



wwPDB EM Validation Summary Report ⓘ

Dec 18, 2022 – 12:21 pm GMT

PDB ID : 7OYA
EMDB ID : EMD-13111
Title : Cryo-EM structure of the 1 hpf zebrafish embryo 80S ribosome
Authors : Leesch, F.; Lorenzo-Orts, L.; Grishkovskaya, I.; Kandolf, S.; Belacic, K.; Meinhart, A.; Haselbach, D.; Pauli, A.
Deposited on : 2021-06-24
Resolution : 3.20 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.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

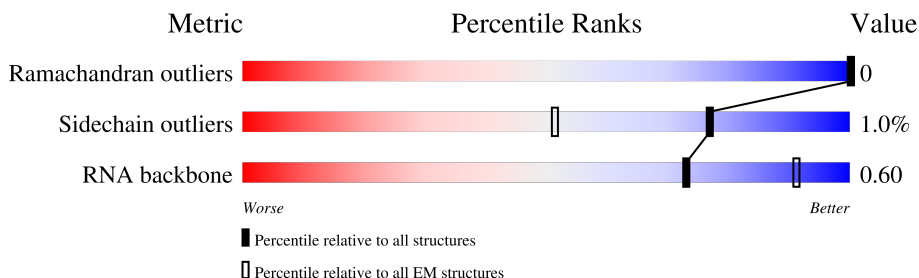
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	22	1939	64% 15% 21%
2	A2	308	68% 32%
3	B2	267	80% 20%
4	C2	280	76% 23%
5	E2	263	99%
6	G2	249	94% 5%
7	H2	194	94% 5%
8	I2	208	89% 10%

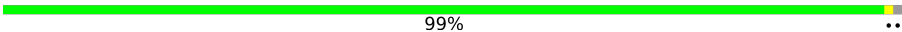




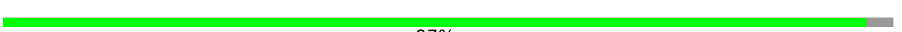






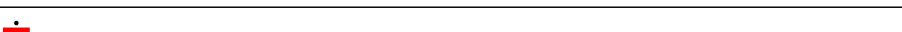

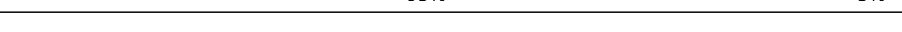
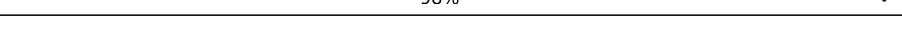
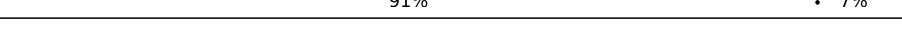
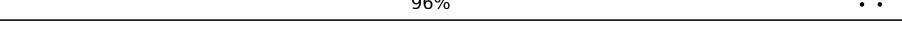



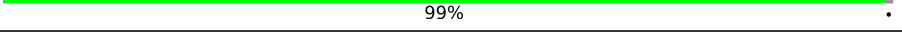


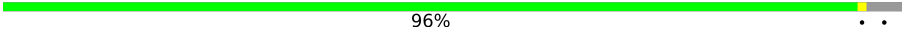
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	J2	194	
10	L2	159	
11	N2	151	
12	O2	151	
13	R2	134	
14	V2	81	
15	W2	130	
16	X2	143	
17	Y2	132	
18	a2	115	
19	b2	84	
20	e2	133	
21	D2	245	
22	F2	204	
23	K2	166	
24	P2	145	
25	Q2	146	
26	U2	119	
27	c2	69	
28	d2	56	
29	g2	317	
30	Z2	124	
31	T2	146	
32	S2	152	
33	i2	347	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	Z1	136	 99% ..
35	b1	64	 77% 23%
36	c1	117	 79% 21%
37	d1	123	 86% 13%
38	e1	135	 93% 7%
39	f1	110	 97% .
40	g1	117	 89% 11%
41	h1	123	 95% ..
42	i1	105	 92% 7%
43	j1	97	 88% 11%
44	k1	70	 99% .
45	o1	106	 96% .
46	p1	92	 98% ..
47	A1	257	 95% 5%
48	B1	403	 98% .
49	C1	375	 91% 7%
50	D1	296	 96% ..
51	E1	265	 76% 22%
52	F1	246	 90% 10%
53	G1	266	 77% 22%
54	H1	192	 99% .
55	J1	178	 93% 6%
56	L1	211	 93% 7%
57	M1	139	 96% ..
58	N1	204	 98% ..

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	O1	205	100%
60	P1	184	82% 17%
61	Q1	182	99%
62	R1	196	84% 15%
63	T1	160	98%
64	U1	141	67% 31%
65	V1	140	92% 8%
66	W1	157	38% 62%
67	X1	155	75% 25%
68	Y1	145	82% 16%
69	l1	51	96%
70	n1	25	96%
71	r1	138	86% 14%
72	l1	215	93% 7%
73	S1	176	99%
74	m1	128	39% 61%
75	a1	148	99%
76	51	4269	64% 14% 22%
77	71	120	94% 6%
78	81	158	82% 18%
79	q1	392	16% 29% 70%
80	v2	858	13% 87%
81	11	155	81% 86% 11%
82	s1	109	13% 14% 84%

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 199905 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	22	1531	Total	C	N	O	P	0	0
			32731	14610	5931	10660	1530		

- Molecule 2 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A2	210	Total	C	N	O	S	0	0
			1665	1061	290	305	9		

- Molecule 3 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B2	213	Total	C	N	O	S	0	0
			1730	1097	310	309	14		

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C2	215	Total	C	N	O	S	0	0
			1669	1080	286	294	9		

- Molecule 5 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E2	261	Total	C	N	O	S	0	0
			2073	1322	385	357	9		

- Molecule 6 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G2	237	Total	C	N	O	S	0	0
			1925	1199	391	328	7		

- Molecule 7 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	H2	186	Total	C	N	O	0	0
			1492	952	276	264		

- Molecule 8 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I2	188	Total	C	N	O	S	0	0
			1531	964	305	257	5		

- Molecule 9 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J2	180	Total	C	N	O	S	0	0
			1492	952	295	243	2		

- Molecule 10 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L2	136	Total	C	N	O	S	0	0
			1110	703	215	186	6		

- Molecule 11 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N2	149	Total	C	N	O	S	0	0
			1200	767	230	202	1		

- Molecule 12 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O2	133	Total	C	N	O	S	0	0
			993	609	194	184	6		

- Molecule 13 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R2	130	Total	C	N	O	S	0	0
			1053	662	194	193	4		

- Molecule 14 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V2	81	Total	C	N	O	S	0	0
			623	384	116	119	4		

- Molecule 15 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W2	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 16 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X2	139	Total	C	N	O	S	0	0
			1083	684	215	181	3		

- Molecule 17 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y2	124	Total	C	N	O	S	0	0
			1011	643	193	170	5		

- Molecule 18 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	a2	98	Total	C	N	O	S	0	0
			782	486	161	130	5		

- Molecule 19 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	b2	82	Total	C	N	O	S	0	0
			645	403	122	113	7		

- Molecule 20 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	e2	50	Total	C	N	O	0	0
			399	244	88	67		

- Molecule 21 is a protein called DNA-(apurinic or apyrimidinic site) lyase.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	D2	218	Total	C	N	O	S	0	0
			1668	1061	298	302	7		

- Molecule 22 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	F2	157	Total	C	N	O	S	0	0
			1234	770	229	230	5		

- Molecule 23 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	K2	94	Total	C	N	O	S	0	0
			771	506	132	128	5		

- Molecule 24 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P2	112	Total	C	N	O	S	0	0
			927	589	170	161	7		

- Molecule 25 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q2	139	Total	C	N	O	S	0	0
			1104	703	207	191	3		

- Molecule 26 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U2	97	Total	C	N	O	S	0	0
			754	473	139	138	4		

- Molecule 27 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c2	62	Total	C	N	O	S	0	0
			482	293	95	92	2		

- Molecule 28 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d2	49	Total	C	N	O	S	0	0
			406	255	83	63	5		

- Molecule 29 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	g2	309	Total	C	N	O	S	0	0
			2388	1505	416	455	12		

- Molecule 30 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Z2	71	Total	C	N	O	0	0
			566	365	103	98		

- Molecule 31 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	T2	137	Total	C	N	O	S	0	0
			1058	667	202	185	4		

- Molecule 32 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	S2	139	Total	C	N	O	S	0	0
			1139	716	226	196	1		

- Molecule 33 is a protein called Zgc:103482.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i2	36	Total	C	N	O	S	0	0
			292	168	65	58	1		

- Molecule 34 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z1	135	Total	C	N	O	S	0	0
			1105	714	208	179	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b1	49	Total	C	N	O	S	0	0
			419	259	92	67	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c1	93	Total	C	N	O	S	0	0
			721	457	127	131	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d1	107	Total	C	N	O	S	0	0
			888	558	172	156	2		

- Molecule 38 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e1	125	Total	C	N	O	S	0	0
			1030	649	212	163	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f1	107	Total	C	N	O	S	0	0
			861	550	171	137	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g1	104	Total	C	N	O	S	0	0
			833	519	172	136	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	h1	120	Total	C	N	O	S	0	0
			991	627	197	165	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i1	98	Total	C	N	O	S	0	0
			801	502	170	125	4		

- Molecule 43 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j1	86	Total	C	N	O	S	0	0
			701	430	155	110	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k1	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 45 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o1	102	Total	C	N	O	S	0	0
			840	526	172	136	6		

- Molecule 46 is a protein called Zgc:171772.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p1	91	Total	C	N	O	S	0	0
			703	444	132	120	7		

- Molecule 47 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	A1	245	Total	C	N	O	S	0	0
			1879	1181	381	310	7		

- Molecule 48 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B1	394	Total	C	N	O	S	0	0
			3181	2021	600	544	16		

- Molecule 49 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	C1	348	Total	C	N	O	S	0	0
			2774	1741	551	464	18		

- Molecule 50 is a protein called Ribosomal protein L5b.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	D1	288	Total	C	N	O	S	0	0
			2337	1482	429	415	11		

- Molecule 51 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	E1	206	Total	C	N	O	S	0	0
			1672	1064	327	274	7		

- Molecule 52 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	F1	222	Total	C	N	O	S	0	0
			1811	1160	346	298	7		

- Molecule 53 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	G1	207	Total	C	N	O	S	0	0
			1683	1076	322	281	4		

- Molecule 54 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	H1	190	Total	C	N	O	S	0	0
			1505	949	279	271	6		

- Molecule 55 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	J1	167	Total	C	N	O	S	0	0
			1348	854	254	235	5		

- Molecule 56 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	L1	197	Total	C	N	O	S	0	0
			1603	1003	335	260	5		

- Molecule 57 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	M1	134	Total	C	N	O	S	0	0
			1094	702	207	180	5		

- Molecule 58 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	N1	202	Total	C	N	O	S	0	0
			1689	1065	352	267	5		

- Molecule 59 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	O1	204	Total	C	N	O	S	0	0
			1662	1073	318	266	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	P1	152	Total	C	N	O	S	0	0
			1235	770	243	213	9		

- Molecule 61 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Q1	180	Total	C	N	O	S	0	0
			1459	917	302	236	4		

- Molecule 62 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	R1	166	Total	C	N	O	S	0	0
			1381	856	300	215	10		

- Molecule 63 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	T1	157	Total	C	N	O	S	0	0
			1283	816	250	213	4		

- Molecule 64 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	U1	97	Total	C	N	O	S	0	0
			792	508	138	144	2		

- Molecule 65 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	V1	129	Total	C	N	O	S	0	0
			970	613	182	170	5		

- Molecule 66 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	W1	60	Total	C	N	O	S	0	0
			503	323	98	80	2		

- Molecule 67 is a protein called Ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	X1	117	Total	C	N	O	S	0	0
			959	614	179	165	1		

- Molecule 68 is a protein called ATPase H⁺ transporting V0 subunit e1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Y1	122	Total	C	N	O	S	0	0
			1024	643	209	169	3		

- Molecule 69 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	l1	49	Total	C	N	O	S	0	0
			434	275	97	61	1		

- Molecule 70 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	n1	24	Total	C	N	O	S	0	0
			231	140	63	26	2		

- Molecule 71 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	r1	118	Total	C	N	O	S	0	0
			943	589	193	159	2		

- Molecule 72 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	I1	201	Total	C	N	O	S	0	0
			1630	1037	315	264	14		

- Molecule 73 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	S1	176	Total	C	N	O	S	0	0
			1457	934	284	230	9		

- Molecule 74 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	m1	50	Total	C	N	O	S	0	0
			413	256	87	64	6		

- Molecule 75 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	a1	147	Total	C	N	O	S	0	0
			1164	740	233	188	3		

- Molecule 76 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	51	3321	Total	C	N	O	P	0	0
			71140	31690	12986	23144	3320		

- Molecule 77 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	71	120	Total	C	N	O	P	0	0
			2563	1145	465	834	119		

- Molecule 78 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	81	158	Total	C	N	O	P	0	0
			3363	1501	600	1104	158		

- Molecule 79 is a protein called Novel protein similar to human proliferation-associated 2G4 protein (PA2G4).

Mol	Chain	Residues	Atoms					AltConf	Trace
79	q1	118	Total	C	N	O	S	0	0
			943	599	165	169	10		

- Molecule 80 is a protein called Eukaryotic translation elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	v2	110	Total	C	N	O	S	0	0
			885	569	147	164	5		

- Molecule 81 is a protein called Eukaryotic translation initiation factor 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	11	138	Total	C	N	O	S	0	0
			1055	656	183	205	11		

- Molecule 82 is a protein called Dap1b.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	s1	17	Total	C	N	O	S	0	0
			139	87	29	22	1		

- Molecule 83 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	a2	1	Total	Zn	0
			1	1	
83	d2	1	Total	Zn	0
			1	1	

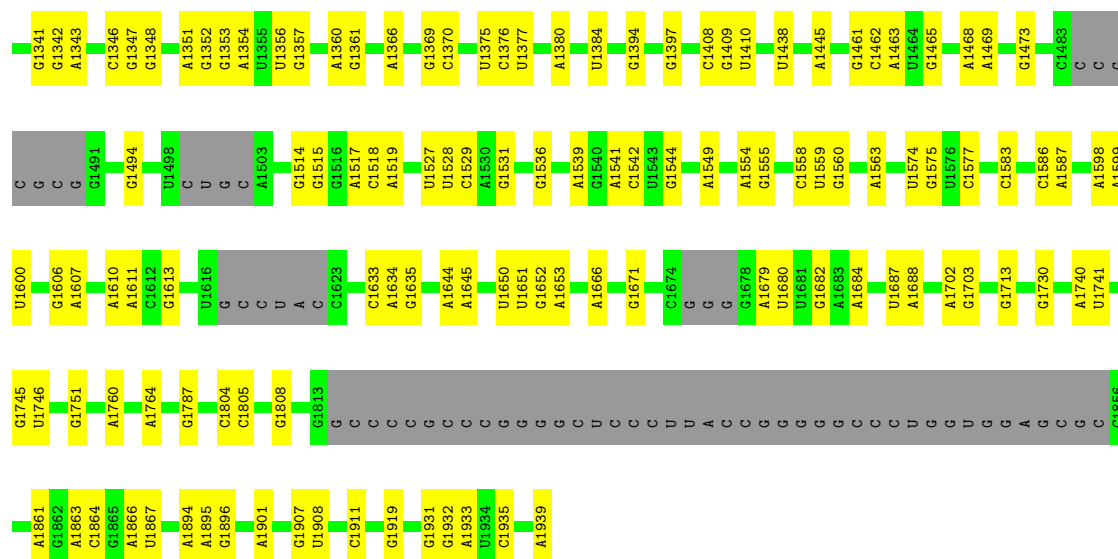
Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
83	g1	1	Total 1	Zn 1	0
83	j1	1	Total 1	Zn 1	0
83	o1	1	Total 1	Zn 1	0
83	p1	1	Total 1	Zn 1	0
83	m1	1	Total 1	Zn 1	0

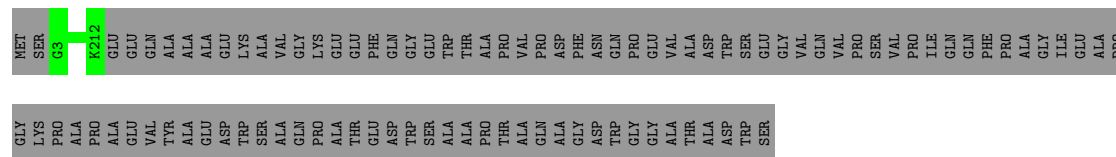
- Molecule 84 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	b1	1	Total 1	Mg 1	0
84	A1	1	Total 1	Mg 1	0
84	B1	1	Total 1	Mg 1	0
84	V1	1	Total 1	Mg 1	0
84	S1	1	Total 1	Mg 1	0
84	m1	1	Total 1	Mg 1	0
84	51	186	Total 186	Mg 186	0
84	71	5	Total 5	Mg 5	0
84	81	5	Total 5	Mg 5	0



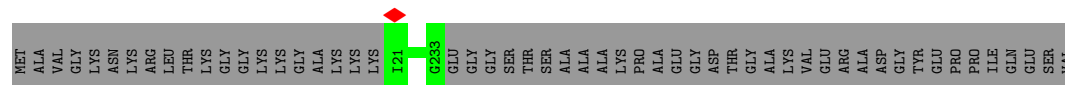
• Molecule 2: 40S ribosomal protein SA

Chain A2: 68% 32%



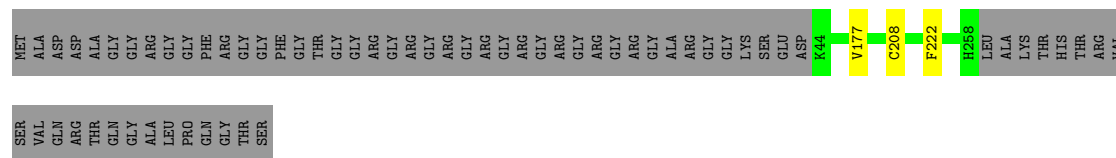
• Molecule 3: 40S ribosomal protein S3a

Chain B2: 80% 20%



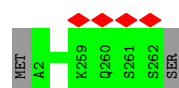
• Molecule 4: 40S ribosomal protein S2

Chain C2: 76% 23%



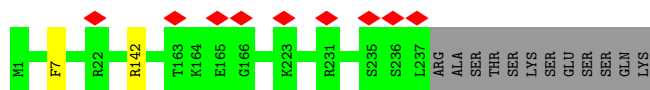
• Molecule 5: 40S ribosomal protein S4, X isoform

Chain E2: 99%



- Molecule 6: 40S ribosomal protein S6

Chain G2:  94% 5%




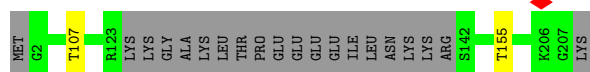
- Molecule 7: 40S ribosomal protein S7

Chain H2:  5% 94%



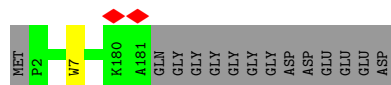
- Molecule 8: 40S ribosomal protein S8

Chain I2:  89% 10%




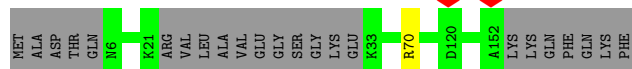
- Molecule 9: 40S ribosomal protein S9

Chain J2:  92% 7%



- Molecule 10: 40S ribosomal protein S11

Chain L2:  85% 14%



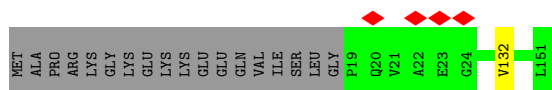
- Molecule 11: 40S ribosomal protein S13

Chain N2:  97%

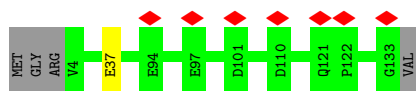


- Molecule 12: Ribosomal protein S14

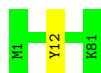
Chain O2:  87% 12%



- Molecule 13: 40S ribosomal protein S17



- Molecule 14: 40S ribosomal protein S21



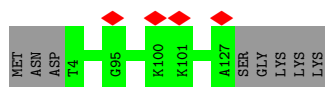
- Molecule 15: 40S ribosomal protein S15a



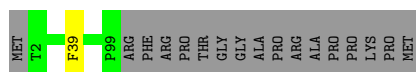
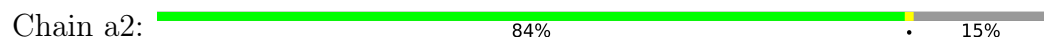
- Molecule 16: 40S ribosomal protein S23



- Molecule 17: 40S ribosomal protein S24

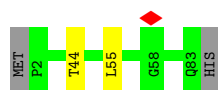


- Molecule 18: 40S ribosomal protein S26

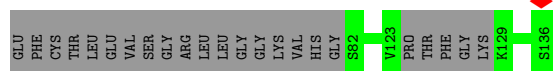
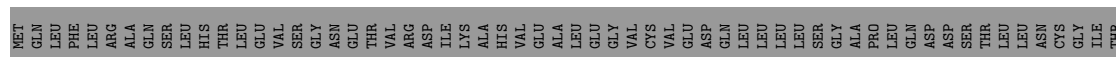


- Molecule 19: 40S ribosomal protein S27

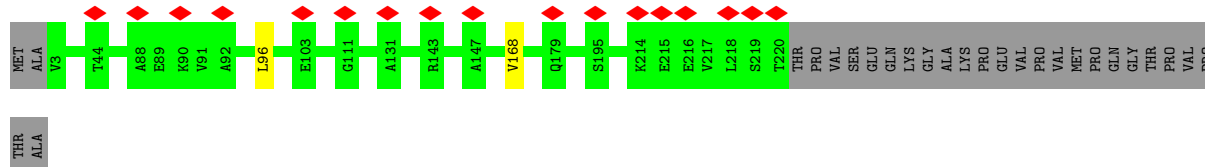
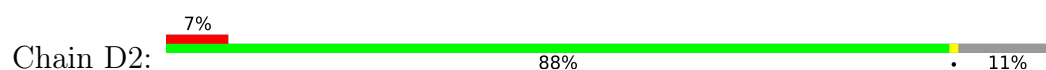




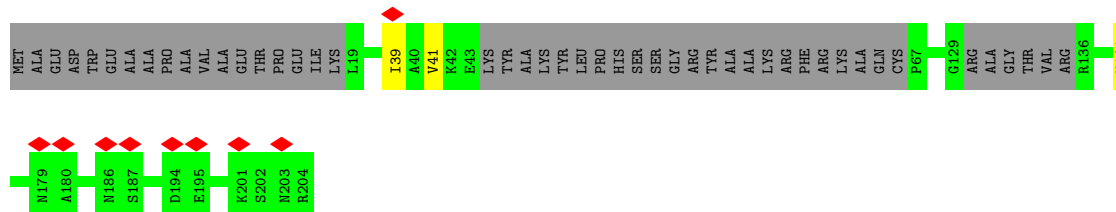
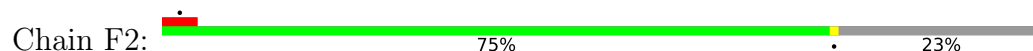
- Molecule 20: 40S ribosomal protein S30



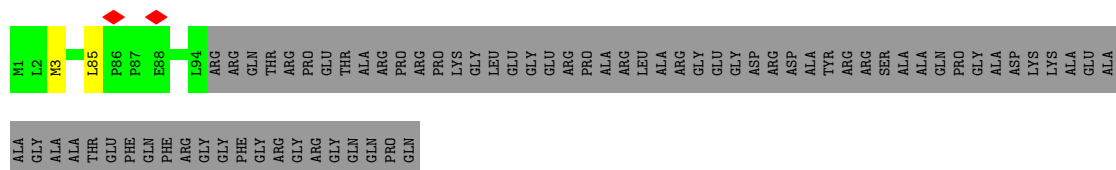
- Molecule 21: DNA-(apurinic or apyrimidinic site) lyase



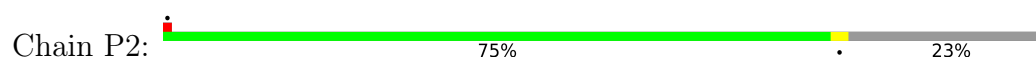
- Molecule 22: Ribosomal protein S5

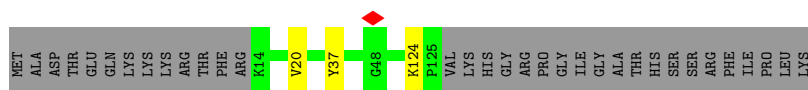


- Molecule 23: Ribosomal protein S10

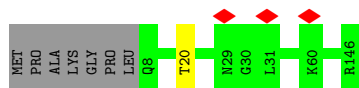


- Molecule 24: 40S ribosomal protein S15

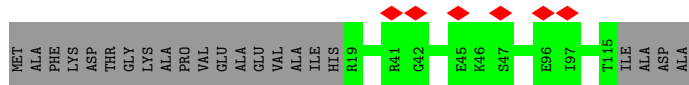
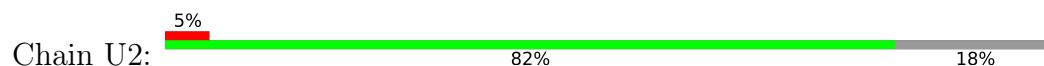




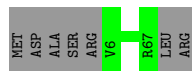
- Molecule 25: Ribosomal protein S16



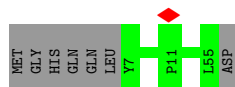
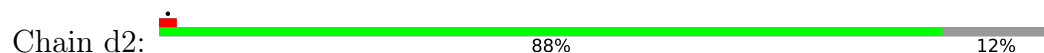
- Molecule 26: 40S ribosomal protein S20



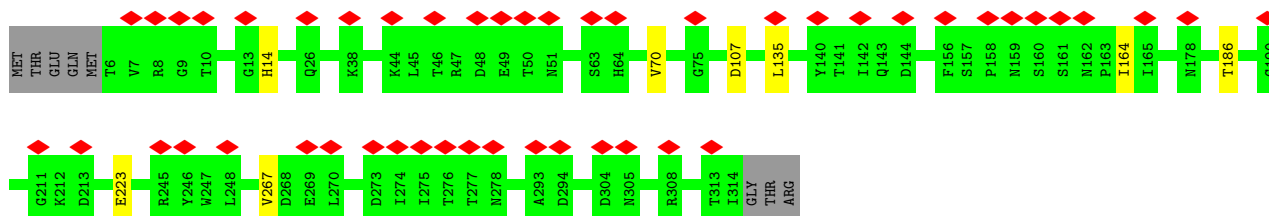
- Molecule 27: 40S ribosomal protein S28



- Molecule 28: 40S ribosomal protein S29



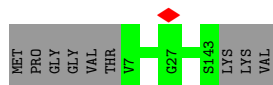
- Molecule 29: Guanine nucleotide-binding protein subunit beta-2-like 1



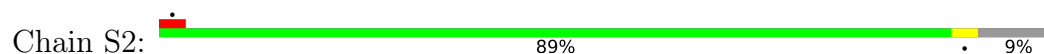
- Molecule 30: 40S ribosomal protein S25



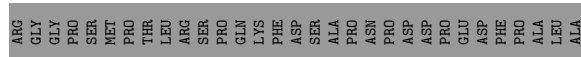
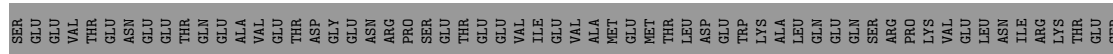
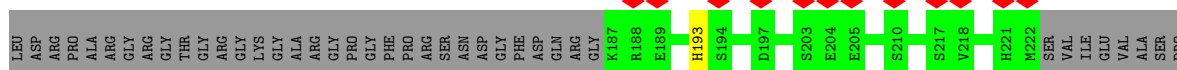
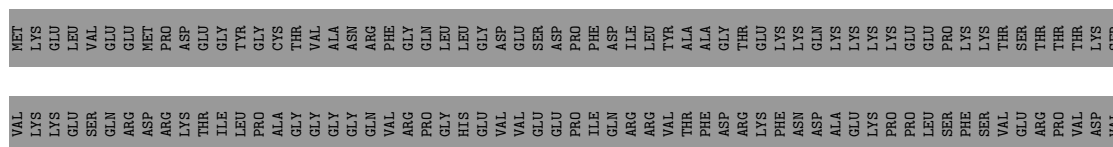
- Molecule 31: 40S ribosomal protein S19



- Molecule 32: 40S ribosomal protein S18



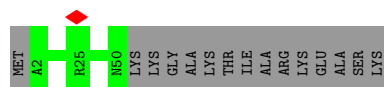
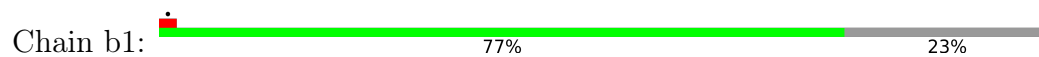
- Molecule 33: Zgc:103482



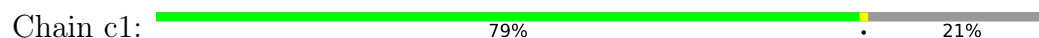
- Molecule 34: 60S ribosomal protein L27



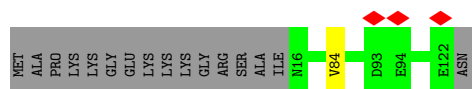
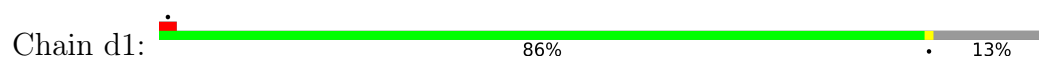
- Molecule 35: 60S ribosomal protein L29



- Molecule 36: 60S ribosomal protein L30



- Molecule 37: 60S ribosomal protein L31



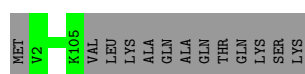
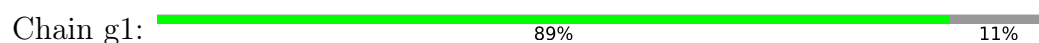
- Molecule 38: Ribosomal protein L32



- Molecule 39: 60S ribosomal protein L35a



- Molecule 40: 60S ribosomal protein L34

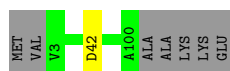


- Molecule 41: 60S ribosomal protein L35




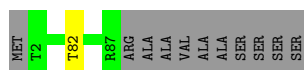
- Molecule 42: 60S ribosomal protein L36

Chain i1:  92% • 7%



- Molecule 43: Ribosomal protein L37

Chain j1:  88% • 11%



- Molecule 44: 60S ribosomal protein L38

Chain k1:  99% •



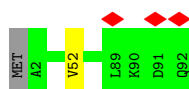
- Molecule 45: 60S ribosomal protein L36a

Chain o1:  96% •



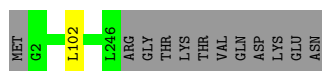
- Molecule 46: Zgc:171772

Chain p1:  98% ••



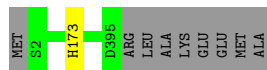
- Molecule 47: 60S ribosomal protein L8

Chain A1:  95% 5%



- Molecule 48: Ribosomal protein L3

Chain B1:  98% •



- Molecule 49: Ribosomal protein L4

ME1	A2	R71	Y122	V217	L240	F257	A349	LYS	ME1	LEU	LYS	PRO	LYS	LYS	LYS	ARG	ARG	VAL	VAL	LYS	LYS	THR	LYS	ALA	LYS	LYS	ALA	GLU	THR	PRO	ALA	GLN	ALA
-----	----	-----	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- MET
GLY
PHE
V4
M73
E186
D215
K258
Q291
ALA
ALA
GLU
GLU
ASP

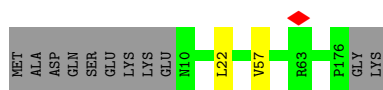
-
- | Amino Acid | Information Content (bits) |
|------------|----------------------------|
| Met | 0.00 |
| Ala | 0.00 |
| Val | 0.00 |
| Leu | 0.00 |
| Ile | 0.00 |
| Pro | 0.00 |
| Thr | 0.00 |
| Lys | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu | 0.00 |
| Phe | 0.00 |
| Thr | 0.00 |
| Val | 0.00 |
| Lys | 0.00 |
| Glu | 0.00 |
| Arg | 0.00 |
| His | 0.00 |
| Gly | 0.00 |
| Ser | 0.00 |
| Asn | 0.00 |
| Asp | 0.00 |
| Glu</ | |

- | | |
|-----|------|
| MET | |
| ALA | |
| GLY | |
| GLU | |
| THR | |
| LYS | |
| LYS | |
| LYS | |
| TLE | |
| PRO | |
| SER | |
| VAL | |
| PRO | |
| GLU | |
| SER | |
| LEU | |
| LEU | |
| LYS | |
| ARG | |
| ARG | |
| GLN | |
| ARG | |
| PHE | |
| ALA | A25 |
| | N97 |
| | N246 |

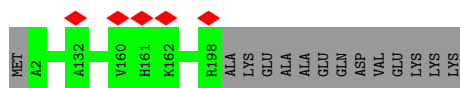
- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GLU | LEU | ALA | THR | LYS | LEU | GLY | MET | PRO | GLY | LYS | LYS | GLY | LYS | VAL | LYS | ALA | PRO | ALA | PRO | SER | VAL | ALA | LYS | LYS | HIS | GLU | VAL | LYS | VAL | VAL | P29 | P137 | ALA | GLU | GLN | LYS | ALA | ALA | GLY | LYS | GLY | ASP | THR | PRO | THR | LYS | ARG | P133 | P175 | T250 | ALA | LYS | LEU | GLU | LYS | ALA | LYS | LYS | ALA | LYS |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- M1 A190
GLU
SER

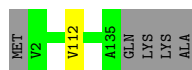
- Chain J1: 93% 6%



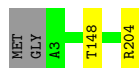
- Molecule 56: 60S ribosomal protein L13



- Molecule 57: 60S ribosomal protein L14



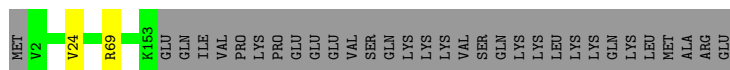
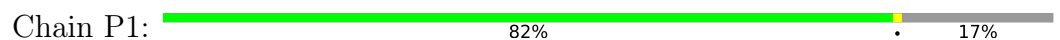
- Molecule 58: Ribosomal protein L15



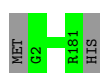
- Molecule 59: 60S ribosomal protein L13a



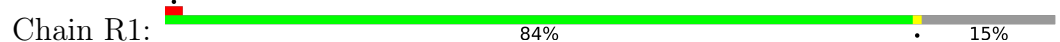
- Molecule 60: 60S ribosomal protein L17

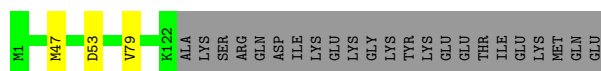


- Molecule 61: Ribosomal protein L18



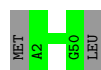
- Molecule 62: 60S ribosomal protein L19





- Molecule 69: Ribosomal protein L39

Chain l1: 96%



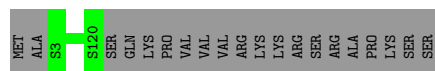
- Molecule 70: 60S ribosomal protein L41

Chain n1: 96%



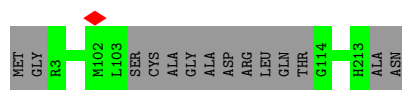
- Molecule 71: 60S ribosomal protein L28

Chain r1: 86% 14%



- Molecule 72: 60S ribosomal protein L10

Chain l1: 93% 7%



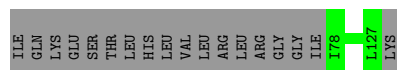
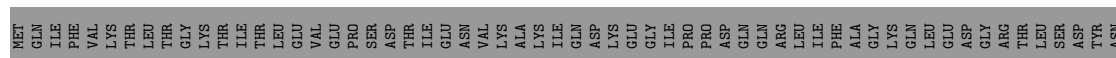
- Molecule 73: 60S ribosomal protein L18a

Chain S1: 99%

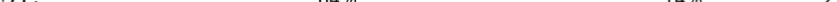


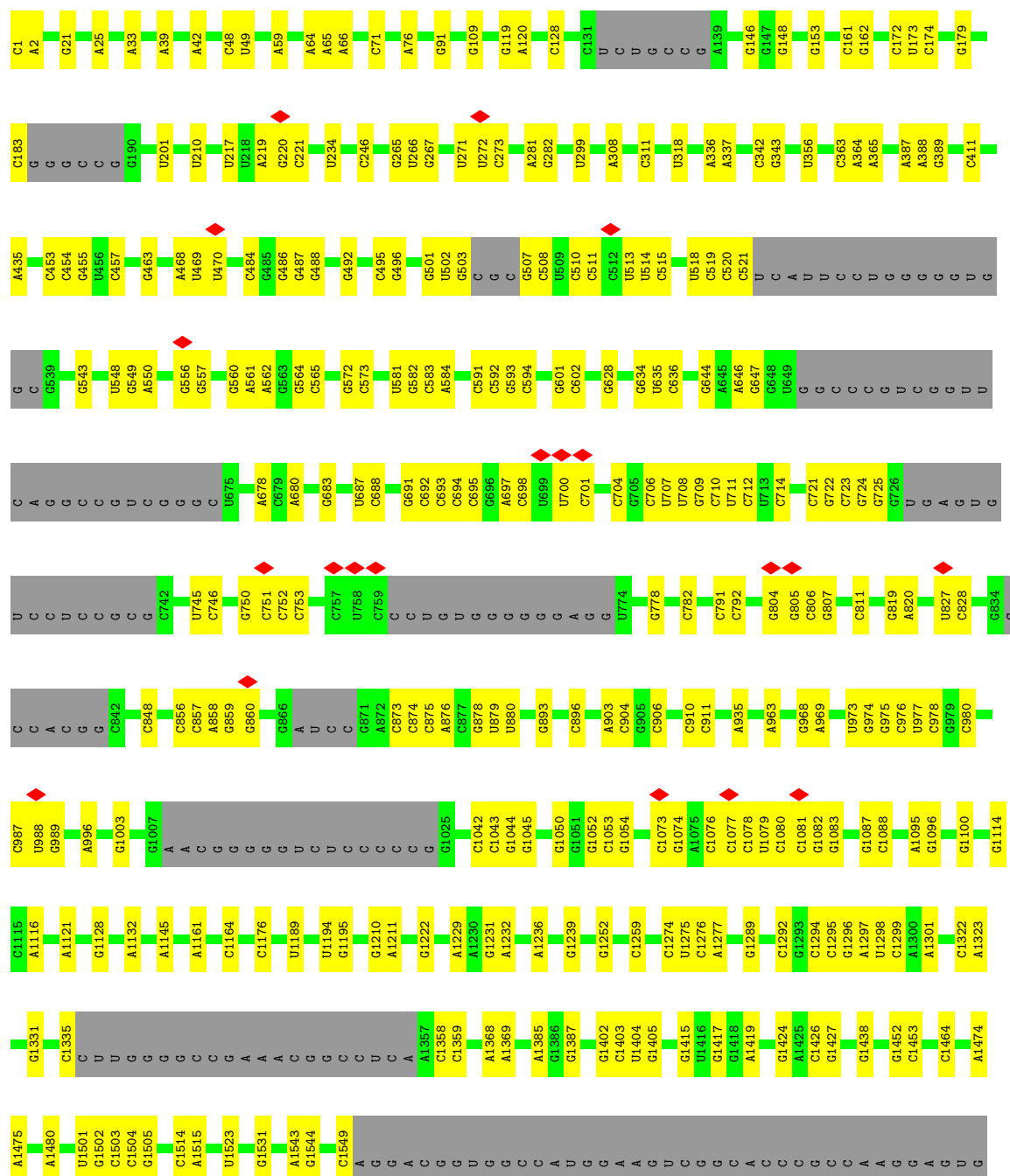
- Molecule 74: 60S ribosomal protein L40

Chain m1: 39% 61%

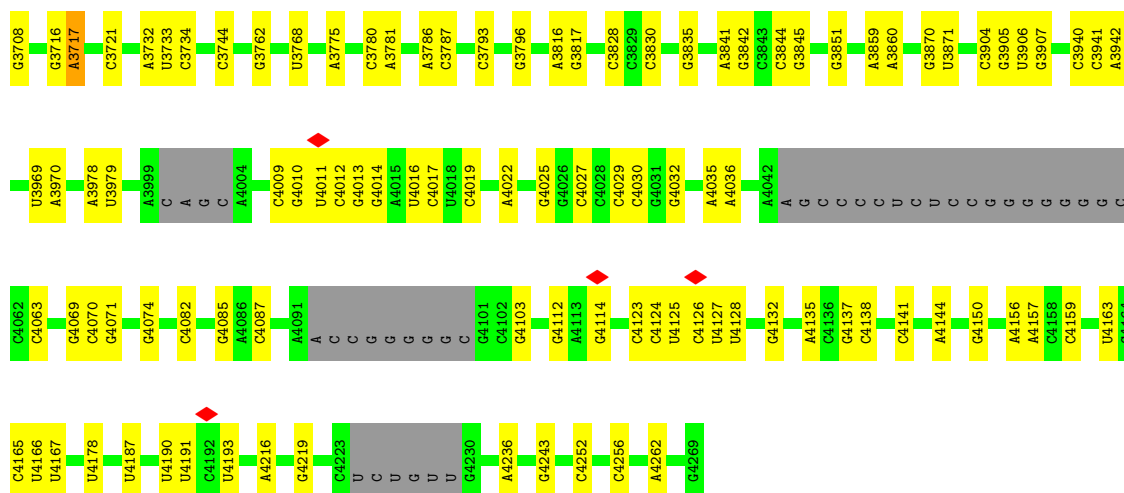


- Molecule 75: 60S ribosomal protein L27a

Chain 51:  64% 14% 22%







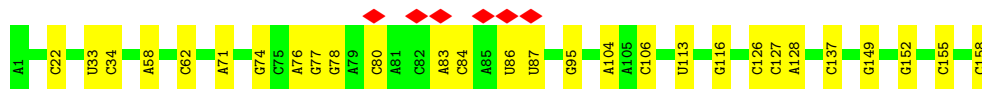
• Molecule 77: 5S rRNA

Chain 71: 94% 6%



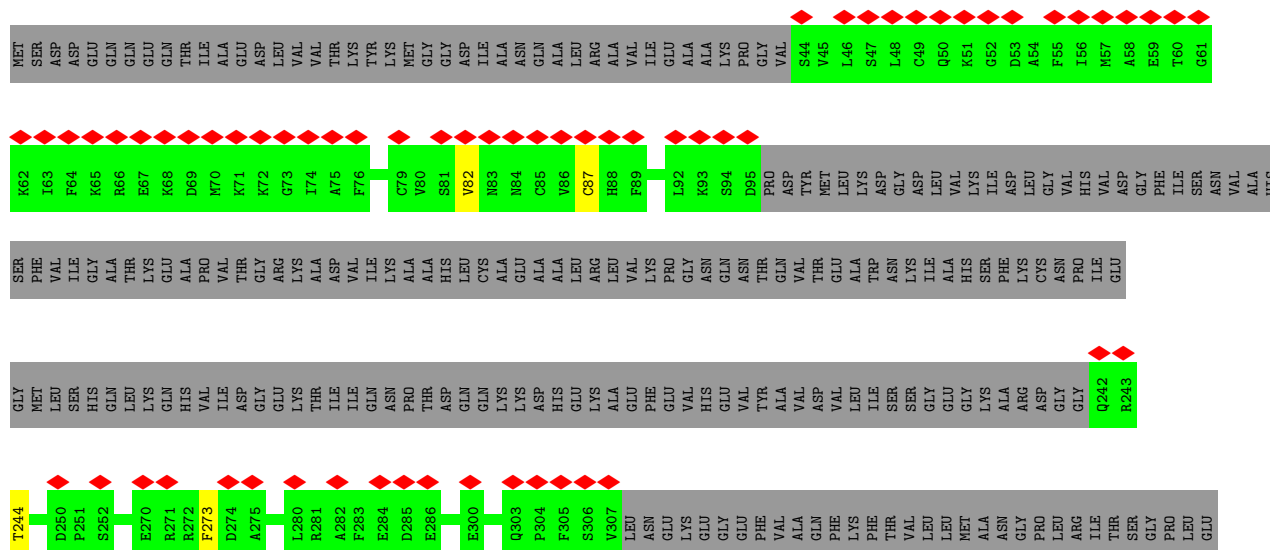
• Molecule 78: 5.8S rRNA

Chain 81: 82% 18%

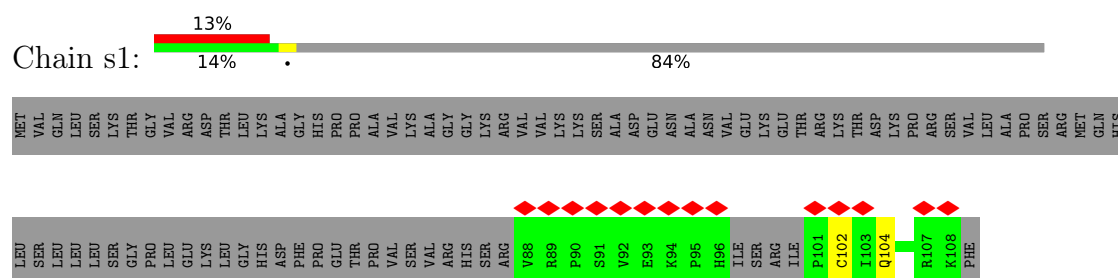


• Molecule 79: Novel protein similar to human proliferation-associated 2G4 protein (PA2G4)

Chain q1: 16% 29% 70%







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	535633	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	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	8.712	Depositor
Minimum map value	-0.551	Depositor
Average map value	0.089	Depositor
Map value standard deviation	0.284	Depositor
Recommended contour level	0.9	Depositor
Map size (Å)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, 5CT

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	22	0.18	0/36607	0.71	5/57041 (0.0%)
2	A2	0.24	0/1703	0.39	0/2313
3	B2	0.23	0/1757	0.41	0/2353
4	C2	0.24	0/1705	0.41	0/2304
5	E2	0.24	0/2113	0.42	0/2842
6	G2	0.23	0/1948	0.40	0/2595
7	H2	0.23	0/1515	0.40	0/2033
8	I2	0.24	0/1558	0.40	0/2081
9	J2	0.23	0/1517	0.38	0/2028
10	L2	0.24	0/1130	0.43	0/1513
11	N2	0.22	0/1223	0.38	0/1644
12	O2	0.24	0/1006	0.44	0/1348
13	R2	0.23	0/1067	0.39	0/1433
14	V2	0.24	0/629	0.41	0/842
15	W2	0.24	0/1051	0.40	0/1406
16	X2	0.24	0/1100	0.42	0/1468
17	Y2	0.24	0/1027	0.42	0/1364
18	a2	0.24	0/795	0.40	0/1066
19	b2	0.23	0/658	0.42	0/884
20	e2	0.23	0/401	0.39	0/526
21	D2	0.24	0/1694	0.43	0/2286
22	F2	0.22	0/1247	0.38	0/1676
23	K2	0.23	0/793	0.38	0/1073
24	P2	0.24	0/943	0.39	0/1260
25	Q2	0.24	0/1121	0.40	0/1501
26	U2	0.23	0/763	0.42	0/1027
27	c2	0.24	0/484	0.44	0/649
28	d2	0.23	0/416	0.38	0/553
29	g2	0.23	0/2445	0.45	0/3335
30	Z2	0.23	0/573	0.41	0/770
31	T2	0.23	0/1076	0.37	0/1445
32	S2	0.23	0/1157	0.40	0/1554

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i2	0.22	0/296	0.39	0/389
34	Z1	0.25	0/1128	0.40	0/1504
35	b1	0.23	0/429	0.36	0/568
36	c1	0.25	0/731	0.40	0/981
37	d1	0.24	0/903	0.41	0/1217
38	e1	0.24	0/1048	0.40	0/1396
39	f1	0.26	0/880	0.43	0/1175
40	g1	0.23	0/843	0.42	0/1123
41	h1	0.22	0/998	0.37	0/1318
42	i1	0.23	0/812	0.36	0/1074
43	j1	0.24	0/715	0.42	0/944
44	k1	0.24	0/575	0.38	0/761
45	o1	0.24	0/853	0.41	0/1125
46	p1	0.24	0/713	0.41	0/945
47	A1	0.25	0/1918	0.43	0/2569
48	B1	0.25	0/3251	0.42	0/4351
49	C1	0.24	0/2828	0.40	0/3797
50	D1	0.24	0/2380	0.38	0/3185
51	E1	0.24	0/1698	0.41	0/2265
52	F1	0.24	0/1842	0.38	0/2460
53	G1	0.24	0/1717	0.39	0/2316
54	H1	0.24	0/1523	0.43	0/2048
55	J1	0.23	0/1371	0.41	0/1833
56	L1	0.23	0/1631	0.40	0/2178
57	M1	0.24	0/1115	0.38	0/1488
58	N1	0.24	0/1731	0.39	0/2314
59	O1	0.24	0/1694	0.38	0/2267
60	P1	0.24	0/1261	0.40	0/1691
61	Q1	0.24	0/1484	0.41	0/1985
62	R1	0.22	0/1397	0.36	0/1849
63	T1	0.24	0/1312	0.40	0/1756
64	U1	0.24	0/806	0.41	0/1081
65	V1	0.25	0/984	0.42	0/1320
66	W1	0.25	0/516	0.39	0/688
67	X1	0.24	0/978	0.40	0/1318
68	Y1	0.23	0/1039	0.40	0/1383
69	l1	0.23	0/444	0.37	0/587
70	n1	0.20	0/232	0.32	0/295
71	r1	0.23	0/956	0.40	0/1279
72	I1	0.25	0/1668	0.40	0/2229
73	S1	0.25	0/1496	0.40	0/2009
74	m1	0.23	0/419	0.41	0/555
75	a1	0.24	0/1196	0.40	0/1601

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	51	0.24	9/79560 (0.0%)	0.70	7/124065 (0.0%)
77	71	0.20	0/2867	0.66	0/4469
78	81	0.19	0/3757	0.69	1/5853 (0.0%)
79	q1	0.24	0/960	0.39	0/1280
80	v2	0.24	0/904	0.40	0/1224
81	11	0.24	0/1053	0.44	0/1411
82	s1	0.37	0/142	0.89	2/189 (1.1%)
All	All	0.23	9/214276 (0.0%)	0.60	15/313921 (0.0%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
76	51	3166	A	O3'-P	-12.87	1.45	1.61
76	51	3168	A	O3'-P	-11.70	1.47	1.61
76	51	3169	C	O3'-P	-11.13	1.47	1.61
76	51	3716	G	O3'-P	-10.02	1.49	1.61
76	51	3656	A	O3'-P	-9.55	1.49	1.61

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	51	3716	G	P-O3'-C3'	16.00	138.91	119.70
76	51	3165	A	O5'-P-OP1	-15.44	91.80	105.70
76	51	3168	A	O5'-P-OP1	-15.11	92.10	105.70
76	51	3717	A	O5'-P-OP2	-7.02	99.38	105.70
1	22	676	U	C2-N1-C1'	6.87	125.95	117.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A2	208/308 (68%)	206 (99%)	2 (1%)	0	100	100
3	B2	211/267 (79%)	203 (96%)	8 (4%)	0	100	100
4	C2	213/280 (76%)	211 (99%)	2 (1%)	0	100	100
5	E2	259/263 (98%)	249 (96%)	10 (4%)	0	100	100
6	G2	235/249 (94%)	228 (97%)	7 (3%)	0	100	100
7	H2	184/194 (95%)	173 (94%)	11 (6%)	0	100	100
8	I2	184/208 (88%)	180 (98%)	4 (2%)	0	100	100
9	J2	178/194 (92%)	177 (99%)	1 (1%)	0	100	100
10	L2	132/159 (83%)	127 (96%)	5 (4%)	0	100	100
11	N2	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
12	O2	131/151 (87%)	127 (97%)	4 (3%)	0	100	100
13	R2	128/134 (96%)	126 (98%)	2 (2%)	0	100	100
14	V2	79/81 (98%)	78 (99%)	1 (1%)	0	100	100
15	W2	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
16	X2	137/143 (96%)	130 (95%)	7 (5%)	0	100	100
17	Y2	122/132 (92%)	118 (97%)	4 (3%)	0	100	100
18	a2	96/115 (84%)	96 (100%)	0	0	100	100
19	b2	80/84 (95%)	78 (98%)	2 (2%)	0	100	100
20	e2	46/133 (35%)	46 (100%)	0	0	100	100
21	D2	216/245 (88%)	208 (96%)	8 (4%)	0	100	100
22	F2	151/204 (74%)	144 (95%)	7 (5%)	0	100	100
23	K2	92/166 (55%)	87 (95%)	5 (5%)	0	100	100
24	P2	110/145 (76%)	107 (97%)	3 (3%)	0	100	100
25	Q2	137/146 (94%)	131 (96%)	6 (4%)	0	100	100
26	U2	95/119 (80%)	92 (97%)	3 (3%)	0	100	100
27	c2	60/69 (87%)	60 (100%)	0	0	100	100
28	d2	47/56 (84%)	47 (100%)	0	0	100	100
29	g2	307/317 (97%)	292 (95%)	15 (5%)	0	100	100
30	Z2	69/124 (56%)	67 (97%)	2 (3%)	0	100	100
31	T2	135/146 (92%)	130 (96%)	5 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	S2	137/152 (90%)	131 (96%)	6 (4%)	0	100	100
33	i2	34/347 (10%)	30 (88%)	4 (12%)	0	100	100
34	Z1	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
35	b1	47/64 (73%)	44 (94%)	3 (6%)	0	100	100
36	c1	91/117 (78%)	90 (99%)	1 (1%)	0	100	100
37	d1	105/123 (85%)	98 (93%)	7 (7%)	0	100	100
38	e1	123/135 (91%)	120 (98%)	3 (2%)	0	100	100
39	f1	105/110 (96%)	103 (98%)	2 (2%)	0	100	100
40	g1	102/117 (87%)	99 (97%)	3 (3%)	0	100	100
41	h1	118/123 (96%)	116 (98%)	2 (2%)	0	100	100
42	i1	96/105 (91%)	93 (97%)	3 (3%)	0	100	100
43	j1	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
44	k1	67/70 (96%)	67 (100%)	0	0	100	100
45	o1	100/106 (94%)	97 (97%)	3 (3%)	0	100	100
46	p1	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
47	A1	243/257 (95%)	234 (96%)	9 (4%)	0	100	100
48	B1	392/403 (97%)	379 (97%)	13 (3%)	0	100	100
49	C1	346/375 (92%)	338 (98%)	8 (2%)	0	100	100
50	D1	286/296 (97%)	283 (99%)	3 (1%)	0	100	100
51	E1	198/265 (75%)	191 (96%)	7 (4%)	0	100	100
52	F1	220/246 (89%)	216 (98%)	4 (2%)	0	100	100
53	G1	203/266 (76%)	196 (97%)	7 (3%)	0	100	100
54	H1	188/192 (98%)	184 (98%)	4 (2%)	0	100	100
55	J1	165/178 (93%)	162 (98%)	3 (2%)	0	100	100
56	L1	195/211 (92%)	191 (98%)	4 (2%)	0	100	100
57	M1	132/139 (95%)	126 (96%)	6 (4%)	0	100	100
58	N1	200/204 (98%)	194 (97%)	6 (3%)	0	100	100
59	O1	202/205 (98%)	201 (100%)	1 (0%)	0	100	100
60	P1	150/184 (82%)	142 (95%)	8 (5%)	0	100	100
61	Q1	178/182 (98%)	169 (95%)	9 (5%)	0	100	100
62	R1	164/196 (84%)	162 (99%)	2 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	T1	155/160 (97%)	148 (96%)	7 (4%)	0	100	100
64	U1	95/141 (67%)	93 (98%)	2 (2%)	0	100	100
65	V1	127/140 (91%)	123 (97%)	4 (3%)	0	100	100
66	W1	58/157 (37%)	57 (98%)	1 (2%)	0	100	100
67	X1	115/155 (74%)	113 (98%)	2 (2%)	0	100	100
68	Y1	120/145 (83%)	118 (98%)	2 (2%)	0	100	100
69	l1	47/51 (92%)	47 (100%)	0	0	100	100
70	n1	22/25 (88%)	22 (100%)	0	0	100	100
71	r1	116/138 (84%)	116 (100%)	0	0	100	100
72	I1	197/215 (92%)	195 (99%)	2 (1%)	0	100	100
73	S1	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
74	m1	48/128 (38%)	48 (100%)	0	0	100	100
75	a1	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
79	q1	114/392 (29%)	110 (96%)	4 (4%)	0	100	100
80	v2	106/858 (12%)	104 (98%)	2 (2%)	0	100	100
81	11	133/155 (86%)	116 (87%)	17 (13%)	0	100	100
82	s1	13/109 (12%)	12 (92%)	1 (8%)	0	100	100
All	All	10994/14099 (78%)	10667 (97%)	327 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A2	179/250 (72%)	179 (100%)	0	100	100
3	B2	194/231 (84%)	194 (100%)	0	100	100
4	C2	181/220 (82%)	178 (98%)	3 (2%)	60	83
5	E2	227/229 (99%)	227 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	G2	208/219 (95%)	206 (99%)	2 (1%)	76	90
7	H2	165/176 (94%)	162 (98%)	3 (2%)	59	82
8	I2	163/181 (90%)	161 (99%)	2 (1%)	71	88
9	J2	160/168 (95%)	159 (99%)	1 (1%)	86	94
10	L2	122/141 (86%)	121 (99%)	1 (1%)	81	93
11	N2	129/130 (99%)	127 (98%)	2 (2%)	62	84
12	O2	103/119 (87%)	102 (99%)	1 (1%)	76	90
13	R2	118/121 (98%)	117 (99%)	1 (1%)	81	93
14	V2	65/65 (100%)	64 (98%)	1 (2%)	65	85
15	W2	112/113 (99%)	112 (100%)	0	100	100
16	X2	111/115 (96%)	110 (99%)	1 (1%)	78	91
17	Y2	108/116 (93%)	108 (100%)	0	100	100
18	a2	86/99 (87%)	85 (99%)	1 (1%)	71	88
19	b2	74/76 (97%)	72 (97%)	2 (3%)	44	75
20	e2	41/112 (37%)	41 (100%)	0	100	100
21	D2	176/204 (86%)	174 (99%)	2 (1%)	73	88
22	F2	135/170 (79%)	132 (98%)	3 (2%)	52	79
23	K2	82/132 (62%)	80 (98%)	2 (2%)	49	77
24	P2	102/130 (78%)	99 (97%)	3 (3%)	42	74
25	Q2	114/119 (96%)	113 (99%)	1 (1%)	78	91
26	U2	87/105 (83%)	87 (100%)	0	100	100
27	c2	54/61 (88%)	54 (100%)	0	100	100
28	d2	42/49 (86%)	42 (100%)	0	100	100
29	g2	263/274 (96%)	255 (97%)	8 (3%)	41	73
30	Z2	61/105 (58%)	58 (95%)	3 (5%)	25	61
31	T2	110/117 (94%)	110 (100%)	0	100	100
32	S2	119/132 (90%)	115 (97%)	4 (3%)	37	70
33	i2	32/296 (11%)	31 (97%)	1 (3%)	40	72
34	Z1	115/116 (99%)	114 (99%)	1 (1%)	78	91
35	b1	45/56 (80%)	45 (100%)	0	100	100
36	c1	78/98 (80%)	77 (99%)	1 (1%)	69	87

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	d1	98/110 (89%)	97 (99%)	1 (1%)	76	90
38	e1	113/121 (93%)	113 (100%)	0	100	100
39	f1	86/88 (98%)	86 (100%)	0	100	100
40	g1	91/102 (89%)	91 (100%)	0	100	100
41	h1	108/110 (98%)	105 (97%)	3 (3%)	43	74
42	i1	83/88 (94%)	82 (99%)	1 (1%)	71	88
43	j1	73/80 (91%)	72 (99%)	1 (1%)	67	86
44	k1	64/65 (98%)	64 (100%)	0	100	100
45	o1	91/95 (96%)	91 (100%)	0	100	100
46	p1	74/75 (99%)	73 (99%)	1 (1%)	67	86
47	A1	189/200 (94%)	188 (100%)	1 (0%)	88	95
48	B1	346/353 (98%)	345 (100%)	1 (0%)	92	96
49	C1	291/313 (93%)	286 (98%)	5 (2%)	60	83
50	D1	244/249 (98%)	241 (99%)	3 (1%)	71	88
51	E1	182/234 (78%)	178 (98%)	4 (2%)	52	79
52	F1	189/210 (90%)	188 (100%)	1 (0%)	88	95
53	G1	181/224 (81%)	180 (99%)	1 (1%)	86	94
54	H1	167/169 (99%)	167 (100%)	0	100	100
55	J1	141/150 (94%)	139 (99%)	2 (1%)	67	86
56	L1	167/178 (94%)	167 (100%)	0	100	100
57	M1	113/117 (97%)	112 (99%)	1 (1%)	78	91
58	N1	171/172 (99%)	169 (99%)	2 (1%)	71	88
59	O1	175/176 (99%)	175 (100%)	0	100	100
60	P1	134/165 (81%)	132 (98%)	2 (2%)	65	85
61	Q1	158/160 (99%)	158 (100%)	0	100	100
62	R1	145/173 (84%)	143 (99%)	2 (1%)	67	86
63	T1	138/140 (99%)	138 (100%)	0	100	100
64	U1	87/127 (68%)	84 (97%)	3 (3%)	37	70
65	V1	101/108 (94%)	101 (100%)	0	100	100
66	W1	52/129 (40%)	52 (100%)	0	100	100
67	X1	105/134 (78%)	105 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	Y1	115/136 (85%)	112 (97%)	3 (3%)	46	76
69	l1	45/47 (96%)	45 (100%)	0	100	100
70	n1	23/24 (96%)	23 (100%)	0	100	100
71	r1	102/120 (85%)	102 (100%)	0	100	100
72	l1	173/182 (95%)	173 (100%)	0	100	100
73	S1	155/155 (100%)	154 (99%)	1 (1%)	86	94
74	m1	46/116 (40%)	46 (100%)	0	100	100
75	a1	121/122 (99%)	120 (99%)	1 (1%)	81	93
79	q1	105/329 (32%)	101 (96%)	4 (4%)	33	67
80	v2	97/731 (13%)	97 (100%)	0	100	100
81	l1	115/129 (89%)	111 (96%)	4 (4%)	36	69
82	s1	17/97 (18%)	17 (100%)	0	100	100
All	All	9632/12048 (80%)	9534 (99%)	98 (1%)	77	90

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	A1	102	LEU
52	F1	97	ASN
49	C1	71	ARG
50	D1	186	GLU
57	M1	112	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 125 such sidechains are listed below:

Mol	Chain	Res	Type
31	T2	127	GLN
68	Y1	65	GLN
47	A1	132	ASN
68	Y1	56	GLN
74	m1	104	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	22	1514/1939 (78%)	281 (18%)	10 (0%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
76	51	3300/4269 (77%)	585 (17%)	36 (1%)
77	71	119/120 (99%)	7 (5%)	0
78	81	157/158 (99%)	27 (17%)	2 (1%)
All	All	5090/6486 (78%)	900 (17%)	48 (0%)

5 of 900 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	22	3	C
1	22	4	C
1	22	17	C
1	22	26	U
1	22	33	G

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
76	51	1080	C
76	51	2205	C
76	51	1231	G
76	51	1795	G
76	51	3044	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
81	5CT	11	51	81	13,14,15	0.70	0	9,15,17	1.21	1 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	5CT	11	51	81	-	5/13/14/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	11	51	5CT	C3-C2-C1	-2.11	107.35	112.16

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	11	51	5CT	C1-C2-C3-C4
81	11	51	5CT	O1-C2-C3-C4
81	11	51	5CT	C2-C1-NZ-CE
81	11	51	5CT	CG-CD-CE-NZ
81	11	51	5CT	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 209 ligands modelled in this entry, 209 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

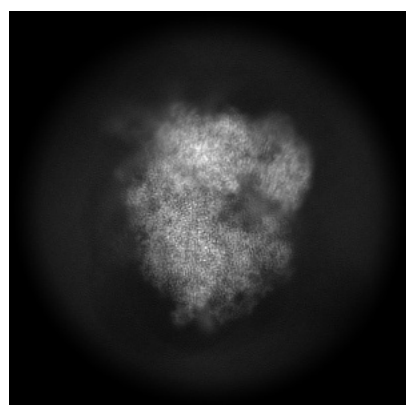
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13111. These allow visual inspection of the internal detail of the map and identification of artifacts.

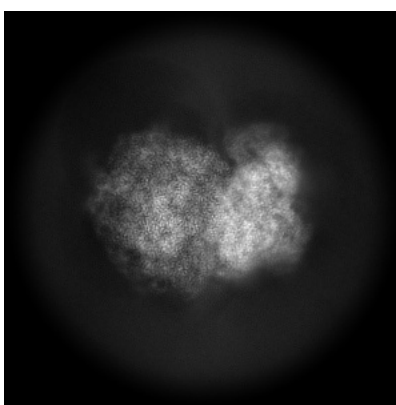
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

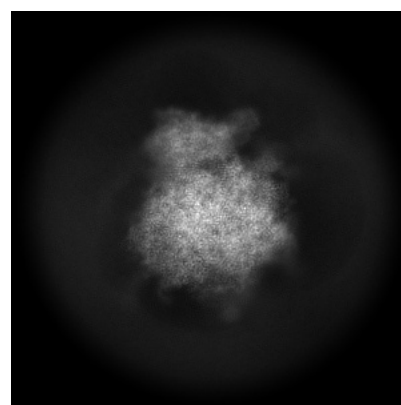
6.1.1 Primary map



X



Y

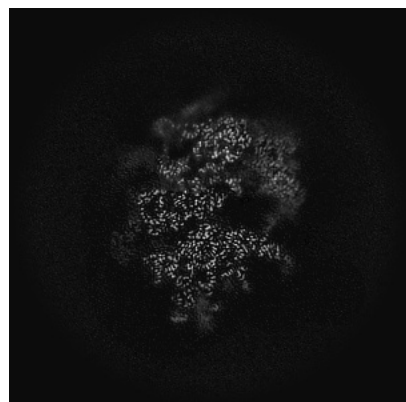


Z

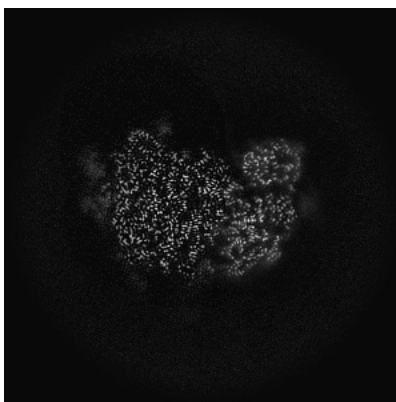
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

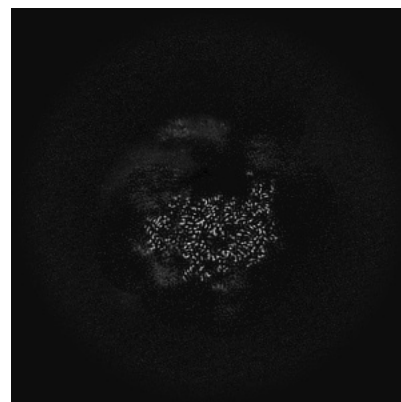
6.2.1 Primary map



X Index: 240



Y Index: 240

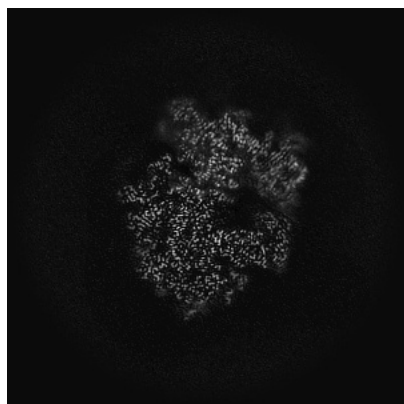


Z Index: 240

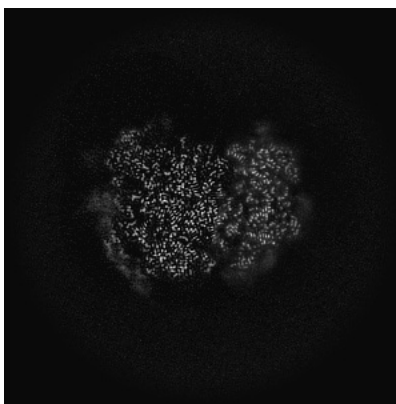
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

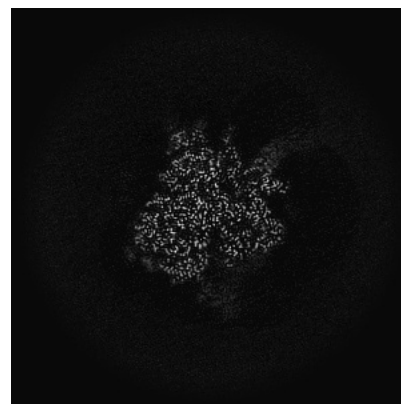
6.3.1 Primary map



X Index: 221



Y Index: 228



Z Index: 202

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

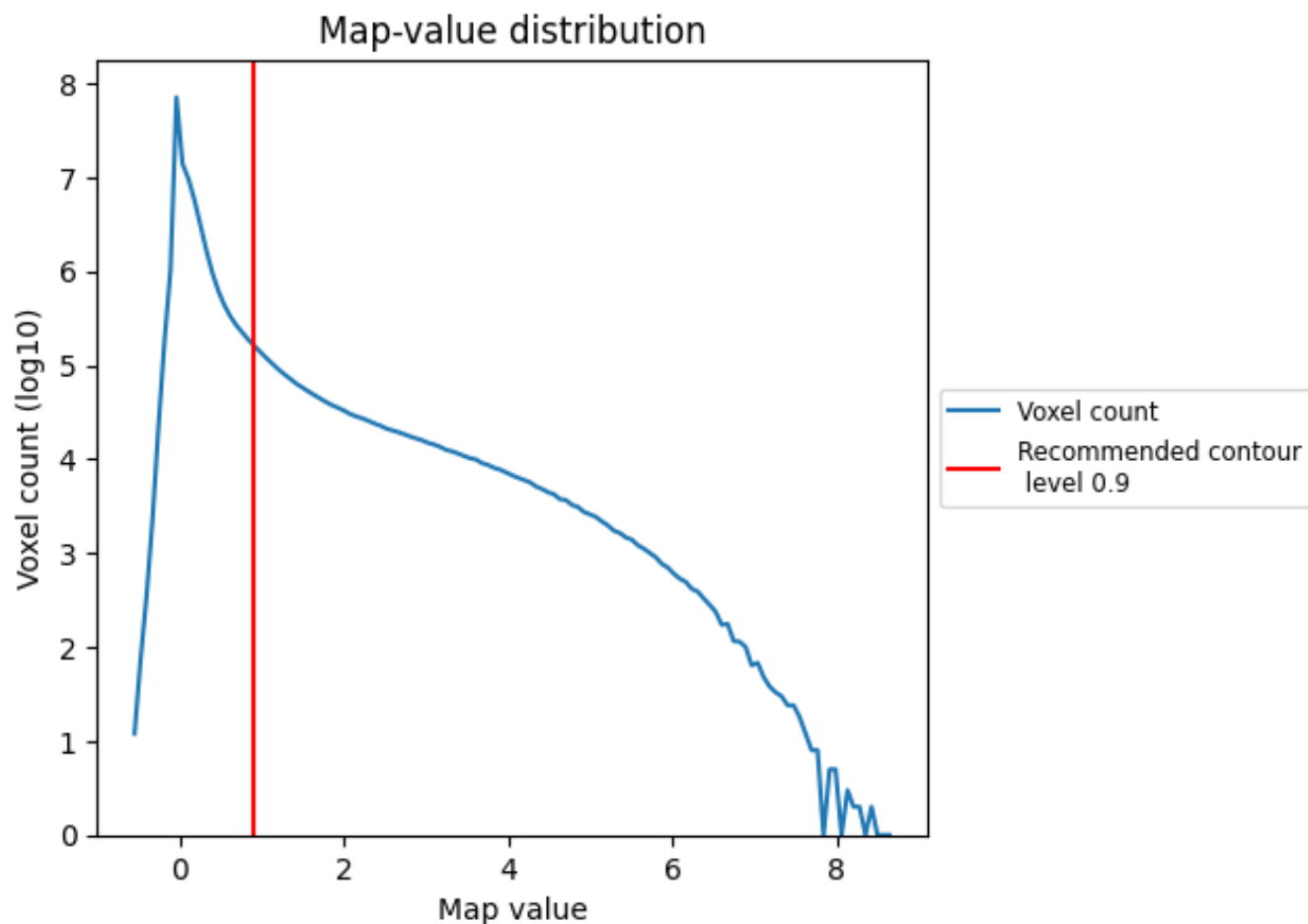
6.5 Mask visualisation

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

7 Map analysis [i](#)

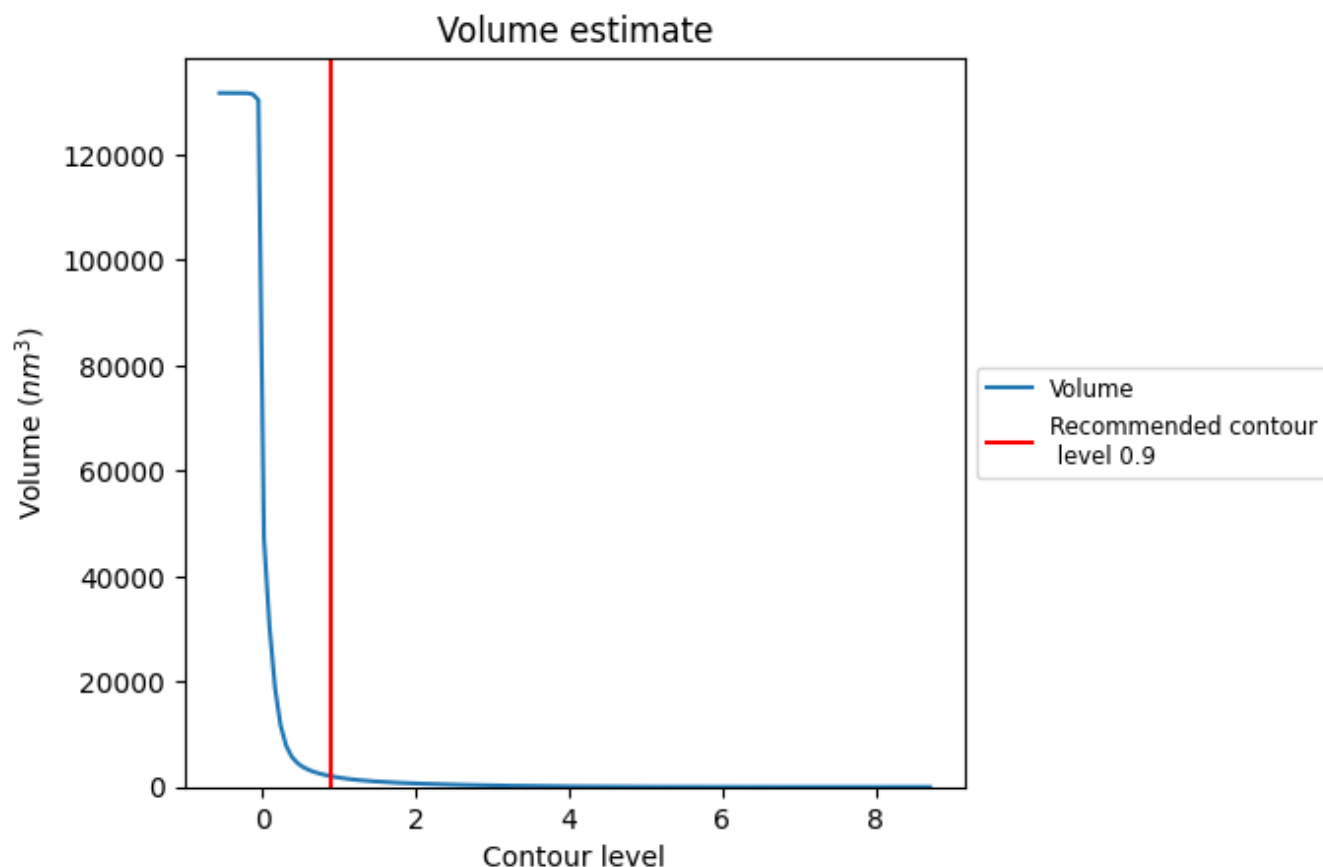
This section contains the results of statistical analysis of the map.

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.

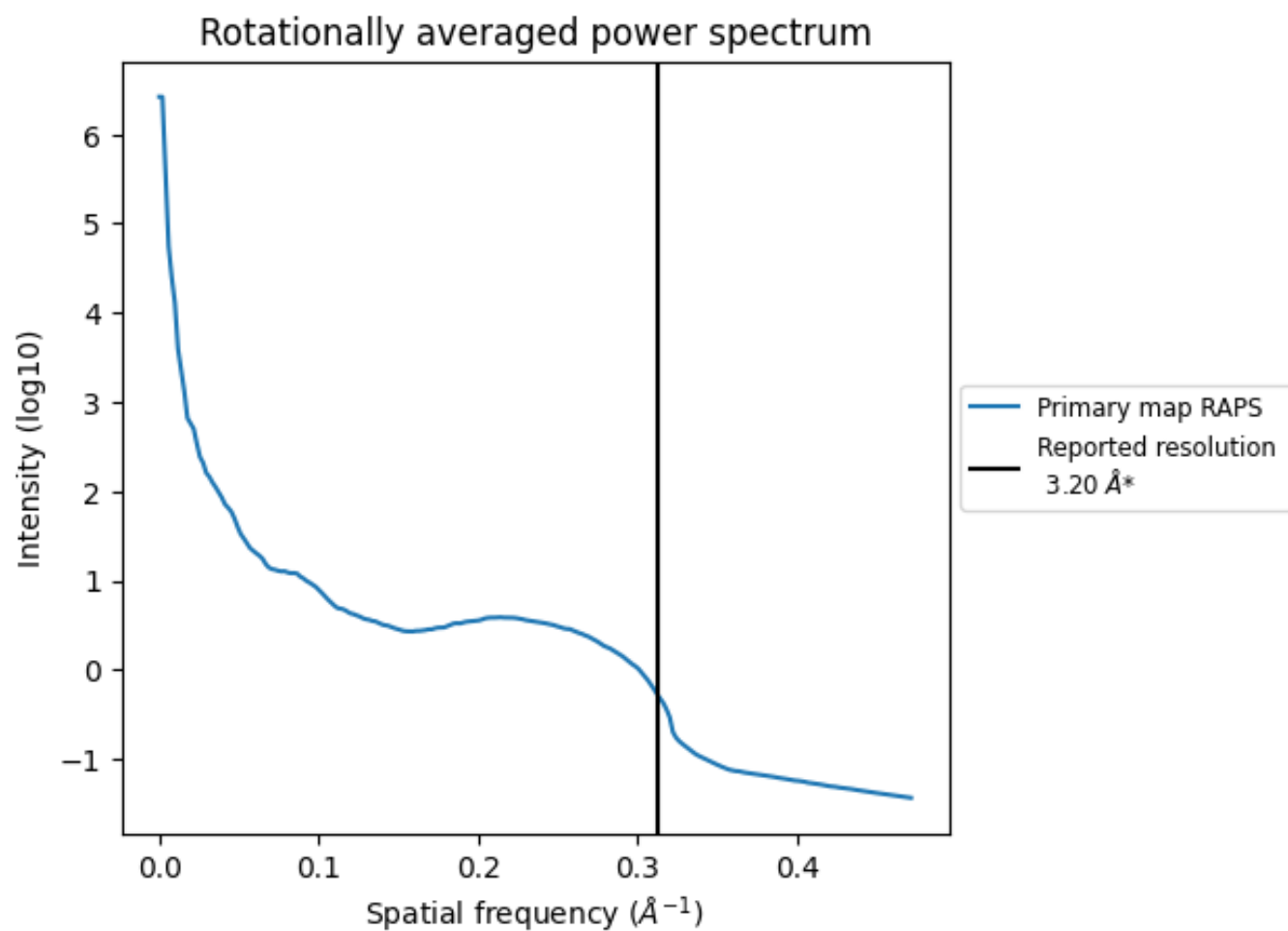
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2042 nm^3 ; this corresponds to an approximate mass of 1844 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 0.312 Å⁻¹

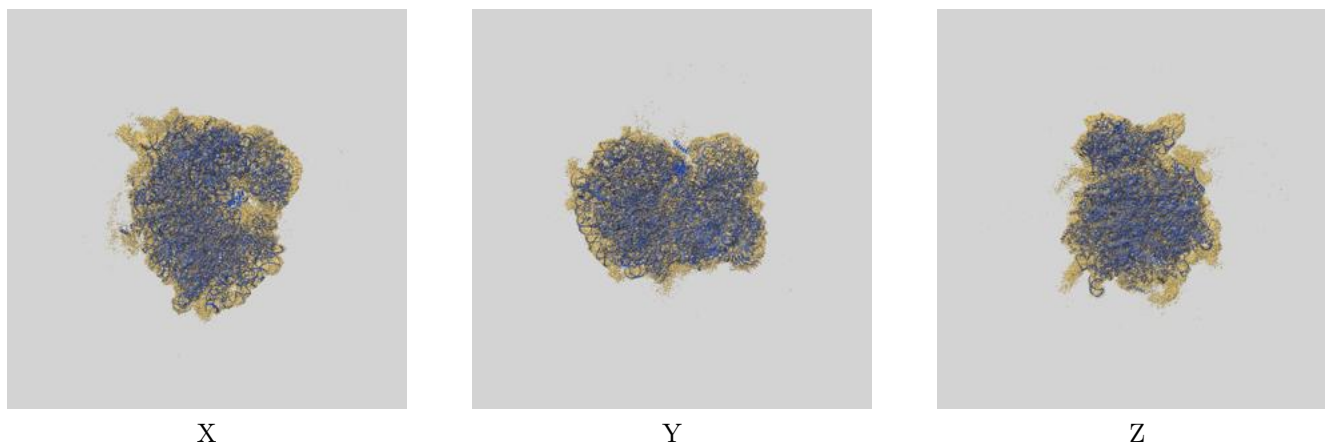
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

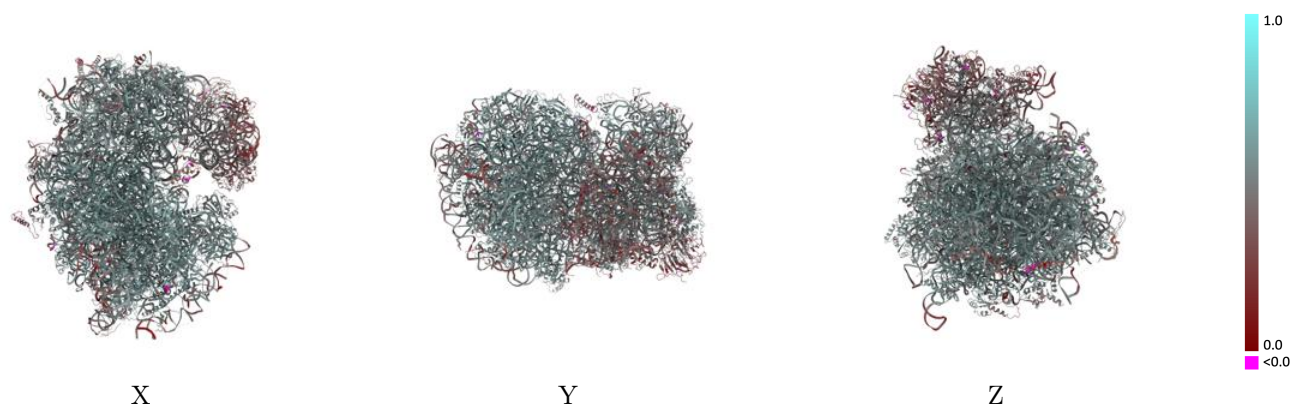
This section contains information regarding the fit between EMDB map EMD-13111 and PDB model 7OYA. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



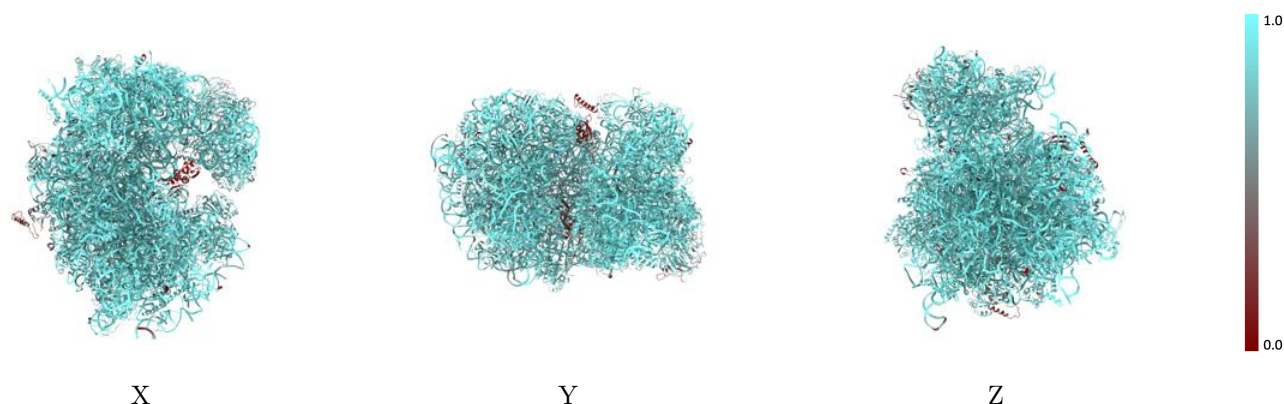
The images above show the 3D surface view of the map at the recommended contour level 0.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



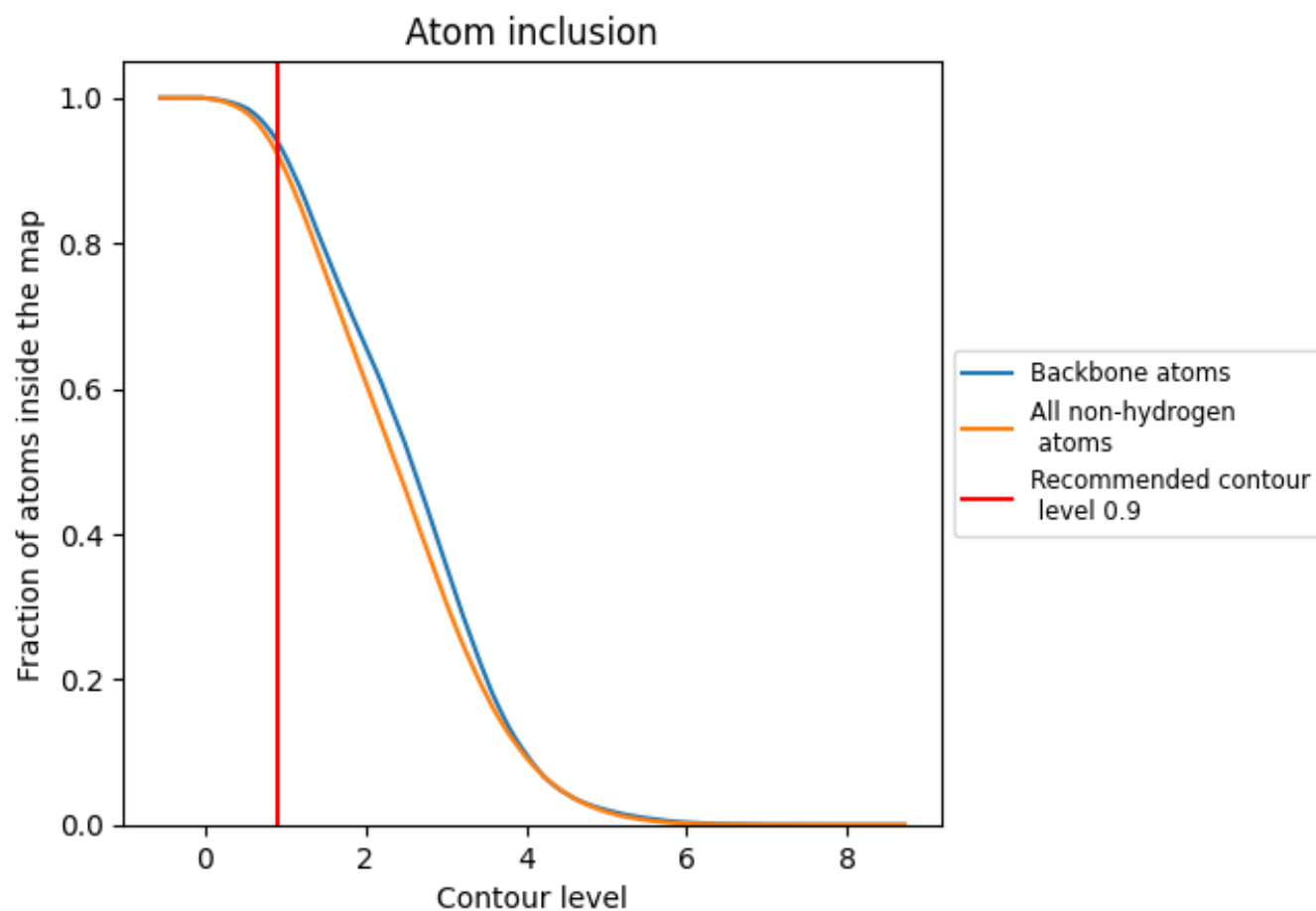
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.9).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9233	 0.5210
11	 0.1372	 0.3190
22	 0.9843	 0.5000
51	 0.9473	 0.5380
71	 0.9840	 0.5730
81	 0.9228	 0.5250
A1	 0.9600	 0.5880
A2	 0.9569	 0.5180
B1	 0.9241	 0.5780
B2	 0.9452	 0.5290
C1	 0.9313	 0.5700
C2	 0.9780	 0.5270
D1	 0.8939	 0.5480
D2	 0.8408	 0.3980
E1	 0.8903	 0.5400
E2	 0.9505	 0.5320
F1	 0.9173	 0.5710
F2	 0.8557	 0.3750
G1	 0.8873	 0.5400
G2	 0.8790	 0.4630
H1	 0.8945	 0.5660
H2	 0.8592	 0.4800
I1	 0.9095	 0.5710
I2	 0.9505	 0.5310
J1	 0.8406	 0.5020
J2	 0.9471	 0.5140
K2	 0.8522	 0.3610
L1	 0.8700	 0.5500
L2	 0.9423	 0.5430
M1	 0.9201	 0.5730
N1	 0.9529	 0.5920
N2	 0.9493	 0.5390
O1	 0.9236	 0.5760
O2	 0.9441	 0.5250
P1	 0.9150	 0.5700















Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
P2	 0.8977	 0.3430
Q1	 0.9235	 0.5730
Q2	 0.8981	 0.3990
R1	 0.8955	 0.5390
R2	 0.8156	 0.4380
S1	 0.9459	 0.5840
S2	 0.8609	 0.3120
T1	 0.8990	 0.5630
T2	 0.9146	 0.4080
U1	 0.7997	 0.4610
U2	 0.8657	 0.3840
V1	 0.8967	 0.5800
V2	 0.9572	 0.5300
W1	 0.8822	 0.5580
W2	 0.9752	 0.5560
X1	 0.8972	 0.5620
X2	 0.9612	 0.5360
Y1	 0.9088	 0.5540
Y2	 0.9094	 0.5030
Z1	 0.9002	 0.5590
Z2	 0.7790	 0.3020
a1	 0.9145	 0.5700
a2	 0.9721	 0.5370
b1	 0.8941	 0.5640
b2	 0.9173	 0.5140
c1	 0.9377	 0.5470
c2	 0.9034	 0.3910
d1	 0.8829	 0.5460
d2	 0.9253	 0.4520
e1	 0.9258	 0.5770
e2	 0.9036	 0.4930
f1	 0.9457	 0.5910
g1	 0.9486	 0.5690
g2	 0.6833	 0.3100
h1	 0.8688	 0.5460
i1	 0.8804	 0.5550
i2	 0.4874	 0.3380
j1	 0.9341	 0.5810
k1	 0.8223	 0.5330
l1	 0.8838	 0.5480
m1	 0.9352	 0.5820
n1	 0.9333	 0.5280

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
o1	 0.9017	 0.5640
p1	 0.9026	 0.5410
q1	 0.3978	 0.3790
r1	 0.9219	 0.5640
s1	 0.2222	 0.3240
v2	 0.0840	 0.3140