wwPDB EM Validation Summary Report (i)

Nov 19, 2022 – 10:00 AM EST

PDB ID	:	7R81
EMDB ID	:	EMD-24307
Title	:	Structure of the translating Neurospora crassa ribosome arrested by cycloheximide
Authors	:	Shen, L.; Su, Z.; Yang, K.; Wu, C.; Becker, T.; Bell-Pedersen, D.; Zhang, J.; Sachs, M.S.
Deposited on	:	2021-06-25
Resolution	:	2.70 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 (i) 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 (1)) were used in the production of this report:

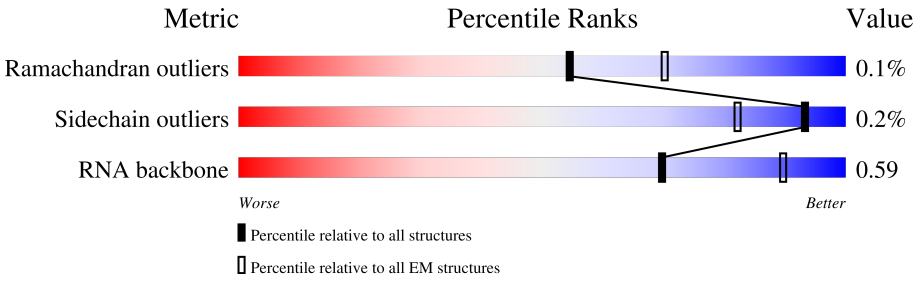
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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 <=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	A1	3338	6% 80% 13% 6%
2	A2	1796	25% 85% 14%
3	B1	120	92% 8%
4	B2	290	48% 72% 28%
5	C1	158	9% 87% 13%
6	C2	256	53% 82% 17%
7	D1	254	96%
8	D2	265	30% 79% 21%

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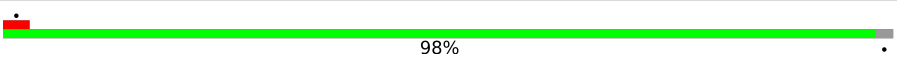
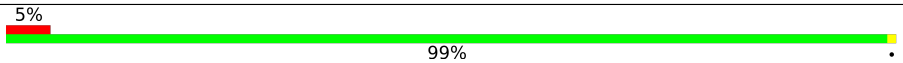
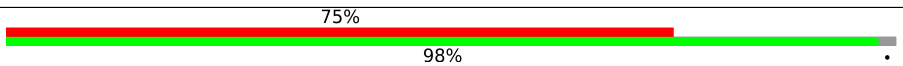
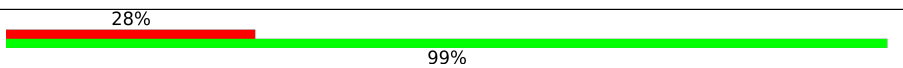
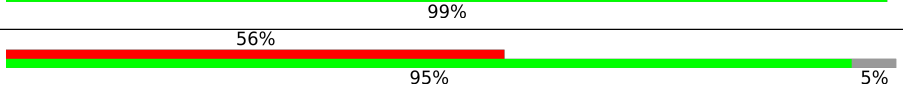
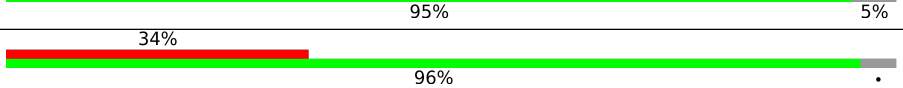
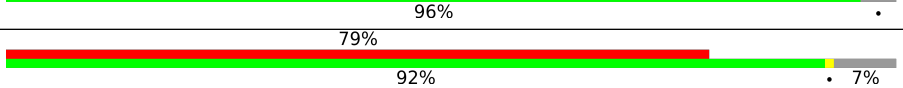
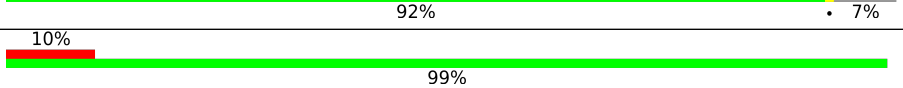
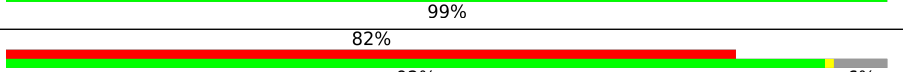
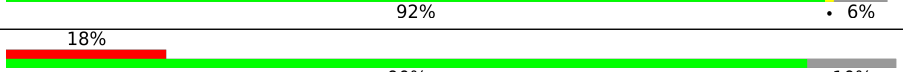
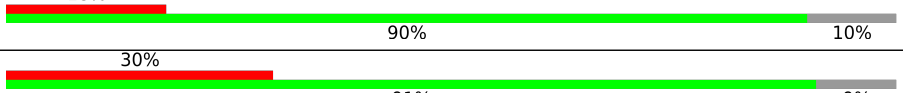
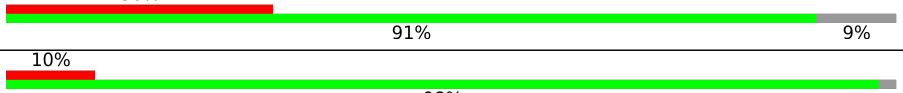
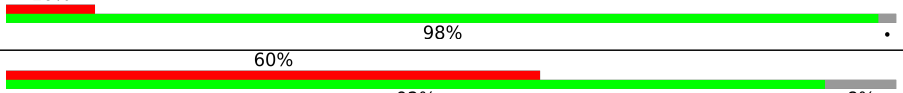
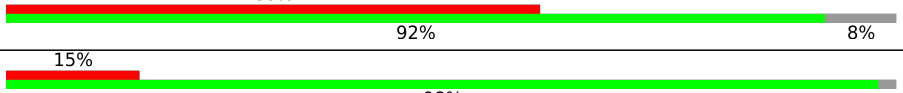
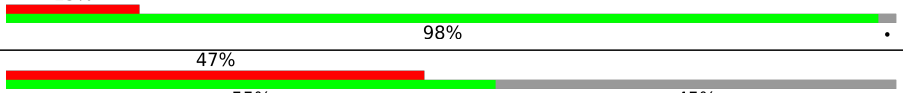
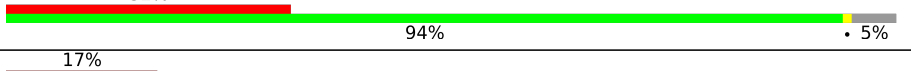
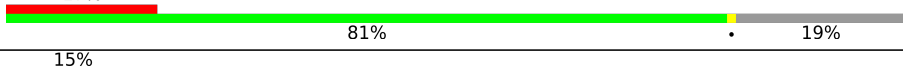
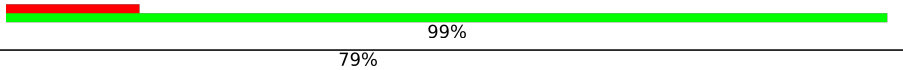
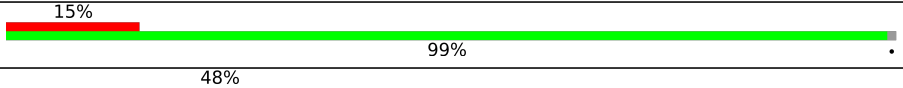
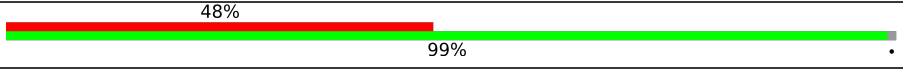
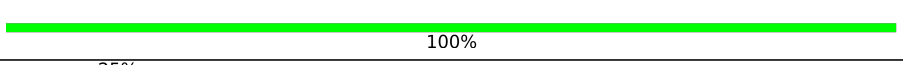
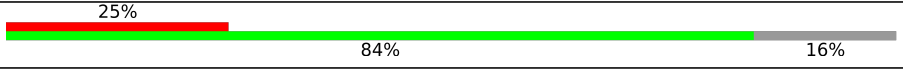
Mol	Chain	Length	Quality of chain
9	E1	392	
10	E2	262	
11	F1	361	
12	F2	261	
13	G1	301	
14	G2	213	
15	H1	202	
16	H2	239	
17	I1	248	
18	I2	202	
19	J1	262	
20	J2	202	
21	K1	193	
22	K2	190	
23	L1	221	
24	L2	163	
25	M1	174	
26	M2	161	
27	N1	214	
28	N2	147	
29	O1	142	
30	O2	151	
31	P1	203	
32	P2	150	
33	Q1	231	

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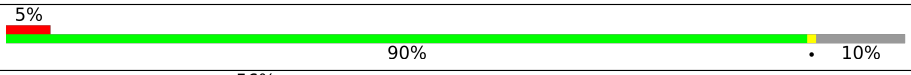
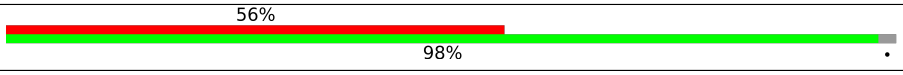
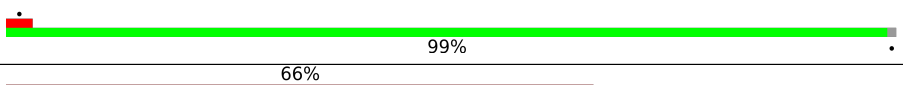
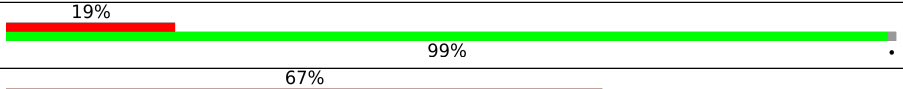
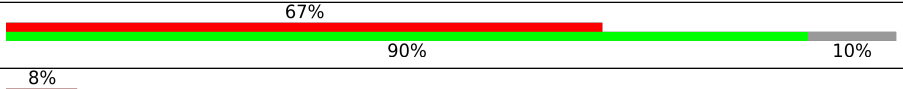
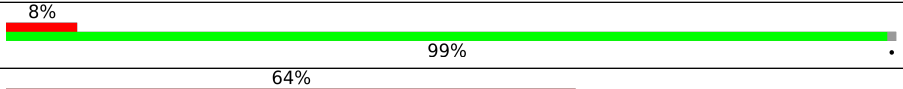
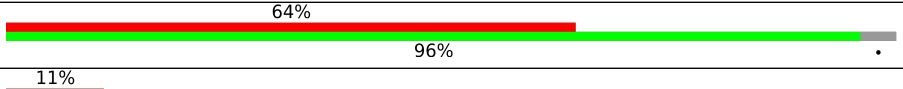
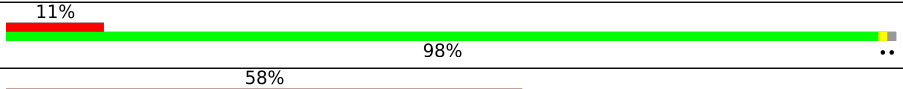
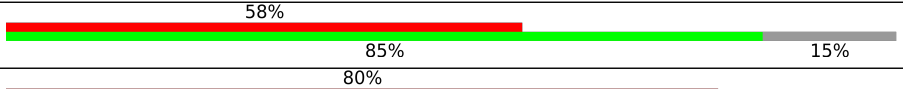
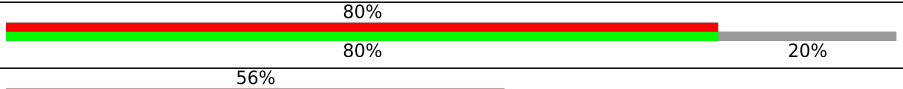
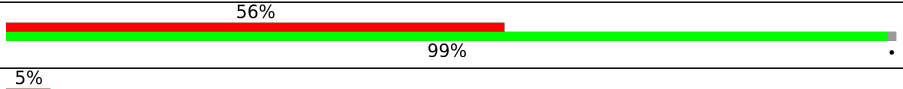
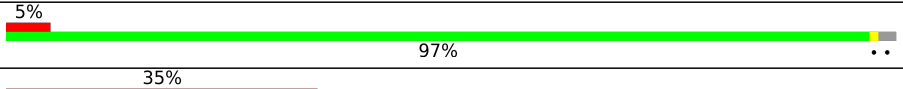
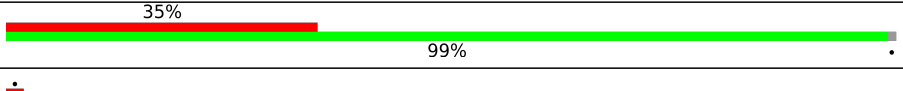
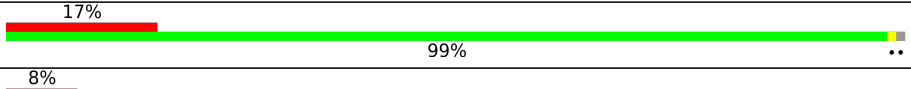
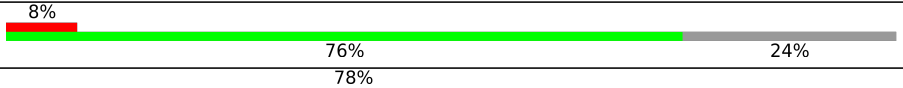
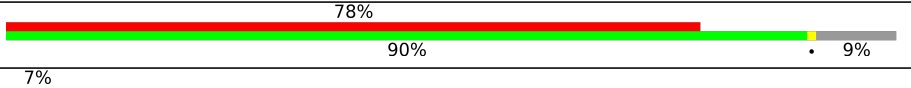
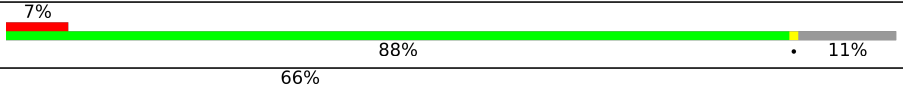
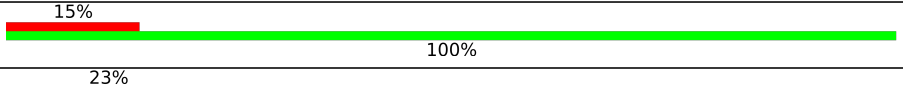
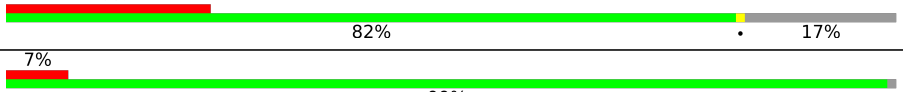
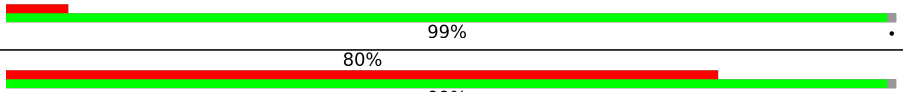
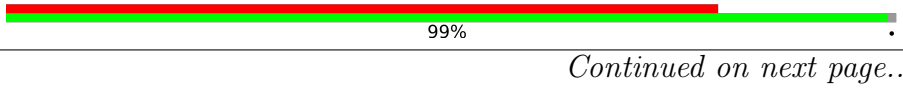
Mol	Chain	Length	Quality of chain
34	Q2	152	
35	R1	186	
36	R2	142	
37	S1	183	
38	S2	146	
39	T1	192	
40	T2	156	
41	U1	174	
42	U2	149	
43	V1	160	
44	V2	117	
45	W1	126	
46	W2	87	
47	X1	139	
48	X2	130	
49	Y1	156	
50	Y2	145	
51	Z1	156	
52	Z2	136	
53	a1	136	
54	a2	97	
55	b1	135	
56	b2	119	
57	c1	149	
58	c2	82	

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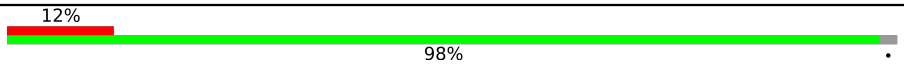
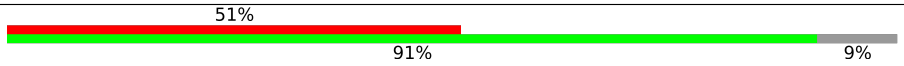
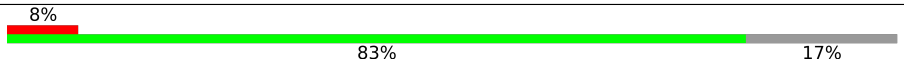
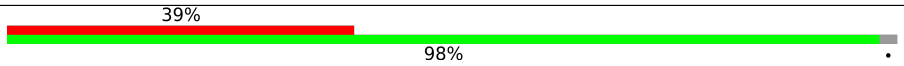
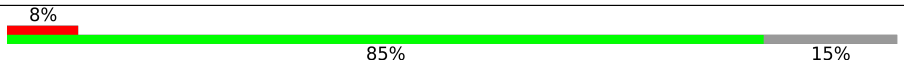
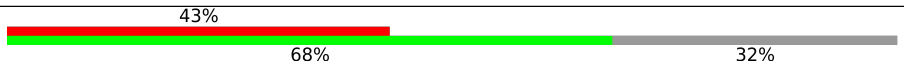
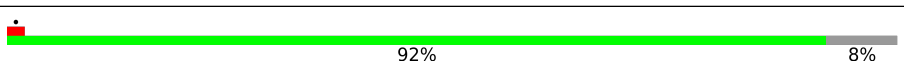
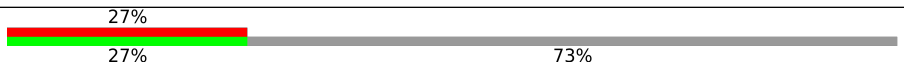
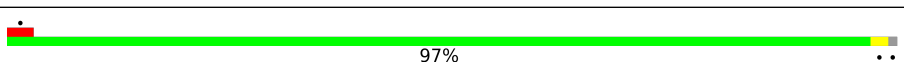
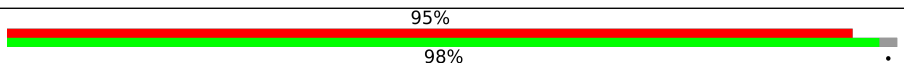
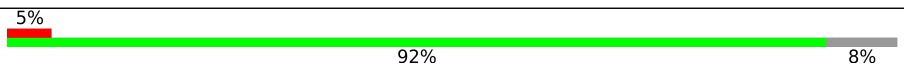
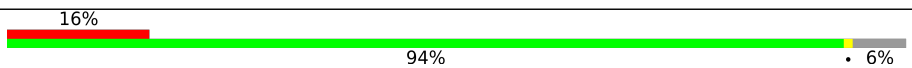
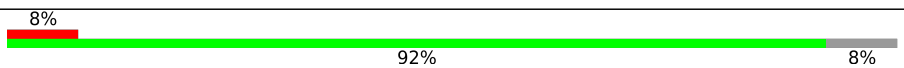
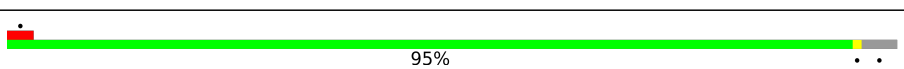
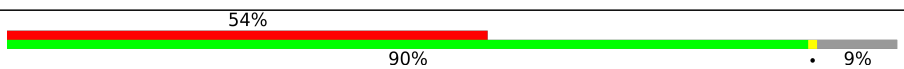
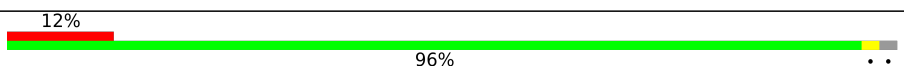
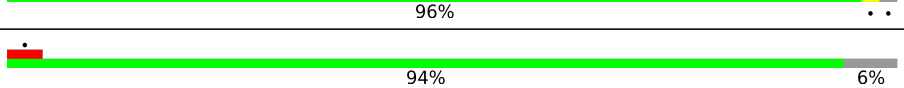
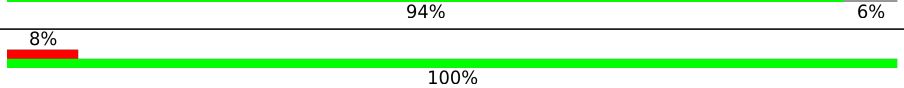
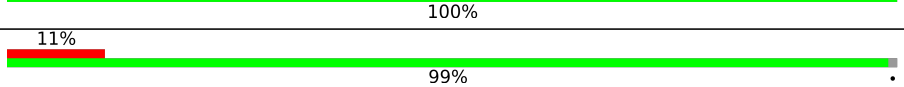
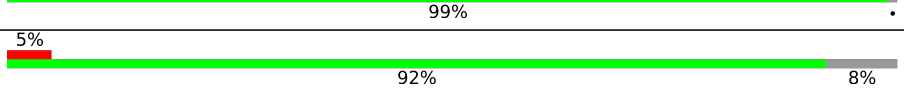
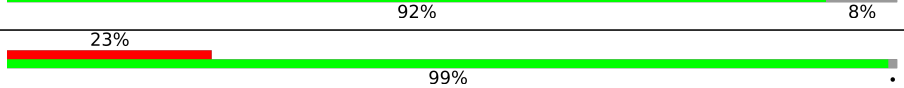
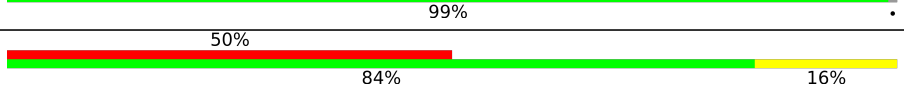
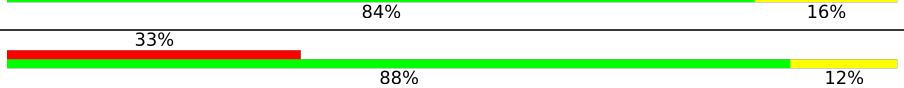
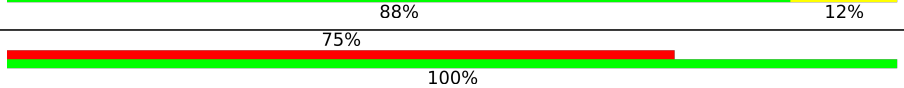
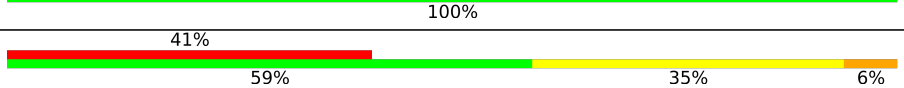
Mol	Chain	Length	Quality of chain
59	d1	65	
60	d2	68	
61	e1	109	
62	e2	56	
63	f1	122	
64	f2	63	
65	g1	131	
66	g2	154	
67	h1	109	
68	h2	316	
69	i1	117	
70	j1	125	
71	k1	104	
72	l1	92	
73	m1	80	
74	n1	51	
75	o1	52	
76	p1	25	
77	q1	106	
78	r1	92	
79	s1	150	
80	t1	76	
80	u1	76	
81	v1	4	
82	w1	17	

2 Entry composition (i)

There are 85 unique types of molecules in this entry. The entry contains 202730 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 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A1	3123	66761	29810	12043	21785	3123	0	0

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A2	1769	37713	16852	6713	12379	1769	0	0

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	B1	120	2554	1141	456	837	120	0	0

- Molecule 4 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	B2	209	1635	1045	289	294	7	0	0

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	C1	158	3360	1503	593	1106	158	0	0

- Molecule 6 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C2	212	1706	1082	314	306	4	0	0

- Molecule 7 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D1	245	Total	C	N	O	S	0	0
			1855	1158	368	326	3		

- Molecule 8 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D2	210	Total	C	N	O	S	0	0
			1612	1036	282	291	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E1	385	Total	C	N	O	S	0	0
			3058	1946	573	529	10		

- Molecule 10 is a protein called Cytoplasmic ribosomal protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E2	224	Total	C	N	O	S	0	0
			1750	1102	319	322	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F1	360	Total	C	N	O	S	0	0
			2727	1711	524	487	5		

- Molecule 12 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F2	256	Total	C	N	O	S	0	0
			2048	1299	385	357	7		

- Molecule 13 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G1	300	Total	C	N	O	S	0	0
			2423	1527	426	467	3		

- Molecule 14 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G2	202	Total	C	N	O	S	0	0
			1586	987	298	294	7		

- Molecule 15 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H1	194	Total	C	N	O	S	0	0
			1521	969	277	274	1		

- Molecule 16 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H2	222	Total	C	N	O	S	0	0
			1782	1116	351	310	5		

- Molecule 17 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I1	247	Total	C	N	O	S	0	0
			2016	1291	369	352	4		

- Molecule 18 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	I2	189	Total	C	N	O	0	0
			1514	955	287	272		

- Molecule 19 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	J1	236	Total	C	N	O	S	0	0
			1882	1206	347	323	6		

- Molecule 20 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	J2	183	Total	C	N	O	S	0	0
			1464	910	293	259	2		

- Molecule 21 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	K1	190	Total	C	N	O	S	0	0
			1504	952	275	273	4		

- Molecule 22 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	K2	174	Total	C	N	O	S	0	0
			1420	900	284	234	2		

- Molecule 23 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L1	217	Total	C	N	O	S	0	0
			1751	1106	340	295	10		

- Molecule 24 is a protein called Probable 40s ribosomal protein s10-b.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L2	90	Total	C	N	O	S	0	0
			753	490	125	135	3		

- Molecule 25 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	M1	165	Total	C	N	O	S	0	0
			1341	839	260	236	6		

- Molecule 26 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	M2	131	Total	C	N	O	S	0	0
			1068	682	206	177	3		

- Molecule 27 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	N1	213	Total	C	N	O	S	0	0
			1675	1046	336	291	2		

- Molecule 28 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	N2	116	Total	C	N	O	S	0	0
			907	566	163	169	9		

- Molecule 29 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	O1	141	Total	C	N	O	S	0	0
			1109	702	212	194	1		

- Molecule 30 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	O2	150	Total	C	N	O	S	0	0
			1179	750	218	208	3		

- Molecule 31 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	P1	202	Total	C	N	O	S	0	0
			1702	1063	359	278	2		

- Molecule 32 is a protein called 40S ribosomal protein S14 (uS11).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	P2	126	Total	C	N	O	S	0	0
			938	574	186	173	5		

- Molecule 33 is a protein called 60S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Q1	199	Total	C	N	O	S	0	0
			1595	1022	301	267	5		

- Molecule 34 is a protein called Ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Q2	127	Total	C	N	O	S	0	0
			1007	639	189	175	4		

- Molecule 35 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	R1	168	Total	C	N	O	S	0	0
			1322	819	269	231	3		

- Molecule 36 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	R2	139	Total	C	N	O	S	0	0
			1089	700	200	187	2		

- Molecule 37 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	S1	182	Total	C	N	O	S	0	0
			1445	912	291	240	2		

- Molecule 38 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	S2	124	Total	C	N	O	S	0	0
			1005	636	182	185	2		

- Molecule 39 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	T1	191	Total	C	N	O	S	0	0
			1563	963	331	265	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	T2	141	Total	C	N	O	S	0	0
			1139	709	227	201	2		

- Molecule 41 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	U1	173	Total	C	N	O	S	0	0
			1429	920	268	237	4		

- Molecule 42 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	U2	143	Total	C	N	O	S	0	0
			1124	701	221	201	1		

- Molecule 43 is a protein called Ribosomal protein Srp1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	V1	159	Total	C	N	O	S	0	0
			1276	807	246	221	2		

- Molecule 44 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V2	99	Total	C	N	O	S	0	0
			786	498	145	140	3		

- Molecule 45 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	W1	101	Total	C	N	O	S	0	0
			816	530	141	144	1		

- Molecule 46 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	W2	86	Total	C	N	O	S	0	0
			668	408	127	130	3		

- Molecule 47 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	X1	136	Total	C	N	O	S	0	0
			1007	638	186	176	7		

- Molecule 48 is a protein called 40S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X2	129	Total	C	N	O	S	0	0
			1035	659	192	180	4		

- Molecule 49 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Y1	61	Total	C	N	O	S	0	0
			525	334	104	86	1		

- Molecule 50 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Y2	144	Total	C	N	O	S	0	0
			1113	701	218	192	2		

- Molecule 51 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	Z1	118	Total	C	N	O	0	0
			941	602	170	169		

- Molecule 52 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Z2	124	Total	C	N	O	S	0	0
			1003	630	197	174	2		

- Molecule 53 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	a1	121	Total	C	N	O	S	0	0
			961	596	189	175	1		

- Molecule 54 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	a2	71	Total	C	N	O	S	0	0
			565	356	105	102	2		

- Molecule 55 is a protein called 60S ribosomal protein L27 (eL27).

Mol	Chain	Residues	Atoms					AltConf	Trace
55	b1	135	Total	C	N	O	S	0	0
			1108	707	206	191	4		

- Molecule 56 is a protein called 40S ribosomal protein S26E.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	b2	99	Total	C	N	O	S	0	0
			793	488	167	131	7		

- Molecule 57 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	c1	148	Total	C	N	O	S	0	0
			1166	738	235	191	2		

- Molecule 58 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	c2	81	Total	C	N	O	S	0	0
			611	386	110	108	7		

- Molecule 59 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	d1	64	Total	C	N	O	0	0
			518	315	113	90		

- Molecule 60 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	d2	62	Total	C	N	O	S	0	0
			491	302	98	90	1		

- Molecule 61 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	e1	91	Total	C	N	O	S	0	0
			681	433	118	125	5		

- Molecule 62 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	e2	55	Total	C	N	O	S	0	0
			446	271	94	77	4		

- Molecule 63 is a protein called 60s ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	f1	104	Total	C	N	O	S	0	0
			854	540	166	145	3		

- Molecule 64 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	f2	43	Total	C	N	O	0	0
			346	216	72	58		

- Molecule 65 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	g1	121	Total	C	N	O	S	0	0
			973	609	199	159	6		

- Molecule 66 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	g2	41	Total	C	N	O	S	0	0
			328	204	59	61	4		

- Molecule 67 is a protein called 60S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	h1	108	Total	C	N	O	S	0	0
			853	541	167	144	1		

- Molecule 68 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	h2	310	Total	C	N	O	S	0	0
			2429	1528	424	468	9		

- Molecule 69 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	i1	108	Total	C	N	O	S	0	0
			853	530	174	145	4		

- Molecule 70 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	j1	118	Total 967	C 613	N 192	O 162	0	0

- Molecule 71 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	k1	96	Total 760	C 473	N 162	O 125	0	0

- Molecule 72 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	l1	88	Total 691	C 424	N 147	O 116	S 4	0	0

- Molecule 73 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	m1	73	Total 585	C 373	N 107	O 103	S 2	0	0

- Molecule 74 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	n1	50	Total 435	C 274	N 97	O 64	0	0

- Molecule 75 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	o1	49	Total 395	C 245	N 83	O 61	S 6	0	0

- Molecule 76 is a protein called hypothetical protein NCU16635 (eL41).

Mol	Chain	Residues	Atoms					AltConf	Trace
76	p1	25	Total 235	C 143	N 63	O 27	S 2	0	0

- Molecule 77 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	q1	105	Total	C	N	O	S	0	0
			827	522	163	137	5		

- Molecule 78 is a protein called 60S ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	r1	85	Total	C	N	O	S	0	0
			647	401	129	112	5		

- Molecule 79 is a protein called Ribosomal_L28e domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
79	s1	149	Total	C	N	O	0	0
			1118	697	222	199		

- Molecule 80 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	t1	76	Total	C	N	O	P	0	0
			1621	723	291	531	76		
80	u1	76	Total	C	N	O	P	0	0
			1621	723	291	531	76		

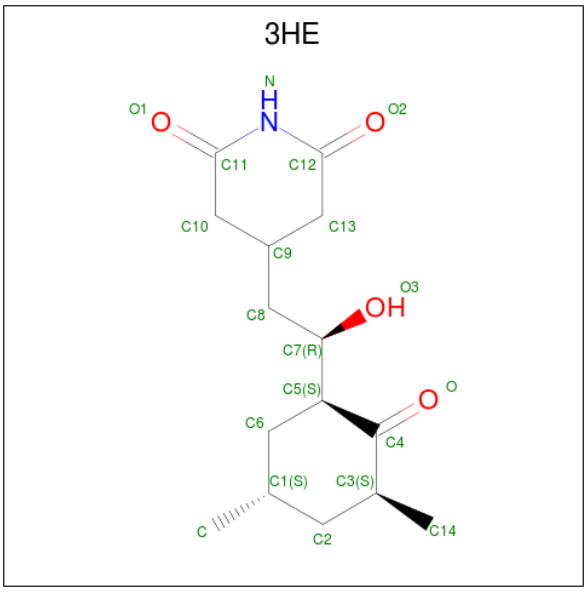
- Molecule 81 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	v1	4	Total	C	N	O	0	0
			20	12	4	4		

- Molecule 82 is a RNA chain called mRNA.

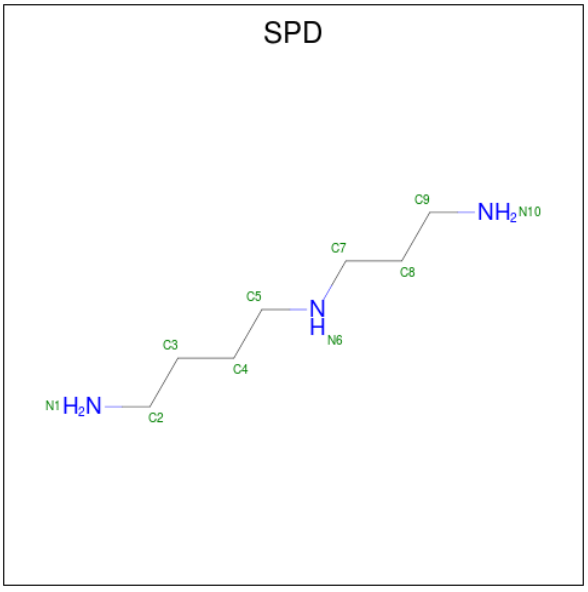
Mol	Chain	Residues	Atoms					AltConf	Trace
82	w1	17	Total	C	N	O	P	0	0
			340	153	34	136	17		

- Molecule 83 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (three-letter code: 3HE) (formula: $C_{15}H_{23}NO_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
83	A1	1	Total	C	N	O	0
			20	15	1	4	

- Molecule 84 is SPERMIDINE (three-letter code: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			AltConf
84	A1	1	Total	C	N	0
			10	7	3	

- Molecule 85 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

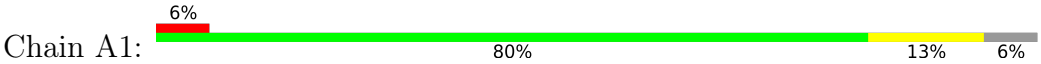
Mol	Chain	Residues	Atoms	AltConf
85	A1	180	Total Mg 180 180	0
85	A2	74	Total Mg 74 74	0
85	F1	1	Total Mg 1 1	0
85	F2	1	Total Mg 1 1	0
85	V1	1	Total Mg 1 1	0
85	Y2	1	Total Mg 1 1	0
85	i1	1	Total Mg 1 1	0
85	u1	1	Total Mg 1 1	0

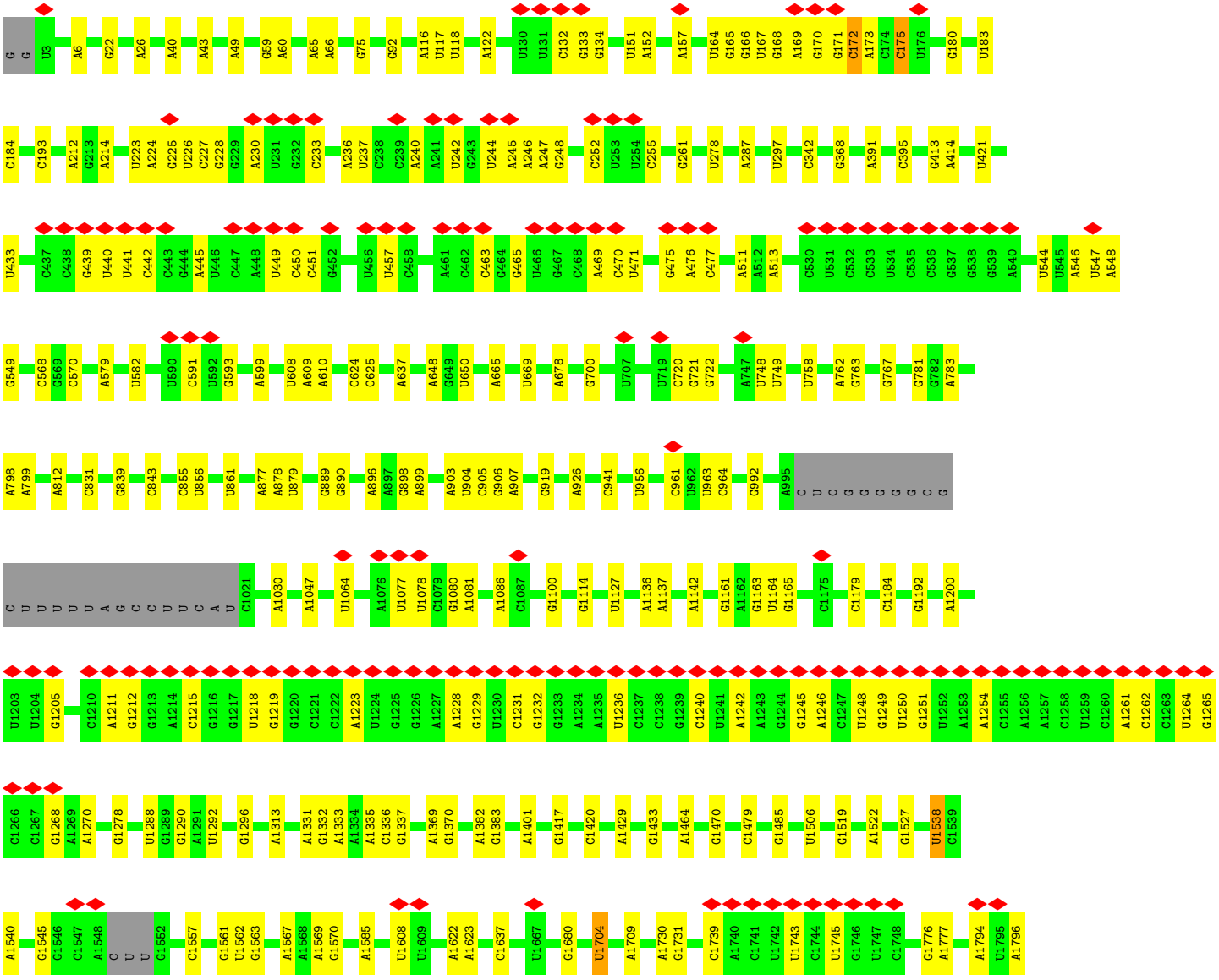
3 Residue-property plots (i)

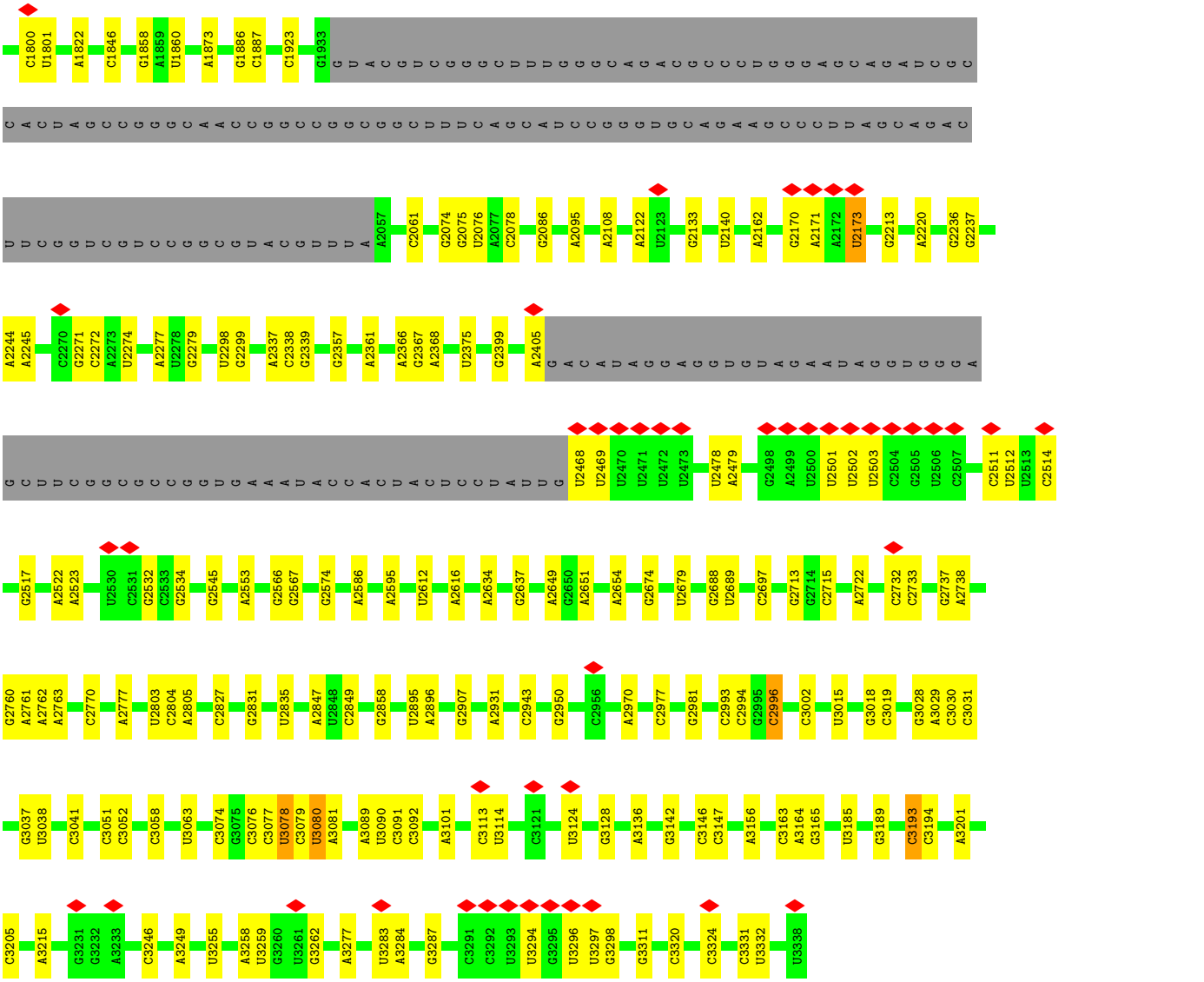
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 26S rRNA

Chain A1:

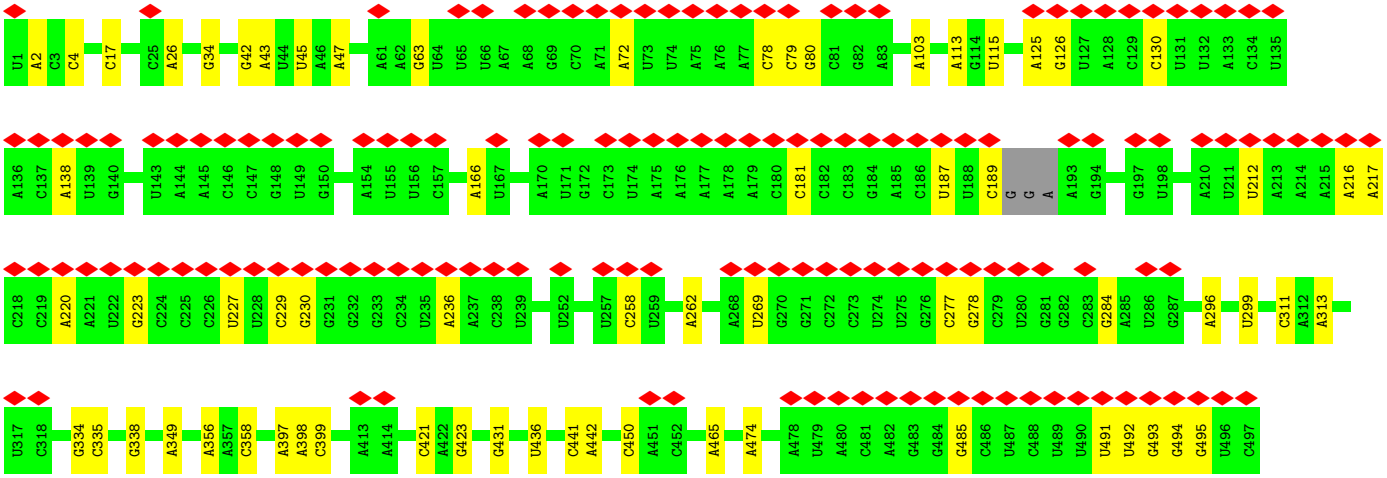


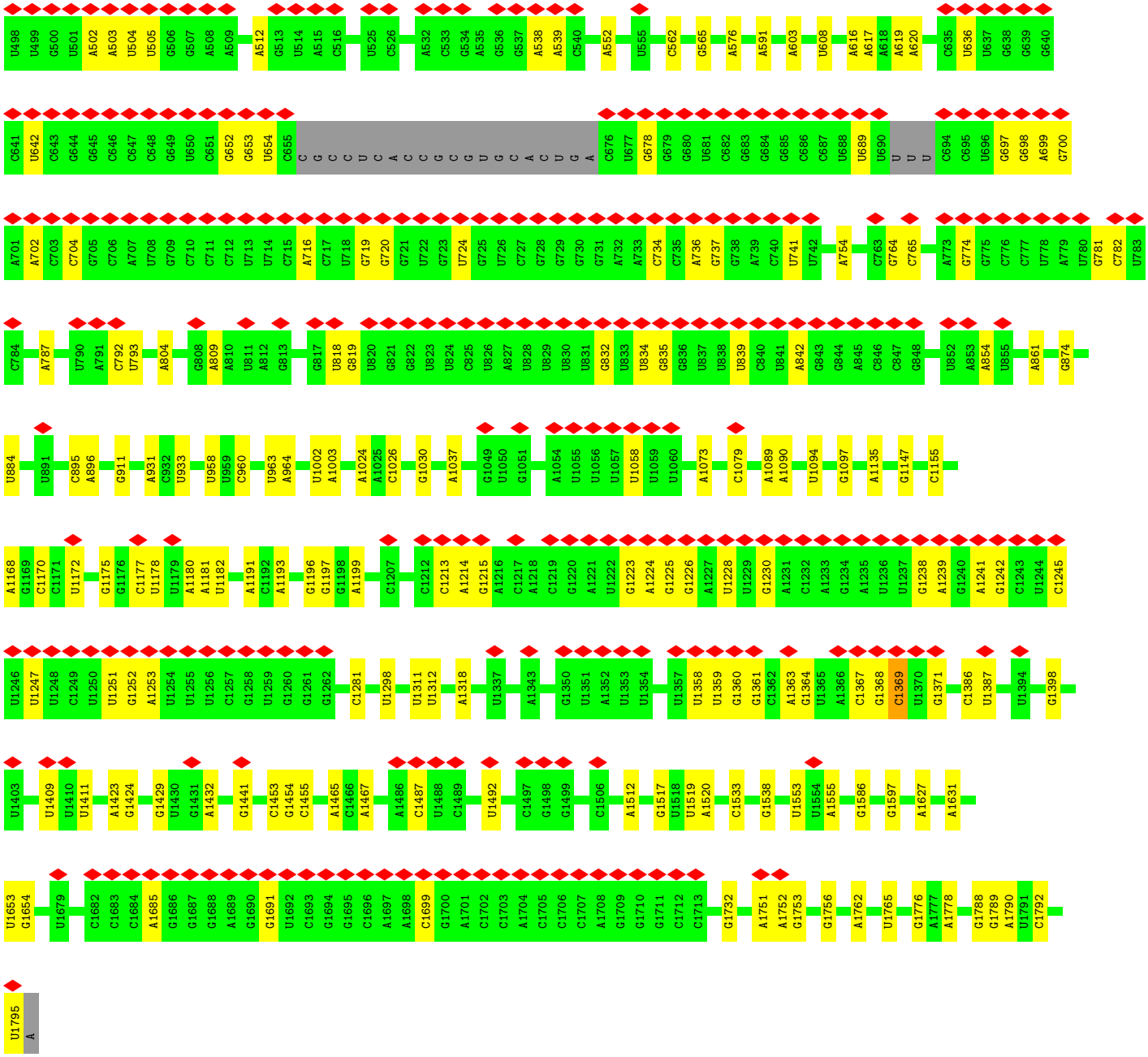




• Molecule 2: 18S rRNA

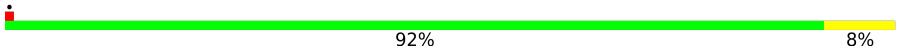
Chain A2:

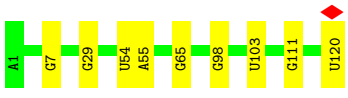




• Molecule 3: 5S rRNA

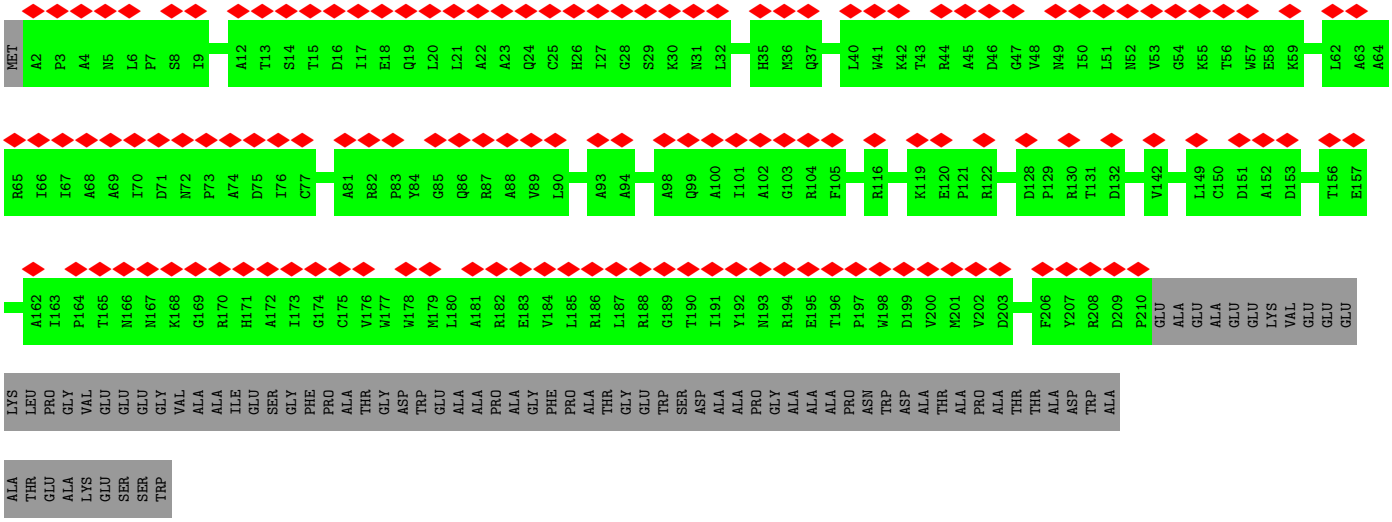
Chain B1:





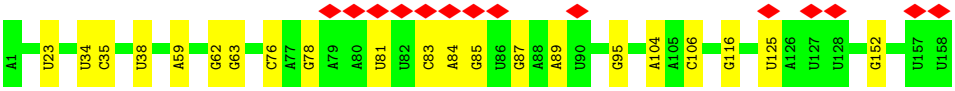
• Molecule 4: 40S ribosomal protein S0

Chain B2:



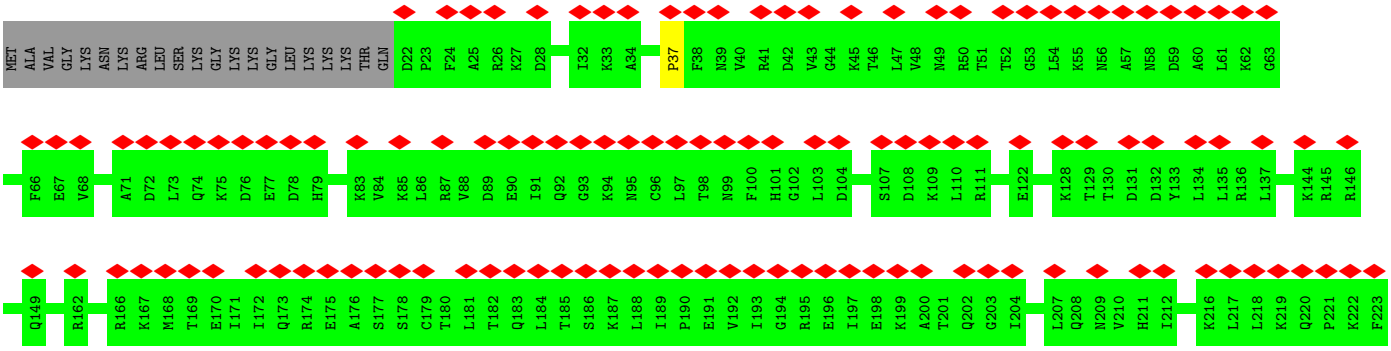
• Molecule 5: 5.8S rRNA

Chain C1:



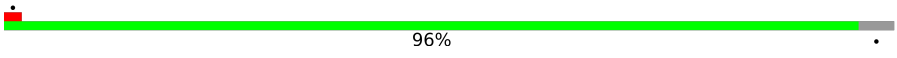
• Molecule 6: 40S ribosomal protein S1

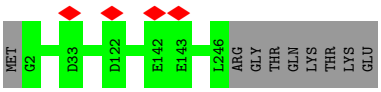
Chain C2:



• Molecule 7: 60S ribosomal protein L2

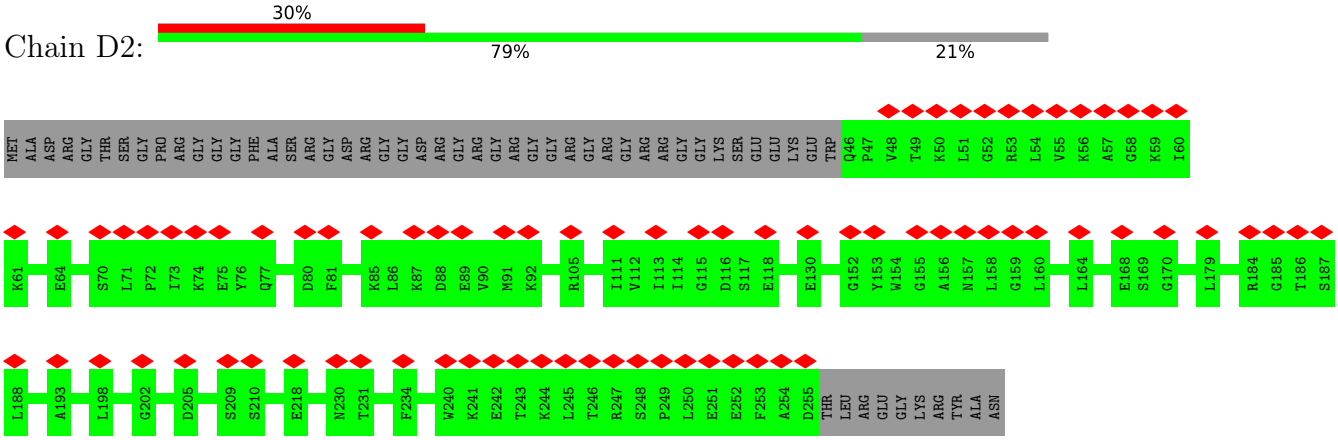
Chain D1:





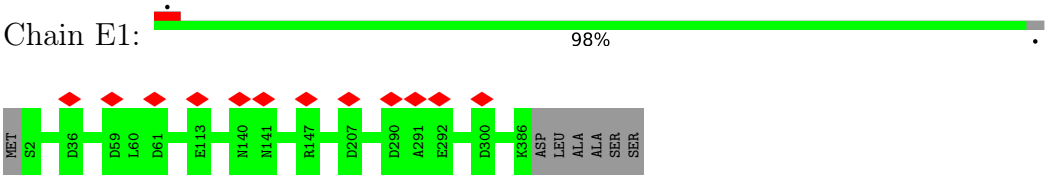
• Molecule 8: 40S ribosomal protein S2

Chain D2:



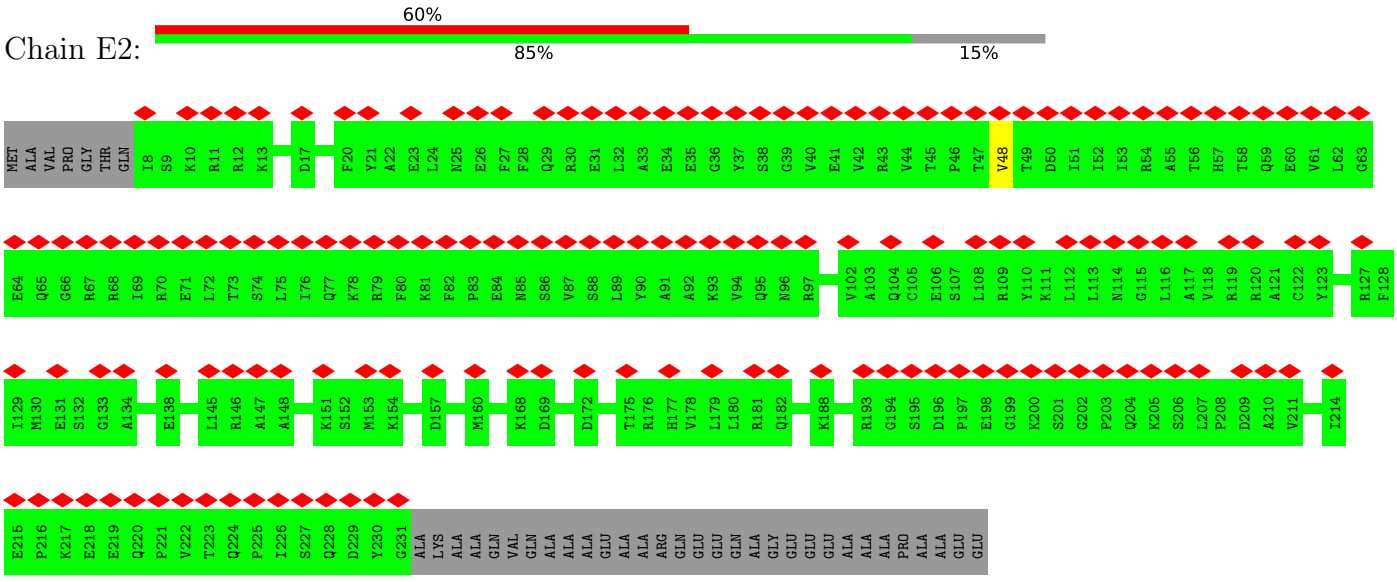
• Molecule 9: 60S ribosomal protein L3

Chain E1:



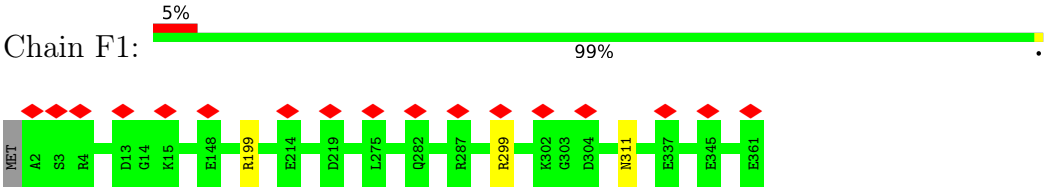
• Molecule 10: Cytoplasmic ribosomal protein 10

Chain E2:



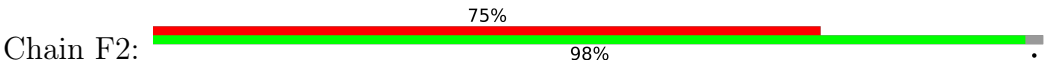
• Molecule 11: 60S ribosomal protein L4-A

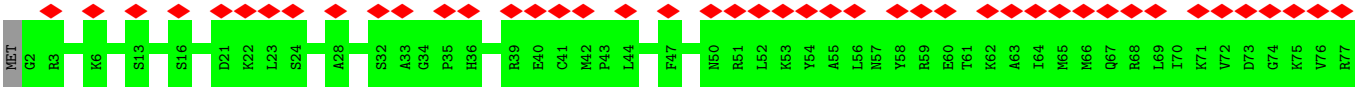
Chain F1:

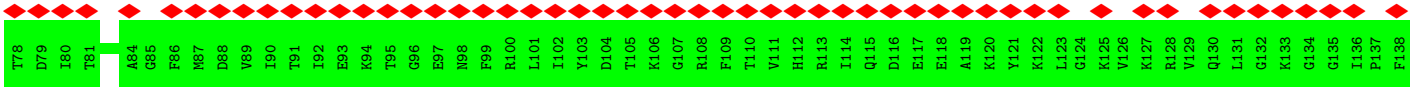


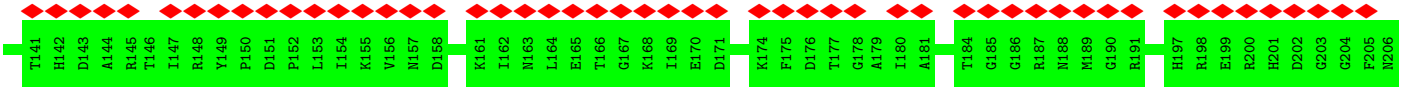
• Molecule 12: 40S ribosomal protein S4

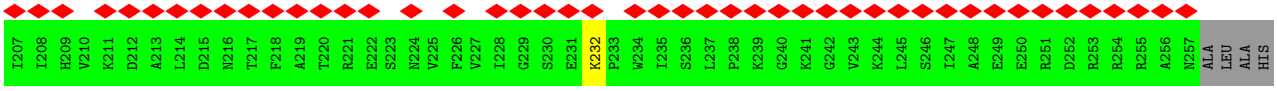
Chain F2:





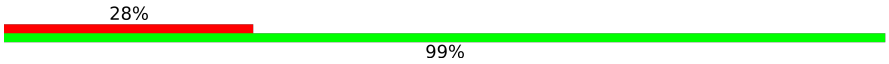


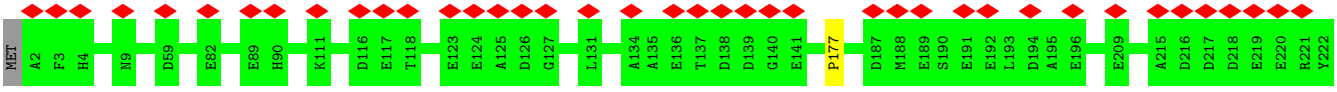


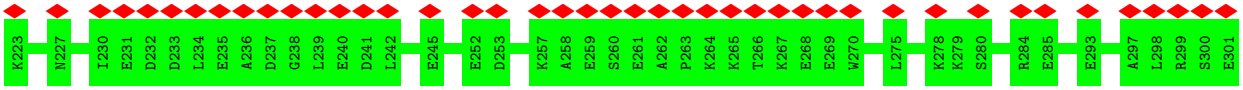


• Molecule 13: 60S ribosomal protein L5

Chain G1:

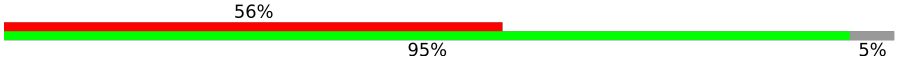


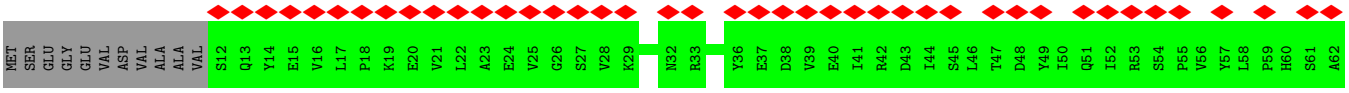


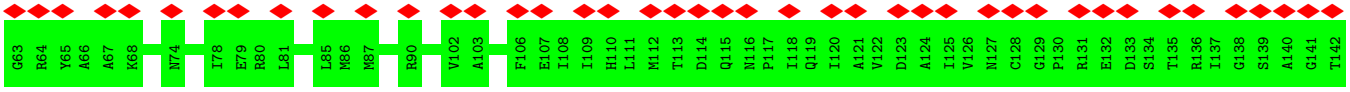


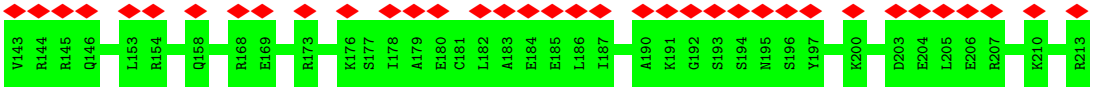
• Molecule 14: 40S ribosomal protein S5

Chain G2:



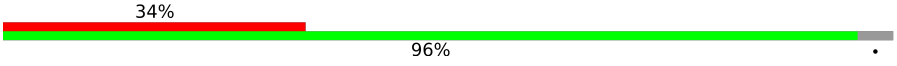


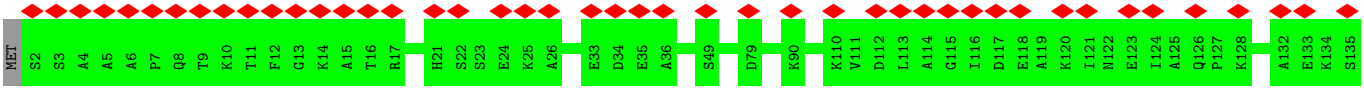


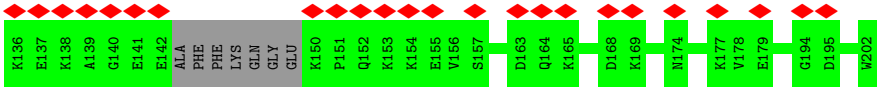


• Molecule 15: 60S ribosomal protein L6

Chain H1:

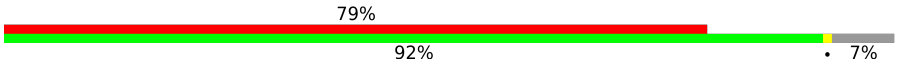


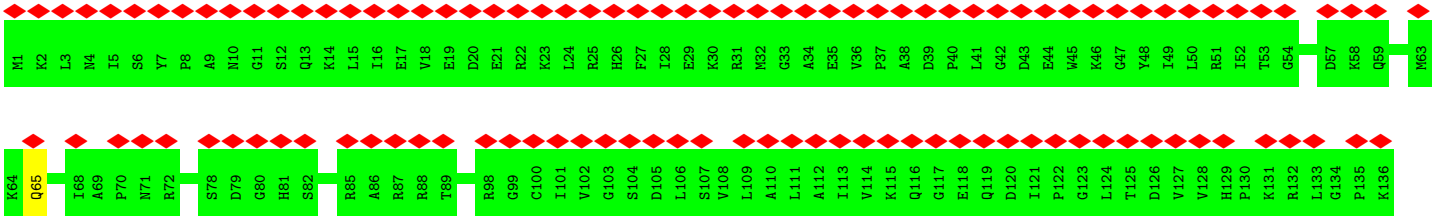




• Molecule 16: 40S ribosomal protein S6

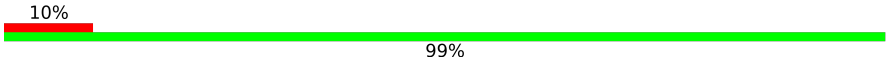
Chain H2:

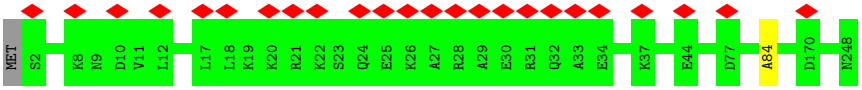




• Molecule 17: 60S ribosomal protein L7

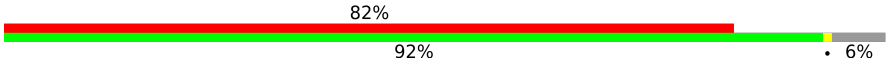
Chain I1:

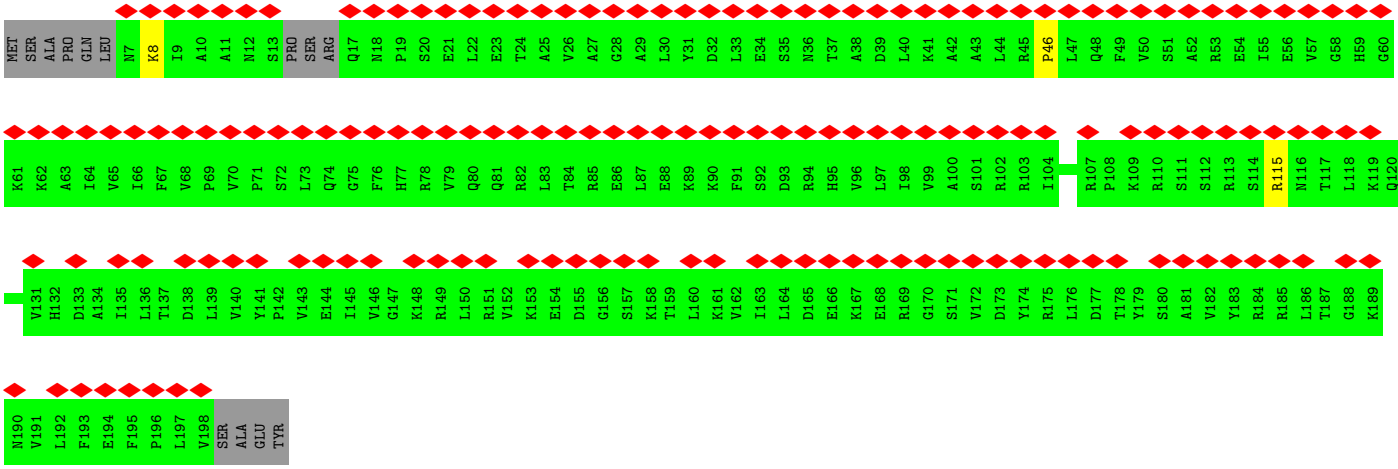




• Molecule 18: 40S ribosomal protein S7

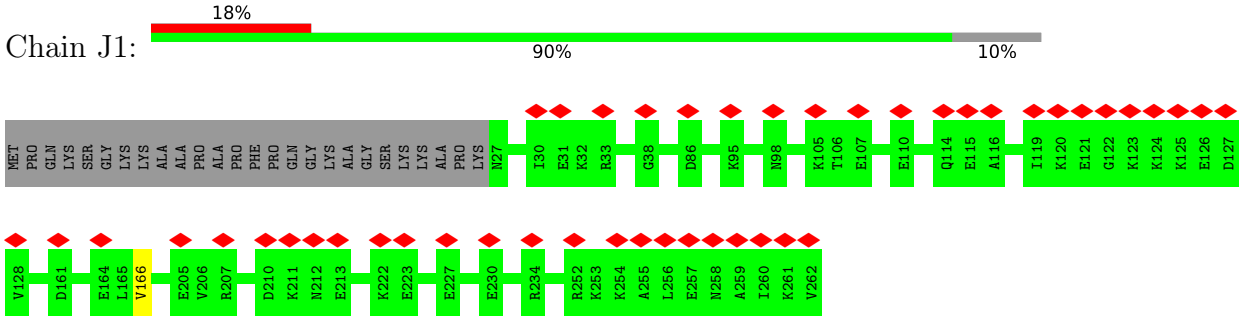
Chain I2:





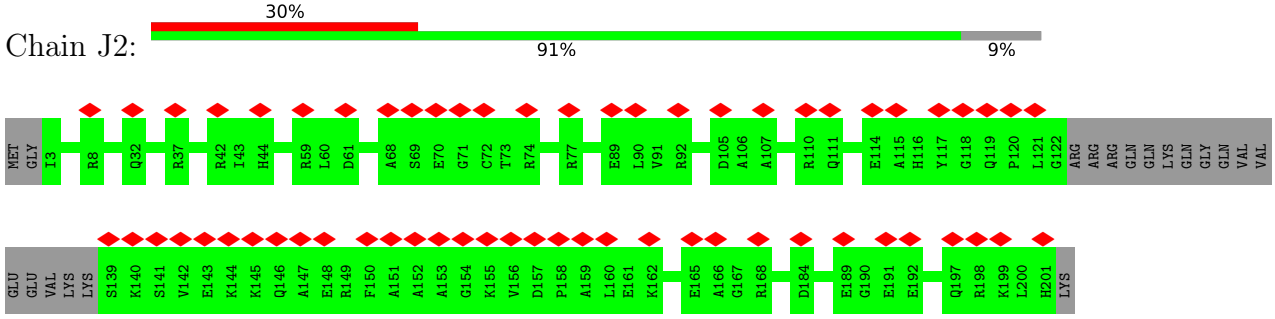
• Molecule 19: 60S ribosomal protein L8

Chain J1:



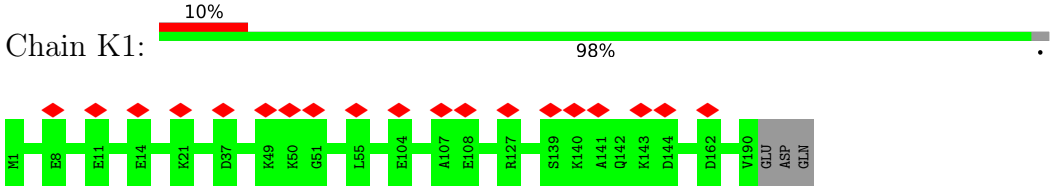
• Molecule 20: 40S ribosomal protein S8

Chain J2:



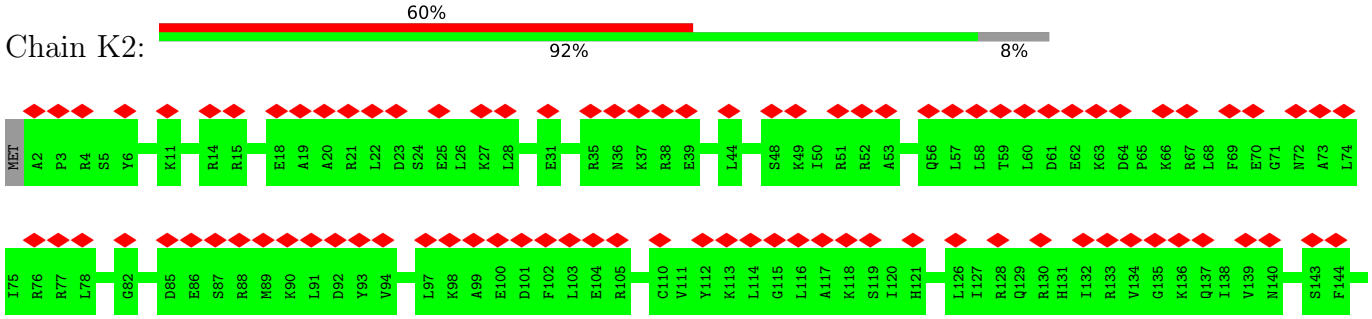
• Molecule 21: 60S ribosomal protein L9

Chain K1:



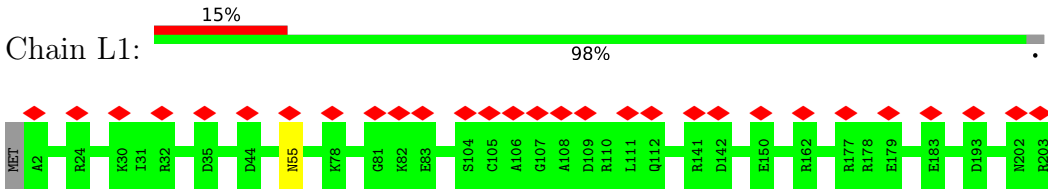
• Molecule 22: 40S ribosomal protein S9

Chain K2:



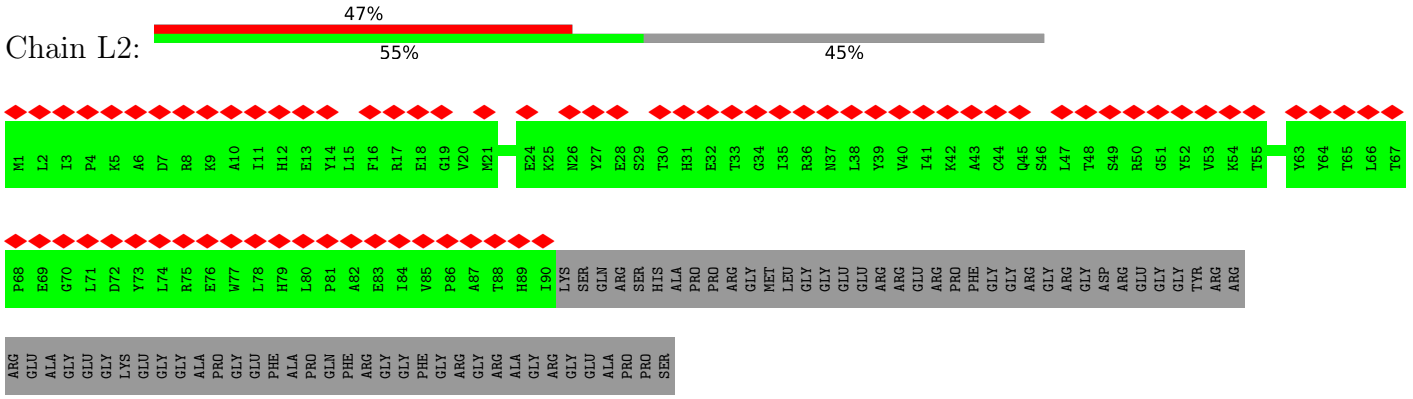
• Molecule 23: 60S ribosomal protein L10

Chain L1:



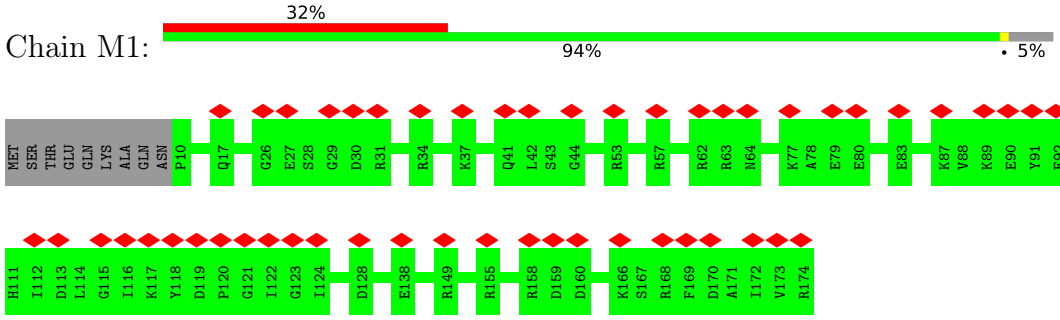
• Molecule 24: Probable 40s ribosomal protein s10-b

Chain L2:



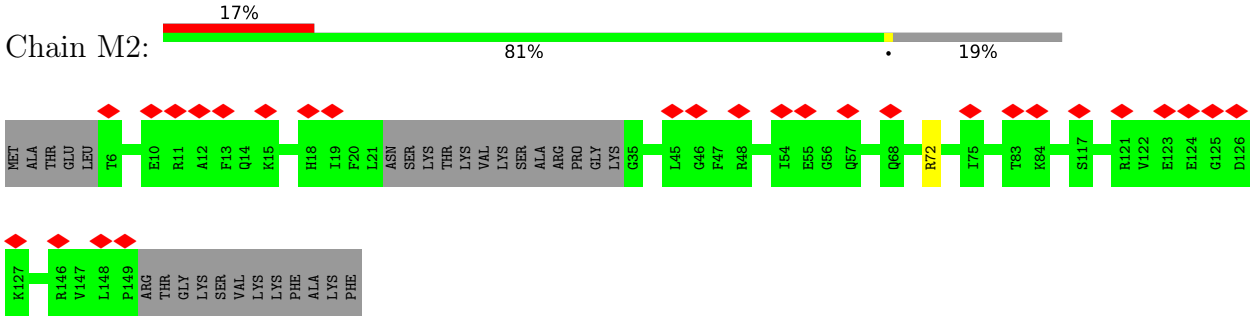
• Molecule 25: 60S ribosomal protein L11

Chain M1:



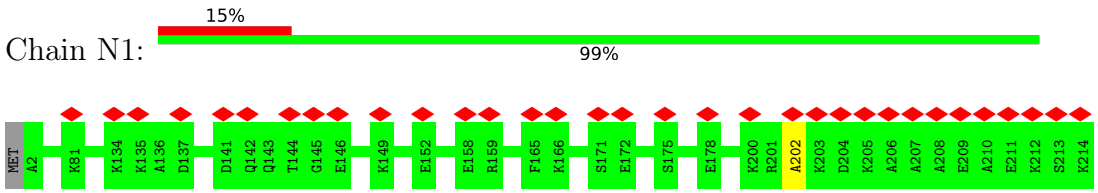
• Molecule 26: 40S ribosomal protein S11

Chain M2:



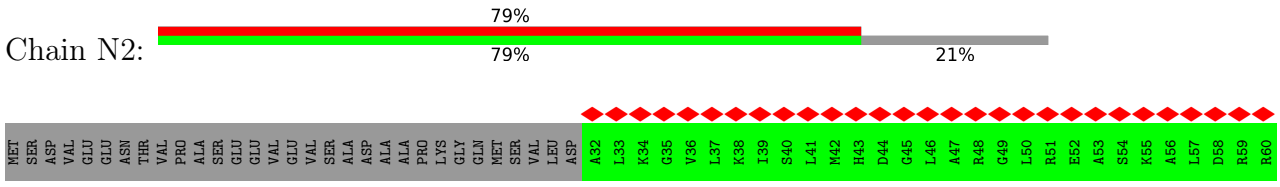
• Molecule 27: 60S ribosomal protein L13

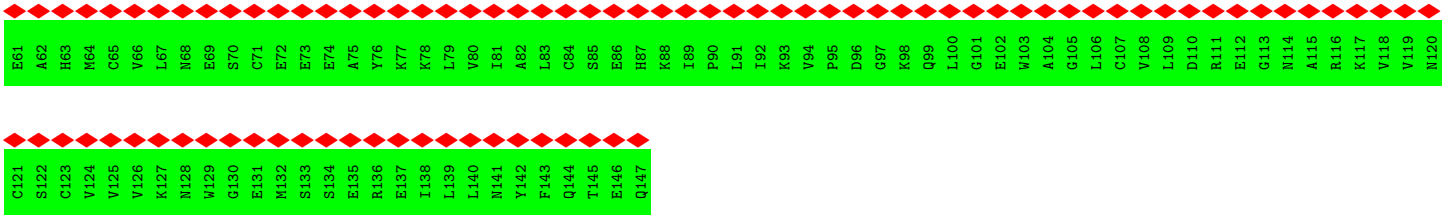
Chain N1:



• Molecule 28: 40S ribosomal protein S12

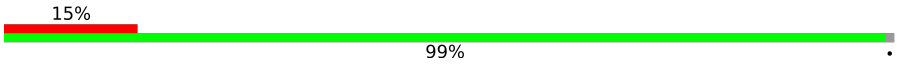
Chain N2:

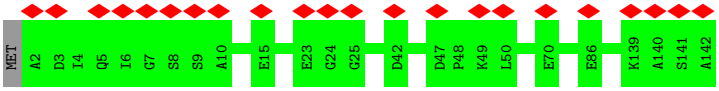




• Molecule 29: Ribosomal protein L14

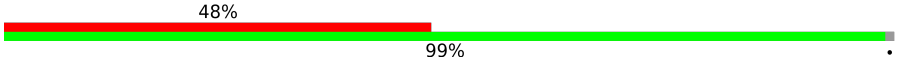
Chain O1:

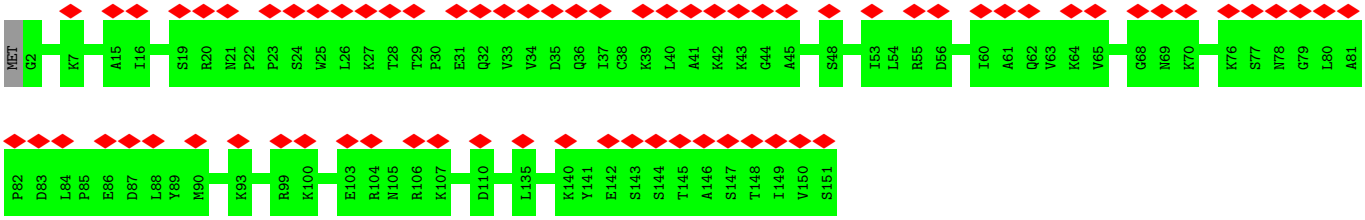




• Molecule 30: 40S ribosomal protein S13

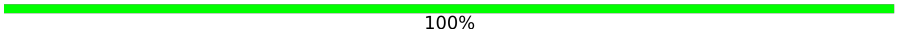
Chain O2:

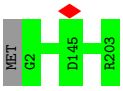




• Molecule 31: 60S ribosomal protein L15

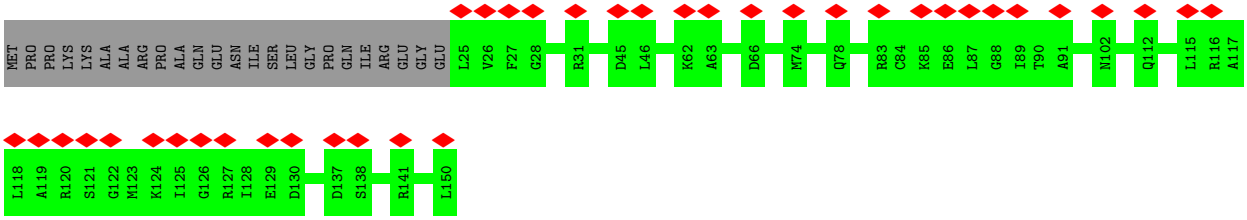
Chain P1:





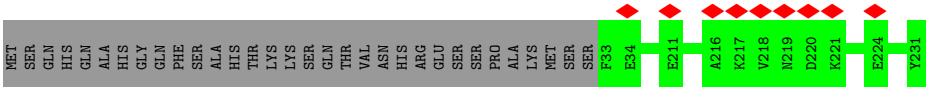
• Molecule 32: 40S ribosomal protein S14 (uS11)

Chain P2:



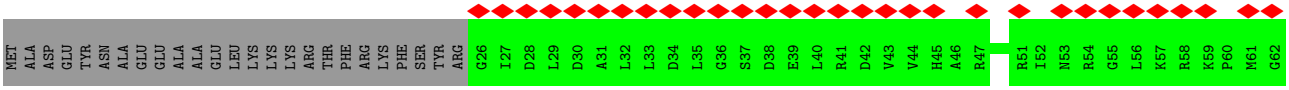
• Molecule 33: 60S ribosomal protein L16

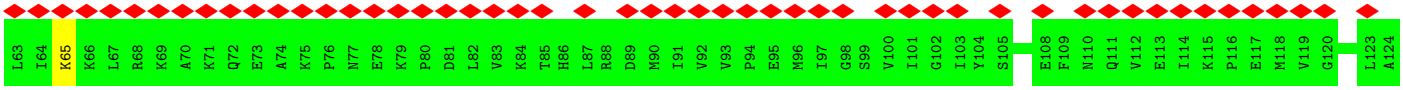
Chain Q1:

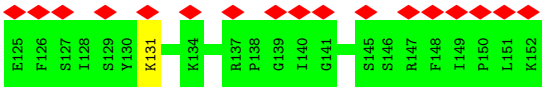


• Molecule 34: Ribosomal protein S12

Chain Q2:

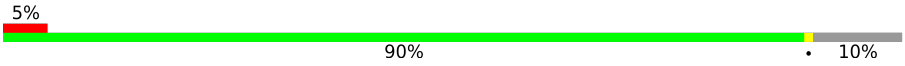


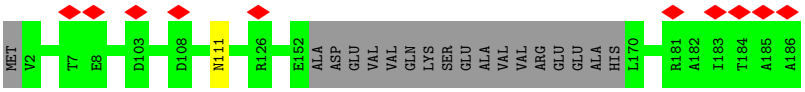




• Molecule 35: 60S ribosomal protein L17

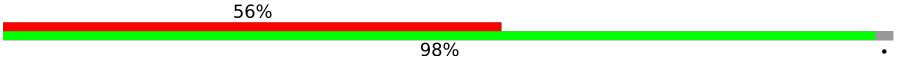
Chain R1:

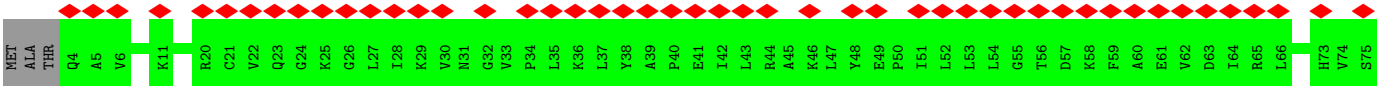


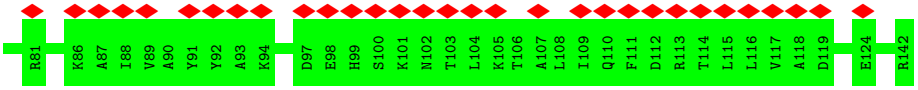


• Molecule 36: 40S ribosomal protein S16

Chain R2:

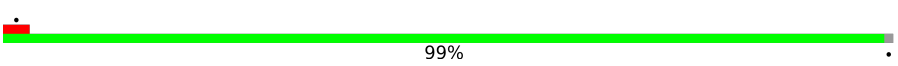


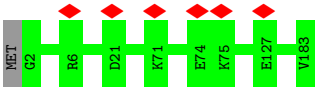




• Molecule 37: 60S ribosomal protein L18

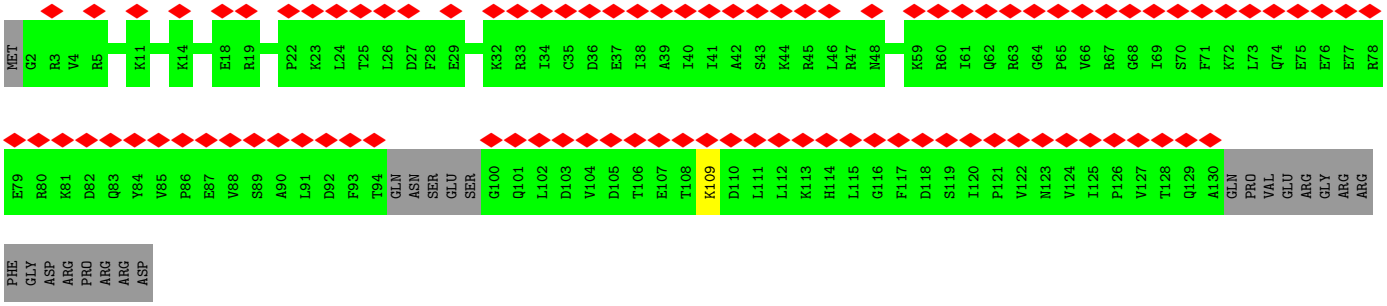
Chain S1:





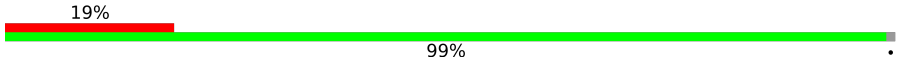
• Molecule 38: 40S ribosomal protein S17

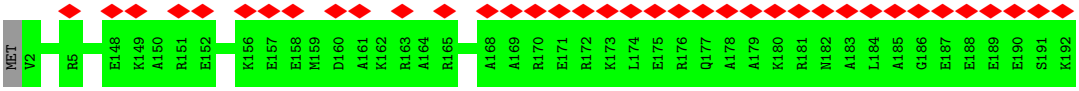
Chain S2:



• Molecule 39: Ribosomal protein L19

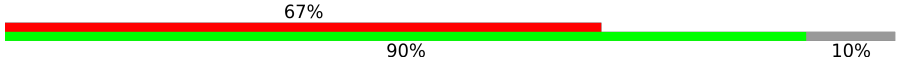
Chain T1:

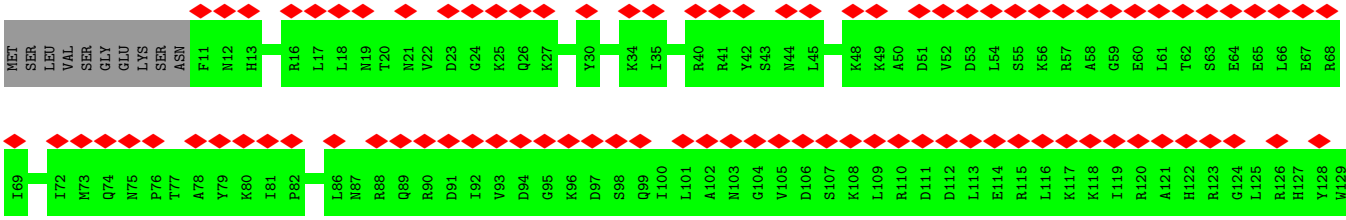




• Molecule 40: 40S ribosomal protein S18

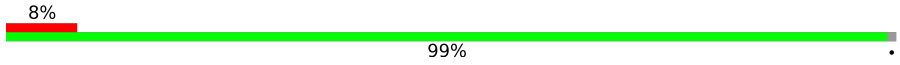
Chain T2:

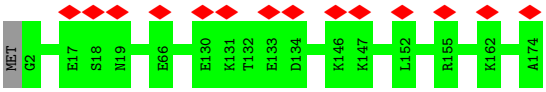




• Molecule 41: 60S ribosomal protein L20

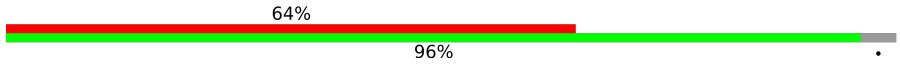
Chain U1:

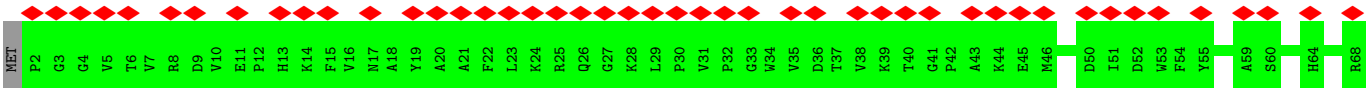


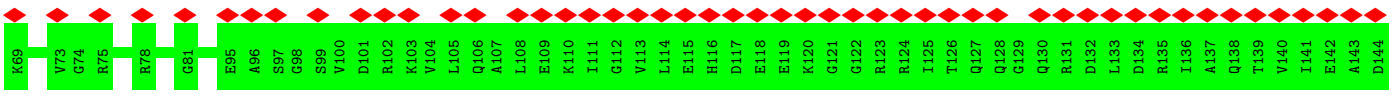


• Molecule 42: 40S ribosomal protein S19

Chain U2:

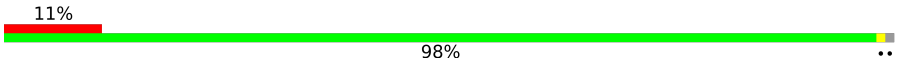


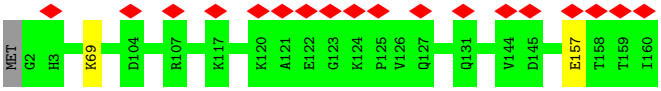




• Molecule 43: Ribosomal protein Srp1

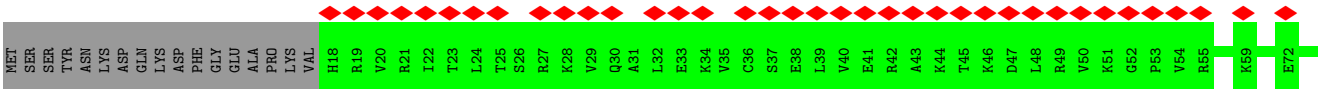
Chain V1:

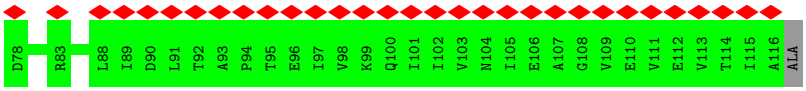




• Molecule 44: 40S ribosomal protein S20

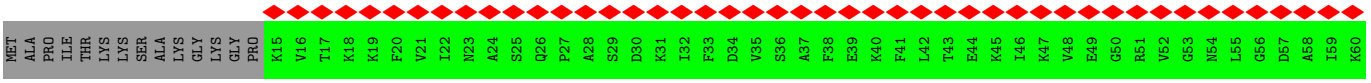
Chain V2:

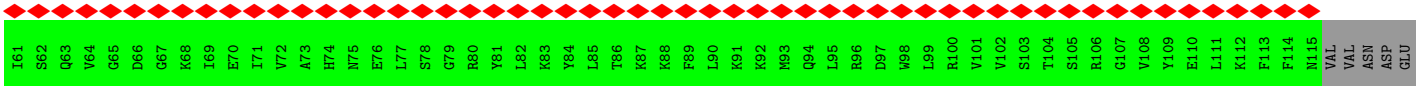




• Molecule 45: 60S ribosomal protein L22

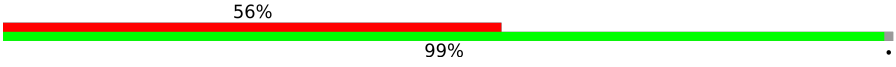
Chain W1:

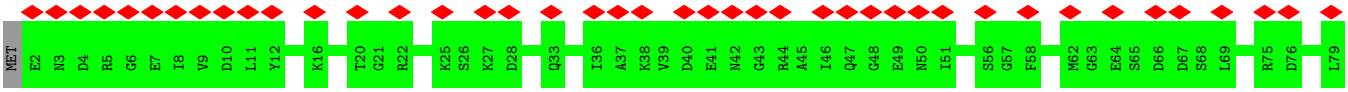


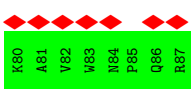


• Molecule 46: 40S ribosomal protein S21

Chain W2:

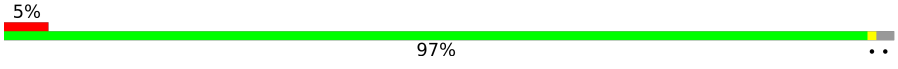


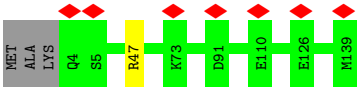




• Molecule 47: 60S ribosomal protein L23

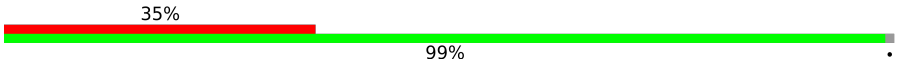
Chain X1:

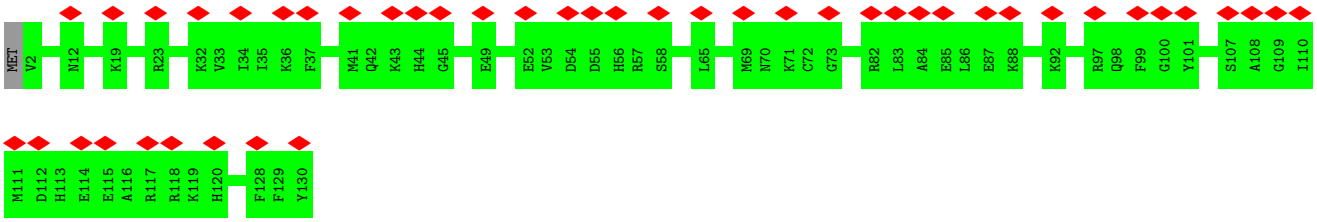




• Molecule 48: 40S ribosomal protein S22

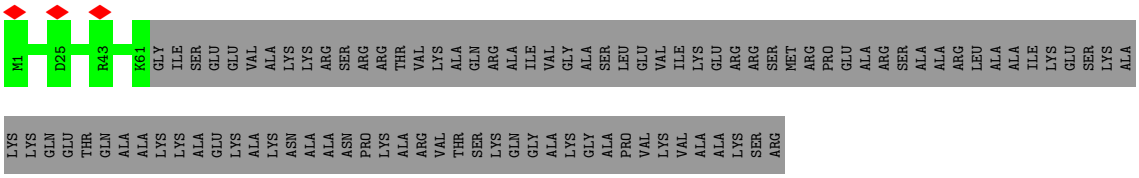
Chain X2:





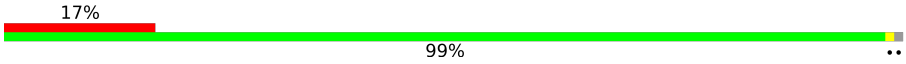
• Molecule 49: 60S ribosomal protein L24

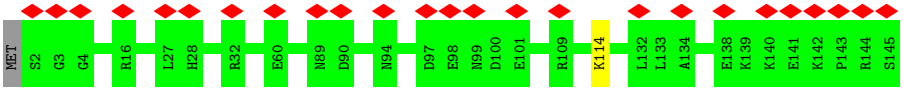
Chain Y1:



• Molecule 50: 40S ribosomal protein S23

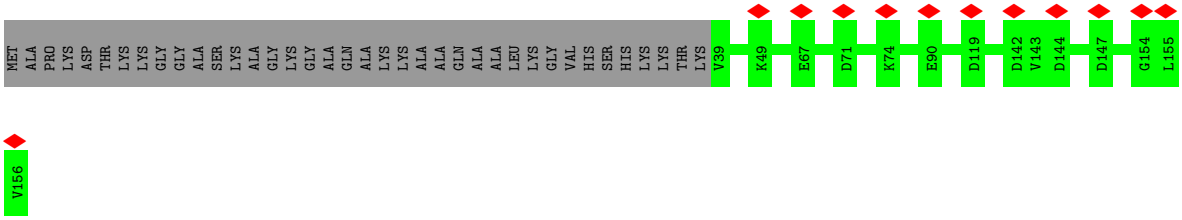
Chain Y2:





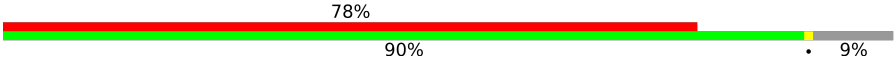
• Molecule 51: 60S ribosomal protein L25

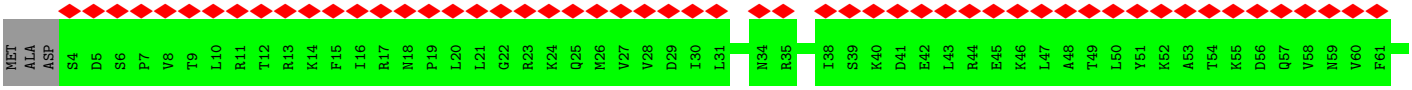
Chain Z1:



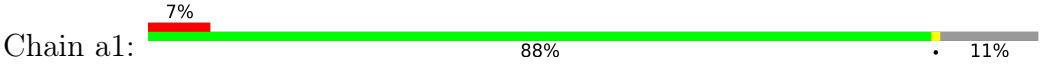
• Molecule 52: 40S ribosomal protein S24

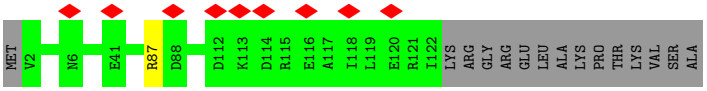
Chain Z2:



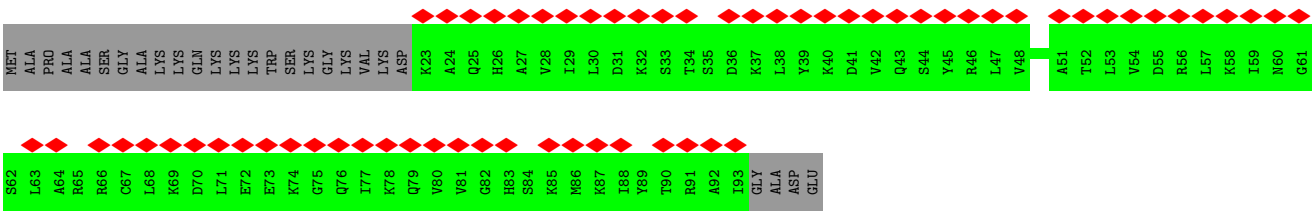


• Molecule 53: Ribosomal protein L26

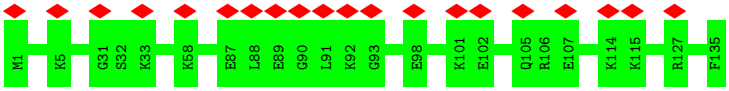




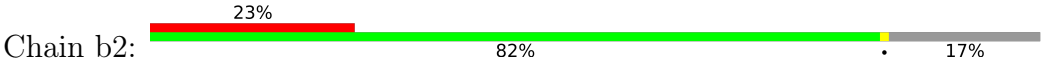
• Molecule 54: 40S ribosomal protein S25

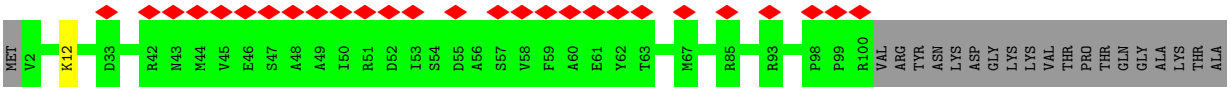


• Molecule 55: 60S ribosomal protein L27 (eL27)

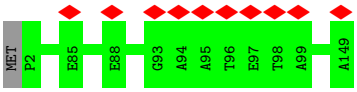


• Molecule 56: 40S ribosomal protein S26E



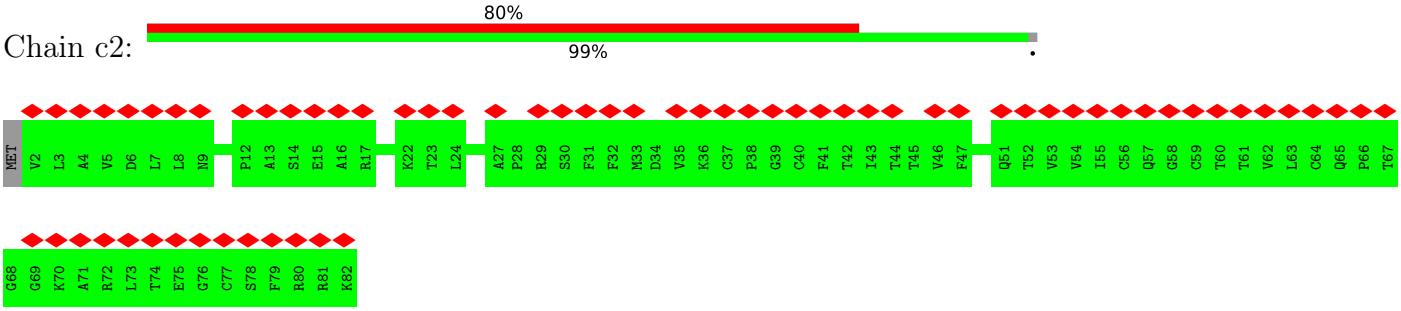


• Molecule 57: 60S ribosomal protein L28



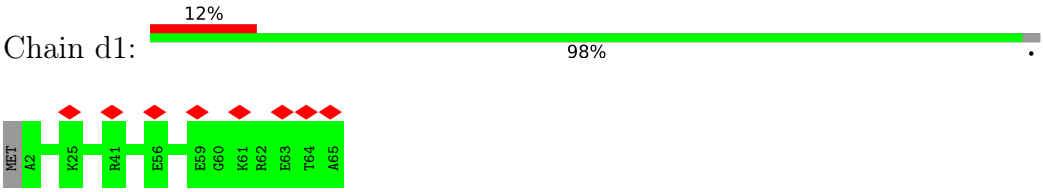
• Molecule 58: 40S ribosomal protein S27

Chain c2:



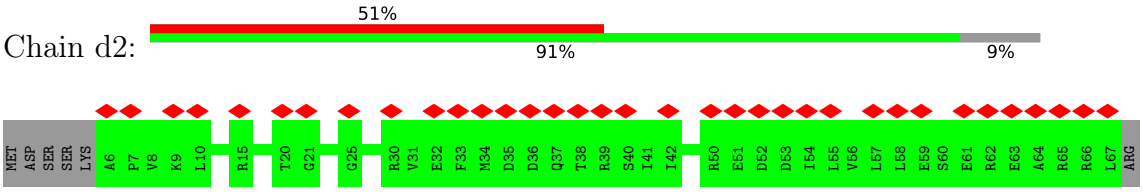
• Molecule 59: 60S ribosomal protein L29

Chain d1:



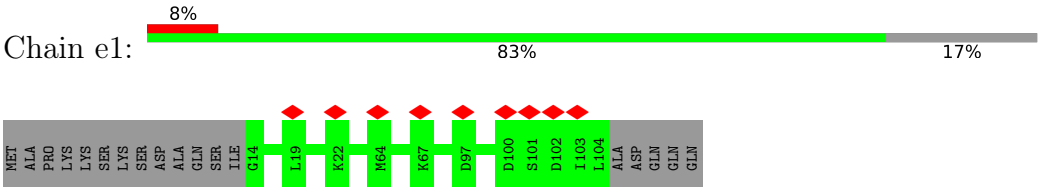
• Molecule 60: 40S ribosomal protein S28

Chain d2:



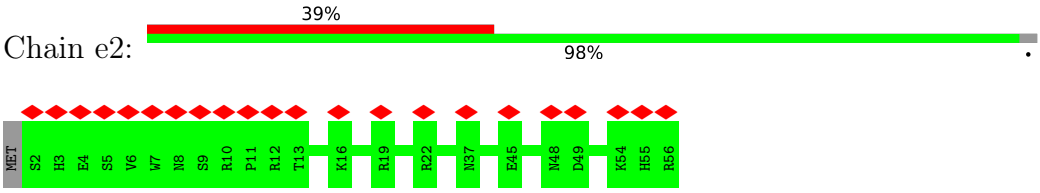
• Molecule 61: 60S ribosomal protein L30

Chain e1:



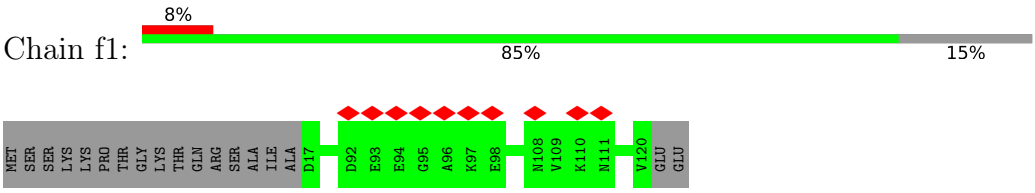
• Molecule 62: 40S ribosomal protein S29

Chain e2:



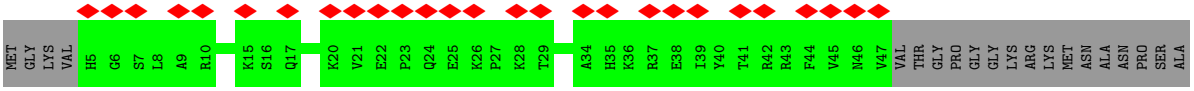
• Molecule 63: 60s ribosomal protein

Chain f1:



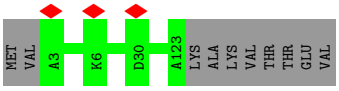
• Molecule 64: 40S ribosomal protein S30

Chain f2:



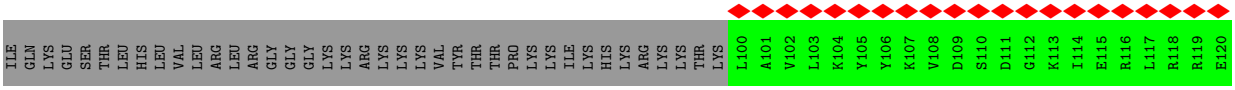
• Molecule 65: 60S ribosomal protein L32

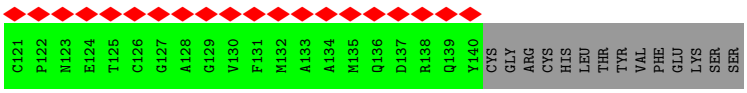
Chain g1:



• Molecule 66: Ubiquitin-40S ribosomal protein S27a

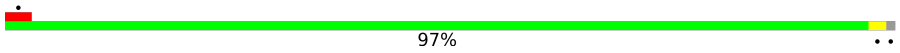
Chain g2:

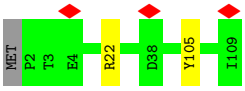




• Molecule 67: 60S ribosomal protein L33

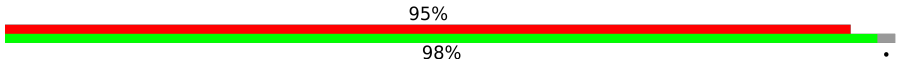
Chain h1:

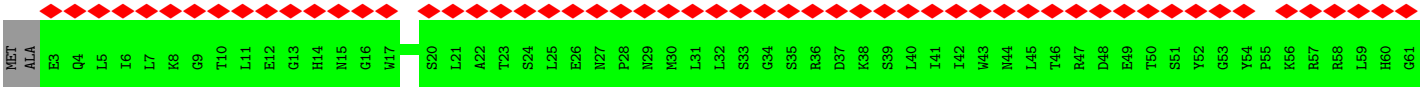


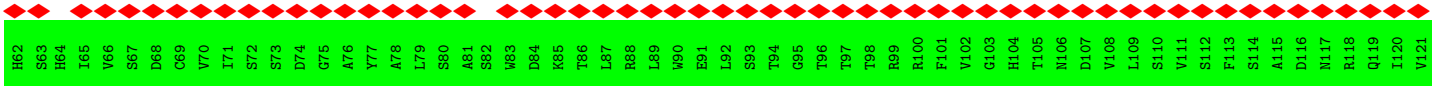


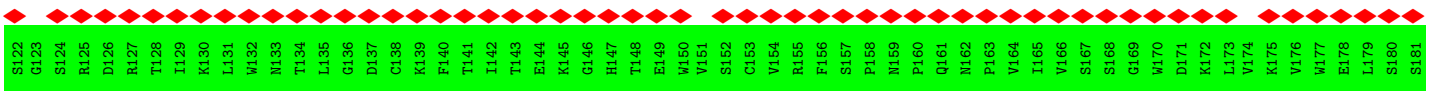
• Molecule 68: Guanine nucleotide-binding protein subunit beta-like protein

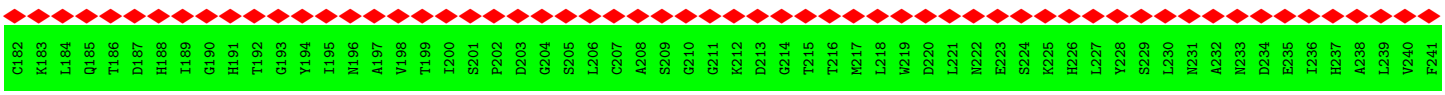
Chain h2:

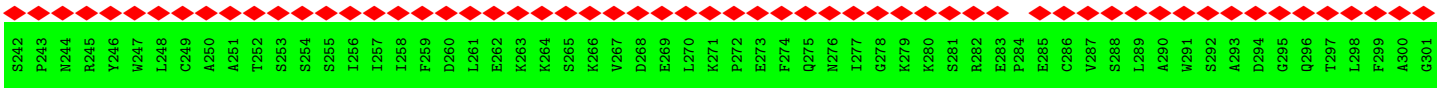


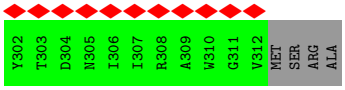






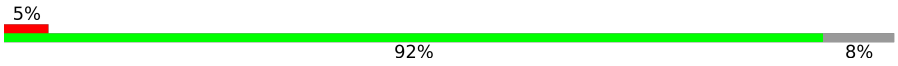


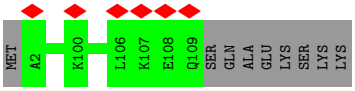




• Molecule 69: 60S ribosomal protein L34

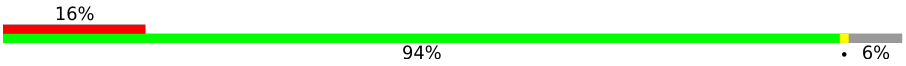
Chain i1:

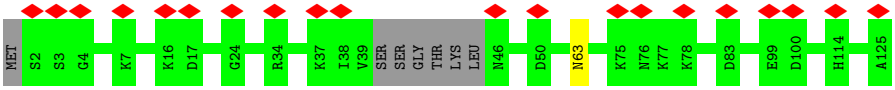




• Molecule 70: 60S ribosomal protein L35

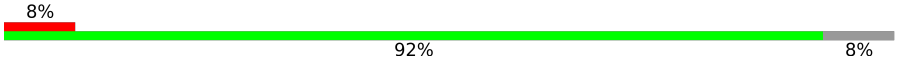
Chain j1:

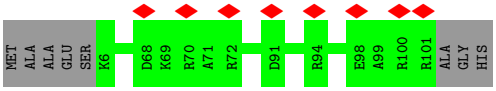




• Molecule 71: 60S ribosomal protein L36

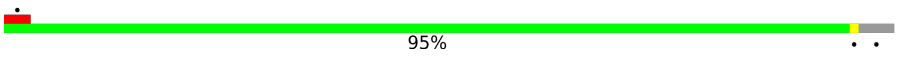
Chain k1:

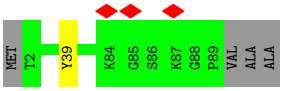




• Molecule 72: Ribosomal protein L37

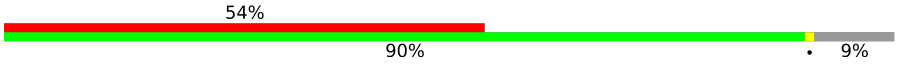
Chain l1:

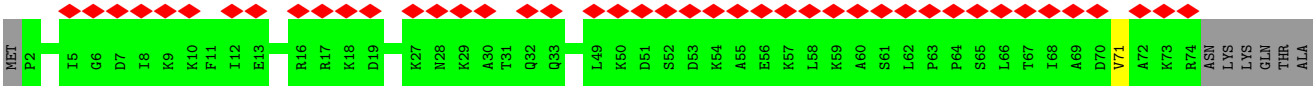




• Molecule 73: 60S ribosomal protein L38

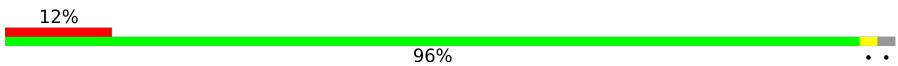
Chain m1:

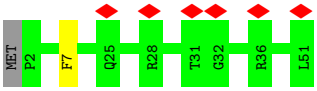




• Molecule 74: 60S ribosomal protein L39

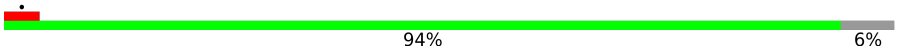
Chain n1:

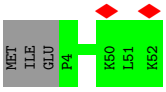




• Molecule 75: 60S ribosomal protein L40

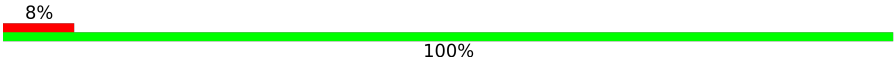
Chain o1:

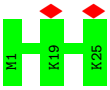




• Molecule 76: hypothetical protein NCU16635 (eL41)

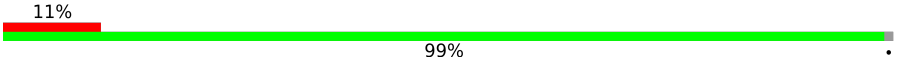
Chain p1:

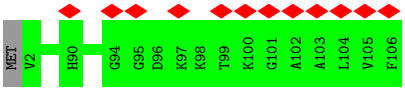




• Molecule 77: 60S ribosomal protein L44

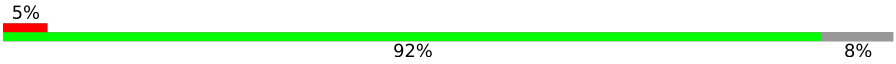
Chain q1:

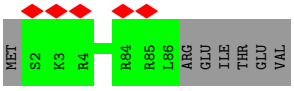




• Molecule 78: 60S ribosomal protein L43

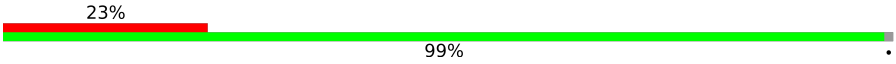
Chain r1:

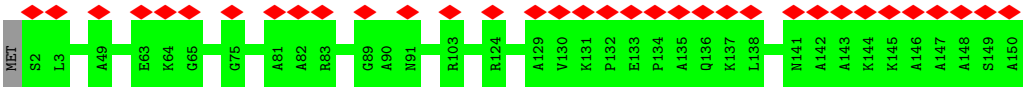




• Molecule 79: Ribosomal_L28e domain-containing protein

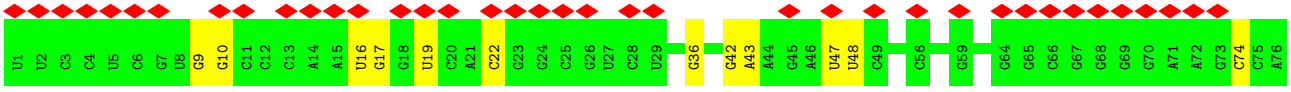
Chain s1:





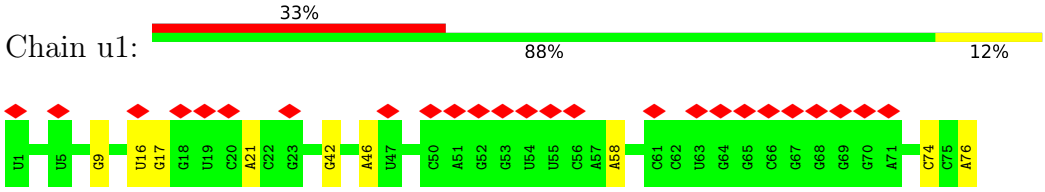
• Molecule 80: tRNA

Chain t1:



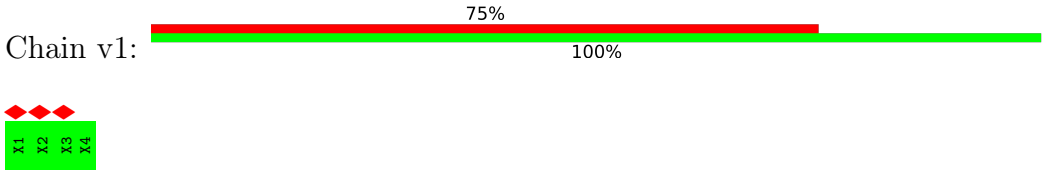
• Molecule 80: tRNA

Chain u1:



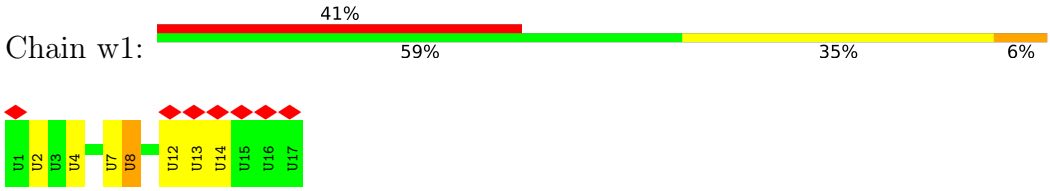
• Molecule 81: Nascent peptide

Chain v1:



• Molecule 82: mRNA

Chain w1:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	196154	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 ($e^-/Å^2$)	32	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.040	Depositor
Minimum map value	-2.001	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.132	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	407.03998, 407.03998, 407.03998	wwPDB
Map dimensions	384, 384, 384	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: SPD, 3HE, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A1	0.36	0/74705	0.81	43/116467 (0.0%)
2	A2	0.24	0/42178	0.76	8/65727 (0.0%)
3	B1	0.28	0/2854	0.77	0/4445
4	B2	0.25	0/1675	0.49	0/2288
5	C1	0.32	0/3756	0.76	0/5849
6	C2	0.26	0/1733	0.55	1/2332 (0.0%)
7	D1	0.29	0/1890	0.55	0/2540
8	D2	0.26	0/1641	0.49	0/2218
9	E1	0.28	0/3127	0.51	0/4201
10	E2	0.25	0/1777	0.53	0/2387
11	F1	0.27	0/2776	0.51	0/3744
12	F2	0.26	0/2088	0.56	0/2806
13	G1	0.26	0/2469	0.50	0/3311
14	G2	0.25	0/1608	0.51	0/2167
15	H1	0.25	0/1549	0.49	0/2084
16	H2	0.25	0/1810	0.55	0/2420
17	I1	0.27	0/2052	0.50	0/2751
18	I2	0.25	0/1536	0.56	0/2069
19	J1	0.26	0/1909	0.49	0/2557
20	J2	0.27	0/1494	0.54	0/2004
21	K1	0.26	0/1523	0.50	0/2048
22	K2	0.24	0/1442	0.56	0/1932
23	L1	0.27	0/1788	0.54	0/2398
24	L2	0.24	0/775	0.47	0/1053
25	M1	0.25	0/1363	0.56	0/1821
26	M2	0.27	0/1092	0.57	0/1468
27	N1	0.26	0/1703	0.54	1/2281 (0.0%)
28	N2	0.24	0/918	0.53	0/1230
29	O1	0.24	0/1125	0.49	0/1508
30	O2	0.24	0/1201	0.47	0/1618
31	P1	0.29	0/1738	0.58	0/2327
32	P2	0.27	0/949	0.57	0/1272

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
33	Q1	0.28	0/1627	0.51	0/2176
34	Q2	0.25	0/1025	0.54	0/1371
35	R1	0.26	0/1342	0.55	0/1799
36	R2	0.25	0/1107	0.50	0/1485
37	S1	0.27	0/1469	0.57	0/1966
38	S2	0.25	0/1018	0.51	0/1367
39	T1	0.25	0/1582	0.53	0/2102
40	T2	0.25	0/1154	0.56	0/1547
41	U1	0.27	0/1464	0.53	0/1970
42	U2	0.23	0/1147	0.50	0/1548
43	V1	0.29	0/1296	0.52	0/1736
44	V2	0.23	0/794	0.53	0/1069
45	W1	0.25	0/829	0.46	0/1107
46	W2	0.25	0/675	0.52	0/905
47	X1	0.28	0/1025	0.51	0/1377
48	X2	0.25	0/1053	0.53	0/1412
49	Y1	0.29	0/537	0.56	0/714
50	Y2	0.25	0/1131	0.50	0/1507
51	Z1	0.25	0/957	0.49	0/1292
52	Z2	0.25	0/1018	0.54	0/1361
53	a1	0.26	0/972	0.56	0/1304
54	a2	0.25	0/569	0.49	0/760
55	b1	0.27	0/1130	0.52	0/1511
56	b2	0.27	0/805	0.59	0/1073
57	c1	0.28	0/1197	0.52	0/1608
58	c2	0.25	0/623	0.51	0/842
59	d1	0.24	0/528	0.50	0/697
60	d2	0.24	0/493	0.60	0/661
61	e1	0.26	0/689	0.47	0/925
62	e2	0.26	0/455	0.53	0/605
63	f1	0.27	0/869	0.53	0/1164
64	f2	0.25	0/353	0.50	0/471
65	g1	0.27	0/990	0.54	0/1319
66	g2	0.24	0/332	0.56	0/443
67	h1	0.30	0/874	0.56	0/1176
68	h2	0.25	0/2486	0.51	0/3378
69	i1	0.28	0/865	0.55	0/1158
70	j1	0.23	0/976	0.49	0/1295
71	k1	0.24	0/766	0.55	0/1016
72	l1	0.28	0/704	0.58	0/933
73	m1	0.26	0/591	0.49	0/786
74	n1	0.24	0/445	0.59	0/592
75	o1	0.25	0/401	0.55	0/528

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	p1	0.24	0/236	0.68	0/300
77	q1	0.27	0/841	0.51	0/1113
78	r1	0.29	0/655	0.55	0/873
79	s1	0.26	0/1134	0.51	0/1523
80	t1	0.21	0/1811	0.76	0/2821
80	u1	0.21	0/1811	0.74	0/2821
82	w1	0.25	0/373	0.99	4/574 (0.7%)
All	All	0.29	0/217468	0.70	57/319404 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
13	G1	0	1
18	I2	0	1
67	h1	0	1
72	l1	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A1	470	C	C2-N1-C1'	8.87	128.56	118.80
1	A1	470	C	N1-C2-O2	8.49	124.00	118.90
1	A1	175	C	N3-C2-O2	-7.79	116.44	121.90
82	w1	8	U	C2-N1-C1'	7.38	126.55	117.70
1	A1	2173	U	C2-N1-C1'	6.91	126.00	117.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	G1	177	PRO	Peptide
18	I2	46	PRO	Peptide
67	h1	105	TYR	Peptide
72	l1	39	TYR	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	
4	B2	207/290 (71%)	200 (97%)	7 (3%)	0	100	100
6	C2	210/256 (82%)	201 (96%)	9 (4%)	0	100	100
7	D1	243/254 (96%)	226 (93%)	17 (7%)	0	100	100
8	D2	208/265 (78%)	197 (95%)	11 (5%)	0	100	100
9	E1	383/392 (98%)	370 (97%)	13 (3%)	0	100	100
10	E2	222/262 (85%)	213 (96%)	8 (4%)	1 (0%)	29	54
11	F1	358/361 (99%)	340 (95%)	18 (5%)	0	100	100
12	F2	254/261 (97%)	240 (94%)	14 (6%)	0	100	100
13	G1	298/301 (99%)	287 (96%)	11 (4%)	0	100	100
14	G2	200/213 (94%)	192 (96%)	8 (4%)	0	100	100
15	H1	190/202 (94%)	170 (90%)	20 (10%)	0	100	100
16	H2	220/239 (92%)	208 (94%)	12 (6%)	0	100	100
17	I1	245/248 (99%)	226 (92%)	18 (7%)	1 (0%)	34	60
18	I2	185/202 (92%)	177 (96%)	8 (4%)	0	100	100
19	J1	234/262 (89%)	221 (94%)	12 (5%)	1 (0%)	34	60
20	J2	179/202 (89%)	176 (98%)	3 (2%)	0	100	100
21	K1	188/193 (97%)	174 (93%)	14 (7%)	0	100	100
22	K2	172/190 (90%)	167 (97%)	5 (3%)	0	100	100
23	L1	215/221 (97%)	205 (95%)	10 (5%)	0	100	100
24	L2	88/163 (54%)	87 (99%)	1 (1%)	0	100	100
25	M1	163/174 (94%)	159 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	M2	127/161 (79%)	119 (94%)	8 (6%)	0	100	100
27	N1	211/214 (99%)	206 (98%)	5 (2%)	0	100	100
28	N2	114/147 (78%)	113 (99%)	1 (1%)	0	100	100
29	O1	139/142 (98%)	134 (96%)	5 (4%)	0	100	100
30	O2	148/151 (98%)	143 (97%)	5 (3%)	0	100	100
31	P1	200/203 (98%)	187 (94%)	13 (6%)	0	100	100
32	P2	124/150 (83%)	120 (97%)	4 (3%)	0	100	100
33	Q1	197/231 (85%)	193 (98%)	4 (2%)	0	100	100
34	Q2	125/152 (82%)	119 (95%)	5 (4%)	1 (1%)	19	43
35	R1	164/186 (88%)	155 (94%)	9 (6%)	0	100	100
36	R2	137/142 (96%)	133 (97%)	4 (3%)	0	100	100
37	S1	180/183 (98%)	174 (97%)	6 (3%)	0	100	100
38	S2	120/146 (82%)	115 (96%)	5 (4%)	0	100	100
39	T1	189/192 (98%)	187 (99%)	2 (1%)	0	100	100
40	T2	139/156 (89%)	127 (91%)	12 (9%)	0	100	100
41	U1	171/174 (98%)	163 (95%)	8 (5%)	0	100	100
42	U2	141/149 (95%)	137 (97%)	4 (3%)	0	100	100
43	V1	157/160 (98%)	153 (98%)	2 (1%)	2 (1%)	12	30
44	V2	97/117 (83%)	95 (98%)	2 (2%)	0	100	100
45	W1	99/126 (79%)	99 (100%)	0	0	100	100
46	W2	84/87 (97%)	80 (95%)	4 (5%)	0	100	100
47	X1	134/139 (96%)	125 (93%)	9 (7%)	0	100	100
48	X2	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
49	Y1	59/156 (38%)	56 (95%)	3 (5%)	0	100	100
50	Y2	142/145 (98%)	139 (98%)	3 (2%)	0	100	100
51	Z1	116/156 (74%)	111 (96%)	5 (4%)	0	100	100
52	Z2	122/136 (90%)	117 (96%)	5 (4%)	0	100	100
53	a1	119/136 (88%)	114 (96%)	5 (4%)	0	100	100
54	a2	69/97 (71%)	68 (99%)	1 (1%)	0	100	100
55	b1	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
56	b2	97/119 (82%)	92 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	c1	146/149 (98%)	130 (89%)	16 (11%)	0	100	100
58	c2	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
59	d1	62/65 (95%)	62 (100%)	0	0	100	100
60	d2	60/68 (88%)	59 (98%)	1 (2%)	0	100	100
61	e1	89/109 (82%)	89 (100%)	0	0	100	100
62	e2	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
63	f1	102/122 (84%)	97 (95%)	5 (5%)	0	100	100
64	f2	41/63 (65%)	40 (98%)	1 (2%)	0	100	100
65	g1	119/131 (91%)	113 (95%)	6 (5%)	0	100	100
66	g2	39/154 (25%)	37 (95%)	2 (5%)	0	100	100
67	h1	106/109 (97%)	100 (94%)	5 (5%)	1 (1%)	17	40
68	h2	308/316 (98%)	292 (95%)	16 (5%)	0	100	100
69	i1	106/117 (91%)	103 (97%)	3 (3%)	0	100	100
70	j1	114/125 (91%)	110 (96%)	4 (4%)	0	100	100
71	k1	94/104 (90%)	91 (97%)	3 (3%)	0	100	100
72	l1	86/92 (94%)	78 (91%)	8 (9%)	0	100	100
73	m1	71/80 (89%)	67 (94%)	3 (4%)	1 (1%)	11	28
74	n1	48/51 (94%)	45 (94%)	2 (4%)	1 (2%)	7	18
75	o1	47/52 (90%)	46 (98%)	1 (2%)	0	100	100
76	p1	23/25 (92%)	23 (100%)	0	0	100	100
77	q1	103/106 (97%)	97 (94%)	6 (6%)	0	100	100
78	r1	83/92 (90%)	79 (95%)	4 (5%)	0	100	100
79	s1	147/150 (98%)	139 (95%)	8 (5%)	0	100	100
All	All	10969/12287 (89%)	10478 (96%)	482 (4%)	9 (0%)	54	78

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	V1	69	LYS
43	V1	157	GLU
67	h1	22	ARG
10	E2	48	VAL
73	m1	71	VAL

5.3.2 Protein sidechains (i)

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	
4	B2	172/225 (76%)	172 (100%)	0	100	100
6	C2	187/224 (84%)	187 (100%)	0	100	100
7	D1	188/196 (96%)	188 (100%)	0	100	100
8	D2	176/211 (83%)	176 (100%)	0	100	100
9	E1	323/328 (98%)	323 (100%)	0	100	100
10	E2	188/209 (90%)	188 (100%)	0	100	100
11	F1	281/282 (100%)	278 (99%)	3 (1%)	73	90
12	F2	219/222 (99%)	218 (100%)	1 (0%)	88	96
13	G1	244/245 (100%)	244 (100%)	0	100	100
14	G2	171/179 (96%)	171 (100%)	0	100	100
15	H1	162/168 (96%)	162 (100%)	0	100	100
16	H2	188/202 (93%)	186 (99%)	2 (1%)	73	90
17	I1	216/217 (100%)	216 (100%)	0	100	100
18	I2	167/178 (94%)	165 (99%)	2 (1%)	71	88
19	J1	201/219 (92%)	201 (100%)	0	100	100
20	J2	146/163 (90%)	146 (100%)	0	100	100
21	K1	168/171 (98%)	168 (100%)	0	100	100
22	K2	151/161 (94%)	151 (100%)	0	100	100
23	L1	181/184 (98%)	180 (99%)	1 (1%)	86	95
24	L2	80/127 (63%)	80 (100%)	0	100	100
25	M1	143/151 (95%)	142 (99%)	1 (1%)	84	94
26	M2	114/139 (82%)	113 (99%)	1 (1%)	78	92
27	N1	172/173 (99%)	172 (100%)	0	100	100
28	N2	99/125 (79%)	99 (100%)	0	100	100
29	O1	115/116 (99%)	115 (100%)	0	100	100
30	O2	131/132 (99%)	131 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	P1	178/179 (99%)	178 (100%)	0	100	100
32	P2	96/115 (84%)	96 (100%)	0	100	100
33	Q1	164/192 (85%)	164 (100%)	0	100	100
34	Q2	109/130 (84%)	108 (99%)	1 (1%)	78	92
35	R1	131/146 (90%)	130 (99%)	1 (1%)	81	93
36	R2	112/114 (98%)	112 (100%)	0	100	100
37	S1	152/153 (99%)	152 (100%)	0	100	100
38	S2	112/132 (85%)	111 (99%)	1 (1%)	78	92
39	T1	159/160 (99%)	159 (100%)	0	100	100
40	T2	123/136 (90%)	123 (100%)	0	100	100
41	U1	153/154 (99%)	153 (100%)	0	100	100
42	U2	117/123 (95%)	117 (100%)	0	100	100
43	V1	134/135 (99%)	134 (100%)	0	100	100
44	V2	90/105 (86%)	90 (100%)	0	100	100
45	W1	89/109 (82%)	89 (100%)	0	100	100
46	W2	71/72 (99%)	71 (100%)	0	100	100
47	X1	104/106 (98%)	103 (99%)	1 (1%)	76	91
48	X2	112/113 (99%)	112 (100%)	0	100	100
49	Y1	55/125 (44%)	55 (100%)	0	100	100
50	Y2	116/117 (99%)	115 (99%)	1 (1%)	78	92
51	Z1	104/128 (81%)	104 (100%)	0	100	100
52	Z2	109/118 (92%)	108 (99%)	1 (1%)	78	92
53	a1	110/122 (90%)	109 (99%)	1 (1%)	78	92
54	a2	63/81 (78%)	63 (100%)	0	100	100
55	b1	122/122 (100%)	122 (100%)	0	100	100
56	b2	87/103 (84%)	86 (99%)	1 (1%)	73	90
57	c1	116/117 (99%)	116 (100%)	0	100	100
58	c2	70/71 (99%)	70 (100%)	0	100	100
59	d1	54/55 (98%)	54 (100%)	0	100	100
60	d2	55/61 (90%)	55 (100%)	0	100	100
61	e1	74/89 (83%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
62	e2	48/49 (98%)	48 (100%)	0	100 100
63	f1	90/105 (86%)	90 (100%)	0	100 100
64	f2	37/51 (72%)	37 (100%)	0	100 100
65	g1	104/113 (92%)	104 (100%)	0	100 100
66	g2	34/138 (25%)	34 (100%)	0	100 100
67	h1	88/89 (99%)	88 (100%)	0	100 100
68	h2	272/276 (99%)	272 (100%)	0	100 100
69	i1	93/101 (92%)	93 (100%)	0	100 100
70	j1	103/109 (94%)	102 (99%)	1 (1%)	76 91
71	k1	78/82 (95%)	78 (100%)	0	100 100
72	l1	73/75 (97%)	73 (100%)	0	100 100
73	m1	64/70 (91%)	64 (100%)	0	100 100
74	n1	45/46 (98%)	45 (100%)	0	100 100
75	o1	44/47 (94%)	44 (100%)	0	100 100
76	p1	23/23 (100%)	23 (100%)	0	100 100
77	q1	87/88 (99%)	87 (100%)	0	100 100
78	r1	68/75 (91%)	68 (100%)	0	100 100
79	s1	112/113 (99%)	112 (100%)	0	100 100
All	All	9387/10280 (91%)	9367 (100%)	20 (0%)	93 98

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	X1	47	ARG
53	a1	87	ARG
70	j1	63	ASN
56	b2	12	LYS
18	I2	8	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
51	Z1	110	GLN
52	Z2	32	HIS
74	n1	17	GLN

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Mol	Chain	Res	Type
54	a2	43	GLN
16	H2	116	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A1	3119/3338 (93%)	419 (13%)	12 (0%)
2	A2	1765/1796 (98%)	244 (13%)	0
3	B1	119/120 (99%)	9 (7%)	0
5	C1	157/158 (99%)	21 (13%)	1 (0%)
80	t1	75/76 (98%)	12 (16%)	0
80	u1	75/76 (98%)	9 (12%)	0
82	w1	16/17 (94%)	6 (37%)	0
All	All	5326/5581 (95%)	720 (13%)	13 (0%)

5 of 720 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A1	6	A
1	A1	22	G
1	A1	26	A
1	A1	40	A
1	A1	43	A

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A1	1136	A
1	A1	1211	A
5	C1	84	A
1	A1	2803	U
1	A1	3080	U

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 262 ligands modelled in this entry, 260 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
84	SPD	A1	8002	-	9,9,9	0.31	0	8,8,8	0.58	0
83	3HE	A1	8001	-	21,21,21	4.31	8 (38%)	19,30,30	5.20	11 (57%)

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
84	SPD	A1	8002	-	-	2/7/7/7	-
83	3HE	A1	8001	-	-	5/8/36/36	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	A1	8001	3HE	O-C4	11.63	1.40	1.21
83	A1	8001	3HE	O1-C11	8.04	1.39	1.23
83	A1	8001	3HE	O2-C12	7.74	1.39	1.23
83	A1	8001	3HE	C12-N	7.65	1.50	1.37
83	A1	8001	3HE	C11-N	6.58	1.48	1.37

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
83	A1	8001	3HE	C11-N-C12	-10.78	112.71	125.78
83	A1	8001	3HE	O-C4-C5	-8.93	110.28	123.28
83	A1	8001	3HE	O-C4-C3	-8.02	110.20	122.15
83	A1	8001	3HE	O2-C12-N	-7.94	107.69	120.28
83	A1	8001	3HE	O2-C12-C13	-7.34	108.33	122.62

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

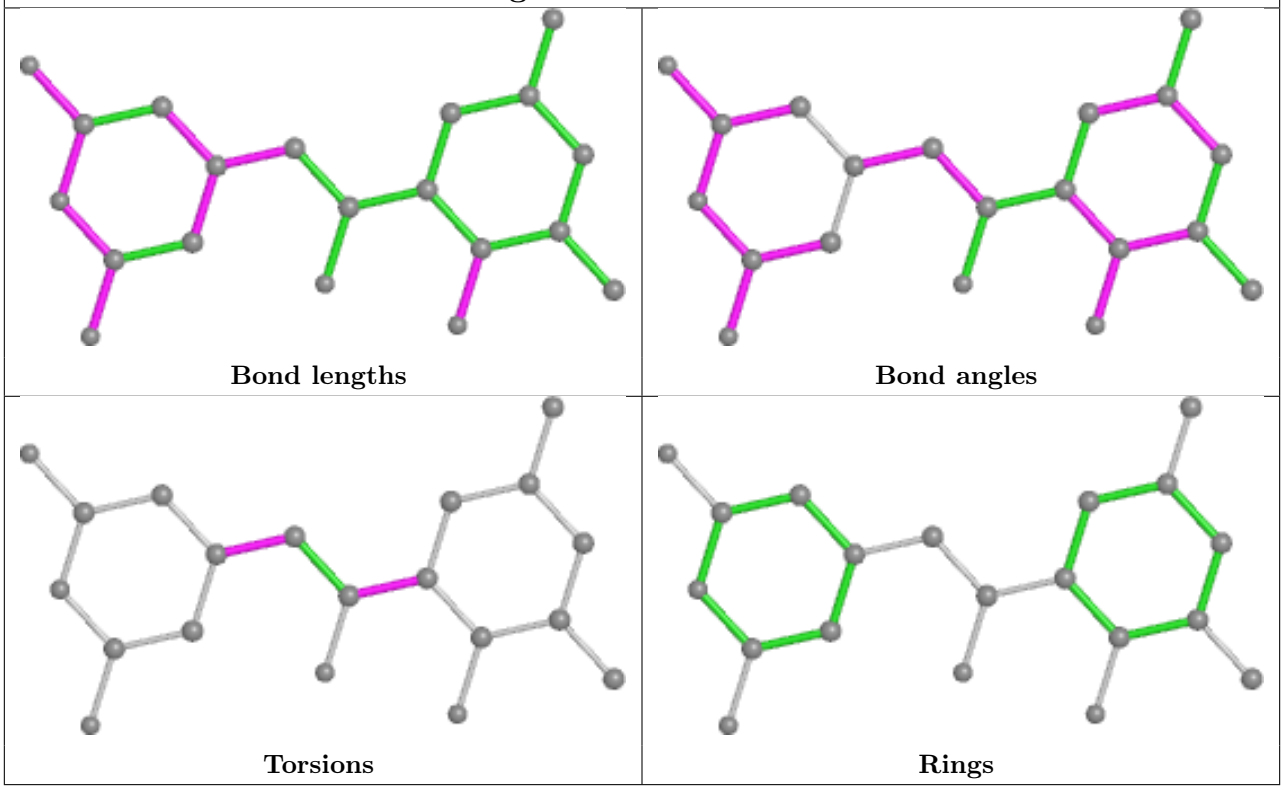
Mol	Chain	Res	Type	Atoms
83	A1	8001	3HE	C6-C5-C7-C8
83	A1	8001	3HE	C6-C5-C7-O3
83	A1	8001	3HE	C7-C8-C9-C10
83	A1	8001	3HE	C7-C8-C9-C13
84	A1	8002	SPD	C3-C4-C5-N6

There are no ring outliers.

No monomer is involved in short contacts.

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

Ligand 3HE A1 8001



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.

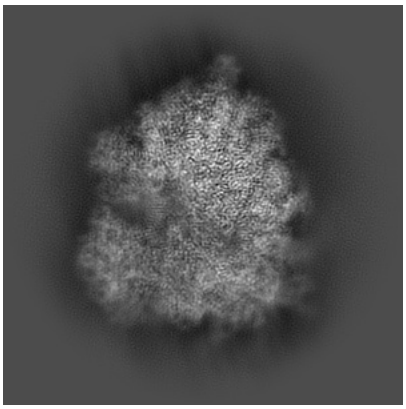
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24307. These allow visual inspection of the internal detail of the map and identification of artifacts.

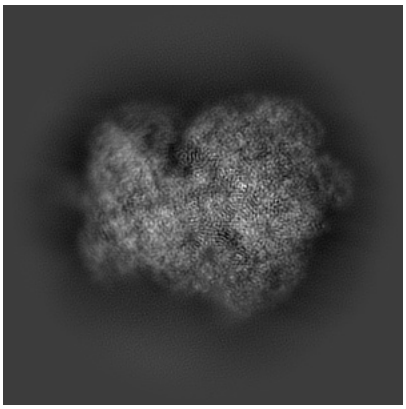
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

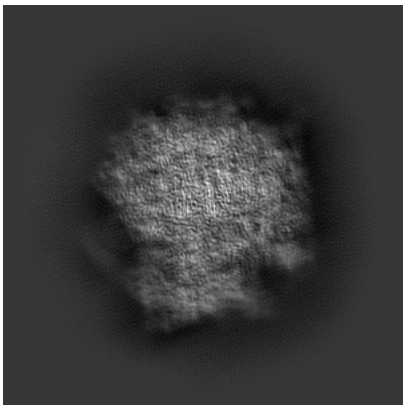
6.1.1 Primary map



X

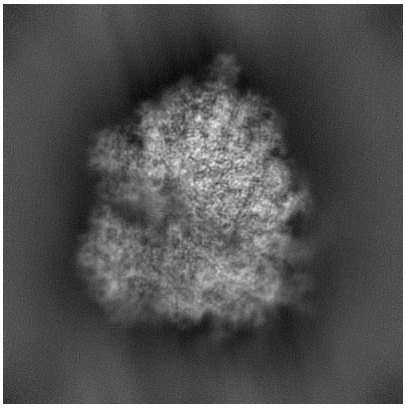


Y

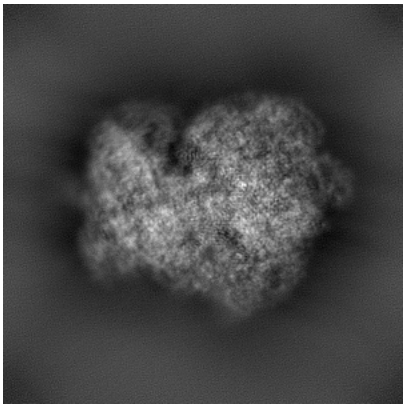


Z

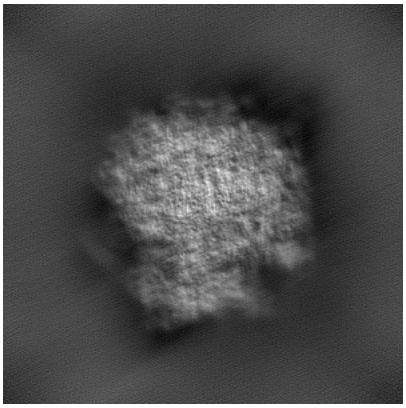
6.1.2 Raw map



X



Y

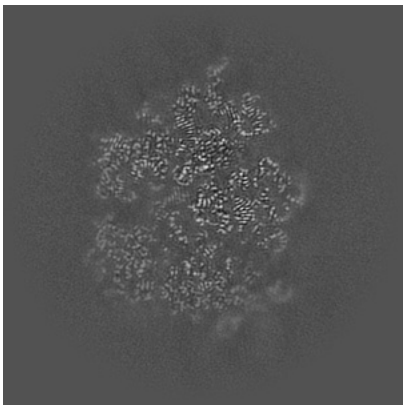


Z

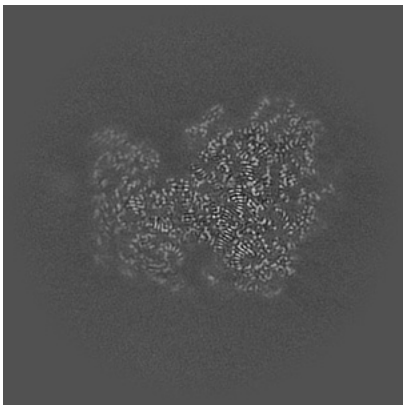
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

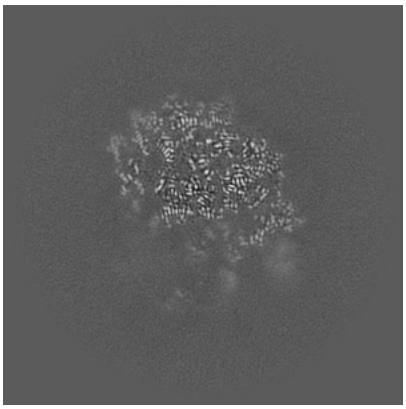
6.2.1 Primary map



X Index: 192

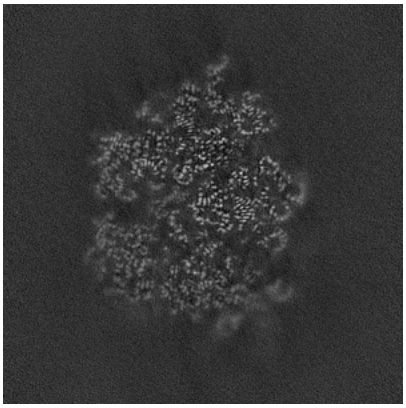


Y Index: 192

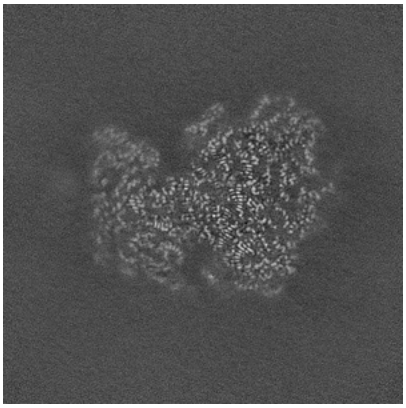


Z Index: 192

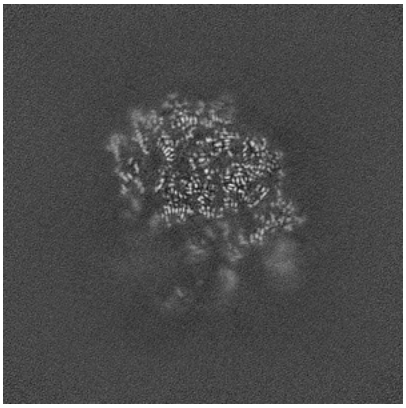
6.2.2 Raw map



X Index: 192



Y Index: 192

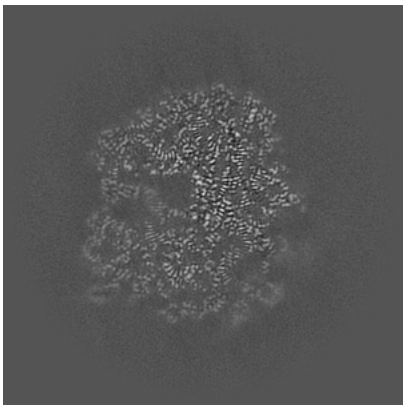


Z Index: 192

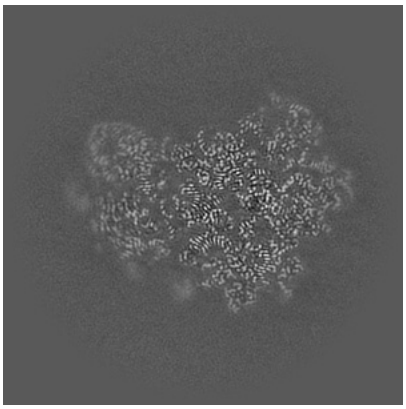
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

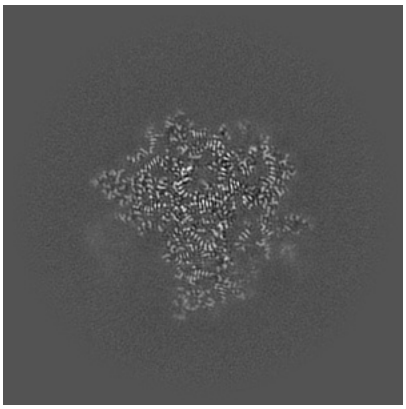
6.3.1 Primary map



X Index: 180

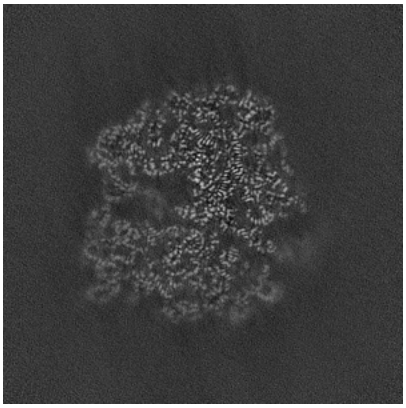


Y Index: 207

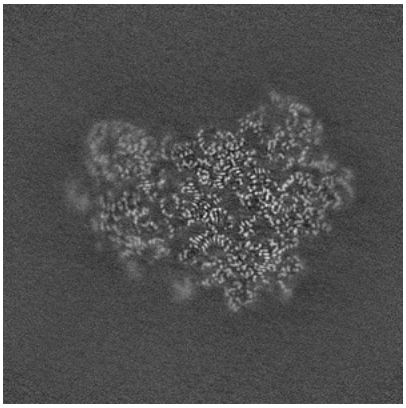


Z Index: 228

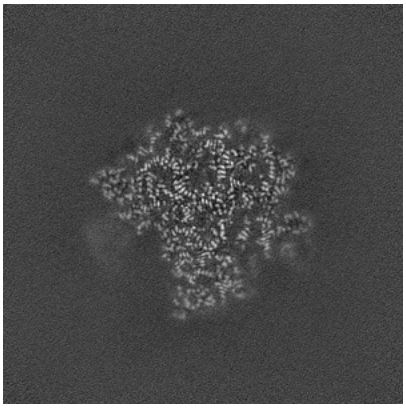
6.3.2 Raw map



X Index: 177



Y Index: 207

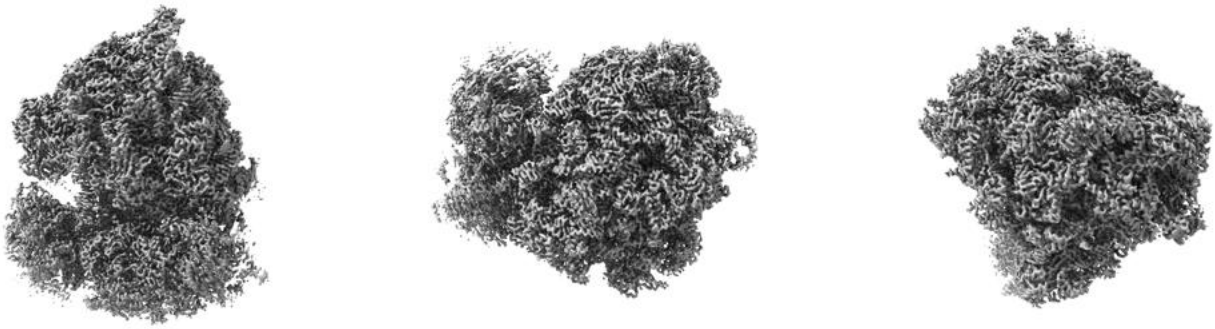


Z Index: 229

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 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map

X Y Z

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

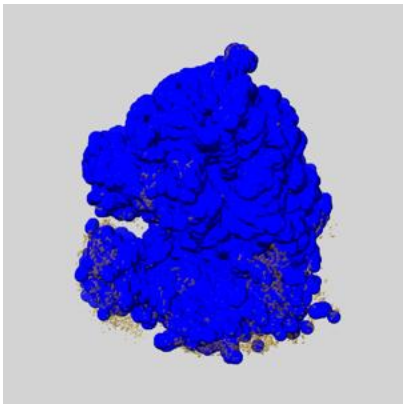
6.5 Mask visualisation (i)

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

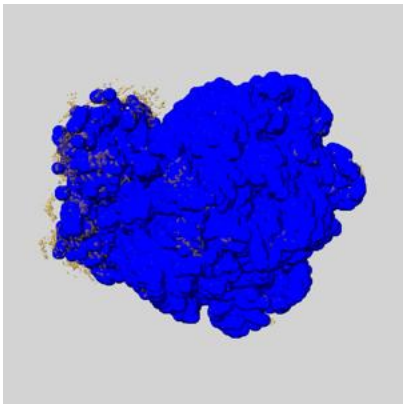
A mask typically either:

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

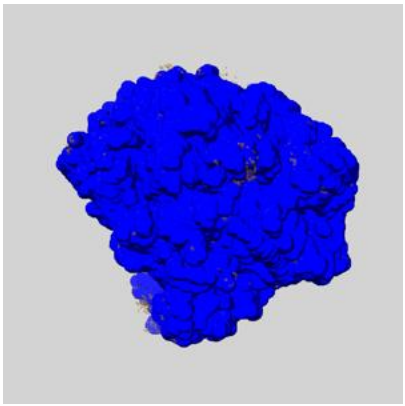
6.5.1 emd_24307_msk_1.map (i)



X



Y

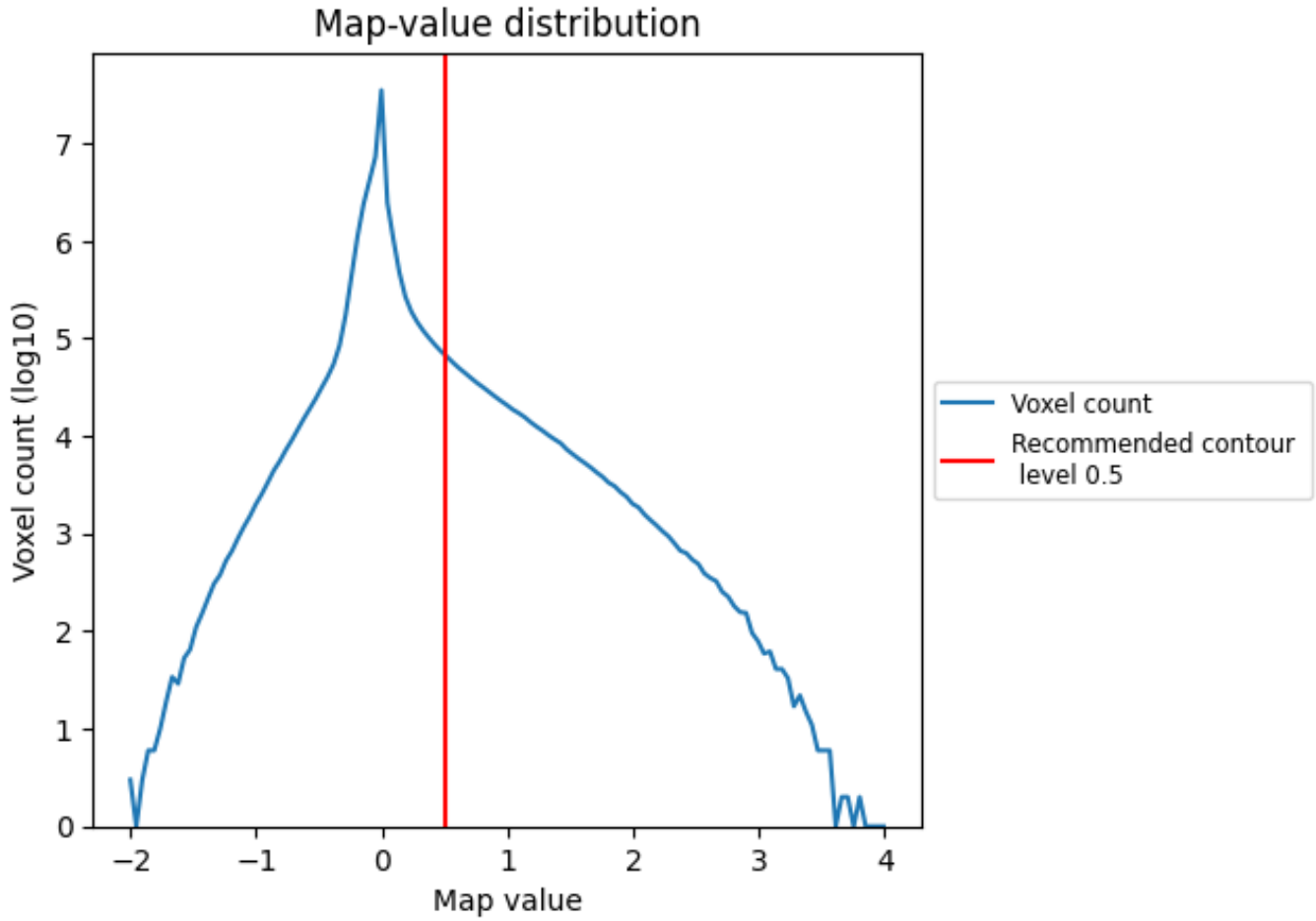


Z

7 Map analysis

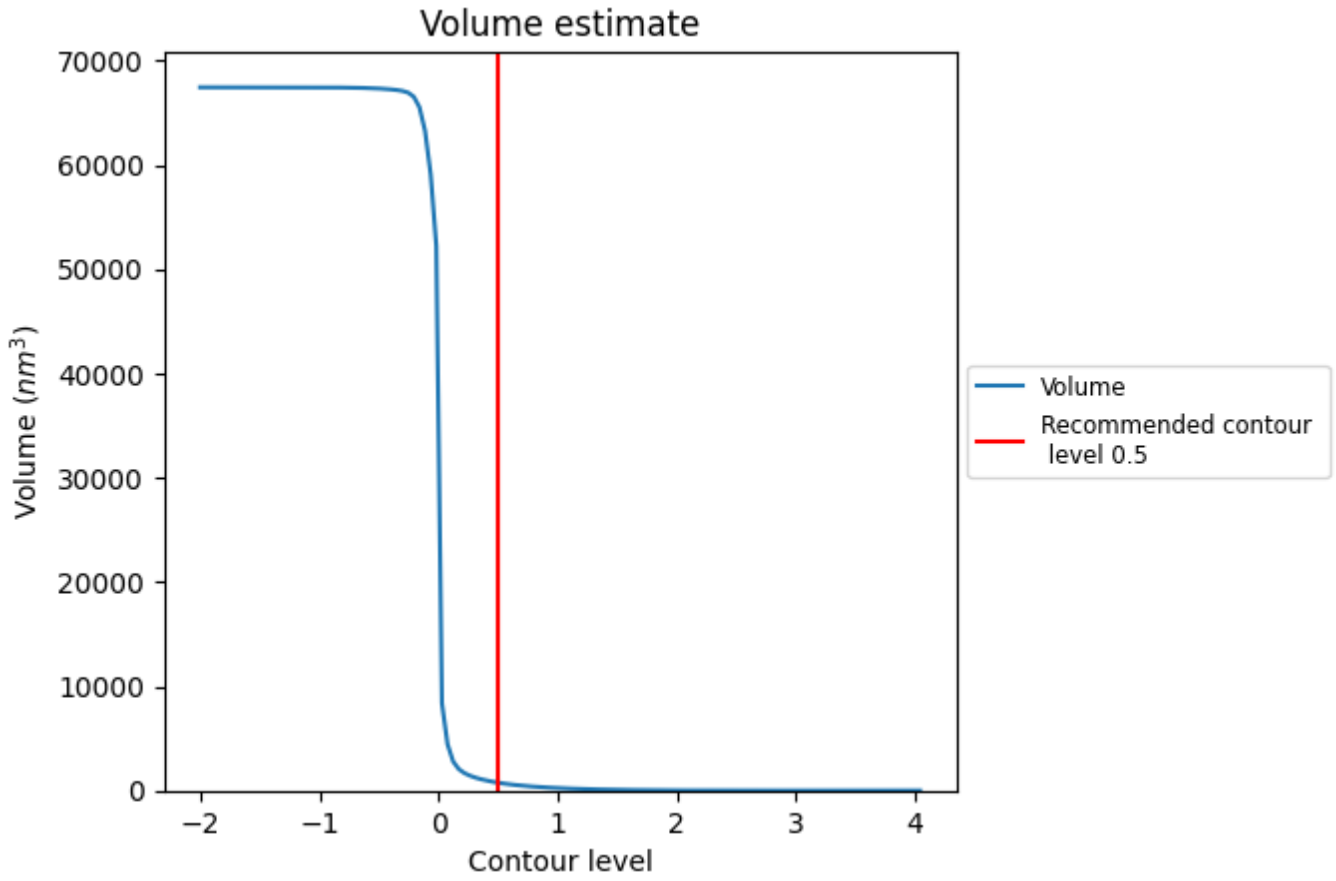
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

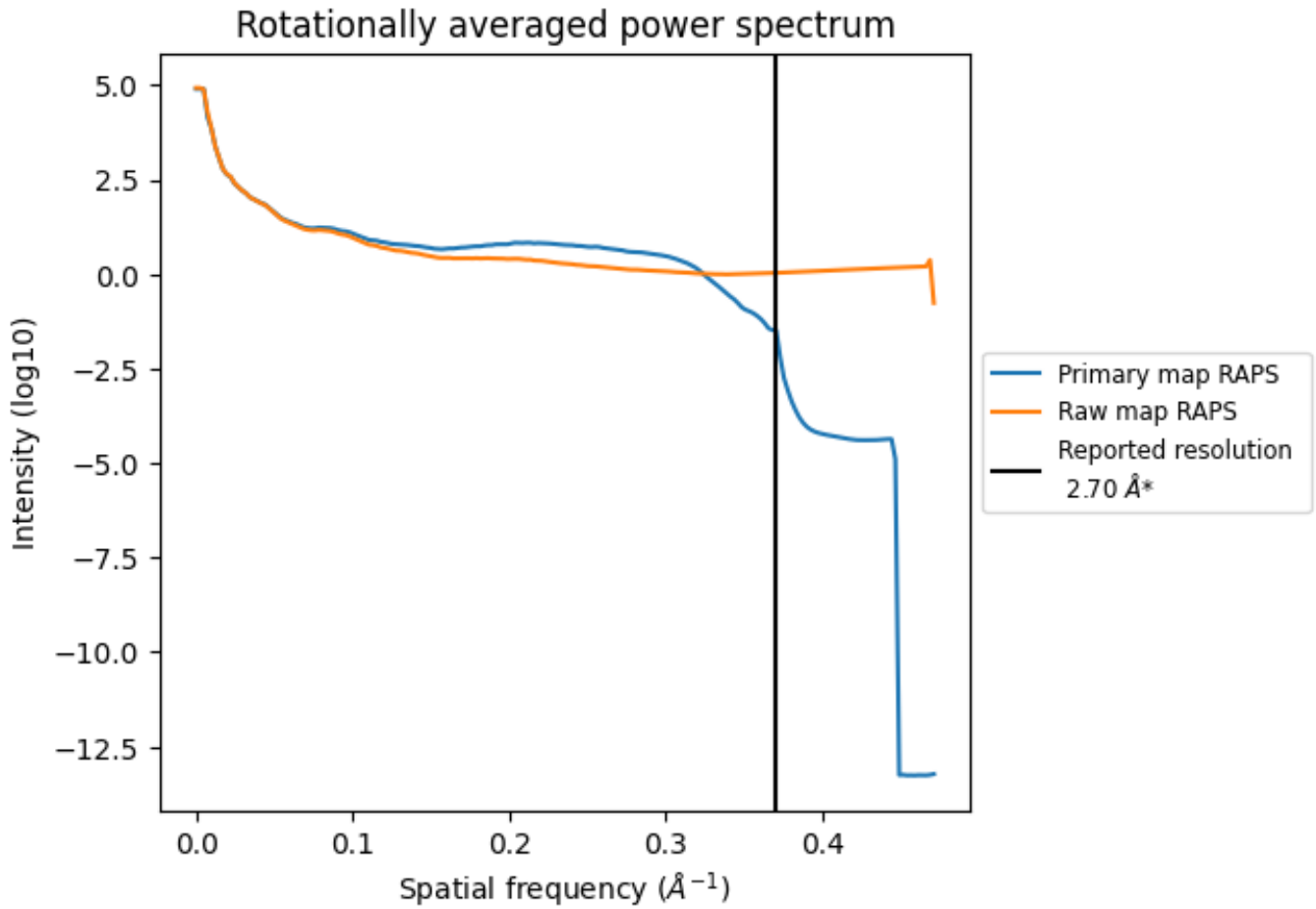
7.2 Volume estimate (i)



The volume at the recommended contour level is 752 nm^3; this corresponds to an approximate mass of 679 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 (i)

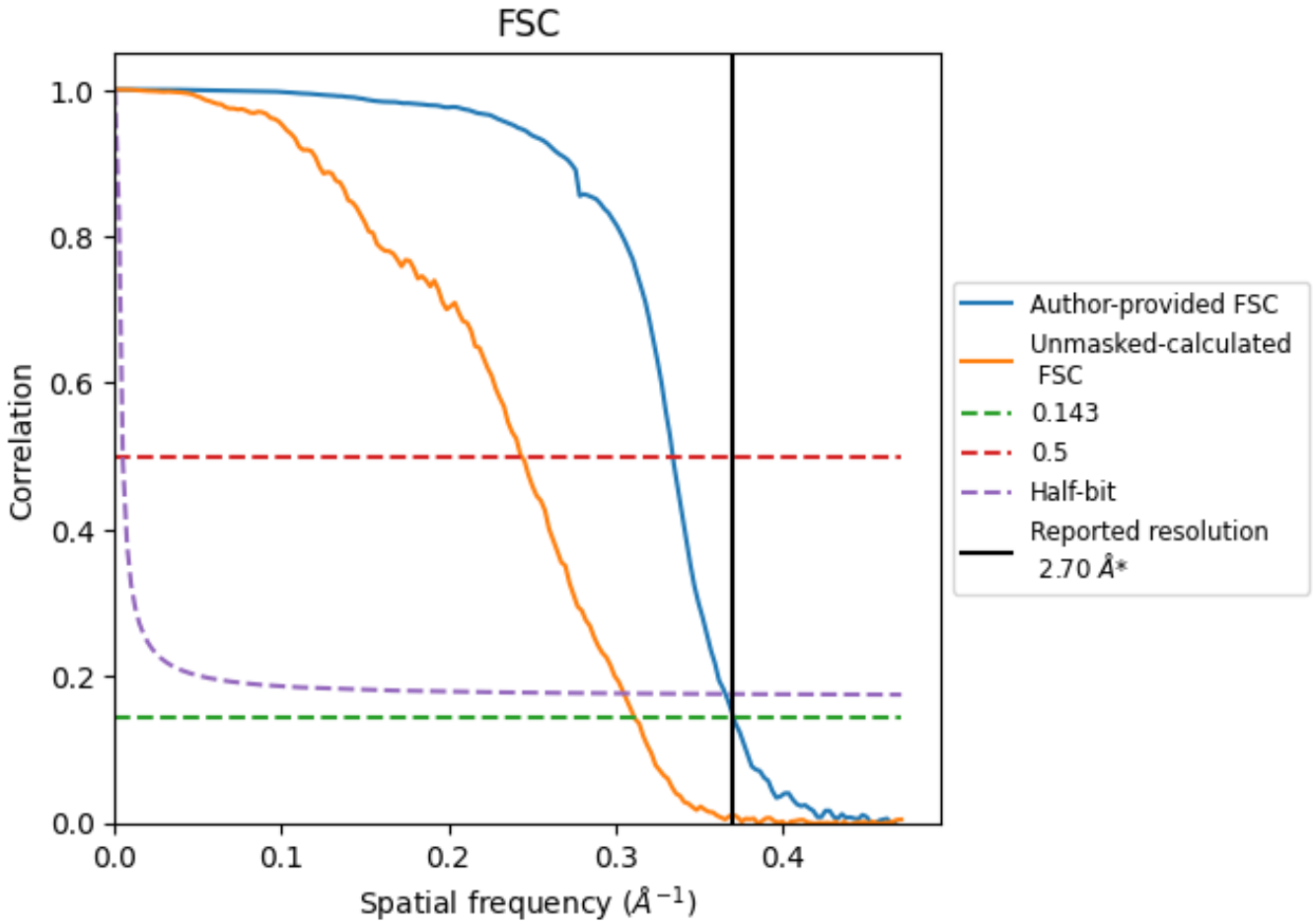


*Reported resolution corresponds to spatial frequency of 0.370 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.370 Å^{-1}

8.2 Resolution estimates (i)

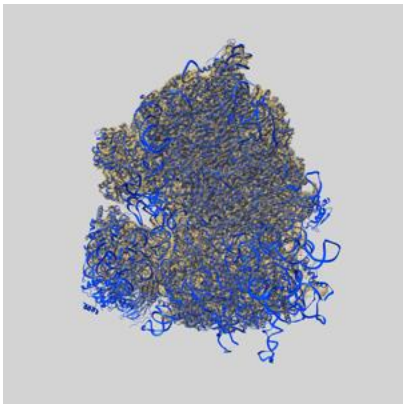
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.69	2.99	2.73
Unmasked-calculated*	3.21	4.10	3.27

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.21 differs from the reported value 2.7 by more than 10 %

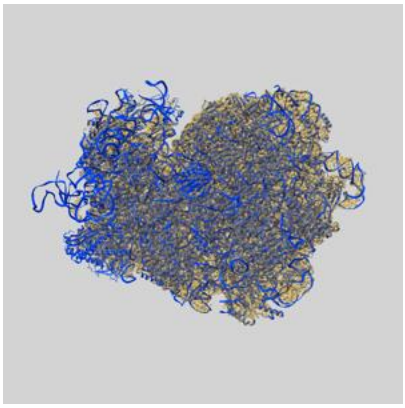
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-24307 and PDB model 7R81. Per-residue inclusion information can be found in section 3 on page 20.

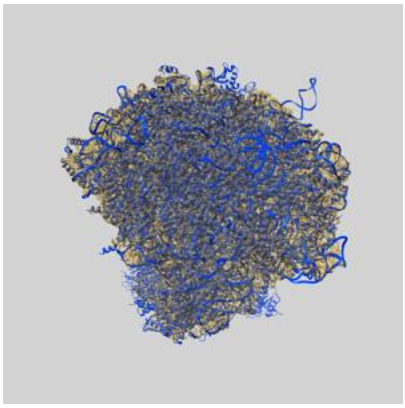
9.1 Map-model overlay



X



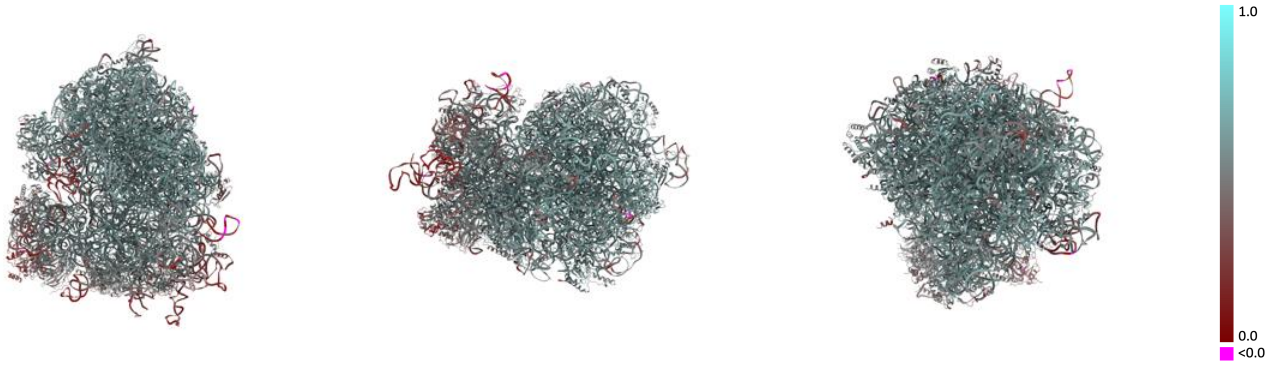
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

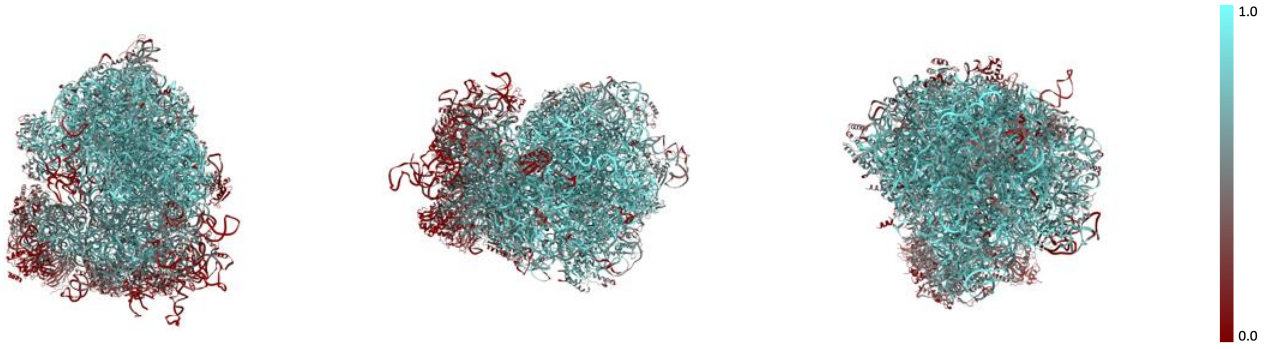
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

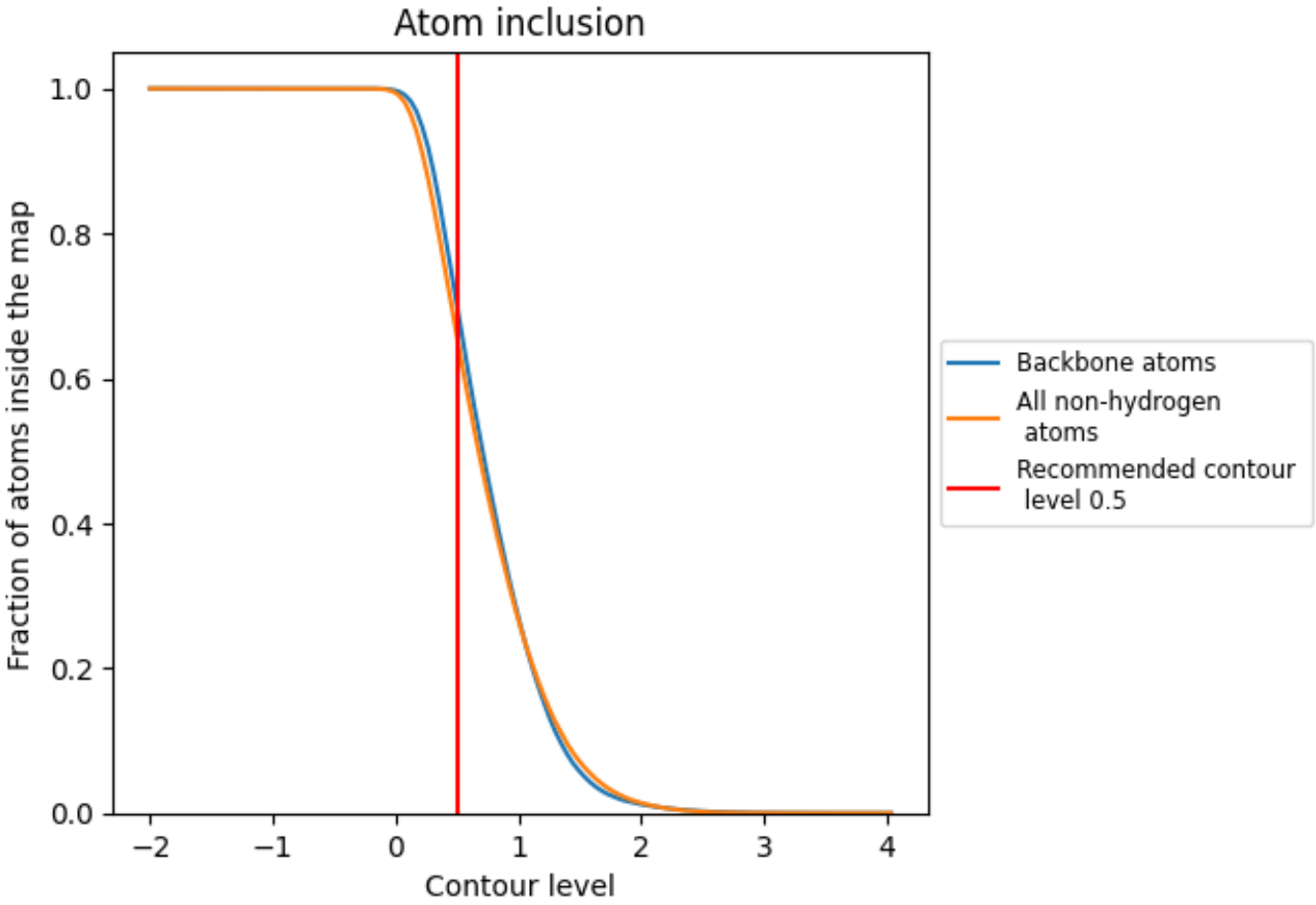
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.5).

9.4 Atom inclusion (i)



At the recommended contour level, 70% of all backbone atoms, 66% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6573	0.5390
A1	0.8444	0.5780
A2	0.6061	0.4900
B1	0.8618	0.5770
B2	0.3199	0.4800
C1	0.8173	0.5650
C2	0.3499	0.4980
D1	0.8181	0.6080
D2	0.4523	0.5170
E1	0.7685	0.5980
E2	0.2685	0.4600
F1	0.7326	0.5830
F2	0.2656	0.4850
G1	0.5689	0.5380
G2	0.3556	0.4860
H1	0.5222	0.5380
H2	0.1851	0.4520
I1	0.7180	0.5720
I2	0.1581	0.4150
J1	0.6047	0.5430
J2	0.5018	0.5280
K1	0.6205	0.5620
K2	0.3243	0.4670
L1	0.6653	0.5600
L2	0.1858	0.4420
M1	0.5000	0.5250
M2	0.5717	0.5500
N1	0.6800	0.5600
N2	0.0000	0.2160
O1	0.6277	0.5590
O2	0.4374	0.5140
P1	0.8444	0.6110
P2	0.5248	0.5260
Q1	0.7696	0.5930
Q2	0.2301	0.4520

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Chain	Atom inclusion	Q-score
R1	0.7761	0.5900
R2	0.3776	0.5090
S1	0.7747	0.6000
S2	0.2370	0.4420
T1	0.6460	0.5410
T2	0.3039	0.4770
U1	0.7469	0.5910
U2	0.3049	0.4810
V1	0.7030	0.5780
V2	0.2725	0.4500
W1	0.0474	0.4640
W2	0.3498	0.4830
X1	0.7325	0.5950
X2	0.4931	0.5250
Y1	0.7510	0.5960
Y2	0.5897	0.5640
Z1	0.6677	0.5750
Z2	0.2027	0.4480
a1	0.7000	0.5720
a2	0.1775	0.4400
b1	0.6474	0.5570
b2	0.5816	0.5280
c1	0.7843	0.6000
c2	0.2429	0.4600
d1	0.7018	0.5730
d2	0.3227	0.5020
e1	0.6771	0.5710
e2	0.4590	0.5160
f1	0.7567	0.5890
f2	0.3254	0.4860
g1	0.7792	0.5980
g2	0.0000	0.2560
h1	0.7956	0.6070
h2	0.0814	0.4240
i1	0.7652	0.5960
j1	0.6322	0.5570
k1	0.6763	0.5650
l1	0.8256	0.6030
m1	0.3962	0.5020
n1	0.7029	0.5700
o1	0.7513	0.5940
p1	0.6822	0.5940

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Chain	Atom inclusion	Q-score
q1	0.7182	0.5780
r1	0.7628	0.5870
s1	0.5925	0.5610
t1	0.4300	0.4890
u1	0.5321	0.5080
v1	0.2000	0.5090
w1	0.4794	0.4360