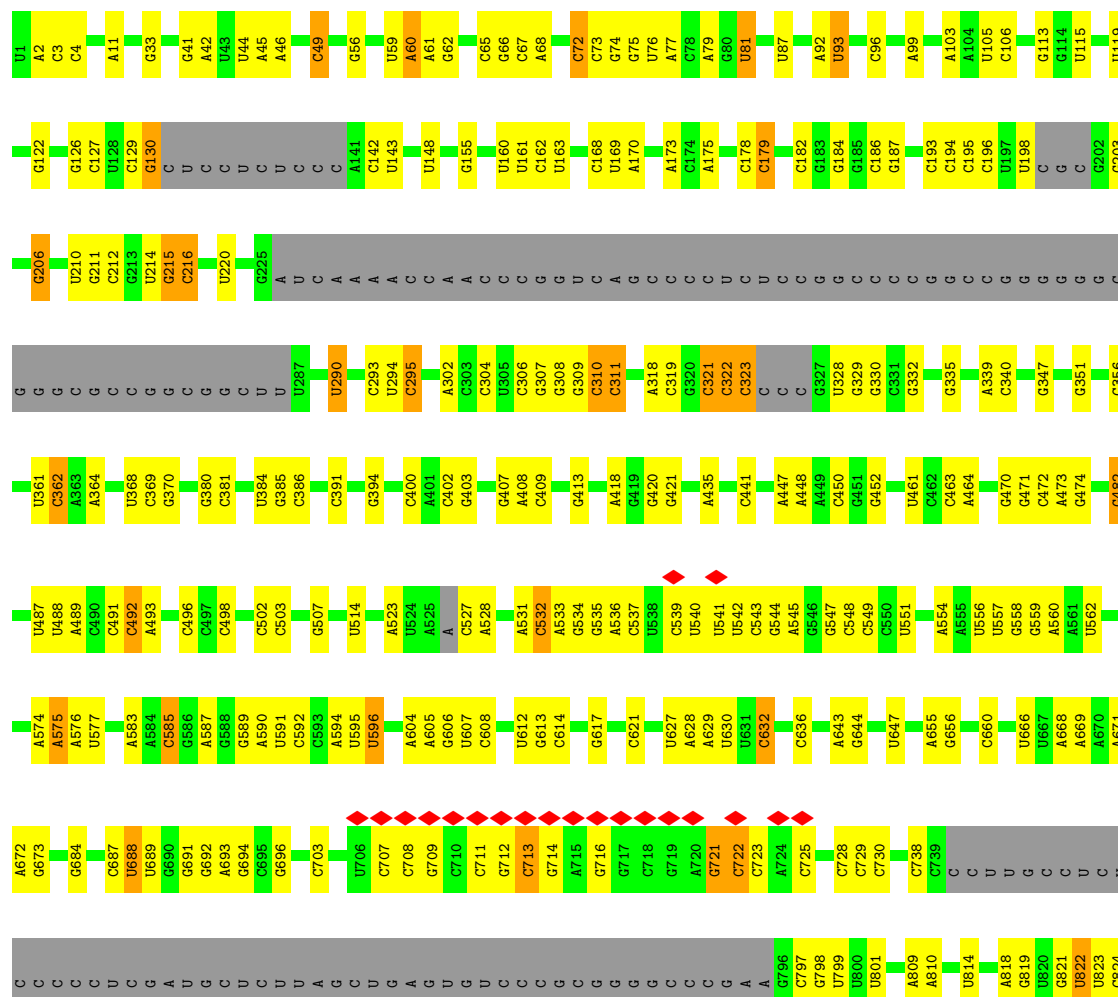
● Molecule 85: 18S ribosomal RNA

Chain S2:  57% 31% 8%





• Molecule 85: 18S ribosomal RNA



A1781	C1698	U1596	A1506	A1402	A1287	A1170	A1023	U906	A827
G1782	A1699	U1599	G1507	C1403	U1288	G1171	A1027	G907	A830
C1783	A1699	G1600	U1508	G1406	U1289	U1172	A1027	A908	A830
A1813	G1709	A1601	G1510	U1407	C1292	A1183	G1043	G909	C833
G1817	A1715	G1604	C1518	U1409	G1294	A1195	U1045	G910	C834
A1823	C1716	G1605	U1619	A1414	G1298	A1204	A1049	C911	C835
A1824	G1717	G1606	U1620	C1415	A1299	G1207	A1050	G912	G
A1825	G1718	A1607	C1521	U1416	U1300	A1208	A1055	A913	A
G1829	U1719	U1608	A1522	C1417	A1301	G1207	U1056	U914	G
U1830	U1720	C1609	C1523	C1418	G1302	A1208	C1057	G915	
A1831	U1721	A1620	C1627	C	C1303	C1215	A1055	A920	C839
A1834	G1722	U1621	U1622	G	U1304	C1216	U1056	A926	C840
U1838	U1725	U1623	A1531	A	C1305	A1217	A1060	C930	C841
G1849	U1728	U1624	C1532	G1422	U1306	C1218	A1062	G933	C842
A1850	U1729	C1627	U1535	G1424	U1307	G1221	A1077	G934	A847
C1852	U1733	G1628	G1536	U1432	C1308	G1224	C1078	C934	C851
C1853	C1742	G1632	U1539	C1433	A1313	C1234	A1082	U939	G855
U1854	G1743	A1633	U1543	C	U1314	U1238	A1083	C950	C856
A1860	A1745	C1635	C1544	C	U1319	U1242	A1084	C953	U857
G1861	U1746	G1636	A1545	A1438	G1320	U1243	C1085	U954	G867
G1862	C1747	A1637	C1547	A1439	G1321	U1251	G1086	A955	G868
A1863	G1748	G1638	C1548	C	U1326	C1261	C1091	C958	A869
U1864	G1749	G1639	U1548	U1441	G1330	A1251	A1082	U958	A872
C1865	C1750	U1643	G1552	G1449	C1331	C1262	C1109	A963	G873
A1869	C1751	C1644	C1553	U1450	A1332	A1263	G1110	U965	G874
	G1752	G1645	A1556	C1453	U1333	G1266	A1113	G970	C877
	C1753	A1647	U1563	A1454	C1341	G1267	U1114	G971	G878
	G1754	G1648	G1567	U1457	U1342	A1268	G971	G880	G879
	C1755	U1652	C1568	G1456	G1348	C1261	U1115	G881	G880
	G1756	G1653	A1569	U1462	U1364	C1264	C1118	U882	U883
	U1761	G1654	G1570	U1463	U1367	A1265	G1126	U884	C884
	C	A1661	C1574	G1466	U1371	C1268	G1130	U885	U885
	G	U1662	G1575	U1473	U1372	G1269	G1131	U886	U886
	C	A1663	U1578	A1474	C1373	G1270	C1132	U887	U887
	C	G1665	A1579	U1477	U1378	C1271	A1133	U888	U888
	C	A1678	A1580	U1477	A1378	G1272	C1139	U889	U889
	G	A1679	U1585	C1482	G1381	G1274	G1141	G	G
	C	G1680	U1586	A1487	A1382	G1275	C1147	U896	U896
	C	C1683	G1587	C1488	C1389	C1276	A1148	U897	U897
	C	A1684	A1588	U1489	C1395	A1277	A1149	U898	U898
	U	U1685	A1589	G1490	A1396	C1278	C1153	U900	U900
	G	G1686	C1591	U1495	U1397	G1283	U1155	U901	G901
	G1777	U1692	A1594	U1505	G1285	G1286	U1156	U904	A904
	C1778	A1695	U1595				G1157	U1018	C905
	G1779							U1022	
	G1780								

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53848	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43.6	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.570	Depositor
Minimum map value	-0.176	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	668.8, 668.8, 668.8	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A4	0.51	0/307	1.12	0/472
2	A5	0.60	0/241	1.46	4/370 (1.1%)
3	B4	0.70	0/1812	1.19	12/2823 (0.4%)
3	D5	0.53	0/1741	1.55	43/2709 (1.6%)
4	B5	0.58	0/1795	1.14	4/2798 (0.1%)
5	CC	0.51	0/1773	1.16	12/2759 (0.4%)
6	L1	0.80	0/3701	1.09	17/5766 (0.3%)
6	L8	1.02	1/3701 (0.0%)	1.14	26/5766 (0.5%)
7	L5	1.03	3/86579 (0.0%)	1.16	640/135047 (0.5%)
7	L6	0.81	3/85637 (0.0%)	1.17	678/133571 (0.5%)
8	L7	1.01	0/2858	1.14	15/4455 (0.3%)
8	L9	0.77	0/2858	1.13	15/4455 (0.3%)
9	LA	0.53	0/1936	0.62	0/2596
9	MA	0.44	0/1924	0.66	1/2581 (0.0%)
10	LB	0.50	0/3251	0.58	0/4352
10	MB	0.42	0/3168	0.61	1/4253 (0.0%)
11	LC	0.48	0/2938	0.58	0/3947
11	MC	0.40	0/2948	0.60	2/3960 (0.1%)
12	LD	0.47	0/2407	0.58	0/3227
12	MD	0.38	0/2333	0.56	0/3139
13	LE	0.43	0/1788	0.60	0/2399
13	ME	0.38	0/1747	0.63	0/2354
14	LF	0.50	0/1905	0.58	0/2539
14	MF	0.43	0/1879	0.66	2/2507 (0.1%)
15	LG	0.43	0/1849	0.61	2/2496 (0.1%)
15	MG	0.38	0/1765	0.63	2/2400 (0.1%)
16	LH	0.44	0/1529	0.59	0/2058
16	MH	0.38	0/1458	0.65	1/1973 (0.1%)
17	LI	0.48	0/1690	0.55	0/2258
17	MI	0.40	0/1619	0.59	0/2170
18	LJ	0.42	0/1352	0.60	0/1813
18	MJ	0.38	0/1249	0.59	0/1690
19	LL	0.44	0/1661	0.55	1/2229 (0.0%)
19	ML	0.39	0/1611	0.57	0/2167

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
20	LM	0.47	0/1145	0.56	0/1536
20	MM	0.43	0/1119	0.61	0/1501
21	LN	0.51	0/1746	0.57	1/2338 (0.0%)
21	MN	0.43	0/1738	0.60	1/2328 (0.0%)
22	LO	0.50	0/1665	0.52	0/2229
22	MO	0.42	0/1645	0.61	3/2205 (0.1%)
23	LP	0.50	0/1260	0.54	0/1692
24	LQ	0.50	0/1526	0.57	0/2038
24	MQ	0.40	0/1517	0.55	0/2030
25	LR	0.44	0/1468	0.53	0/1945
25	MR	0.36	0/1428	0.63	1/1897 (0.1%)
26	LS	0.52	0/1492	0.55	0/2003
26	MS	0.42	0/1476	0.60	2/1983 (0.1%)
27	LT	0.47	0/1310	0.57	0/1752
27	MT	0.41	0/1296	0.57	0/1734
28	LU	0.42	0/813	0.60	0/1093
28	MU	0.37	0/782	0.63	0/1057
29	LV	0.49	0/985	0.56	0/1323
29	MV	0.44	0/968	0.58	0/1303
30	LW	0.44	0/820	0.56	0/1104
30	MW	0.36	0/798	0.52	0/1081
31	LX	0.46	0/998	0.54	0/1341
31	MX	0.39	0/967	0.65	1/1304 (0.1%)
32	LY	0.48	0/1128	0.58	0/1500
32	MY	0.40	0/1101	0.56	0/1469
33	LZ	0.48	0/1130	0.56	0/1507
33	MZ	0.40	0/1105	0.52	0/1475
34	La	0.48	0/1183	0.55	0/1582
34	Ma	0.39	0/1173	0.57	1/1568 (0.1%)
35	Lb	0.41	0/600	0.57	0/796
35	Mb	0.36	0/509	0.50	0/675
36	Lc	0.50	0/752	0.54	0/1011
36	Mc	0.39	0/726	0.63	0/977
37	Ld	0.47	0/889	0.54	0/1198
37	Md	0.39	0/871	0.57	0/1176
38	Le	0.52	0/1067	0.59	0/1425
38	Me	0.41	0/1063	0.55	0/1418
39	Lf	0.52	0/891	0.63	0/1194
39	Mf	0.45	0/883	0.69	1/1185 (0.1%)
40	Lg	0.50	0/899	0.58	0/1200
40	Mg	0.40	0/861	0.61	0/1153
41	Lh	0.44	0/1014	0.53	0/1340
41	Mh	0.34	0/983	0.53	0/1304

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
42	Li	0.38	0/824	0.55	0/1093
42	Mi	0.34	0/808	0.56	0/1074
43	Lj	0.51	0/720	0.61	0/952
43	Mj	0.41	0/716	0.54	0/948
44	Lk	0.45	0/548	0.60	0/730
44	Mk	0.39	0/534	0.63	0/712
45	Ll	0.44	0/454	0.57	0/599
45	Ml	0.38	0/450	0.52	0/595
46	Lm	0.45	0/431	0.54	0/570
46	Mm	0.38	0/399	0.53	0/532
47	Ln	0.47	0/231	0.50	0/294
47	Mn	0.33	0/231	0.54	0/294
48	Lo	0.48	0/861	0.59	0/1137
48	Mo	0.40	0/787	0.62	1/1042 (0.1%)
49	Lp	0.53	0/706	0.60	0/939
49	Mp	0.44	0/699	0.58	0/931
50	Lr	0.48	0/1012	0.60	0/1358
50	Mr	0.38	0/997	0.57	2/1341 (0.1%)
51	MP	0.40	0/1229	0.59	1/1655 (0.1%)
52	RA	0.36	0/1612	0.56	1/2203 (0.0%)
52	SA	0.43	0/1708	0.58	0/2324
53	RB	0.36	0/1654	0.59	0/2227
53	SB	0.44	0/1745	0.63	0/2337
54	RC	0.40	0/1626	0.62	0/2211
54	SC	0.46	0/1697	0.58	0/2301
55	RD	0.38	0/1499	0.63	1/2041 (0.0%)
55	SD	0.38	0/1606	0.58	1/2181 (0.0%)
56	RE	0.34	0/1933	0.58	0/2623
56	SE	0.43	0/2014	0.61	0/2726
57	RF	0.35	0/1385	0.61	1/1870 (0.1%)
57	SF	0.38	0/1437	0.62	1/1936 (0.1%)
58	RG	0.31	0/1570	0.56	0/2112
58	SG	0.34	0/1657	0.57	0/2247
59	RH	0.32	0/1362	0.58	0/1831
59	SH	0.40	0/1295	0.57	0/1763
60	RI	0.32	0/1477	0.57	0/1990
60	SI	0.43	0/1603	0.57	0/2161
61	RJ	0.35	0/1432	0.63	0/1926
61	SJ	0.39	0/1456	0.55	0/1957
62	RK	0.34	0/759	0.60	0/1036
62	SK	0.40	0/750	0.56	1/1026 (0.1%)
63	RL	0.36	0/1159	0.61	0/1555
63	SL	0.47	0/1163	0.54	0/1562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
64	RN	0.33	0/1223	0.57	1/1644 (0.1%)
64	SN	0.42	0/1206	0.58	0/1626
65	RO	0.36	0/1016	0.66	1/1363 (0.1%)
65	SO	0.44	0/982	0.62	0/1320
66	RP	0.36	0/1020	0.65	0/1369
66	SP	0.38	0/995	0.54	0/1344
67	RQ	0.34	0/1096	0.61	0/1473
67	SQ	0.40	0/1089	0.60	0/1465
68	RR	0.31	0/890	0.65	1/1207 (0.1%)
68	SR	0.38	0/955	0.61	0/1294
69	RS	0.35	0/1098	0.60	0/1480
69	SS	0.40	0/1136	0.63	0/1528
70	RT	0.33	0/1012	0.53	0/1371
70	ST	0.37	0/1100	0.52	0/1479
71	RU	0.29	0/758	0.61	1/1023 (0.1%)
71	SU	0.35	0/722	0.60	0/983
72	RV	0.35	0/596	0.55	0/800
72	SV	0.42	0/625	0.57	0/837
73	RW	0.34	0/1044	0.53	0/1398
73	SW	0.47	0/1043	0.60	0/1396
74	RX	0.33	0/1066	0.65	1/1434 (0.1%)
74	SX	0.45	0/1096	0.62	0/1467
75	RY	0.33	0/871	0.59	0/1169
75	SY	0.36	0/944	0.56	0/1271
76	RZ	0.31	0/493	0.73	2/672 (0.3%)
76	SZ	0.39	0/565	0.68	1/764 (0.1%)
77	Ra	0.35	0/775	0.55	0/1042
77	Sa	0.46	0/794	0.58	0/1065
78	Rb	0.33	0/631	0.64	0/853
78	Sb	0.39	0/632	0.61	0/851
79	Rc	0.34	0/432	0.78	0/582
79	Sc	0.42	0/474	0.68	1/638 (0.2%)
80	Rd	0.34	0/430	0.52	0/573
80	Sd	0.43	0/443	0.53	0/589
81	Re	0.34	0/390	0.58	0/515
81	Se	0.38	0/431	0.55	0/570
82	Rf	0.26	0/485	0.55	1/661 (0.2%)
83	Rg	0.30	0/1993	0.61	0/2730
83	Sg	0.35	0/2227	0.69	0/3059
84	Rh	0.29	0/270	0.48	0/359
85	S2	0.91	6/40905 (0.0%)	1.24	450/63753 (0.7%)
85	S3	0.70	4/40701 (0.0%)	1.23	386/63428 (0.6%)
All	All	0.74	17/449690 (0.0%)	1.02	2345/663456 (0.4%)

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
9	LA	0	1
9	MA	0	2
11	MC	0	1
12	LD	0	1
12	MD	0	1
13	LE	0	1
13	ME	0	1
15	MG	0	1
16	LH	0	1
17	LI	0	2
17	MI	0	1
18	MJ	0	1
19	LL	0	2
19	ML	0	1
20	MM	0	1
24	LQ	0	1
26	MS	0	2
27	LT	0	1
29	MV	0	1
31	MX	0	1
39	Lf	0	1
48	Mo	0	1
51	MP	0	1
52	RA	0	1
52	SA	0	1
53	SB	0	1
54	SC	0	1
58	SG	0	2
66	RP	0	1
67	SQ	0	1
68	RR	0	1
69	SS	0	1
71	RU	0	1
71	SU	0	2
74	SX	0	2
76	RZ	0	1
78	Rb	0	1
78	Sb	0	2
79	Rc	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
83	Rg	0	2
83	Sg	0	1
All	All	0	51

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	L8	62	A	N9-C4	-7.77	1.33	1.37
85	S3	216	C	N3-C4	-7.53	1.28	1.33
85	S2	926	A	C6-N1	-7.27	1.30	1.35
85	S3	215	G	C6-N1	-7.13	1.34	1.39
85	S2	536	A	N9-C4	6.03	1.41	1.37

The worst 5 of 2345 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	S3	310	C	N3-C4-N4	-23.33	101.67	118.00
85	S3	215	G	N1-C6-O6	-21.95	106.73	119.90
7	L6	468	U	C5-C4-O4	20.43	138.16	125.90
85	S3	310	C	C5-C4-N4	19.96	134.17	120.20
7	L6	468	U	N3-C4-O4	-18.11	106.72	119.40

There are no chirality outliers.

5 of 51 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	LA	46	LYS	Peptide
12	LD	119	TYR	Peptide
13	LE	278	THR	Peptide
16	LH	187	VAL	Peptide
17	LI	14	ASN	Peptide

5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
9	LA	246/257 (96%)	224 (91%)	22 (9%)	0	100	100
9	MA	246/257 (96%)	219 (89%)	27 (11%)	0	100	100
10	LB	393/403 (98%)	362 (92%)	29 (7%)	2 (0%)	25	61
10	MB	389/403 (96%)	353 (91%)	36 (9%)	0	100	100
11	LC	362/427 (85%)	335 (92%)	25 (7%)	2 (1%)	22	57
11	MC	363/427 (85%)	341 (94%)	20 (6%)	2 (1%)	22	57
12	LD	291/297 (98%)	270 (93%)	18 (6%)	3 (1%)	13	46
12	MD	291/297 (98%)	270 (93%)	19 (6%)	2 (1%)	19	54
13	LE	213/288 (74%)	191 (90%)	22 (10%)	0	100	100
13	ME	214/288 (74%)	201 (94%)	12 (6%)	1 (0%)	25	61
14	LF	223/248 (90%)	211 (95%)	12 (5%)	0	100	100
14	MF	223/248 (90%)	211 (95%)	12 (5%)	0	100	100
15	LG	225/266 (85%)	206 (92%)	18 (8%)	1 (0%)	30	66
15	MG	225/266 (85%)	206 (92%)	19 (8%)	0	100	100
16	LH	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
16	MH	187/192 (97%)	166 (89%)	21 (11%)	0	100	100
17	LI	202/214 (94%)	185 (92%)	16 (8%)	1 (0%)	25	61
17	MI	199/214 (93%)	178 (89%)	21 (11%)	0	100	100
18	LJ	167/178 (94%)	161 (96%)	6 (4%)	0	100	100
18	MJ	165/178 (93%)	155 (94%)	10 (6%)	0	100	100
19	LL	203/211 (96%)	184 (91%)	18 (9%)	1 (0%)	25	61
19	ML	202/211 (96%)	182 (90%)	19 (9%)	1 (0%)	25	61
20	LM	137/215 (64%)	127 (93%)	8 (6%)	2 (2%)	8	36
20	MM	134/215 (62%)	126 (94%)	7 (5%)	1 (1%)	19	54
21	LN	201/204 (98%)	194 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	MN	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
22	LO	198/203 (98%)	193 (98%)	5 (2%)	0	100	100
22	MO	199/203 (98%)	191 (96%)	8 (4%)	0	100	100
23	LP	151/154 (98%)	142 (94%)	9 (6%)	0	100	100
24	LQ	185/188 (98%)	170 (92%)	15 (8%)	0	100	100
24	MQ	185/188 (98%)	174 (94%)	11 (6%)	0	100	100
25	LR	174/196 (89%)	173 (99%)	1 (1%)	0	100	100
25	MR	173/196 (88%)	171 (99%)	2 (1%)	0	100	100
26	LS	173/176 (98%)	159 (92%)	14 (8%)	0	100	100
26	MS	173/176 (98%)	158 (91%)	13 (8%)	2 (1%)	11	41
27	LT	157/160 (98%)	144 (92%)	12 (8%)	1 (1%)	22	57
27	MT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
28	LU	99/128 (77%)	94 (95%)	5 (5%)	0	100	100
28	MU	99/128 (77%)	92 (93%)	7 (7%)	0	100	100
29	LV	129/140 (92%)	118 (92%)	11 (8%)	0	100	100
29	MV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
30	LW	111/157 (71%)	101 (91%)	7 (6%)	3 (3%)	4	22
30	MW	111/157 (71%)	104 (94%)	7 (6%)	0	100	100
31	LX	118/156 (76%)	114 (97%)	4 (3%)	0	100	100
31	MX	118/156 (76%)	105 (89%)	13 (11%)	0	100	100
32	LY	132/145 (91%)	119 (90%)	13 (10%)	0	100	100
32	MY	132/145 (91%)	119 (90%)	13 (10%)	0	100	100
33	LZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
33	MZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
34	La	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
34	Ma	142/148 (96%)	127 (89%)	15 (11%)	0	100	100
35	Lb	73/159 (46%)	67 (92%)	6 (8%)	0	100	100
35	Mb	61/159 (38%)	56 (92%)	5 (8%)	0	100	100
36	Lc	95/115 (83%)	92 (97%)	2 (2%)	1 (1%)	12	44
36	Mc	91/115 (79%)	85 (93%)	6 (7%)	0	100	100
37	Ld	105/125 (84%)	99 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	Md	105/125 (84%)	98 (93%)	7 (7%)	0	100	100
38	Le	126/135 (93%)	119 (94%)	7 (6%)	0	100	100
38	Me	125/135 (93%)	120 (96%)	5 (4%)	0	100	100
39	Lf	107/110 (97%)	101 (94%)	6 (6%)	0	100	100
39	Mf	107/110 (97%)	97 (91%)	9 (8%)	1 (1%)	14	49
40	Lg	112/117 (96%)	104 (93%)	8 (7%)	0	100	100
40	Mg	108/117 (92%)	99 (92%)	9 (8%)	0	100	100
41	Lh	119/123 (97%)	115 (97%)	4 (3%)	0	100	100
41	Mh	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
42	Li	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
42	Mi	99/105 (94%)	95 (96%)	4 (4%)	0	100	100
43	Lj	84/88 (96%)	78 (93%)	6 (7%)	0	100	100
43	Mj	84/88 (96%)	82 (98%)	2 (2%)	0	100	100
44	Lk	67/70 (96%)	60 (90%)	7 (10%)	0	100	100
44	Mk	67/70 (96%)	59 (88%)	8 (12%)	0	100	100
45	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
45	Ml	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
46	Lm	50/128 (39%)	50 (100%)	0	0	100	100
46	Mm	48/128 (38%)	43 (90%)	5 (10%)	0	100	100
47	Ln	22/25 (88%)	22 (100%)	0	0	100	100
47	Mn	22/25 (88%)	22 (100%)	0	0	100	100
48	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
48	Mo	96/106 (91%)	88 (92%)	8 (8%)	0	100	100
49	Lp	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
49	Mp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
50	Lr	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
50	Mr	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
51	MP	151/184 (82%)	137 (91%)	14 (9%)	0	100	100
52	RA	210/295 (71%)	196 (93%)	13 (6%)	1 (0%)	25	61
52	SA	214/295 (72%)	204 (95%)	9 (4%)	1 (0%)	25	61
53	RB	212/264 (80%)	202 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	SB	211/264 (80%)	205 (97%)	6 (3%)	0	100	100
54	RC	215/293 (73%)	205 (95%)	10 (5%)	0	100	100
54	SC	217/293 (74%)	207 (95%)	10 (5%)	0	100	100
55	RD	207/243 (85%)	189 (91%)	17 (8%)	1 (0%)	25	61
55	SD	219/243 (90%)	193 (88%)	26 (12%)	0	100	100
56	RE	255/263 (97%)	236 (92%)	19 (8%)	0	100	100
56	SE	260/263 (99%)	238 (92%)	22 (8%)	0	100	100
57	RF	176/204 (86%)	165 (94%)	11 (6%)	0	100	100
57	SF	185/204 (91%)	167 (90%)	17 (9%)	1 (0%)	25	61
58	RG	203/249 (82%)	186 (92%)	17 (8%)	0	100	100
58	SG	229/249 (92%)	206 (90%)	21 (9%)	2 (1%)	14	49
59	RH	168/194 (87%)	150 (89%)	18 (11%)	0	100	100
59	SH	179/194 (92%)	164 (92%)	15 (8%)	0	100	100
60	RI	183/208 (88%)	173 (94%)	10 (6%)	0	100	100
60	SI	204/208 (98%)	193 (95%)	11 (5%)	0	100	100
61	RJ	174/194 (90%)	165 (95%)	7 (4%)	2 (1%)	12	44
61	SJ	177/194 (91%)	168 (95%)	9 (5%)	0	100	100
62	RK	93/165 (56%)	82 (88%)	11 (12%)	0	100	100
62	SK	94/165 (57%)	86 (92%)	8 (8%)	0	100	100
63	RL	136/158 (86%)	124 (91%)	12 (9%)	0	100	100
63	SL	140/158 (89%)	129 (92%)	11 (8%)	0	100	100
64	RN	148/151 (98%)	132 (89%)	16 (11%)	0	100	100
64	SN	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
65	RO	133/151 (88%)	120 (90%)	13 (10%)	0	100	100
65	SO	132/151 (87%)	118 (89%)	14 (11%)	0	100	100
66	RP	123/145 (85%)	112 (91%)	9 (7%)	2 (2%)	8	34
66	SP	126/145 (87%)	120 (95%)	6 (5%)	0	100	100
67	RQ	139/146 (95%)	130 (94%)	9 (6%)	0	100	100
67	SQ	140/146 (96%)	127 (91%)	13 (9%)	0	100	100
68	RR	123/135 (91%)	106 (86%)	16 (13%)	1 (1%)	16	51
68	SR	129/135 (96%)	114 (88%)	15 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	RS	136/152 (90%)	117 (86%)	19 (14%)	0	100	100
69	SS	139/152 (91%)	119 (86%)	20 (14%)	0	100	100
70	RT	139/145 (96%)	130 (94%)	9 (6%)	0	100	100
70	ST	141/145 (97%)	137 (97%)	4 (3%)	0	100	100
71	RU	96/119 (81%)	85 (88%)	11 (12%)	0	100	100
71	SU	99/119 (83%)	88 (89%)	11 (11%)	0	100	100
72	RV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
72	SV	81/83 (98%)	73 (90%)	8 (10%)	0	100	100
73	RW	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
73	SW	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
74	RX	139/143 (97%)	123 (88%)	15 (11%)	1 (1%)	19	54
74	SX	139/143 (97%)	128 (92%)	9 (6%)	2 (1%)	9	37
75	RY	111/133 (84%)	106 (96%)	5 (4%)	0	100	100
75	SY	121/133 (91%)	113 (93%)	8 (7%)	0	100	100
76	RZ	68/125 (54%)	59 (87%)	9 (13%)	0	100	100
76	SZ	73/125 (58%)	66 (90%)	7 (10%)	0	100	100
77	Ra	97/101 (96%)	89 (92%)	8 (8%)	0	100	100
77	Sa	97/101 (96%)	84 (87%)	13 (13%)	0	100	100
78	Rb	81/84 (96%)	66 (82%)	14 (17%)	1 (1%)	11	41
78	Sb	81/84 (96%)	72 (89%)	9 (11%)	0	100	100
79	Rc	59/69 (86%)	48 (81%)	11 (19%)	0	100	100
79	Sc	61/69 (88%)	53 (87%)	8 (13%)	0	100	100
80	Rd	50/56 (89%)	46 (92%)	4 (8%)	0	100	100
80	Sd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
81	Re	47/59 (80%)	40 (85%)	7 (15%)	0	100	100
81	Se	55/59 (93%)	50 (91%)	5 (9%)	0	100	100
82	Rf	68/132 (52%)	58 (85%)	10 (15%)	0	100	100
83	Rg	259/317 (82%)	220 (85%)	39 (15%)	0	100	100
83	Sg	304/317 (96%)	244 (80%)	58 (19%)	2 (1%)	19	54
84	Rh	35/156 (22%)	33 (94%)	2 (6%)	0	100	100
All	All	21776/25012 (87%)	20084 (92%)	1648 (8%)	44 (0%)	45	77

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	LC	111	TRP
12	LD	113	PHE
17	LI	213	HIS
20	LM	96	GLU
36	Lc	23	LYS

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	
9	LA	190/199 (96%)	188 (99%)	2 (1%)	70	87
9	MA	187/199 (94%)	185 (99%)	2 (1%)	70	87
10	LB	343/349 (98%)	343 (100%)	0	100	100
10	MB	324/349 (93%)	324 (100%)	0	100	100
11	LC	299/348 (86%)	297 (99%)	2 (1%)	81	91
11	MC	301/348 (86%)	301 (100%)	0	100	100
12	LD	241/250 (96%)	240 (100%)	1 (0%)	89	95
12	MD	218/250 (87%)	217 (100%)	1 (0%)	86	94
13	LE	191/252 (76%)	188 (98%)	3 (2%)	58	82
13	ME	179/252 (71%)	177 (99%)	2 (1%)	70	87
14	LF	194/215 (90%)	194 (100%)	0	100	100
14	MF	187/215 (87%)	187 (100%)	0	100	100
15	LG	188/223 (84%)	188 (100%)	0	100	100
15	MG	167/223 (75%)	167 (100%)	0	100	100
16	LH	167/171 (98%)	166 (99%)	1 (1%)	84	93
16	MH	150/171 (88%)	149 (99%)	1 (1%)	81	91
17	LI	172/181 (95%)	171 (99%)	1 (1%)	84	93
17	MI	156/181 (86%)	156 (100%)	0	100	100
18	LJ	136/149 (91%)	136 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	MJ	113/149 (76%)	113 (100%)	0	100	100
19	LL	164/177 (93%)	163 (99%)	1 (1%)	84	93
19	ML	152/177 (86%)	151 (99%)	1 (1%)	81	91
20	LM	114/161 (71%)	113 (99%)	1 (1%)	75	89
20	MM	110/161 (68%)	110 (100%)	0	100	100
21	LN	171/172 (99%)	170 (99%)	1 (1%)	84	93
21	MN	169/172 (98%)	167 (99%)	2 (1%)	67	86
22	LO	170/174 (98%)	169 (99%)	1 (1%)	84	93
22	MO	163/174 (94%)	162 (99%)	1 (1%)	84	93
23	LP	132/135 (98%)	130 (98%)	2 (2%)	60	83
24	LQ	161/165 (98%)	161 (100%)	0	100	100
24	MQ	159/165 (96%)	159 (100%)	0	100	100
25	LR	150/175 (86%)	150 (100%)	0	100	100
25	MR	141/175 (81%)	141 (100%)	0	100	100
26	LS	156/157 (99%)	156 (100%)	0	100	100
26	MS	151/157 (96%)	150 (99%)	1 (1%)	81	91
27	LT	135/140 (96%)	135 (100%)	0	100	100
27	MT	130/140 (93%)	128 (98%)	2 (2%)	60	83
28	LU	84/115 (73%)	84 (100%)	0	100	100
28	MU	77/115 (67%)	77 (100%)	0	100	100
29	LV	99/107 (92%)	99 (100%)	0	100	100
29	MV	94/107 (88%)	94 (100%)	0	100	100
30	LW	61/126 (48%)	60 (98%)	1 (2%)	58	82
30	MW	54/126 (43%)	53 (98%)	1 (2%)	52	79
31	LX	107/133 (80%)	106 (99%)	1 (1%)	75	89
31	MX	98/133 (74%)	96 (98%)	2 (2%)	50	78
32	LY	123/135 (91%)	123 (100%)	0	100	100
32	MY	116/135 (86%)	116 (100%)	0	100	100
33	LZ	117/118 (99%)	117 (100%)	0	100	100
33	MZ	109/118 (92%)	109 (100%)	0	100	100
34	La	118/121 (98%)	117 (99%)	1 (1%)	79	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Ma	116/121 (96%)	115 (99%)	1 (1%)	75	89
35	Lb	59/126 (47%)	59 (100%)	0	100	100
35	Mb	49/126 (39%)	49 (100%)	0	100	100
36	Lc	79/97 (81%)	78 (99%)	1 (1%)	65	85
36	Mc	76/97 (78%)	76 (100%)	0	100	100
37	Ld	94/110 (86%)	94 (100%)	0	100	100
37	Md	88/110 (80%)	88 (100%)	0	100	100
38	Le	113/121 (93%)	113 (100%)	0	100	100
38	Me	113/121 (93%)	113 (100%)	0	100	100
39	Lf	87/89 (98%)	87 (100%)	0	100	100
39	Mf	85/89 (96%)	85 (100%)	0	100	100
40	Lg	93/100 (93%)	92 (99%)	1 (1%)	70	87
40	Mg	88/100 (88%)	87 (99%)	1 (1%)	70	87
41	Lh	108/110 (98%)	108 (100%)	0	100	100
41	Mh	100/110 (91%)	100 (100%)	0	100	100
42	Li	81/89 (91%)	79 (98%)	2 (2%)	42	73
42	Mi	79/89 (89%)	76 (96%)	3 (4%)	28	62
43	Lj	73/75 (97%)	72 (99%)	1 (1%)	62	83
43	Mj	72/75 (96%)	71 (99%)	1 (1%)	62	83
44	Lk	57/65 (88%)	56 (98%)	1 (2%)	54	80
44	Mk	52/65 (80%)	52 (100%)	0	100	100
45	Ll	47/48 (98%)	47 (100%)	0	100	100
45	Ml	46/48 (96%)	46 (100%)	0	100	100
46	Lm	47/116 (40%)	47 (100%)	0	100	100
46	Mm	42/116 (36%)	42 (100%)	0	100	100
47	Ln	23/24 (96%)	23 (100%)	0	100	100
47	Mn	23/24 (96%)	23 (100%)	0	100	100
48	Lo	90/94 (96%)	89 (99%)	1 (1%)	70	87
48	Mo	79/94 (84%)	78 (99%)	1 (1%)	65	85
49	Lp	71/75 (95%)	70 (99%)	1 (1%)	62	83
49	Mp	70/75 (93%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	Lr	107/121 (88%)	107 (100%)	0	100	100
50	Mr	103/121 (85%)	102 (99%)	1 (1%)	73	88
51	MP	124/163 (76%)	123 (99%)	1 (1%)	79	90
52	RA	147/243 (60%)	145 (99%)	2 (1%)	62	83
52	SA	170/243 (70%)	168 (99%)	2 (1%)	67	86
53	RB	162/231 (70%)	162 (100%)	0	100	100
53	SB	191/231 (83%)	191 (100%)	0	100	100
54	RC	155/225 (69%)	155 (100%)	0	100	100
54	SC	175/225 (78%)	173 (99%)	2 (1%)	70	87
55	RD	126/202 (62%)	125 (99%)	1 (1%)	79	90
55	SD	145/202 (72%)	144 (99%)	1 (1%)	81	91
56	RE	176/225 (78%)	175 (99%)	1 (1%)	84	93
56	SE	196/225 (87%)	194 (99%)	2 (1%)	73	88
57	RF	133/170 (78%)	131 (98%)	2 (2%)	60	83
57	SF	139/170 (82%)	139 (100%)	0	100	100
58	RG	137/218 (63%)	136 (99%)	1 (1%)	81	91
58	SG	138/218 (63%)	137 (99%)	1 (1%)	81	91
59	RH	134/174 (77%)	133 (99%)	1 (1%)	81	91
59	SH	109/174 (63%)	109 (100%)	0	100	100
60	RI	141/180 (78%)	140 (99%)	1 (1%)	81	91
60	SI	149/180 (83%)	149 (100%)	0	100	100
61	RJ	140/168 (83%)	138 (99%)	2 (1%)	62	83
61	SJ	143/168 (85%)	143 (100%)	0	100	100
62	RK	68/136 (50%)	68 (100%)	0	100	100
62	SK	65/136 (48%)	64 (98%)	1 (2%)	60	83
63	RL	124/142 (87%)	122 (98%)	2 (2%)	58	82
63	SL	121/142 (85%)	120 (99%)	1 (1%)	79	90
64	RN	127/131 (97%)	126 (99%)	1 (1%)	79	90
64	SN	123/131 (94%)	123 (100%)	0	100	100
65	RO	103/119 (87%)	102 (99%)	1 (1%)	73	88
65	SO	95/119 (80%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	RP	103/130 (79%)	102 (99%)	1 (1%)	73	88
66	SP	96/130 (74%)	95 (99%)	1 (1%)	73	88
67	RQ	105/121 (87%)	104 (99%)	1 (1%)	73	88
67	SQ	102/121 (84%)	102 (100%)	0	100	100
68	RR	77/122 (63%)	77 (100%)	0	100	100
68	SR	84/122 (69%)	84 (100%)	0	100	100
69	RS	103/132 (78%)	102 (99%)	1 (1%)	73	88
69	SS	110/132 (83%)	109 (99%)	1 (1%)	75	89
70	RT	82/115 (71%)	81 (99%)	1 (1%)	67	86
70	ST	105/115 (91%)	104 (99%)	1 (1%)	73	88
71	RU	78/107 (73%)	78 (100%)	0	100	100
71	SU	68/107 (64%)	67 (98%)	1 (2%)	60	83
72	RV	53/67 (79%)	53 (100%)	0	100	100
72	SV	62/67 (92%)	62 (100%)	0	100	100
73	RW	110/113 (97%)	110 (100%)	0	100	100
73	SW	110/113 (97%)	108 (98%)	2 (2%)	54	80
74	RX	101/115 (88%)	101 (100%)	0	100	100
74	SX	109/115 (95%)	109 (100%)	0	100	100
75	RY	79/115 (69%)	79 (100%)	0	100	100
75	SY	86/115 (75%)	85 (99%)	1 (1%)	67	86
76	RZ	40/103 (39%)	38 (95%)	2 (5%)	20	53
76	SZ	56/103 (54%)	56 (100%)	0	100	100
77	Ra	79/88 (90%)	79 (100%)	0	100	100
77	Sa	83/88 (94%)	83 (100%)	0	100	100
78	Rb	64/76 (84%)	64 (100%)	0	100	100
78	Sb	65/76 (86%)	64 (98%)	1 (2%)	60	83
79	Rc	41/62 (66%)	41 (100%)	0	100	100
79	Sc	51/62 (82%)	51 (100%)	0	100	100
80	Rd	42/49 (86%)	42 (100%)	0	100	100
80	Sd	44/49 (90%)	44 (100%)	0	100	100
81	Re	37/48 (77%)	37 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
81	Se	39/48 (81%)	37 (95%)	2 (5%)	20	53
82	Rf	30/108 (28%)	29 (97%)	1 (3%)	33	67
83	Rg	167/275 (61%)	167 (100%)	0	100	100
83	Sg	199/275 (72%)	198 (100%)	1 (0%)	86	94
84	Rh	17/140 (12%)	17 (100%)	0	100	100
All	All	17231/21296 (81%)	17136 (99%)	95 (1%)	82	93

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	RF	127	ARG
76	RZ	60	LYS
59	RH	85	LYS
64	RN	46	THR
52	SA	212	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 223 such sidechains are listed below:

Mol	Chain	Res	Type
27	MT	77	ASN
83	Sg	191	HIS
55	RD	165	ASN
83	Sg	62	HIS
64	SN	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A4	13/14 (92%)	7 (53%)	0
2	A5	10/11 (90%)	4 (40%)	0
3	B4	75/76 (98%)	23 (30%)	0
3	D5	70/76 (92%)	37 (52%)	2 (2%)
4	B5	74/75 (98%)	22 (29%)	0
5	CC	74/75 (98%)	27 (36%)	2 (2%)
6	L1	155/157 (98%)	37 (23%)	2 (1%)
6	L8	155/157 (98%)	30 (19%)	2 (1%)
7	L5	3594/5227 (68%)	867 (24%)	22 (0%)
7	L6	3553/5227 (67%)	900 (25%)	13 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	L7	119/121 (98%)	13 (10%)	0
8	L9	119/121 (98%)	16 (13%)	0
85	S2	1706/1869 (91%)	543 (31%)	20 (1%)
85	S3	1693/1869 (90%)	504 (29%)	14 (0%)
All	All	11410/15075 (75%)	3030 (26%)	77 (0%)

5 of 3030 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A4	39	U
1	A4	40	U
1	A4	41	U
1	A4	42	U
1	A4	46	U

5 of 77 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	S2	1519	U
85	S3	1395	C
85	S2	1597	C
85	S3	604	A
85	S3	1824	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

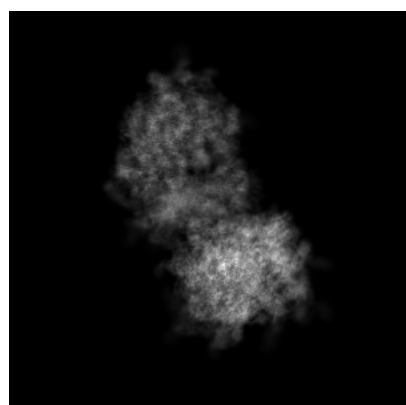
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14181. These allow visual inspection of the internal detail of the map and identification of artifacts.

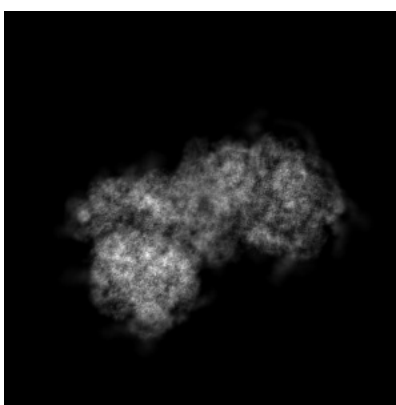
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

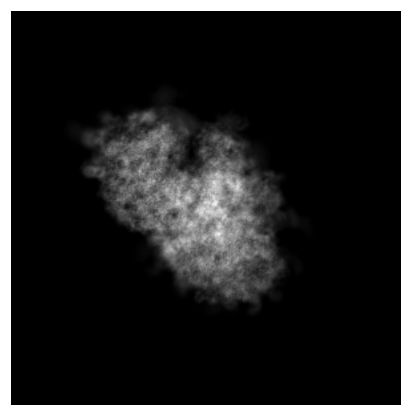
6.1.1 Primary map



X



Y

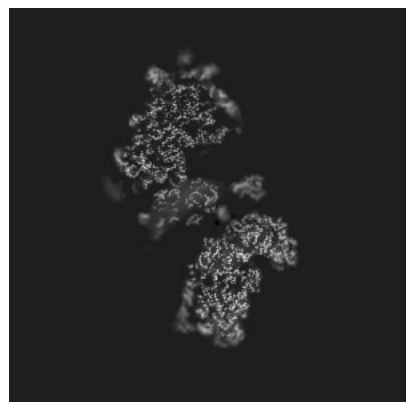


Z

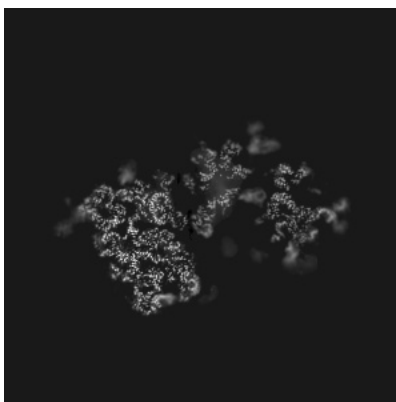
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

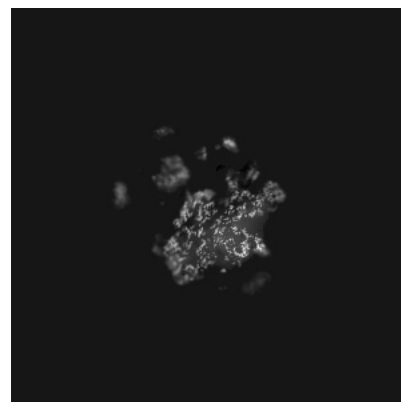
6.2.1 Primary map



X Index: 320



Y Index: 320

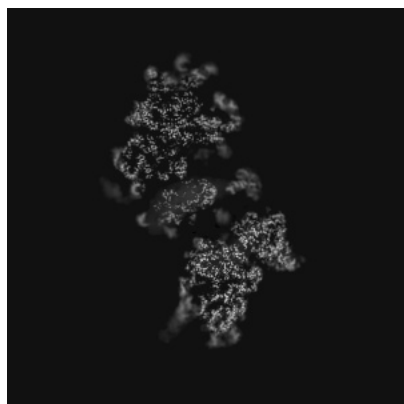


Z Index: 320

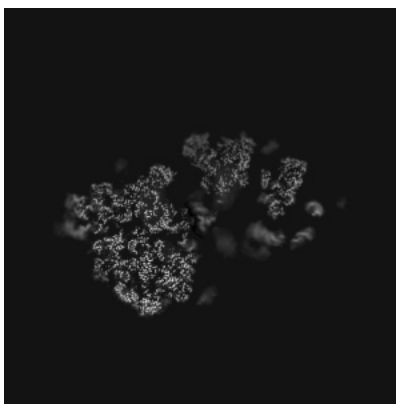
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 327



Y Index: 336

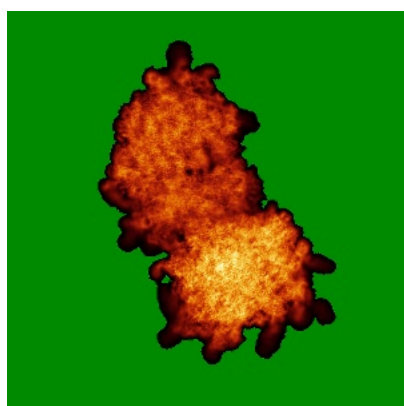


Z Index: 231

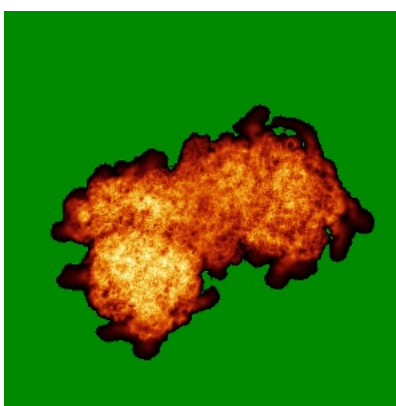
The images above show the largest variance slices of the map in three orthogonal directions.

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

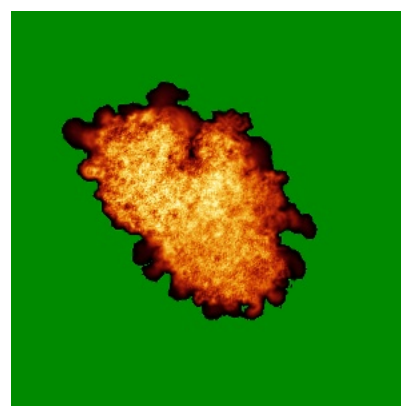
6.4.1 Primary map



X



Y

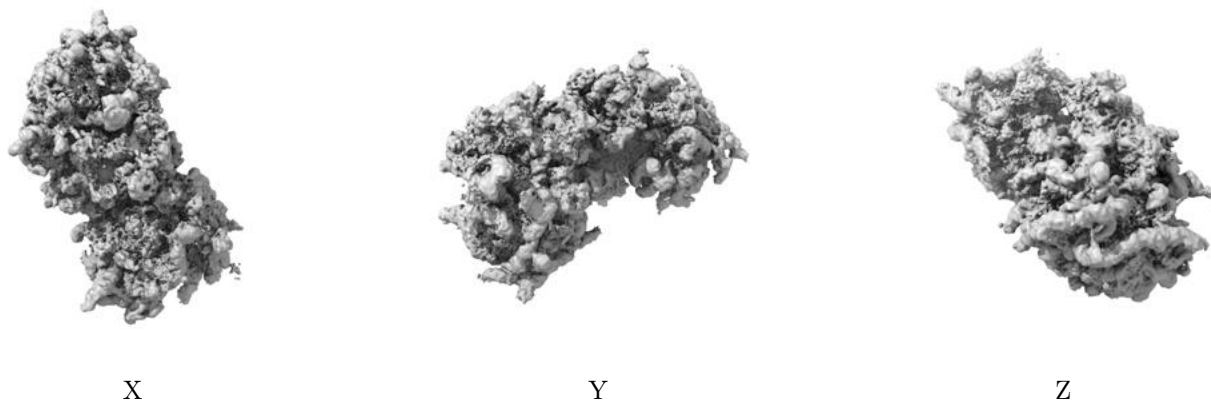


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

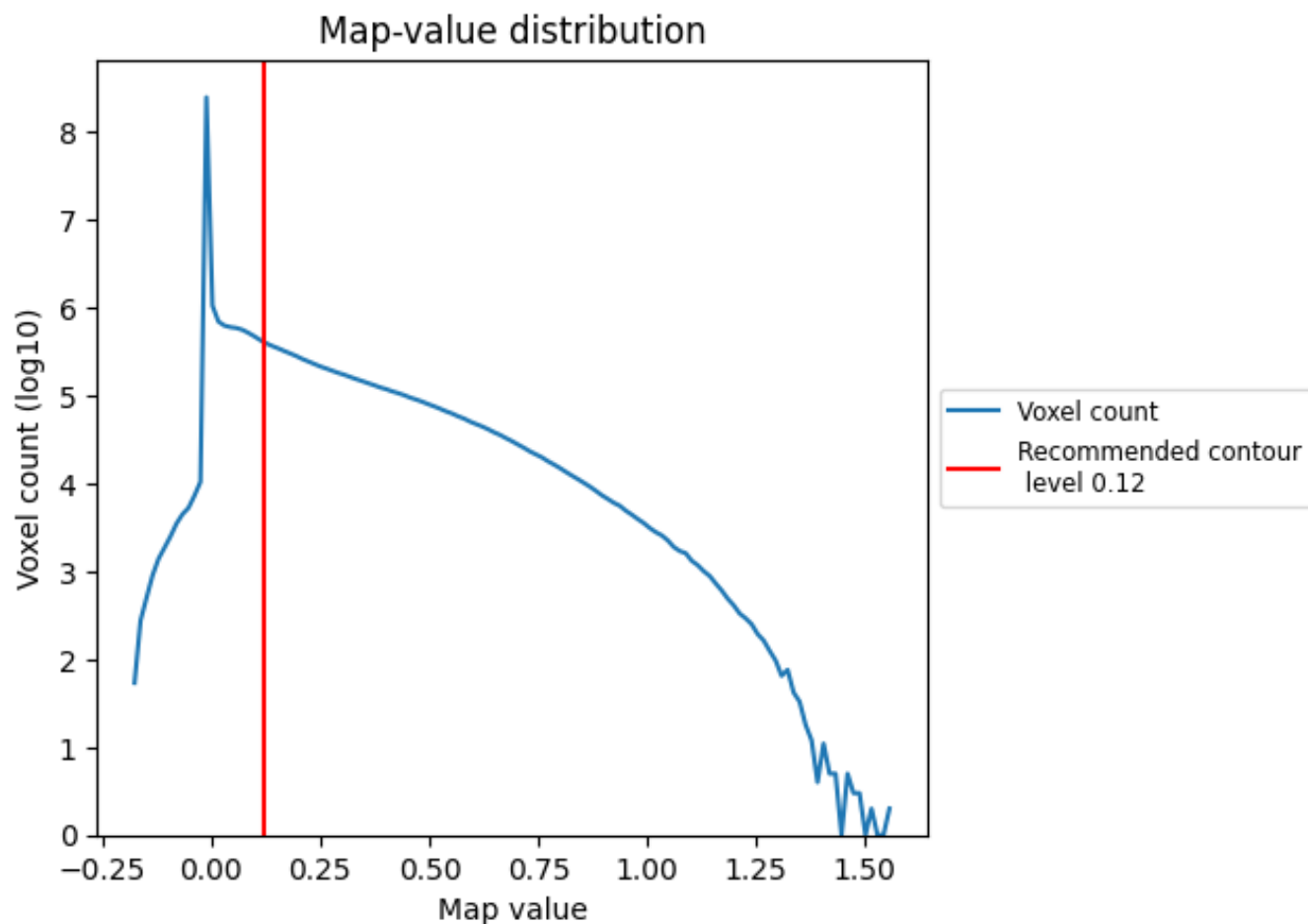
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

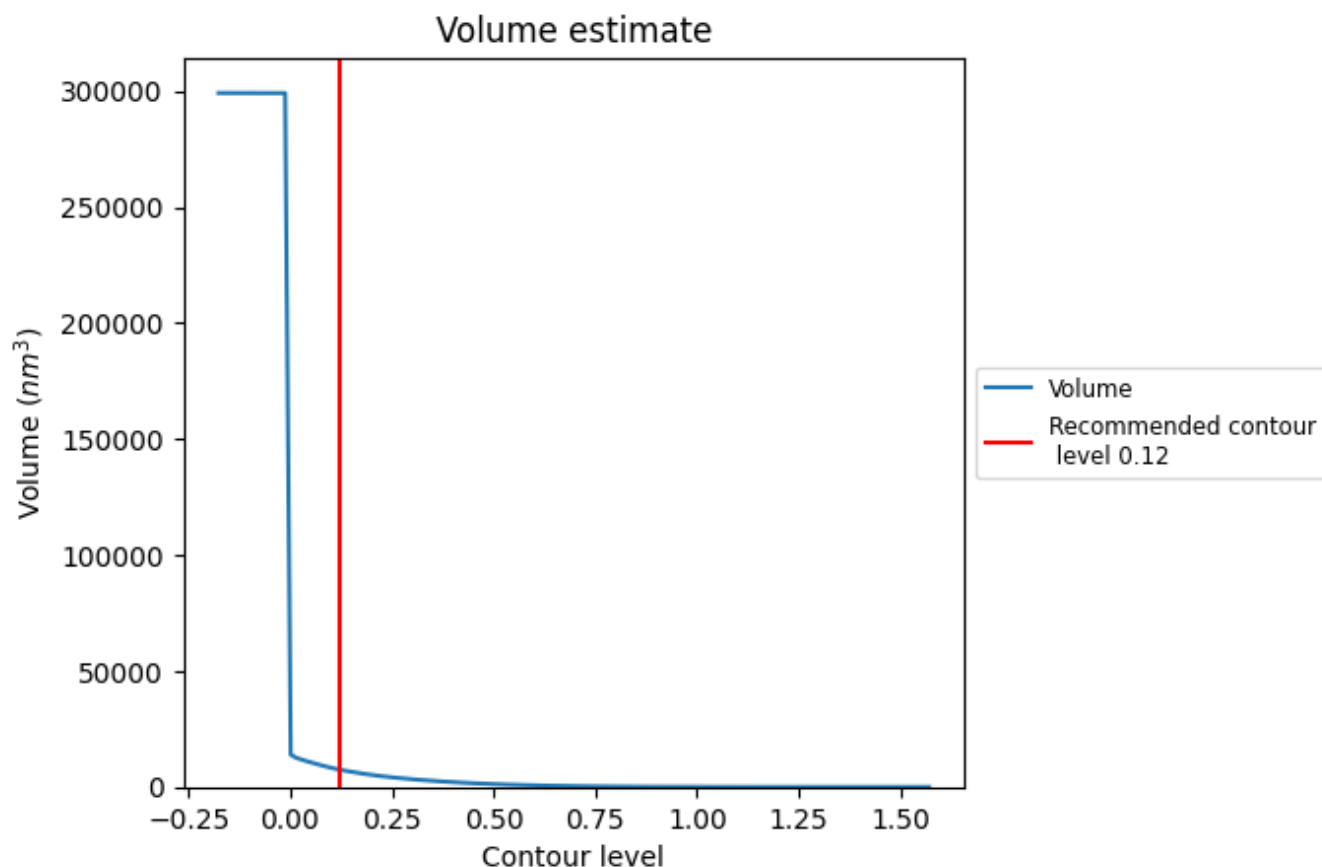
This section contains the results of statistical analysis of the map.

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.

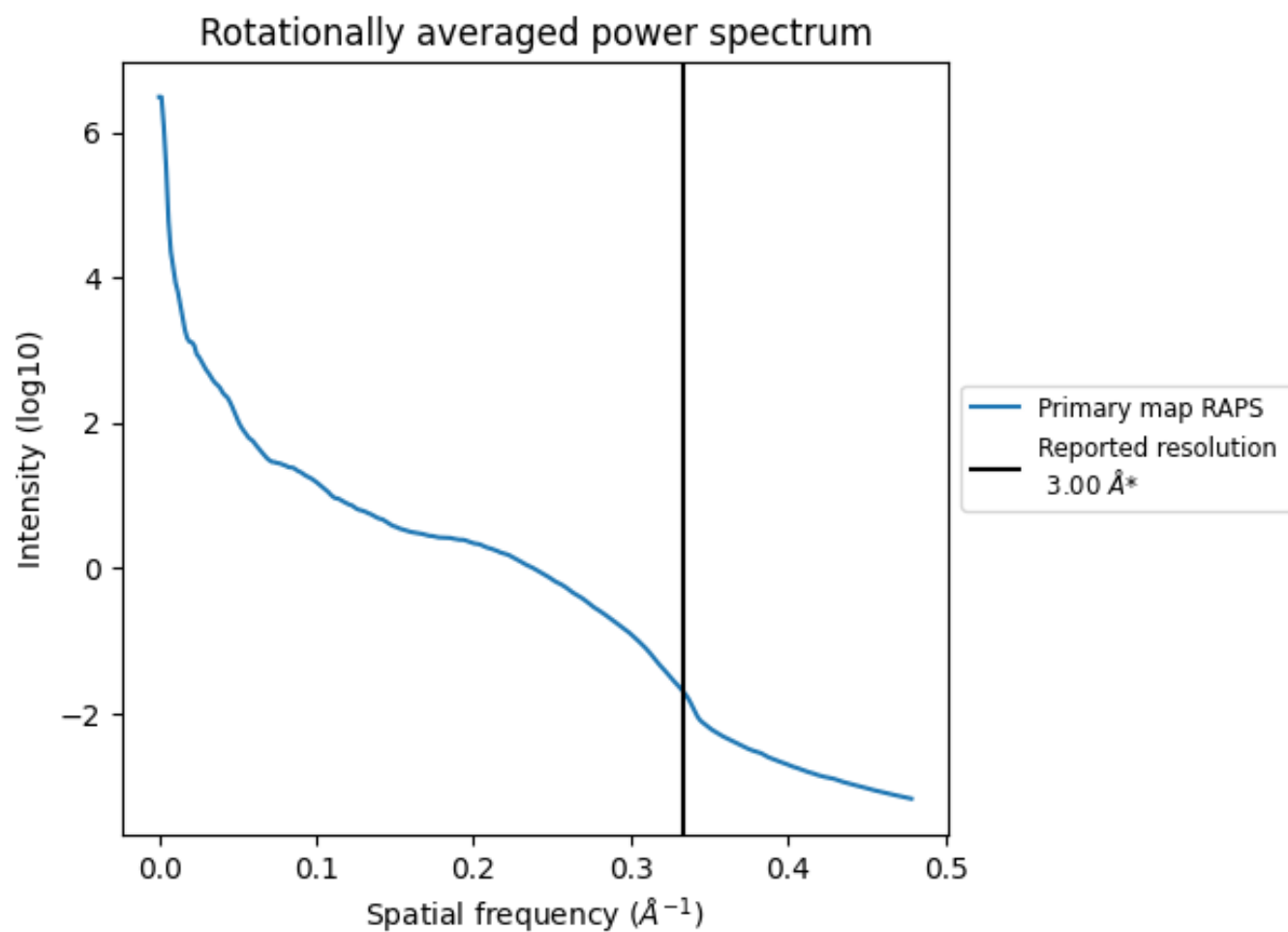
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 7521 nm³; this corresponds to an approximate mass of 6794 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 ⓘ

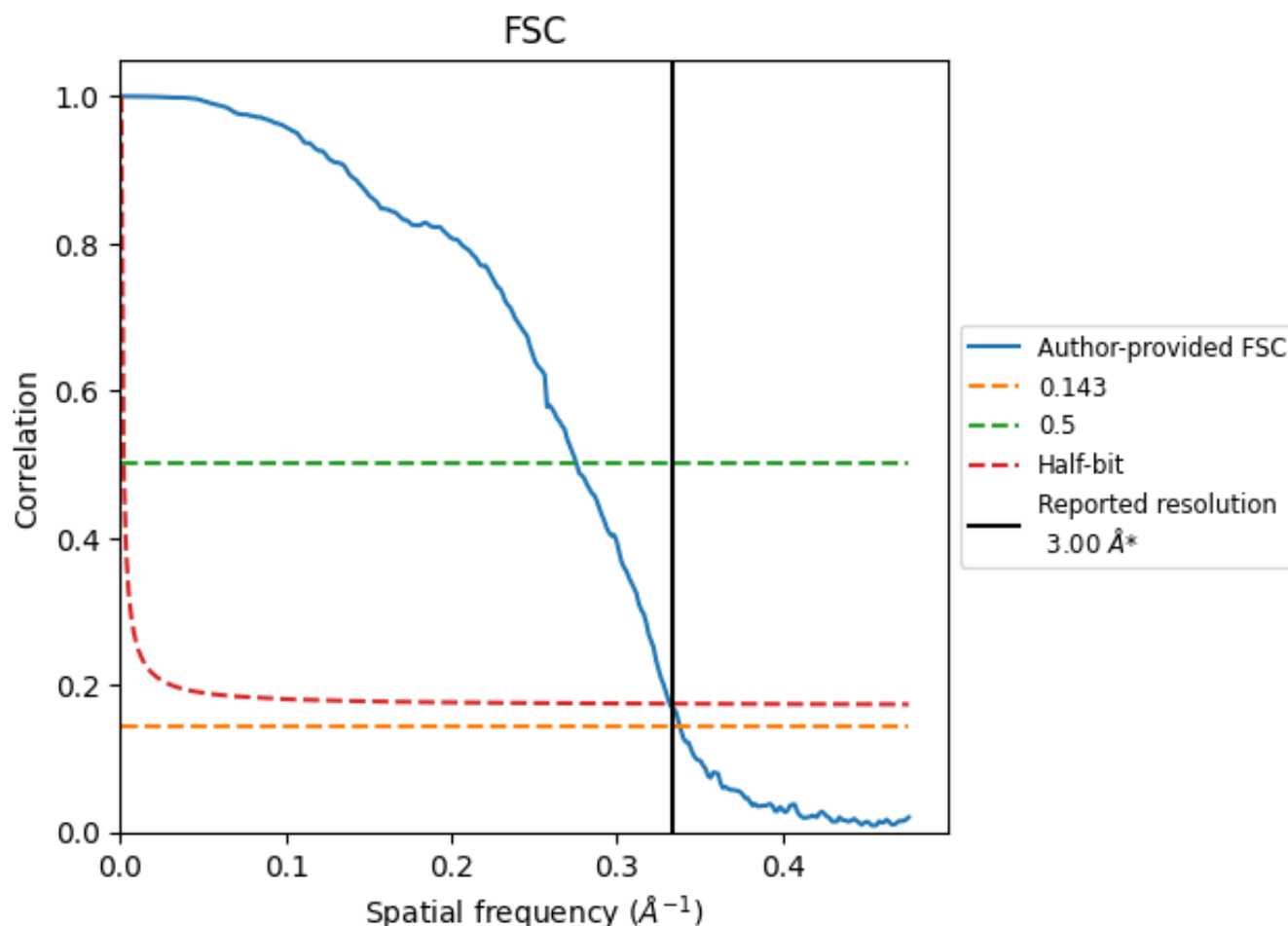


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

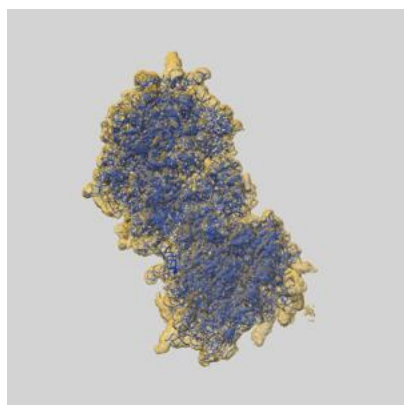
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.96	3.63	3.01
Unmasked-calculated*	-	-	-

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

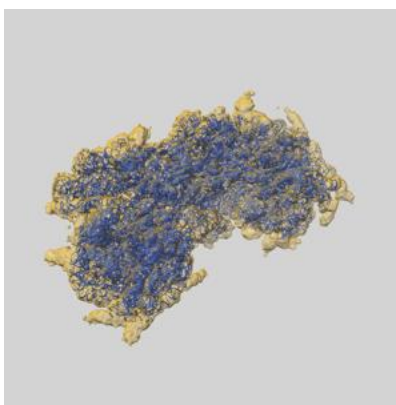
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14181 and PDB model 7QVP. Per-residue inclusion information can be found in section [3](#) on page [26](#).

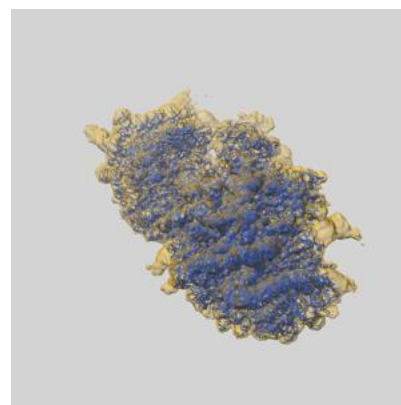
9.1 Map-model overlay [i](#)



X



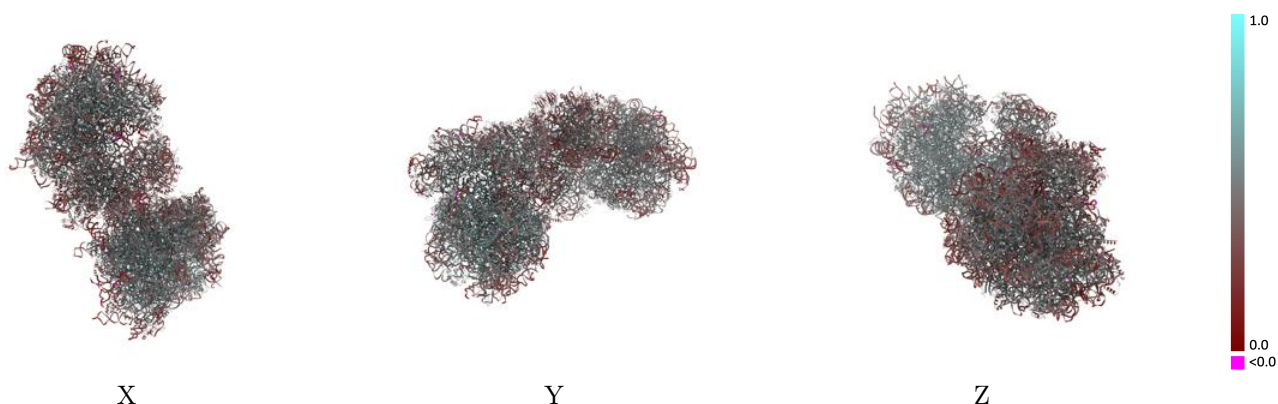
Y



Z

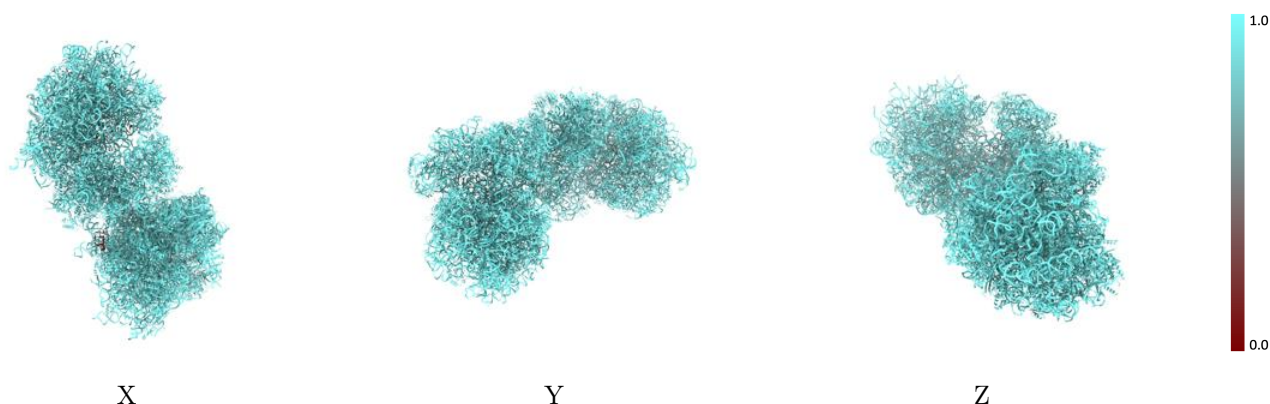
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



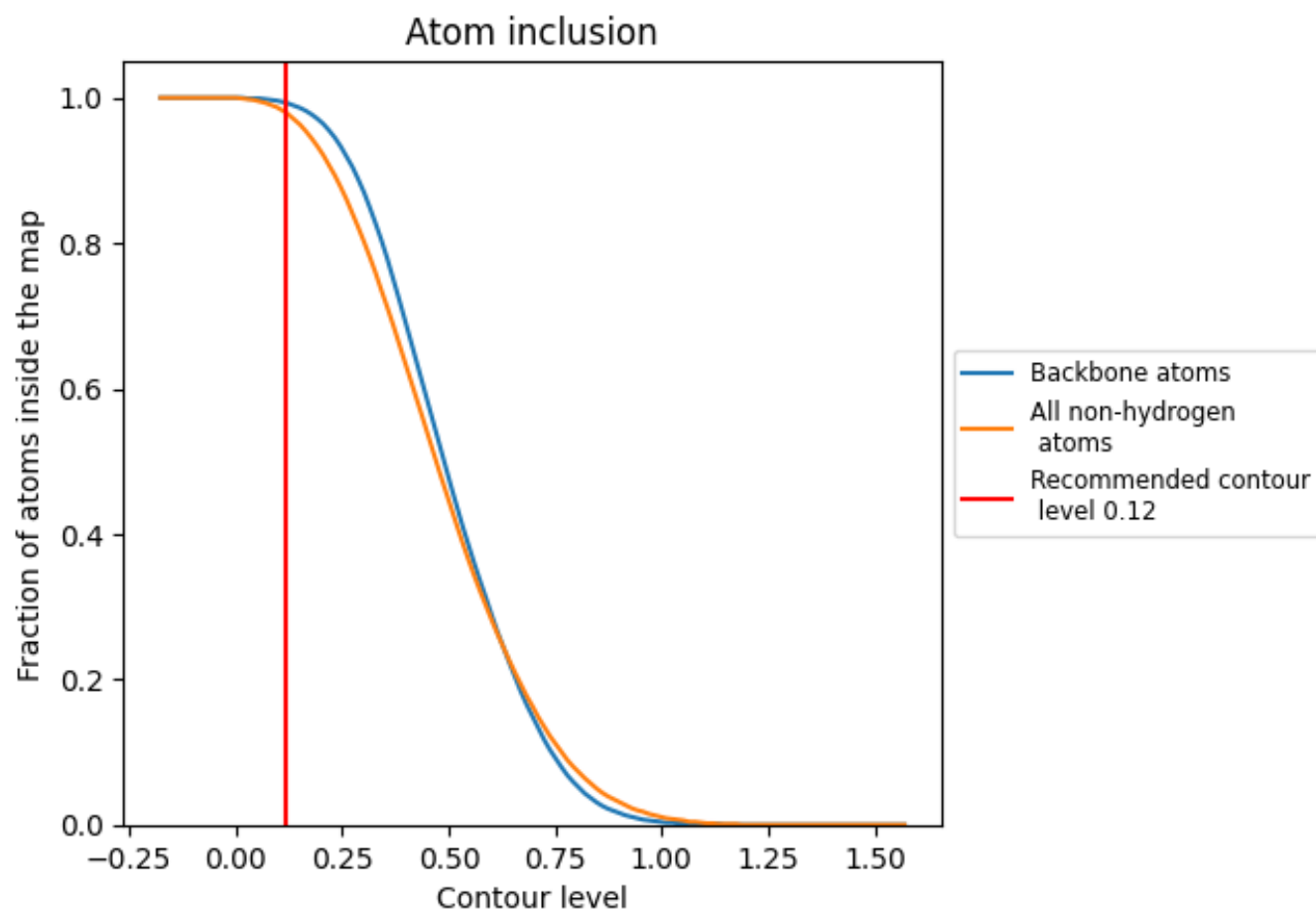
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9790	 0.4490
A4	 0.8540	 0.3350
A5	 0.9860	 0.3950
B4	 0.9830	 0.4260
B5	 0.9860	 0.3010
CC	 0.8660	 0.2510
D5	 0.7960	 0.1770
L1	 0.9870	 0.4450
L5	 0.9970	 0.4900
L6	 0.9910	 0.4420
L7	 1.0000	 0.5190
L8	 0.9930	 0.4970
L9	 0.9990	 0.4420
LA	 0.9840	 0.5510
LB	 0.9830	 0.5220
LC	 0.9850	 0.5210
LD	 0.9960	 0.4660
LE	 0.9880	 0.4810
LF	 0.9830	 0.5130
LG	 0.9540	 0.4520
LH	 0.9860	 0.4930
LI	 0.9760	 0.5120
LJ	 0.9770	 0.4570
LL	 0.9740	 0.5010
LM	 0.9910	 0.4810
LN	 0.9850	 0.5500
LO	 0.9890	 0.5220
LP	 0.9840	 0.5360
LQ	 0.9830	 0.5380
LR	 0.9830	 0.4920
LS	 0.9930	 0.5330
LT	 0.9720	 0.5030
LU	 0.9860	 0.4480
LV	 0.9780	 0.5380
LW	 0.9730	 0.4080























































































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Chain	Atom inclusion	Q-score
LX	 0.9800	 0.5070
LY	 0.9900	 0.4970
LZ	 0.9920	 0.4820
La	 0.9900	 0.5360
Lb	 0.9480	 0.4570
Lc	 0.9660	 0.4990
Ld	 0.9780	 0.5040
Le	 0.9800	 0.5450
Lf	 0.9830	 0.5460
Lg	 0.9670	 0.5120
Lh	 0.9750	 0.4760
Li	 0.9680	 0.4760
Lj	 0.9930	 0.5360
Lk	 0.9660	 0.4500
Ll	 0.9670	 0.5220
Lm	 0.9760	 0.5050
Ln	 0.9670	 0.5420
Lo	 0.9560	 0.5180
Lp	 0.9620	 0.5210
Lr	 0.9880	 0.5200
MA	 0.8940	 0.4880
MB	 0.9550	 0.4770
MC	 0.9370	 0.4690
MD	 0.9830	 0.4140
ME	 0.9810	 0.4330
MF	 0.9230	 0.4560
MG	 0.9480	 0.3970
MH	 0.9470	 0.4350
MI	 0.9410	 0.4500
MJ	 0.9730	 0.4280
ML	 0.9410	 0.4440
MM	 0.9670	 0.4310
MN	 0.9210	 0.4970
MO	 0.9220	 0.4660
MP	 0.9550	 0.4920
MQ	 0.9150	 0.4880
MR	 0.9430	 0.4210
MS	 0.9540	 0.4810
MT	 0.9260	 0.4530
MU	 0.9810	 0.3800
MV	 0.9150	 0.4870
MW	 0.8780	 0.3850





















































































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Chain	Atom inclusion	Q-score
MX	 0.9270	 0.4360
MY	 0.9690	 0.4400
MZ	 0.9690	 0.4350
Ma	 0.9470	 0.4820
Mb	 0.9360	 0.4500
Mc	 0.9460	 0.4250
Md	 0.9390	 0.4540
Me	 0.9070	 0.4890
Mf	 0.9520	 0.4910
Mg	 0.9000	 0.4680
Mh	 0.9500	 0.4280
Mi	 0.9520	 0.4110
Mj	 0.9430	 0.5000
Mk	 0.9480	 0.3940
ML	 0.8500	 0.4650
Mm	 0.9420	 0.4720
Mn	 0.8520	 0.3940
Mo	 0.9360	 0.4780
Mp	 0.8930	 0.4930
Mr	 0.9630	 0.4740
RA	 0.9860	 0.3930
RB	 0.9540	 0.4130
RC	 0.9490	 0.4300
RD	 0.9230	 0.3520
RE	 0.9270	 0.3620
RF	 0.9210	 0.3530
RG	 0.9540	 0.3130
RH	 0.9710	 0.3220
RI	 0.9500	 0.3380
RJ	 0.9160	 0.3250
RK	 0.9220	 0.2950
RL	 0.9320	 0.3920
RN	 0.9150	 0.3670
RO	 0.9210	 0.3980
RP	 0.9670	 0.3710
RQ	 0.9260	 0.3500
RR	 0.9580	 0.3350
RS	 0.9620	 0.3640
RT	 0.9680	 0.3550
RU	 0.9160	 0.3300
RV	 0.9600	 0.4210
RW	 0.9710	 0.3980





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Chain	Atom inclusion	Q-score
RX	 0.9850	 0.4020
RY	 0.9360	 0.3000
RZ	 0.9600	 0.2930
Ra	 0.9730	 0.4230
Rb	 0.9840	 0.3760
Rc	 0.9190	 0.3660
Rd	 0.9280	 0.3820
Re	 0.8960	 0.3560
Rf	 0.9790	 0.2200
Rg	 0.9800	 0.2750
Rh	 0.9850	 0.2510
S2	 0.9970	 0.4600
S3	 0.9810	 0.3930
SA	 0.9840	 0.4550
SB	 0.9230	 0.4720
SC	 0.9860	 0.4890
SD	 0.9760	 0.4260
SE	 0.9900	 0.4710
SF	 0.9590	 0.4180
SG	 0.9950	 0.3960
SH	 0.9920	 0.4360
SI	 0.9880	 0.4840
SJ	 0.9850	 0.4520
SK	 0.9850	 0.3710
SL	 0.9720	 0.5210
SN	 0.9630	 0.4870
SO	 0.9600	 0.5020
SP	 0.9880	 0.4060
SQ	 0.9780	 0.4370
SR	 0.9730	 0.4260
SS	 0.9850	 0.4190
ST	 0.9880	 0.4130
SU	 0.9970	 0.4220
SV	 0.9900	 0.4700
SW	 0.9850	 0.5060
SX	 0.9780	 0.5110
SY	 0.9880	 0.4140
SZ	 0.9710	 0.3980
Sa	 0.9770	 0.5030
Sb	 0.9640	 0.4480
Sc	 0.9430	 0.4460
Sd	 0.9810	 0.4560

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Chain	Atom inclusion	Q-score
Se	 0.9470	 0.4330
Sg	 0.9740	 0.3650