



wwPDB EM Validation Summary Report ⓘ

Jun 26, 2026 – 07:00 AM EDT

PDB ID : 7LS1 / pdb_00007ls1
EMDB ID : EMD-23500
Title : 80S ribosome from mouse bound to eEF2 (Class II)
Authors : Loerch, S.; Smith, P.R.; Kunder, N.; Stanowick, A.D.; Lou, T.-F.; Campbell, Z.T.
Deposited on : 2021-02-17
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

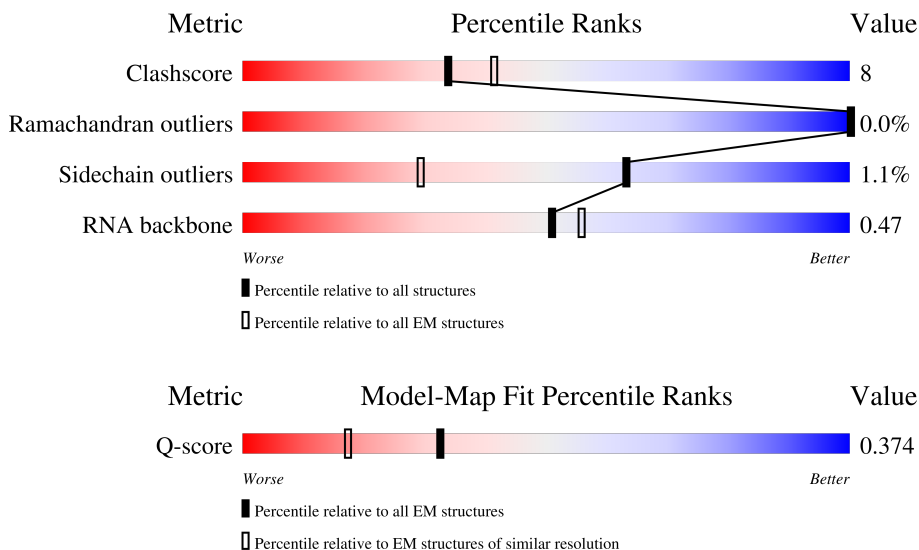
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.30 Å.

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








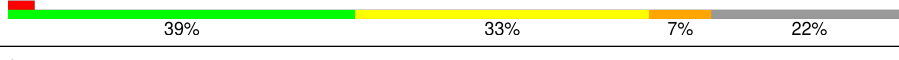



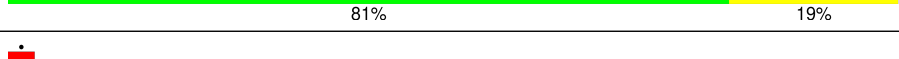
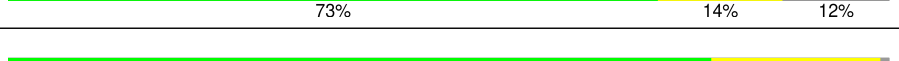
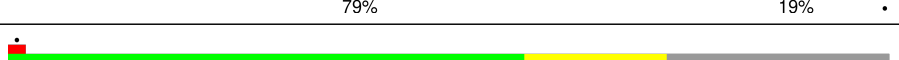
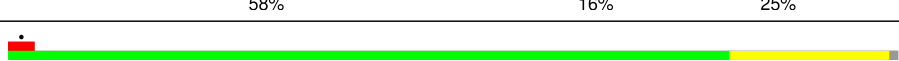
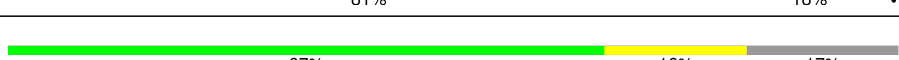
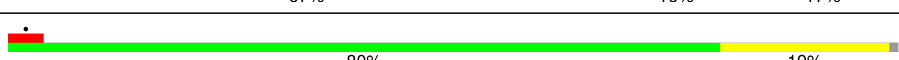
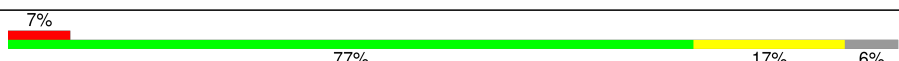
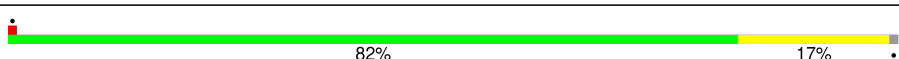
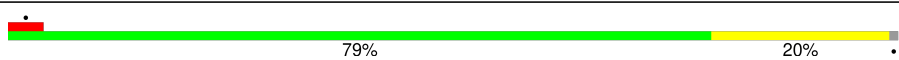



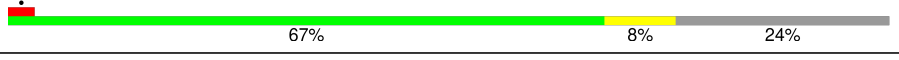
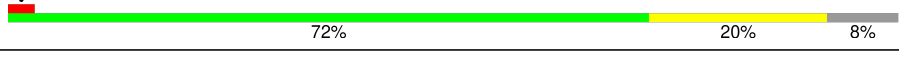
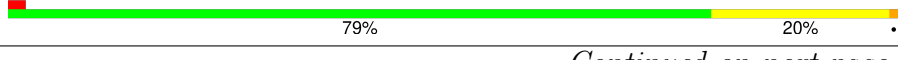

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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

Mol	Chain	Length	Quality of chain
1	A1	270	
2	B1	266	
3	C1	192	

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Mol	Chain	Length	Quality of chain
4	D1	214	 7% 79% 17%
5	E1	178	 7% 78% 19%
6	F1	211	 82% 16%
7	G1	217	 56% 8% 36%
8	H1	204	 73% 27%
9	A2	4731	 39% 33% 7% 22%
10	B2	121	 56% 40%
11	C2	174	 49% 33% 7% 10%
12	D2	257	 5% 73% 25%
13	E2	403	 5% 81% 19%
14	F2	419	 73% 14% 12%
15	G2	297	 79% 19%
16	H2	296	 58% 16% 25%
17	I2	203	 81% 18%
18	J2	184	 67% 16% 17%
19	K2	188	 80% 19%
20	L2	196	 7% 77% 17% 6%
21	M2	176	 82% 17%
22	N2	160	 79% 20%
23	O2	128	 69% 10% 21%
24	P2	140	 5% 71% 21% 8%
25	Q2	157	 25% 67% 8% 24%
26	R2	156	 67% 8% 24%
27	S2	145	 72% 20% 8%
28	T2	136	 79% 20%

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Mol	Chain	Length	Quality of chain
29	U2	148	81% 18%
30	V2	160	58% 15% 28%
31	W2	115	58% 23% 18%
32	X2	125	61% 25% 14%
33	Y2	135	77% 18% 5%
34	Z2	110	85% 14%
35	a2	117	79% 18%
36	b2	123	83% 15%
37	c2	105	84% 12%
38	d2	97	49% 39% 11%
39	e2	70	77% 20%
40	f2	51	78% 20%
41	g2	128	36% 5% 59%
42	h2	25	84% 12%
43	i2	106	77% 20%
44	j2	92	76% 21%
45	k2	137	71% 20% 9%
46	m2	1871	40% 44% 8% 8%
47	n2	75	37% 44% 19%
48	p2	264	64% 17% 19%
49	q2	243	77% 16% 7%
50	r2	263	76% 24%
51	w2	158	78% 18%
52	z2	135	86% 13%
53	o2	295	53% 19% 27%

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Mol	Chain	Length	Quality of chain
54	s2	204	
55	v2	165	
56	x2	145	
57	y2	146	
58	A3	152	
59	B3	145	
60	C3	119	
61	D3	83	
62	E3	143	
63	F3	115	
64	G3	69	
65	H3	56	
66	I3	317	
67	J3	293	
68	K3	249	
69	L3	194	
70	M3	132	
71	N3	151	
72	O3	151	
73	P3	130	
74	Q3	133	
75	R3	125	
76	S3	84	
77	T3	133	
78	U3	156	

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Mol	Chain	Length	Quality of chain
79	m	858	
80	j	317	
81	k	165	
82	A	386	
83	t	194	
84	u	208	
85	L1	217	

2 Entry composition [i](#)

There are 89 unique types of molecules in this entry. The entry contains 227065 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A1	222	1851	1190	356	297	8	1	0

- Molecule 2 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B1	241	1934	1233	373	324	4	1	0

- Molecule 3 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C1	190	1519	956	284	273	6	0	0

- Molecule 4 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D1	208	1690	1073	327	278	12	0	0

- Molecule 5 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E1	174	1397	880	260	251	6	0	0

- Molecule 6 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F1	207	1676	1048	344	280	4	0	0

- Molecule 7 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G1	139	1143	732	221	183	7	0	0

- Molecule 8 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H1	203	1701	1072	359	266	4	0	0

- Molecule 9 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	A2	3707	79546	35474	14505	25861	3706	0	0

- Molecule 10 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
10	B2	120	2558	1141	456	842	119	0	0

- Molecule 11 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	C2	156	3315	1481	585	1094	155	0	0

- Molecule 12 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	D2	251	1921	1204	393	318	6	0	0

- Molecule 13 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	E2	402	3238	2060	609	555	14	0	0

- Molecule 14 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F2	367	Total	C	N	O	S	0	0
			2928	1842	583	488	15		

- Molecule 15 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G2	293	Total	C	N	O	S	0	0
			2385	1506	440	425	14		

- Molecule 16 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H2	221	Total	C	N	O	S	0	0
			1789	1145	342	298	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I2	201	Total	C	N	O	S	0	0
			1640	1055	320	259	6		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J2	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K2	186	Total	C	N	O	S	0	0
			1511	946	313	248	4		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L2	184	Total	C	N	O	S	0	0
			1542	955	332	246	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	M2	175	1450	924	283	233	10	0	0

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	N2	159	1298	823	253	216	6	0	0

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	O2	101	825	529	144	150	2	0	0

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	P2	129	969	613	182	169	5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Q2	119	974	610	201	159	4	0	0

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	R2	118	967	618	181	167	1	0	0

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	S2	134	1115	700	226	186	3	0	0

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	T2	135	1107	714	208	182	3	0	0

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	U2	147	1164	736	239	185	4	0	0

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	V2	116	936	591	196	144	5	0	0

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	W2	94	732	465	130	131	6	0	0

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	X2	107	888	560	171	155	2	0	0

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Y2	128	1053	667	216	165	5	0	0

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Z2	109	876	555	174	143	4	0	0

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a2	114	Total	C	N	O	S	0	0
			906	565	187	148	6		

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b2	120	Total	C	N	O	S	0	0
			1001	634	201	165	1		

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c2	102	Total	C	N	O	S	0	0
			829	517	173	134	5		

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d2	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e2	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f2	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g2	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h2	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i2	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j2	89	Total	C	N	O	S	0	0
			694	436	133	118	7		

- Molecule 45 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k2	125	Total	C	N	O	S	0	0
			1001	621	207	168	5		

- Molecule 46 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m2	1723	Total	C	N	O	P	0	0
			36795	16430	6601	12042	1722		

- Molecule 47 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n2	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p2	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q2	226	Total	C	N	O	S	0	0
			1756	1119	316	314	7		

- Molecule 50 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r2	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 51 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w2	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 52 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	z2	134	Total	C	N	O	S	0	0
			1080	678	201	197	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	o2	214	Total	C	N	O	S	0	0
			1694	1077	297	312	8		

- Molecule 54 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	s2	189	Total	C	N	O	S	0	0
			1496	934	285	270	7		

- Molecule 55 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v2	96	Total	C	N	O	S	0	0
			811	528	146	132	5		

- Molecule 56 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x2	130	Total	C	N	O	S	0	0
			1073	681	205	180	7		

- Molecule 57 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y2	144	Total	C	N	O	S	0	0
			1143	726	216	198	3		

- Molecule 58 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	A3	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 59 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B3	141	Total	C	N	O	S	0	0
			1104	691	215	196	2		

- Molecule 60 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	C3	102	Total	C	N	O	S	0	0
			807	507	153	143	4		

- Molecule 61 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	D3	83	Total	C	N	O	S	0	0
			638	392	119	122	5		

- Molecule 62 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	E3	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 63 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	F3	100	Total	C	N	O	S	1	0
			811	506	169	131	5		

- Molecule 64 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	G3	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 65 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	H3	54	Total	C	N	O	S	0	0
			455	284	93	73	5		

- Molecule 66 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	I3	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 67 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	J3	222	Total	C	N	O	S	0	0
			1725	1116	298	302	9		

- Molecule 68 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	K3	227	Total	C	N	O	S	0	0
			1840	1149	367	317	7		

- Molecule 69 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	L3	184	Total	C	N	O	S	0	0
			1518	964	305	247	2		

- Molecule 70 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	M3	122	Total	C	N	O	S	0	0
			942	593	164	177	8		

- Molecule 71 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	N3	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 72 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	O3	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
73	P3	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Q3	129	Total	C	N	O	S	0	0
			1049	662	206	176	5		

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	R3	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 76 is a protein called 40S ribosomal protein S27-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	S3	83	Total	C	N	O	S	0	0
			652	409	121	115	7		

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	T3	55	Total	C	N	O	S	0	0
			438	271	95	71	1		

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	U3	62	Total	C	N	O	S	0	0
			505	317	96	85	7		

- Molecule 79 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	m	824	Total	C	N	O	S	0	0
			6433	4087	1104	1199	43		

- Molecule 80 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	j	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 81 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	k	153	Total	C	N	O	S	0	0
			1159	721	218	217	3		

- Molecule 82 is a protein called Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	A	61	Total	C	N	O	0	0
			486	289	94	103		

- Molecule 83 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	t	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 84 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
84	u	206	1686	1058	332	291	5	0	0

- Molecule 85 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
85	L1	206	1660	1061	300	291	8	0	0

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	d2	1	Total	Zn	0
			1	1	
86	g2	1	Total	Zn	0
			1	1	
86	i2	1	Total	Zn	0
			1	1	
86	j2	1	Total	Zn	0
			1	1	
86	F3	1	Total	Zn	0
			1	1	
86	H3	1	Total	Zn	0
			1	1	
86	U3	1	Total	Zn	0
			1	1	

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

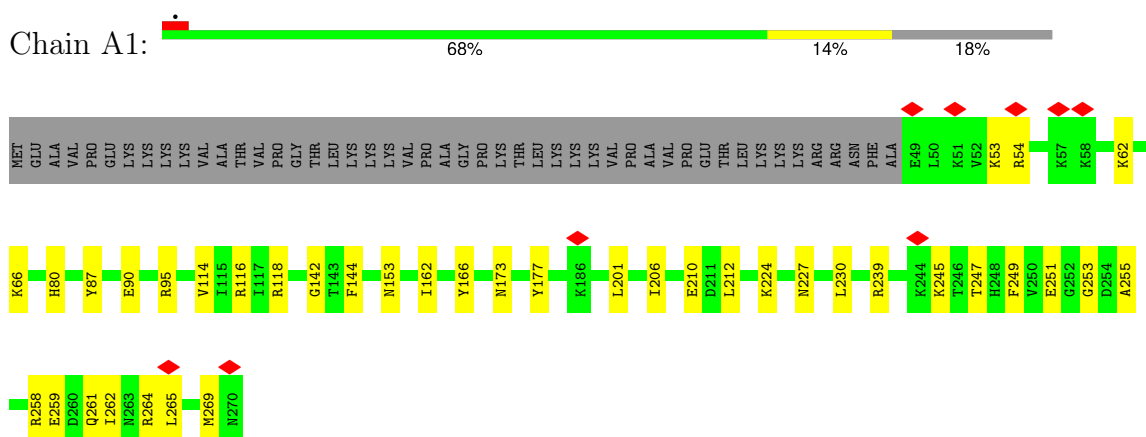
Mol	Chain	Residues	Atoms		AltConf
87	H3	1	Total	Mg	0
			1	1	

- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

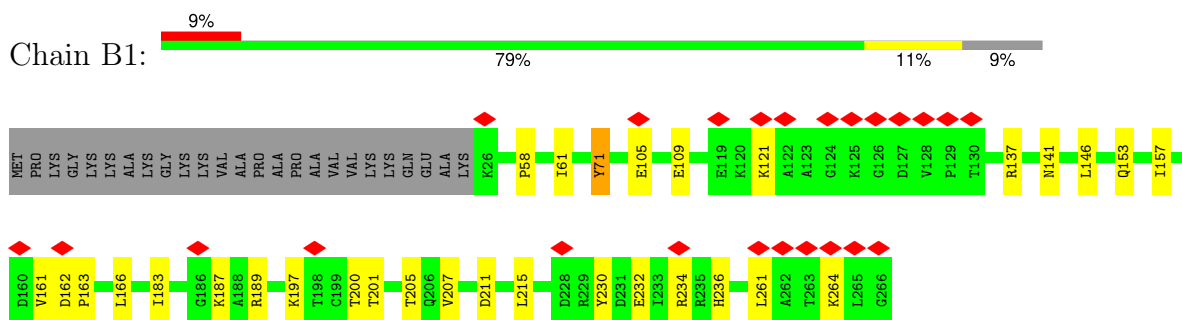
3 Residue-property plots [i](#)

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.

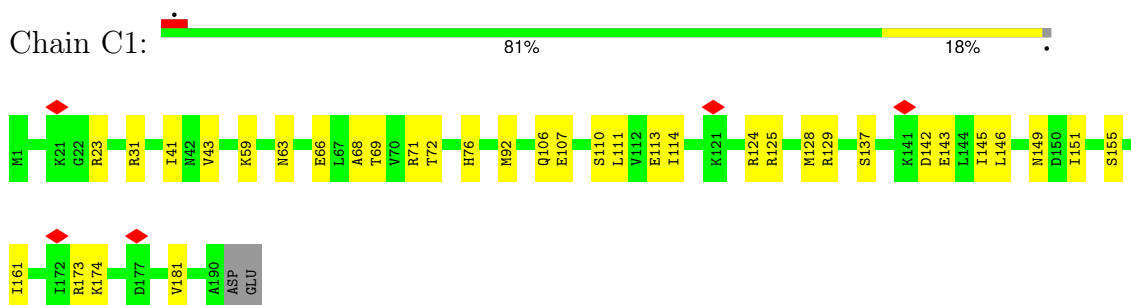
- Molecule 1: 60S ribosomal protein L7



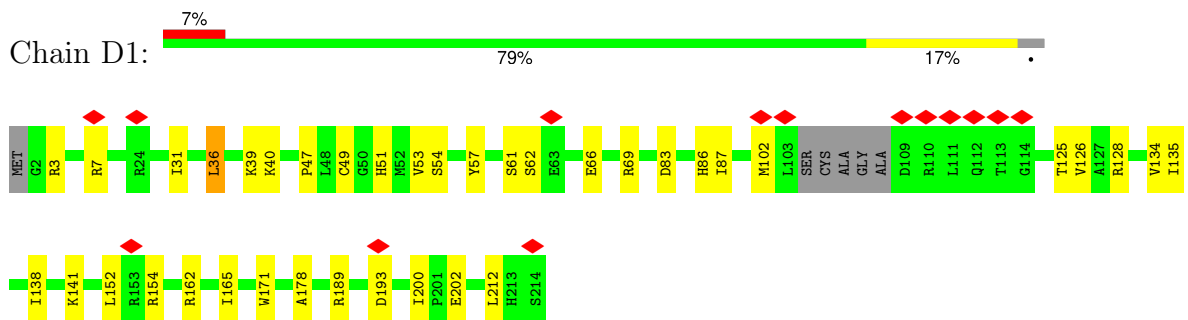
- Molecule 2: 60S ribosomal protein L7a



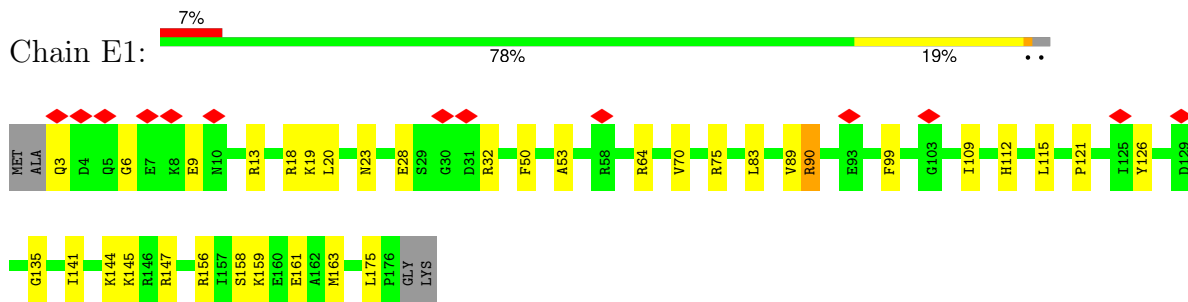
- Molecule 3: 60S ribosomal protein L9



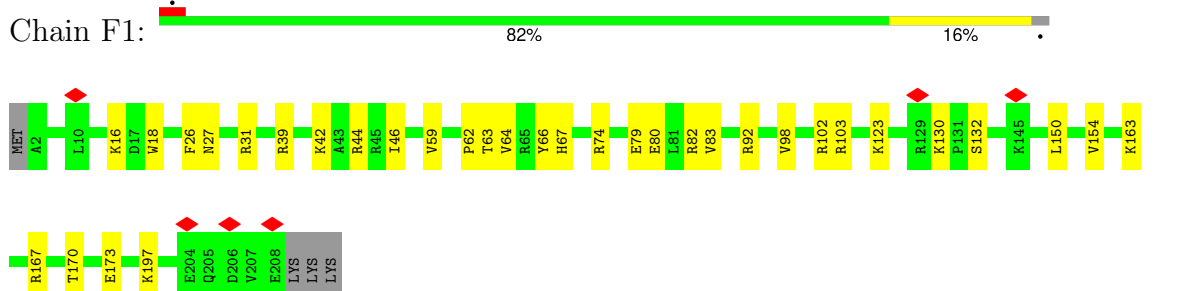
• Molecule 4: 60S ribosomal protein L10-like



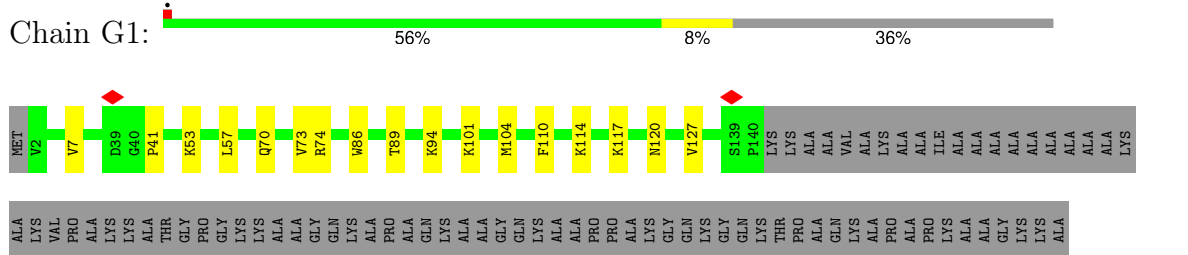
• Molecule 5: 60S ribosomal protein L11



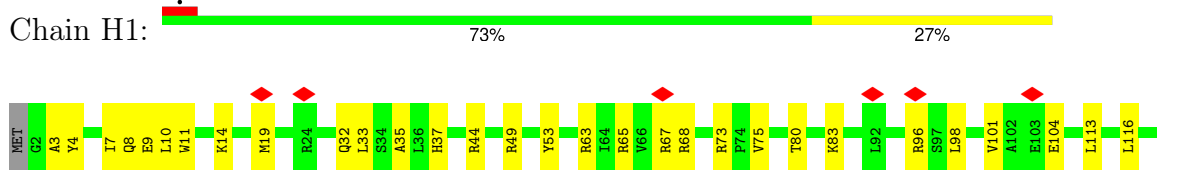
• Molecule 6: 60S ribosomal protein L13



• Molecule 7: 60S ribosomal protein L14

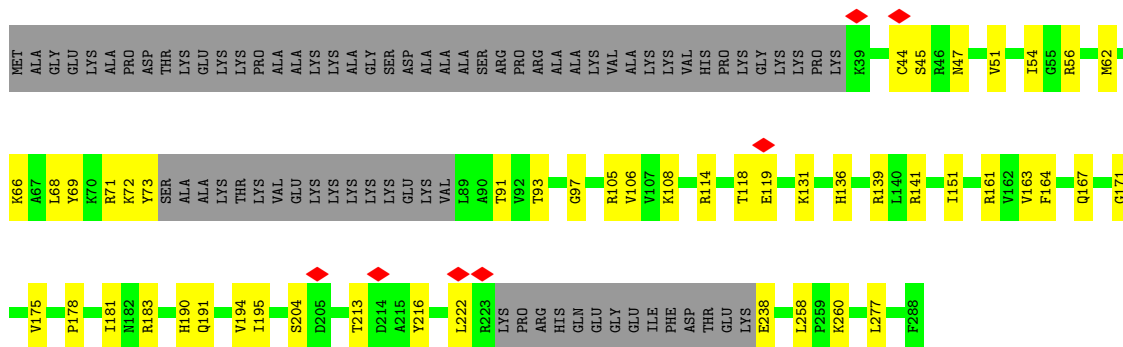


• Molecule 8: 60S ribosomal protein L15

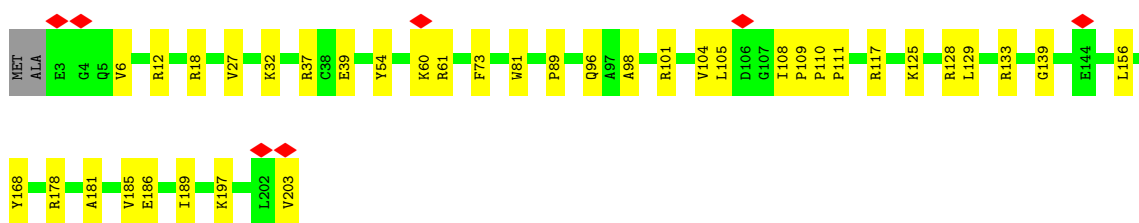
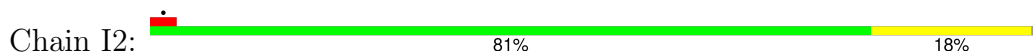


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U2036	G1904	G1824	U1752	G1671	U	G1439	A1337	A1176	C1085	C1015
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G2039	G1906	G1826	U1761	A1673	U1598	G1443	G1339	U1178	G1087	U1017
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G2041	C1908	G1828	G1763	U1678	C1524	A1445	C1348	G1179	G1089	G1019
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A2119	C	G				U1441	G1260	G1260	G1155	G
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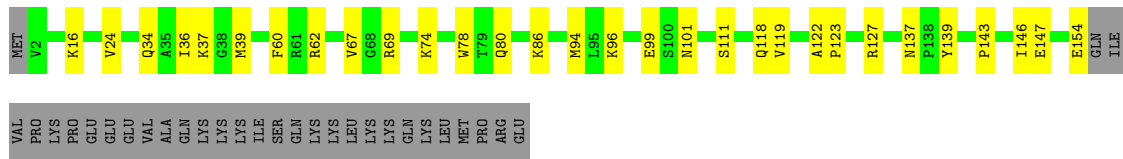
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A3460	G3464	A3546	U3620	G3746	U3824	G3915	U3996	U3996	A4163	A4242	A4339	G4434
A3461	G3465	G3547	A3621	A3747	G3825	C3916	C3997	C3997	A4164	G4247	A4340	C4435
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A3463	G3468	C3549	A3623	G3749	G3827	G3918	U3999	U3999	G4166	U4249	A4342	C4437
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A3465	U3470	A3551	G3625	C3751	C3829	A3920	C4001	C4001	A4168	G4251	A4344	U4439
A3466	G3471	C3552	G3626	C3752	A3830	A3921	U4002	U4002	A4169	A4252	A4345	C4439
A3467	A3472	G3553	G3627	C3753	G3831	A3922	U4003	U4003	C4170	U4253	A4346	G4440
A3468	A3473	A3554	A3628	G3754	G3832	G3923	U4004	U4004	A4171	A4254	A4347	C4441
A3469	A3474	A3555	G3629	A3755	G3833	G3924	U4005	U4005	C4172	C4255	A4348	G4442
A3470	G3475	A3556	G3630	G3756	G3834	A3925	U4006	U4006	A4173	G4256	A4349	G
A3471	A3477	A3557	C3631	C3757	G3835	A3926	U4007	U4007	C4174	G4257	A4350	G
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A3475	A3482	A3561	C3635	A3761	G3839	A3930	A4101	A4101	C4178	U4272	A4354	G
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A3478	A3485	A3564	C3638	C3764	U3842	A3933	U4104	U4104	U4183	G4275	A4357	G
A3479	A3486	A3565	C3639	A3765	G3843	A3934	U4105	U4105	C4188	A4276	A4358	G
A3480	A3487	A3566	C3640	C3766	U3844	A3935	C4106	C4106	C4189	A4277	A4359	G
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A3521	A3528	A3607	C3681	A3805	U3885	A3976	U4147	U4147	U4230	U4318	A4400	G
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A3525	A3532	A3611	C3685	A3809	U3889	A3980	U4151	U4151	U4234	U4322	A4404	G
A3526	A3533	A3612	C3686	A3810	U3890	A3981	U4152	U4152	U4235	U4323	A4405	G
A3527	A3534	A3613	C3687	A3811	U3891	A3982	U4153	U4153	U4236	U4324	A4406	G
A3528	A3535	A3614	C3688	A3812	U3892	A3983	U4154	U4154	U4237	U4325	A4407	G
A3529	A3536	A3615	C3689	A3813	U3893	A3984	U4155	U4155	U4238	U4326	A4408	G
A3530	A3537	A3616	C3690	A3814	U3894	A3985	U4156	U4156	U4239	U4327	A4409	G
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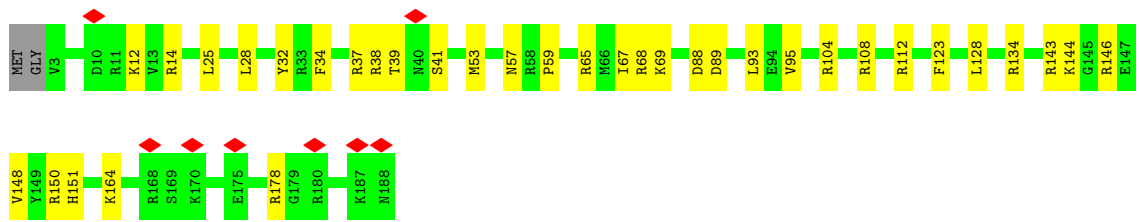
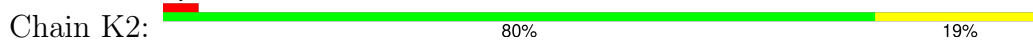
• Molecule 17: 60S ribosomal protein L13a



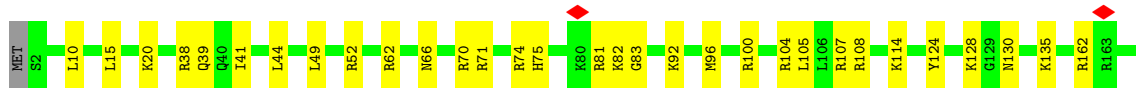
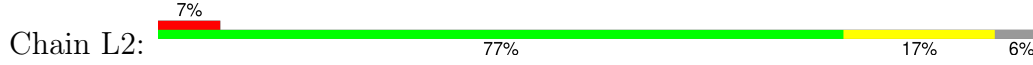
• Molecule 18: 60S ribosomal protein L17

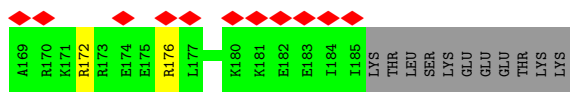


• Molecule 19: 60S ribosomal protein L18

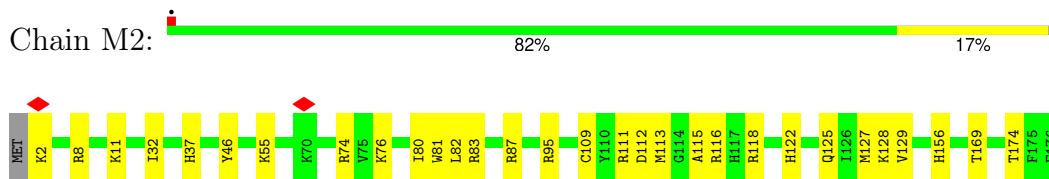


• Molecule 20: 60S ribosomal protein L19

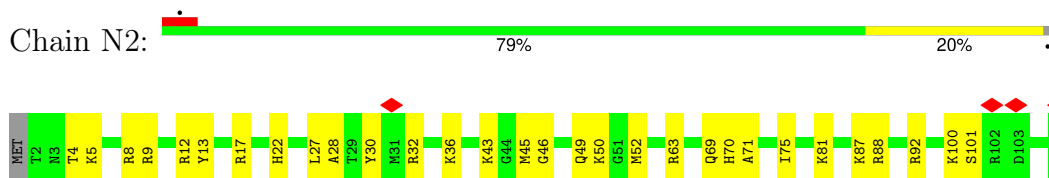




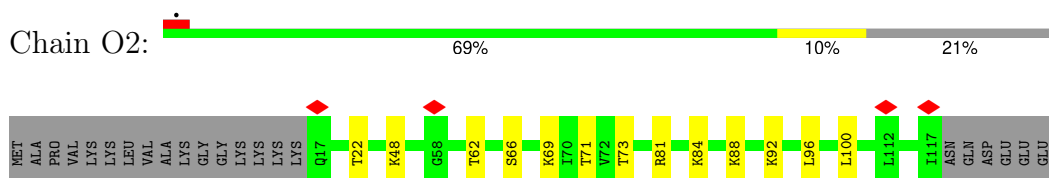
• Molecule 21: 60S ribosomal protein L18a



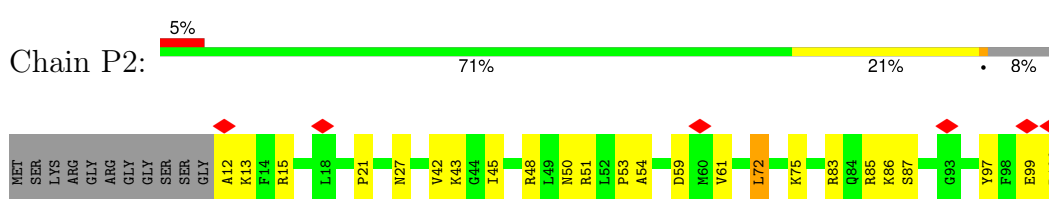
• Molecule 22: 60S ribosomal protein L21



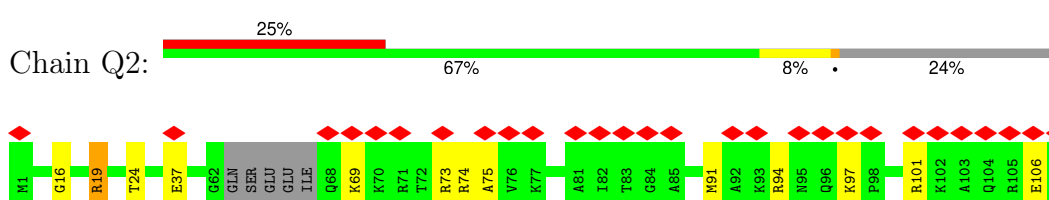
• Molecule 23: 60S ribosomal protein L22



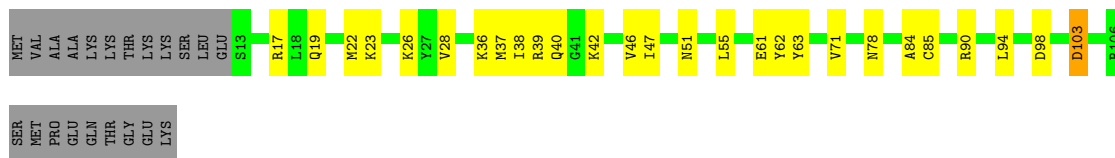
• Molecule 24: 60S ribosomal protein L23



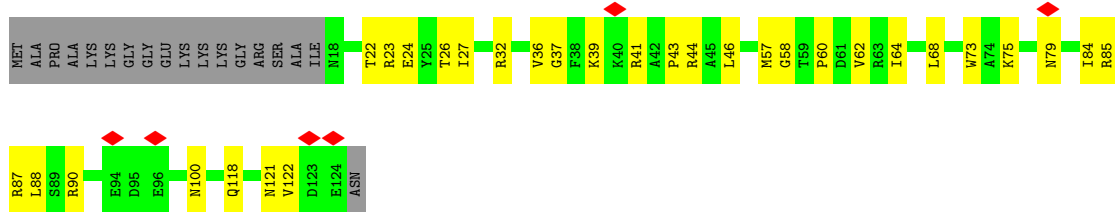
• Molecule 25: 60S ribosomal protein L24



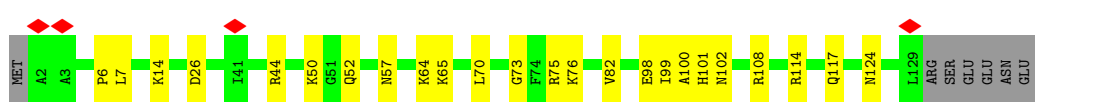
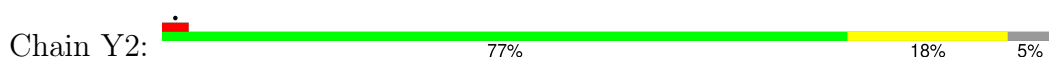
• Molecule 31: 60S ribosomal protein L30



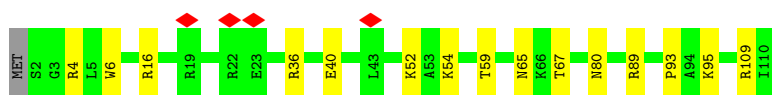
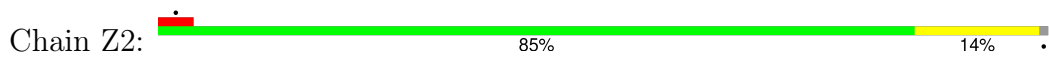
• Molecule 32: 60S ribosomal protein L31



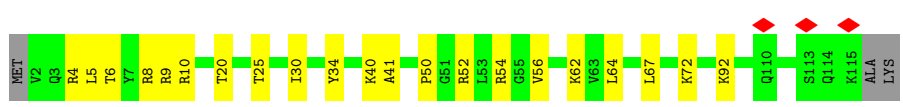
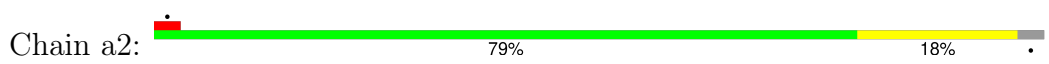
• Molecule 33: 60S ribosomal protein L32



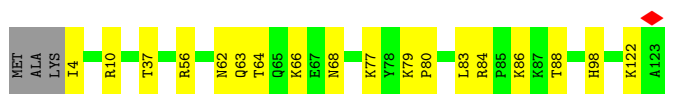
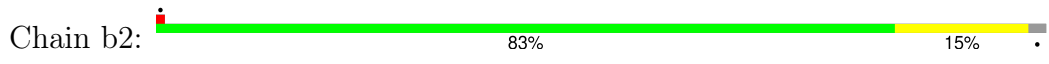
• Molecule 34: 60S ribosomal protein L35a



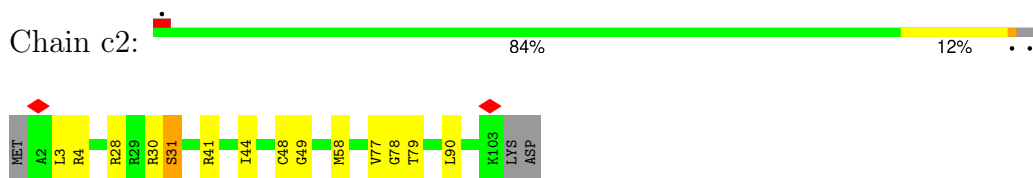
• Molecule 35: 60S ribosomal protein L34



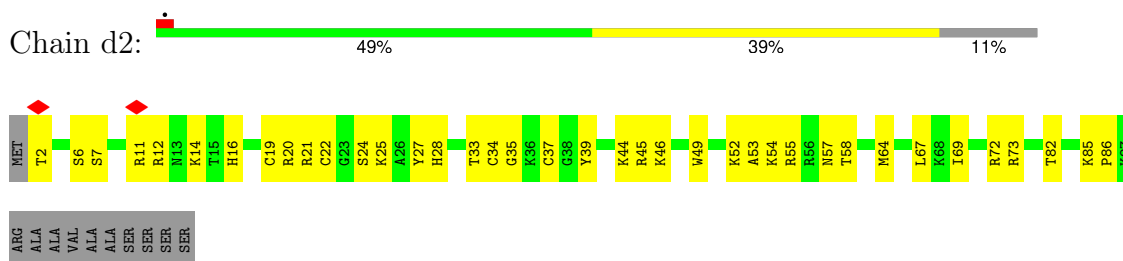
• Molecule 36: 60S ribosomal protein L35



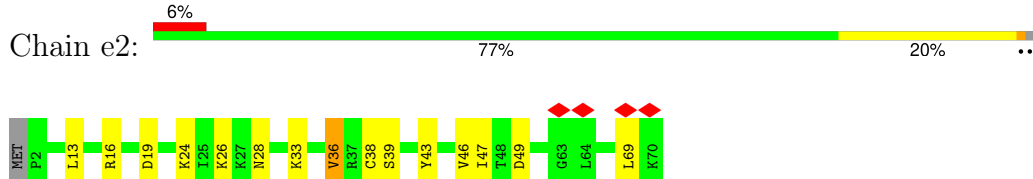
• Molecule 37: 60S ribosomal protein L36



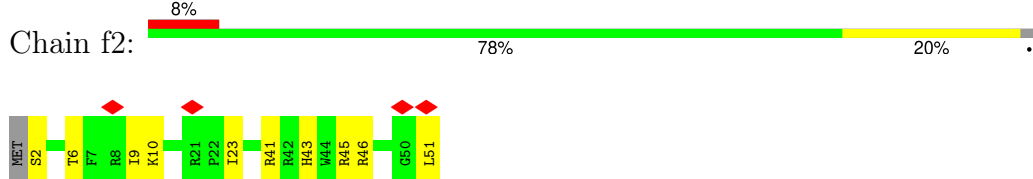
• Molecule 38: 60S ribosomal protein L37



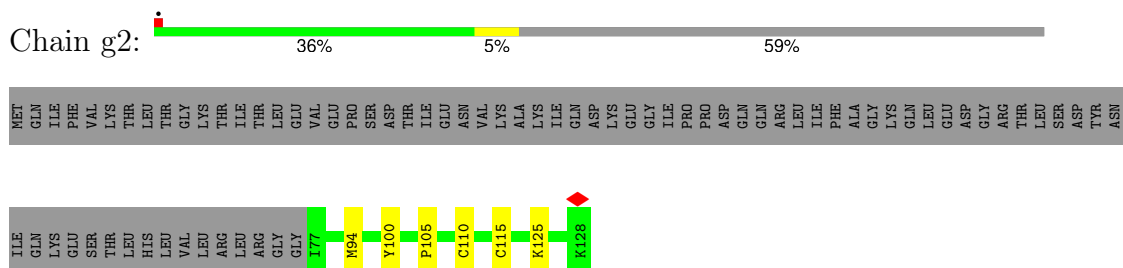
• Molecule 39: 60S ribosomal protein L38



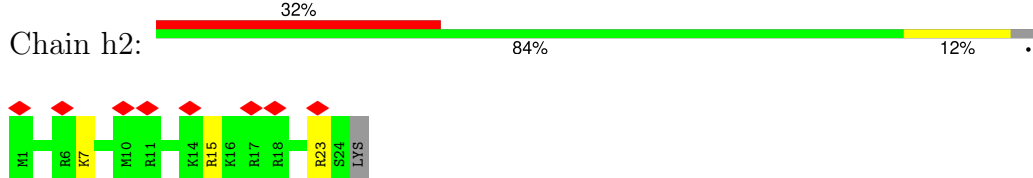
• Molecule 40: 60S ribosomal protein L39

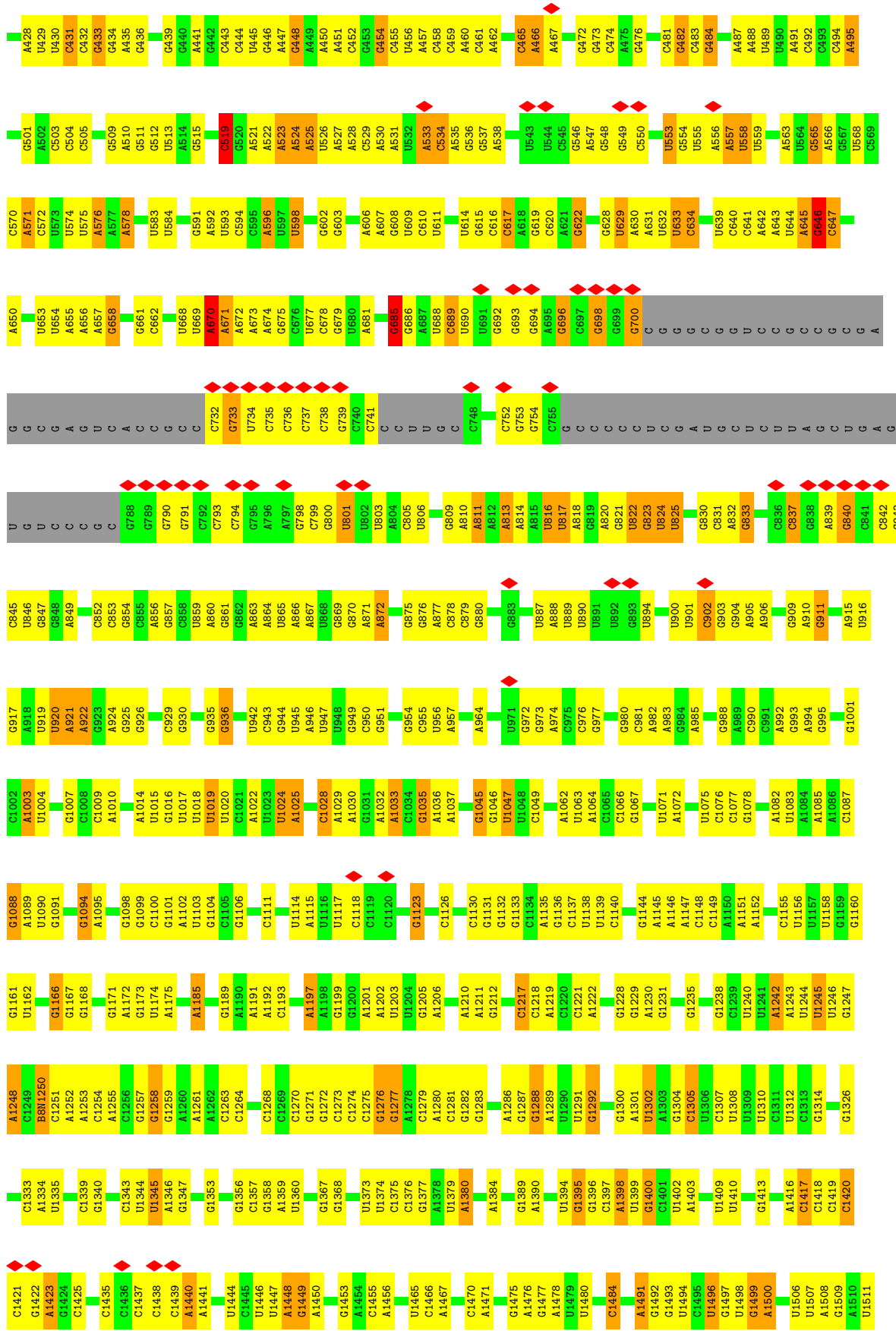


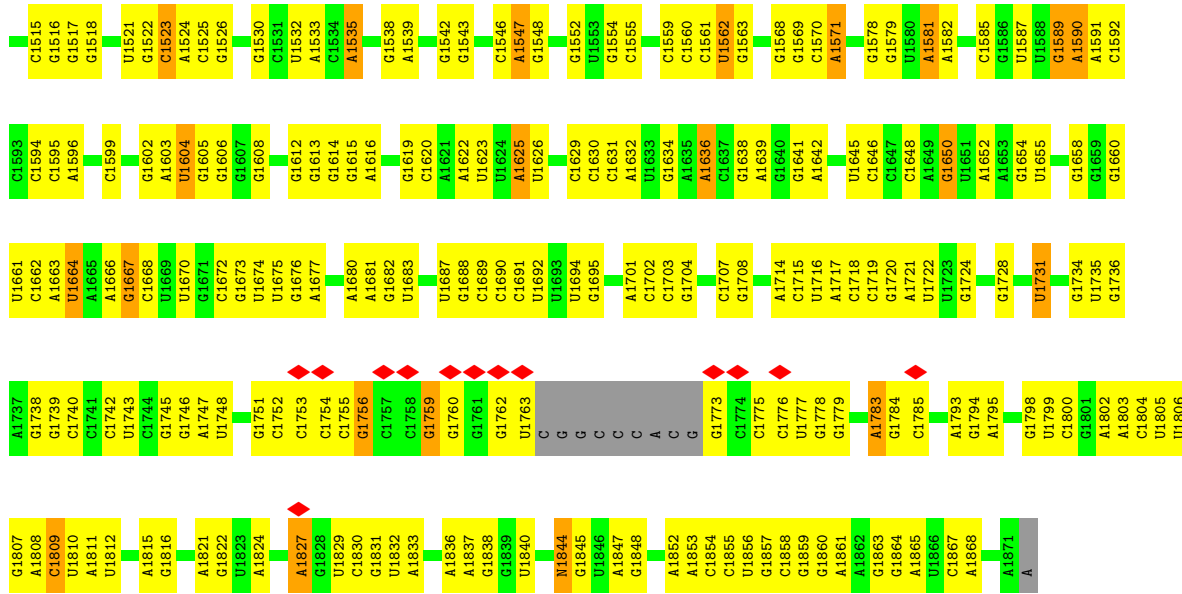
• Molecule 41: Ubiquitin-60S ribosomal protein L40



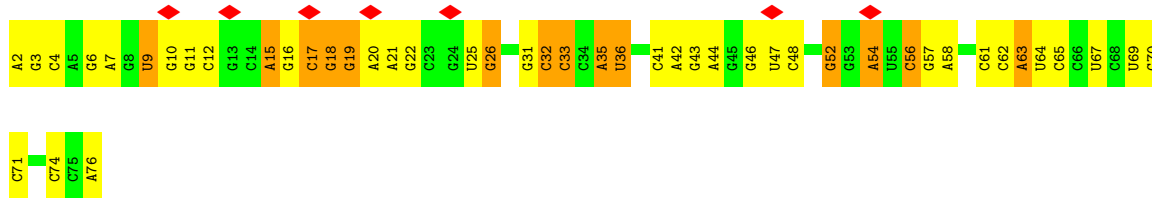
• Molecule 42: 60S ribosomal protein L41



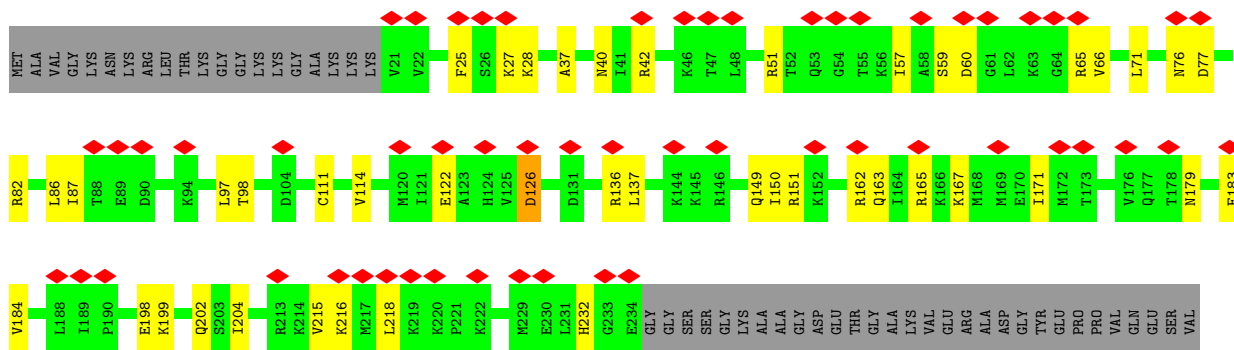




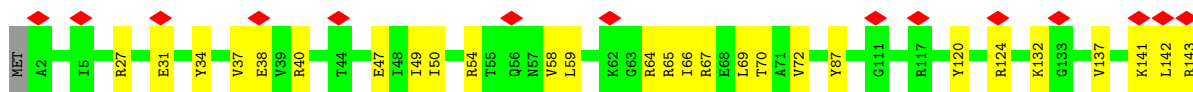
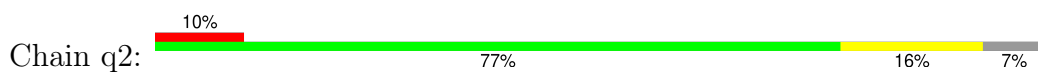
• Molecule 47: tRNA

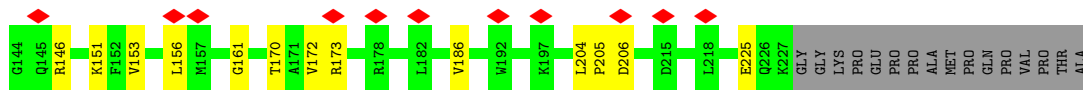


• Molecule 48: 40S ribosomal protein S3a

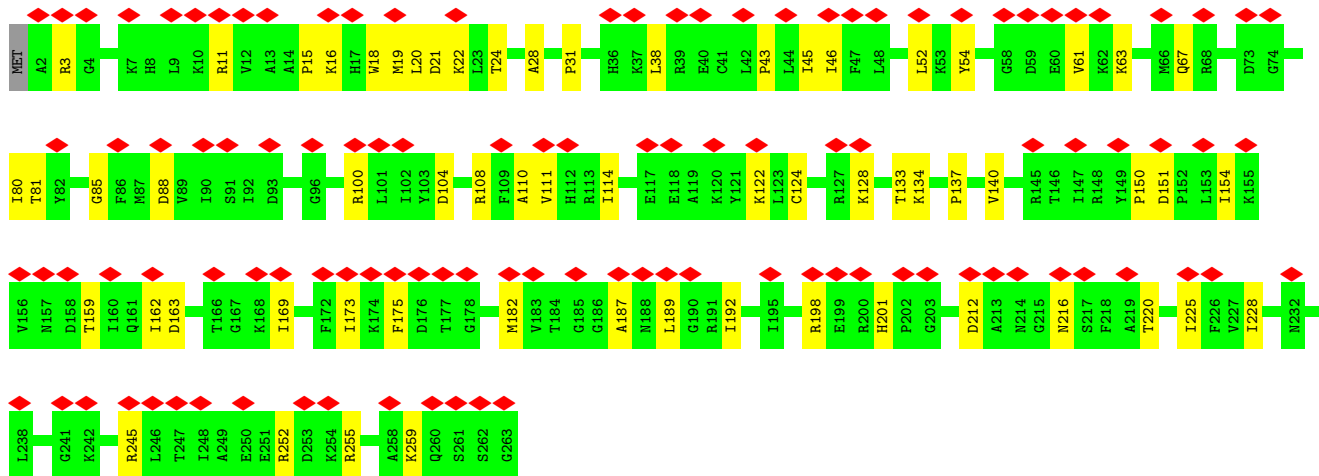
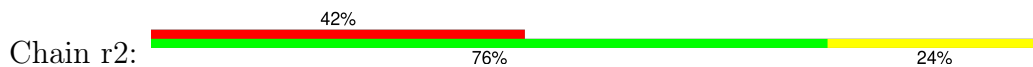


• Molecule 49: 40S ribosomal protein S3

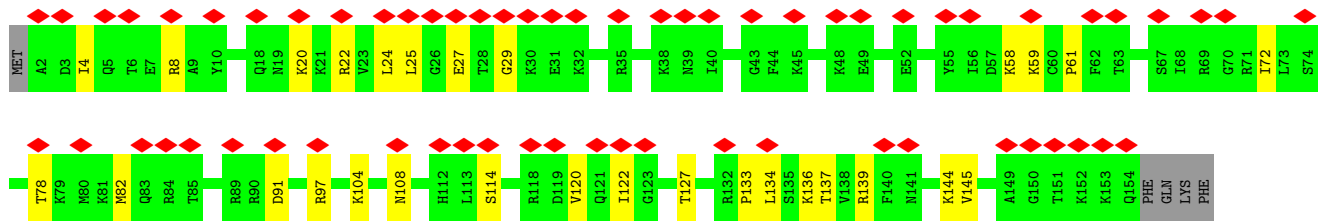
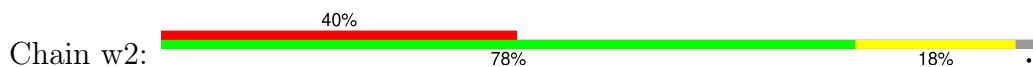




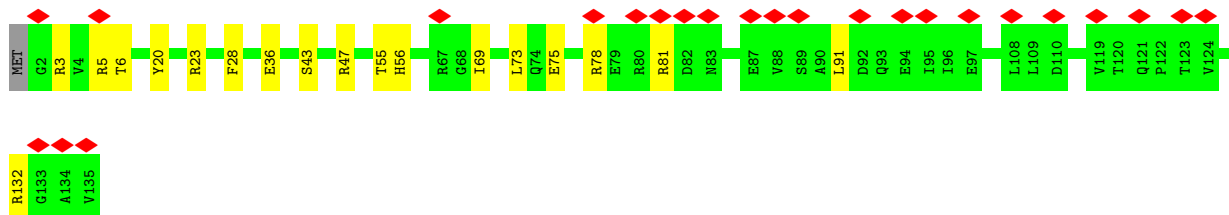
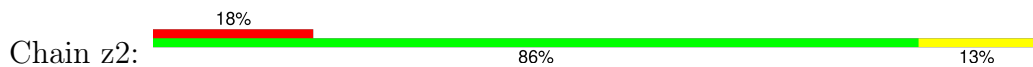
• Molecule 50: 40S ribosomal protein S4, X isoform



• Molecule 51: 40S ribosomal protein S11

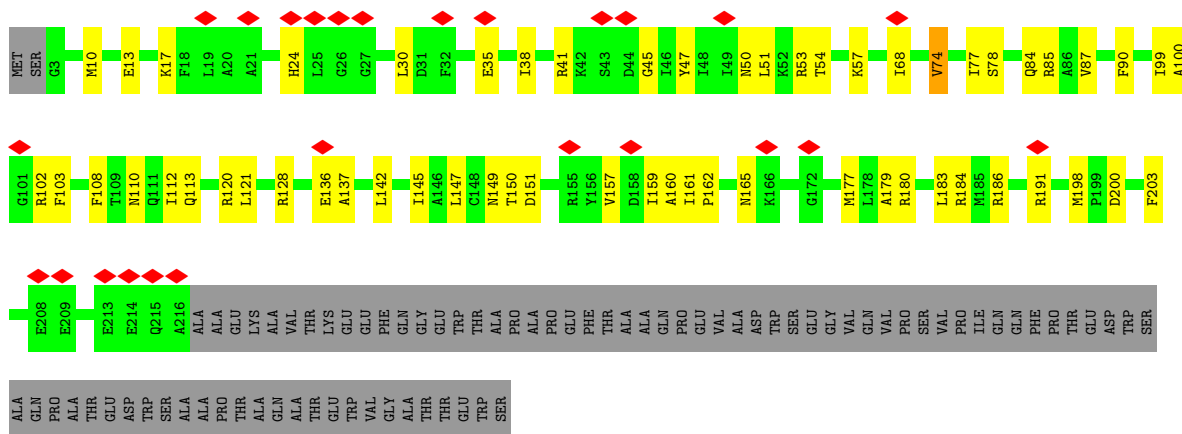


• Molecule 52: 40S ribosomal protein S17

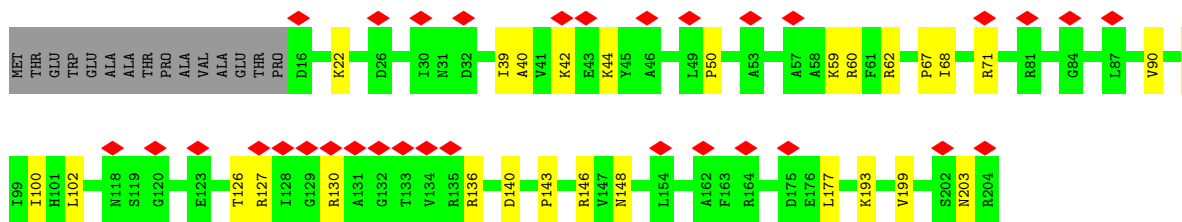
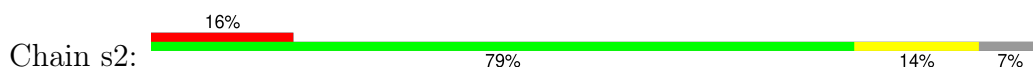


• Molecule 53: 40S ribosomal protein SA

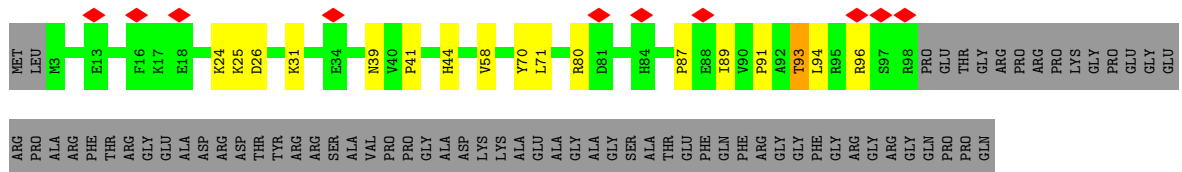




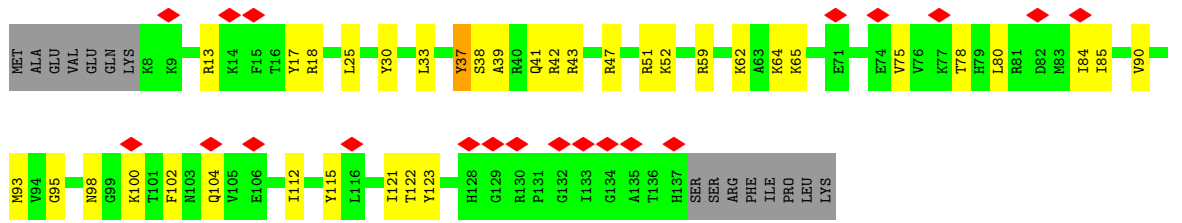
• Molecule 54: 40S ribosomal protein S5



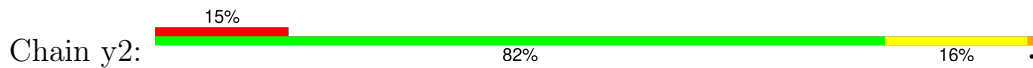
• Molecule 55: 40S ribosomal protein S10

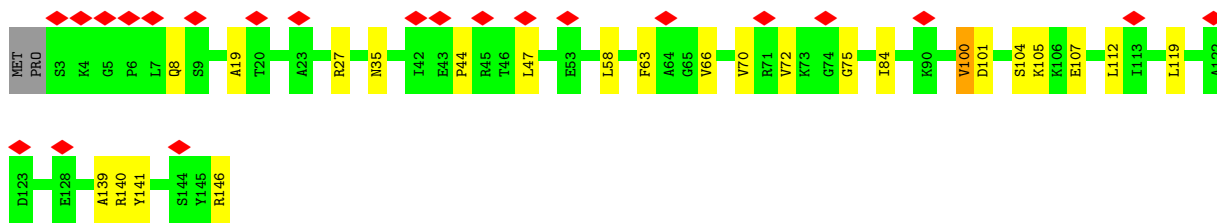


• Molecule 56: 40S ribosomal protein S15

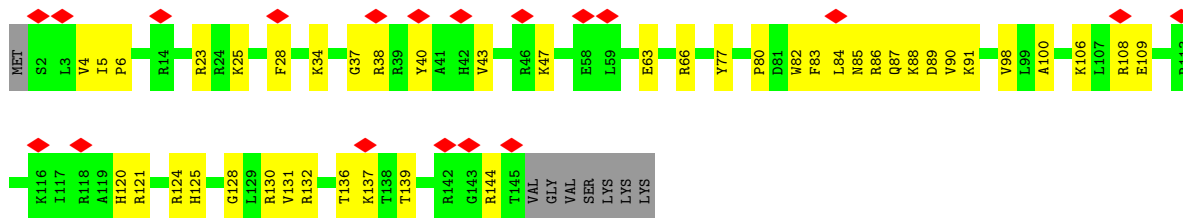


• Molecule 57: 40S ribosomal protein S16

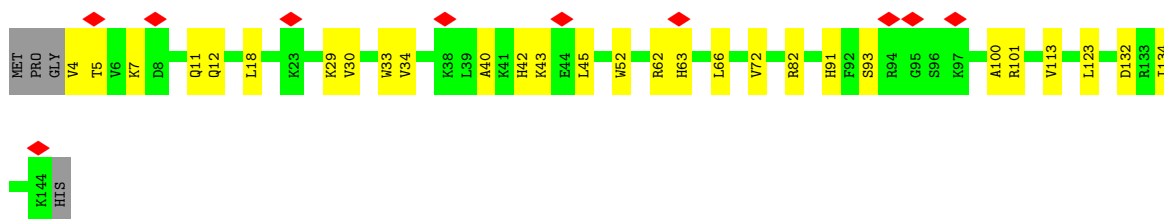
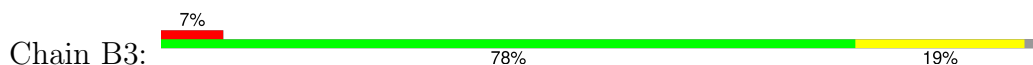




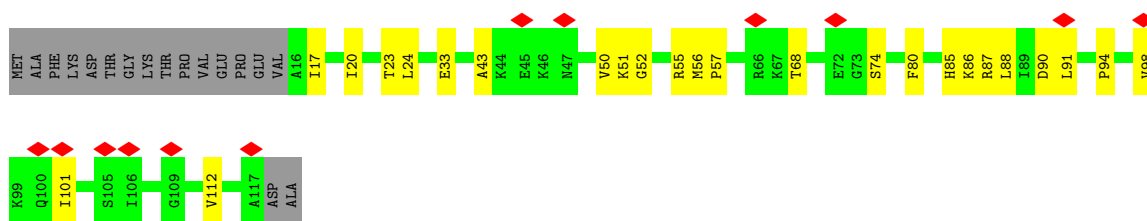
• Molecule 58: 40S ribosomal protein S18



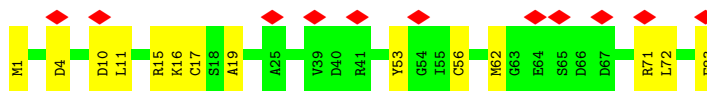
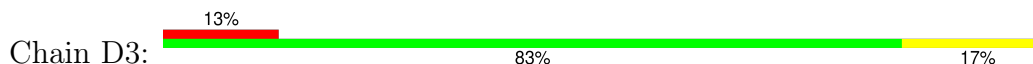
• Molecule 59: 40S ribosomal protein S19



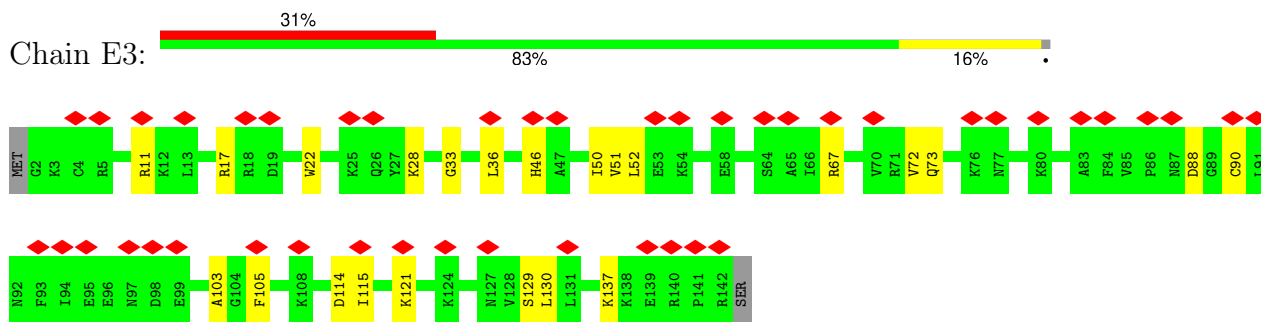
• Molecule 60: 40S ribosomal protein S20



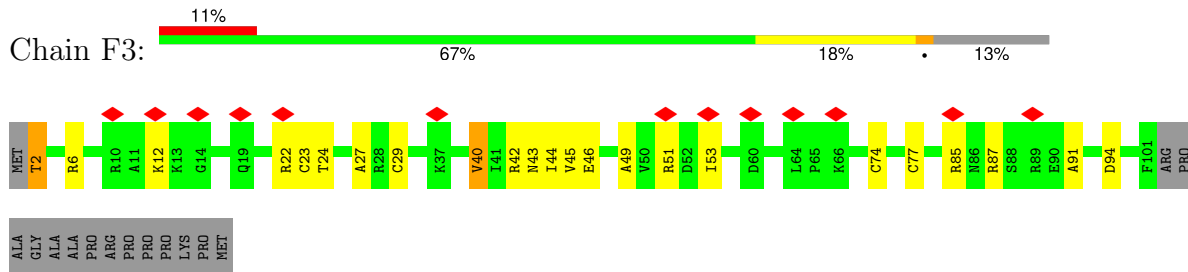
• Molecule 61: 40S ribosomal protein S21



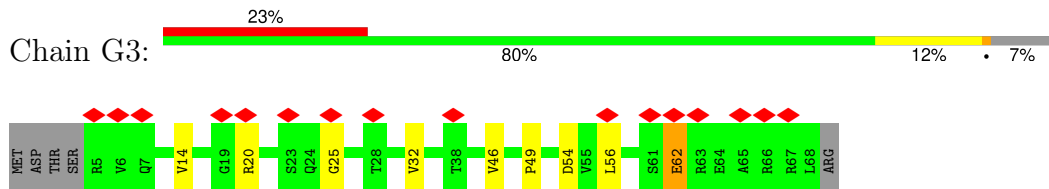
• Molecule 62: 40S ribosomal protein S23



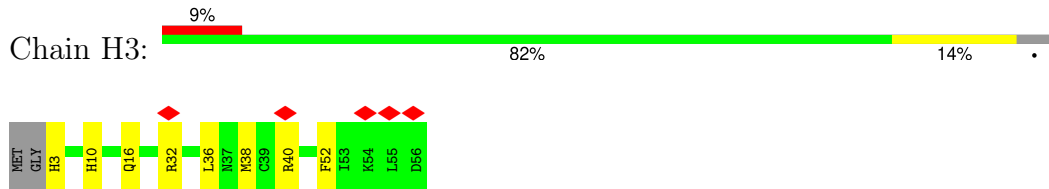
• Molecule 63: 40S ribosomal protein S26



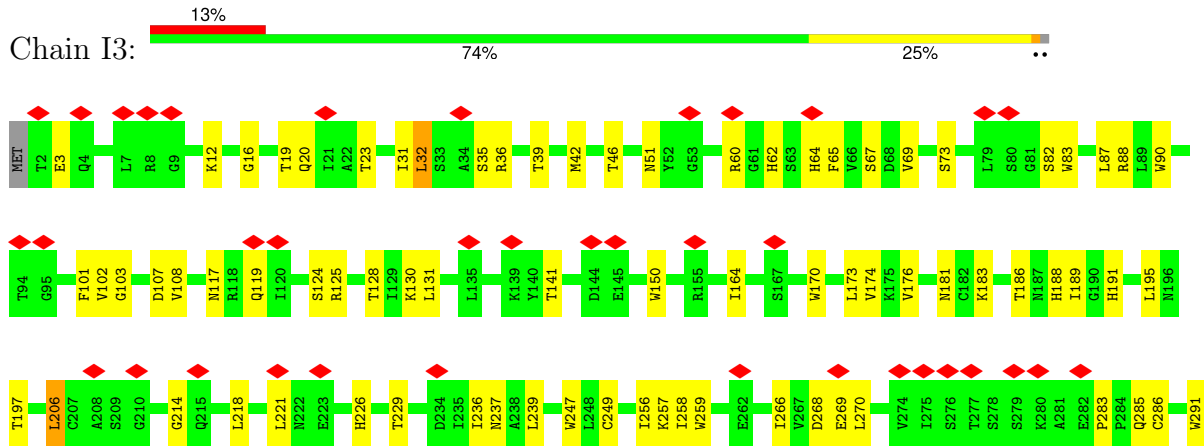
• Molecule 64: 40S ribosomal protein S28

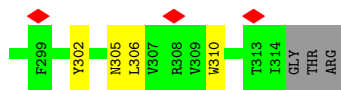


• Molecule 65: 40S ribosomal protein S29

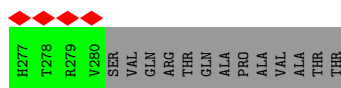
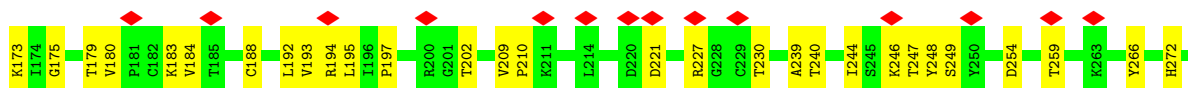
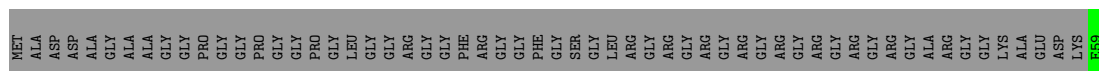


• Molecule 66: Receptor of activated protein C kinase 1

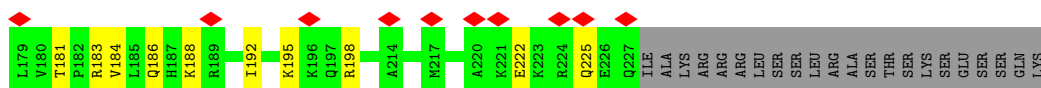
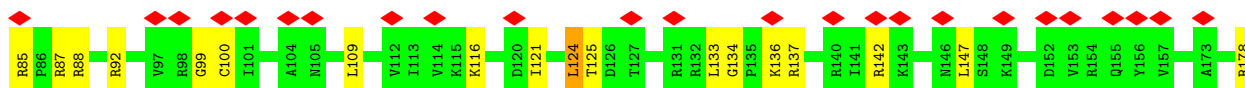
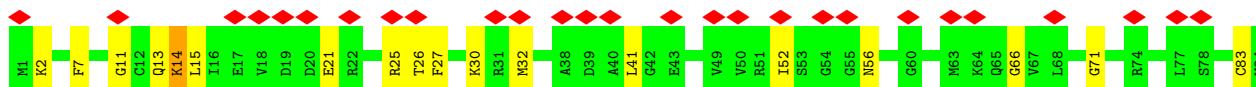




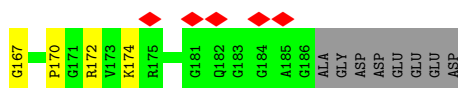
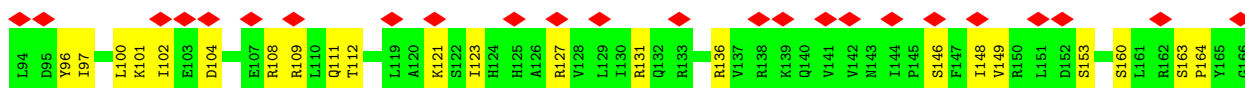
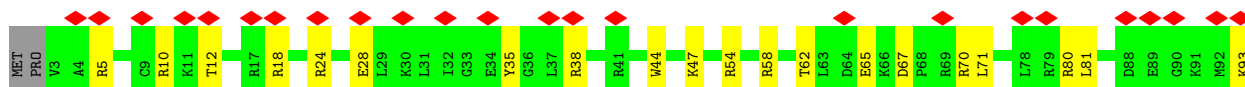
• Molecule 67: 40S ribosomal protein S2



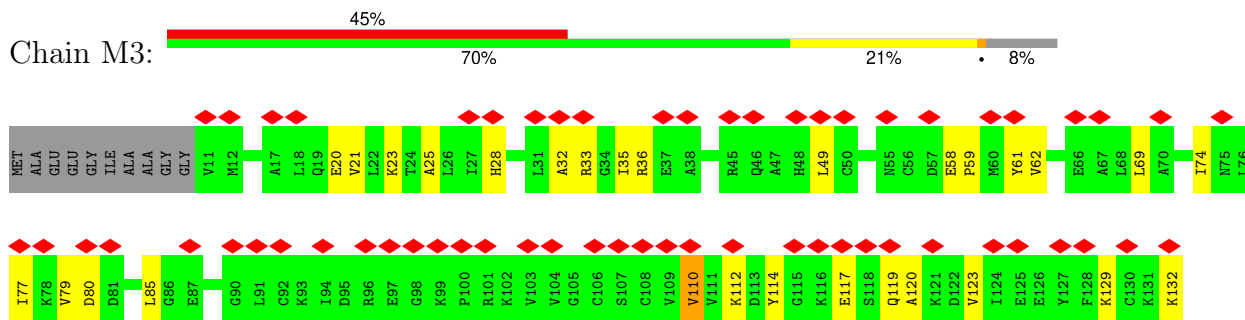
• Molecule 68: 40S ribosomal protein S6



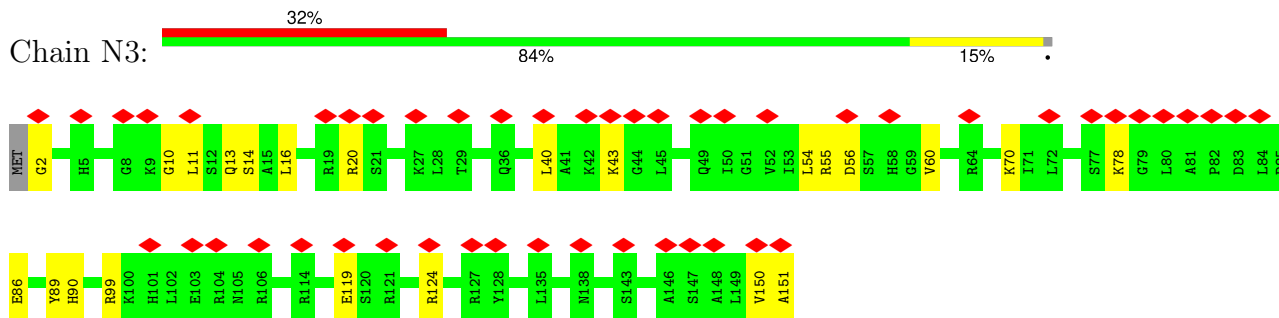
• Molecule 69: 40S ribosomal protein S9



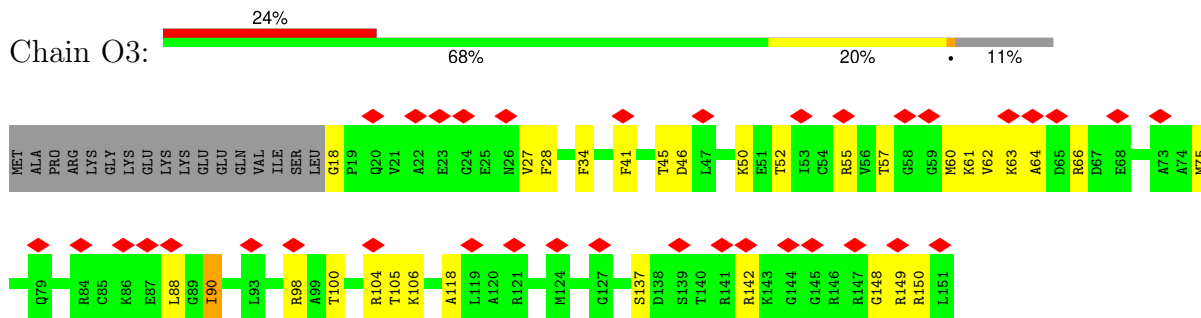
• Molecule 70: 40S ribosomal protein S12



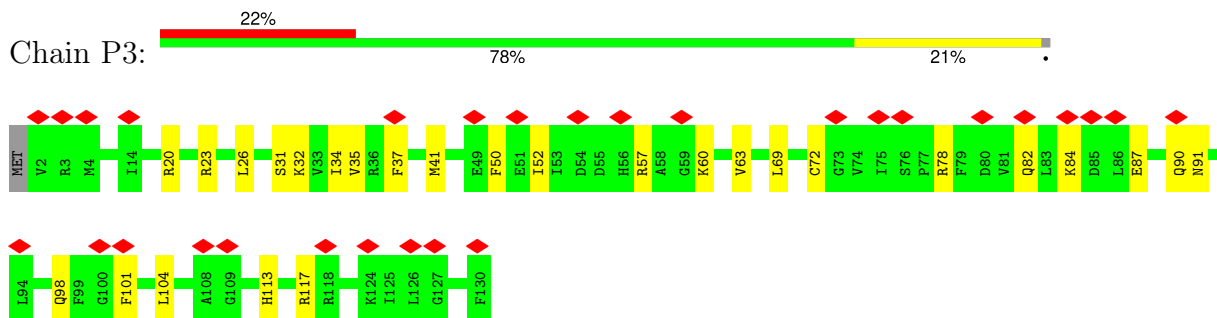
• Molecule 71: 40S ribosomal protein S13



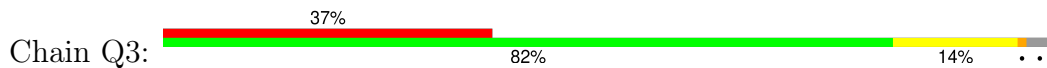
• Molecule 72: 40S ribosomal protein S14

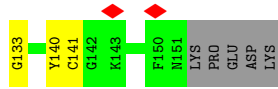


• Molecule 73: 40S ribosomal protein S15a

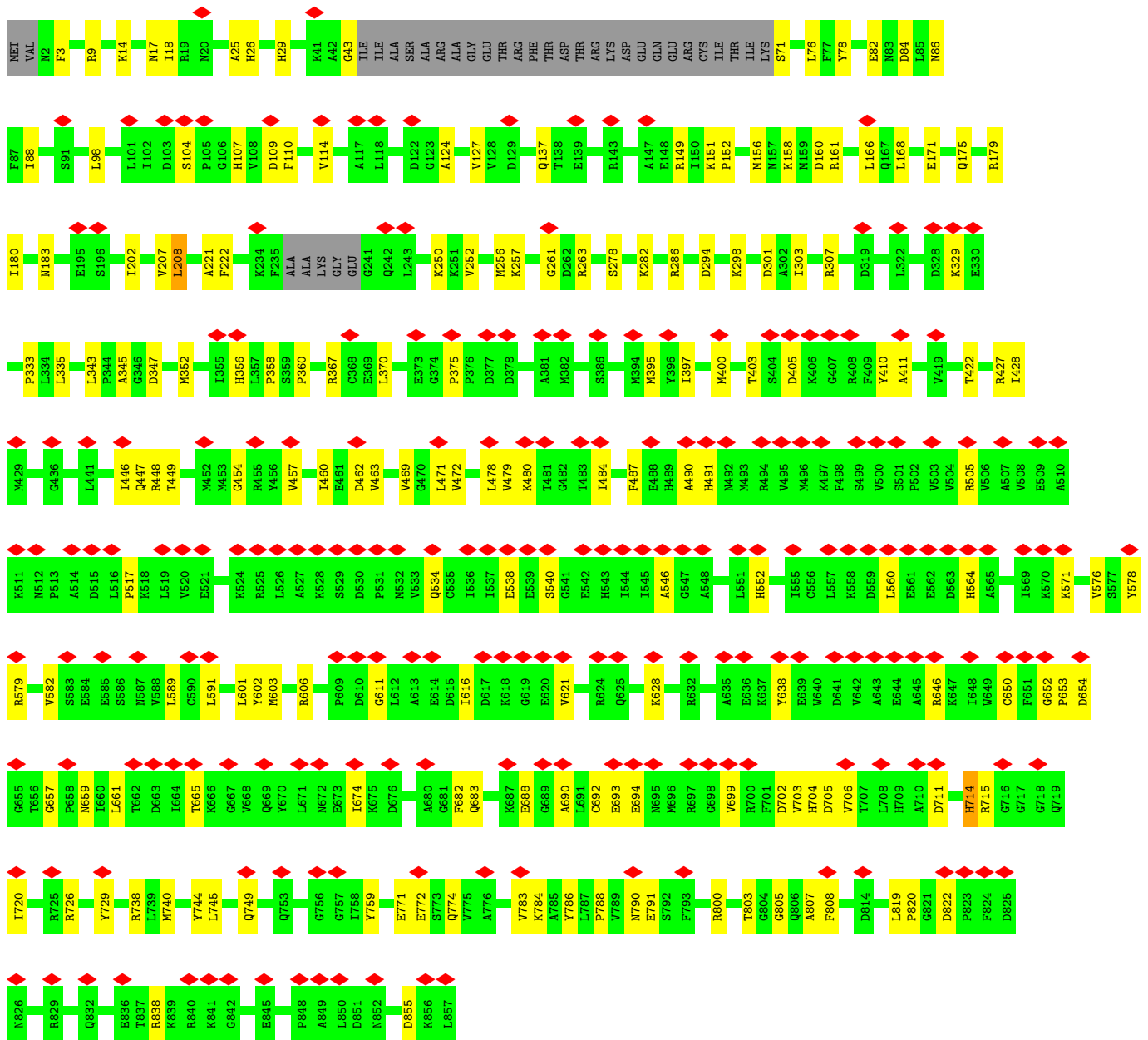
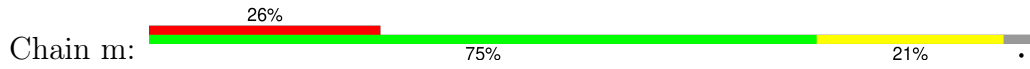


• Molecule 74: 40S ribosomal protein S24





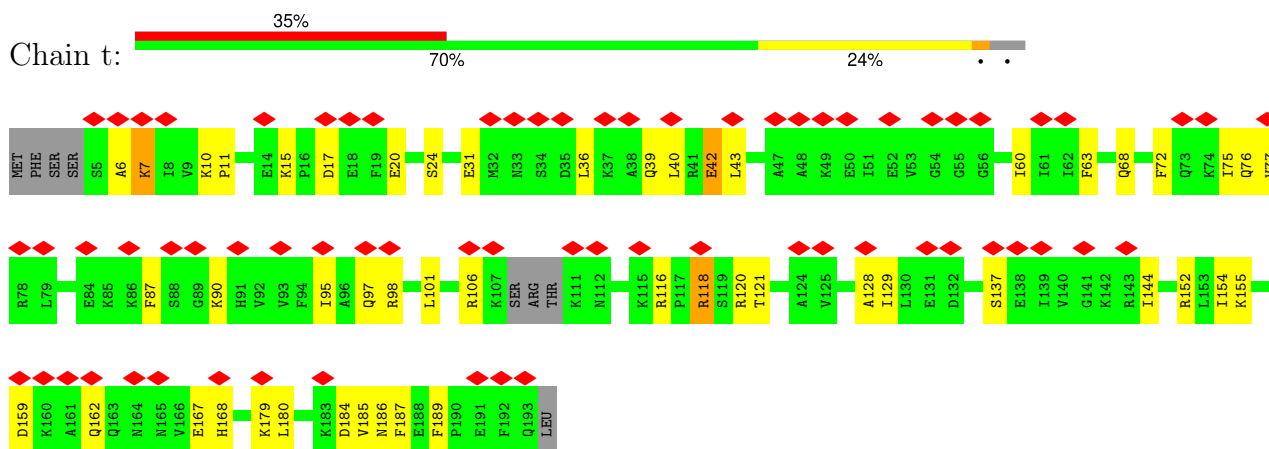
• Molecule 79: Elongation factor 2



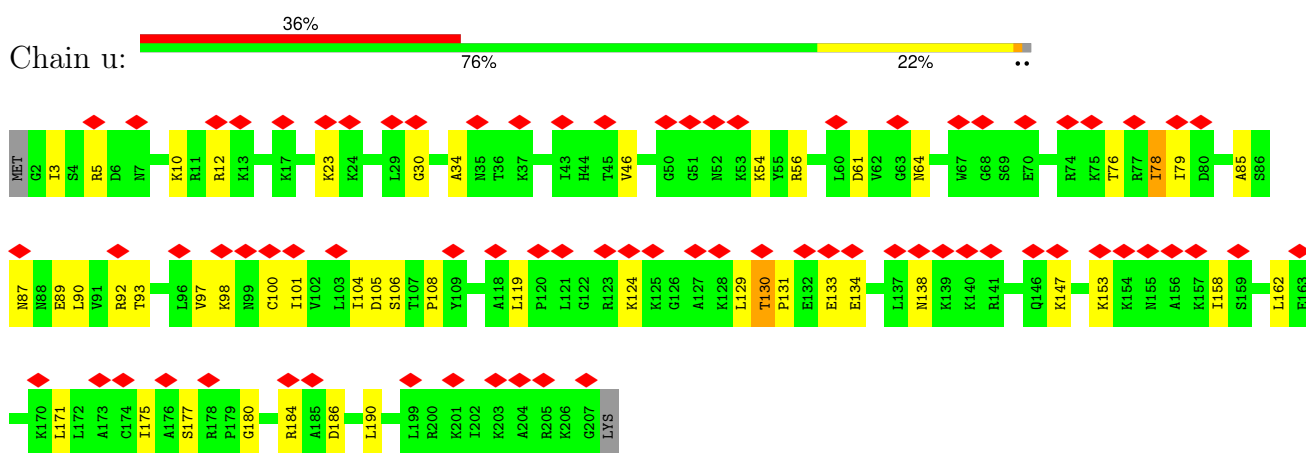
• Molecule 80: 60S acidic ribosomal protein P0



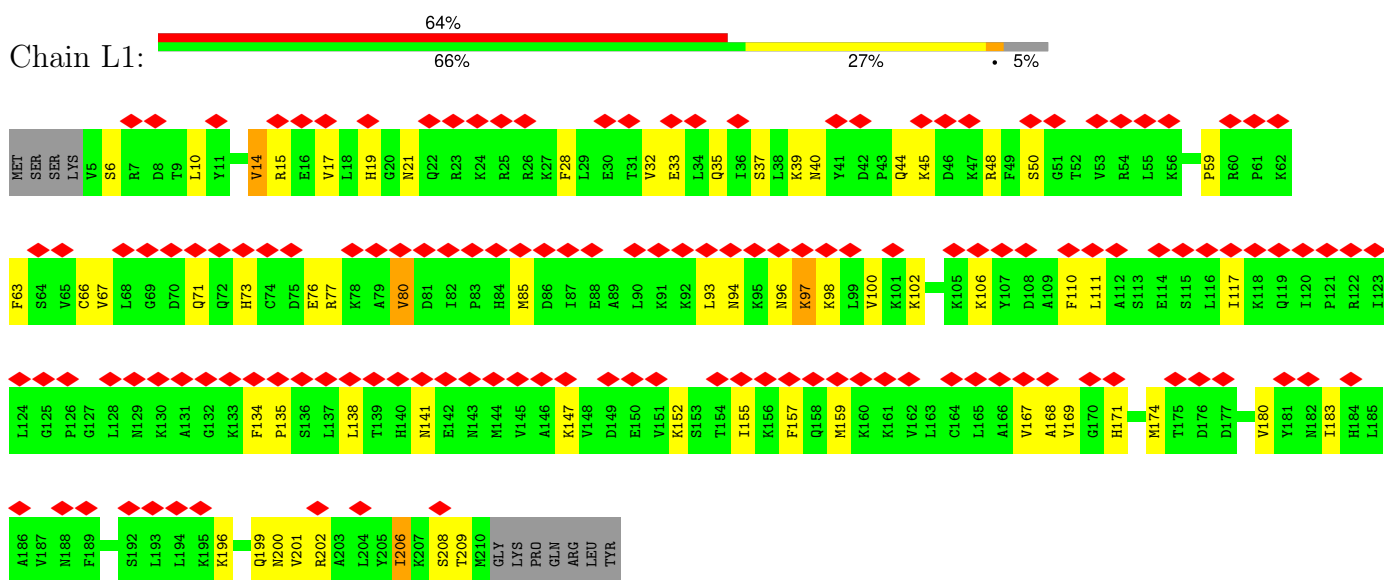
• Molecule 83: 40S ribosomal protein S7



• Molecule 84: 40S ribosomal protein S8



• Molecule 85: 60S ribosomal protein L10a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11878	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	27.769	Depositor
Minimum map value	-16.146	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	1.100	Depositor
Recommended contour level	4.8	Depositor
Map size (\AA)	814.07996, 814.07996, 814.07996	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: B8N, OMC, I4U, GDP, MLZ, 1MA, B9H, 2MG, B9B, B8Q, MG, B8T, ZN, MHG, DDE, P7G, UR3, 5MC, 4AC, A2M, E7G, 6MZ, OMG, OMU, B8W, G7M, PSU

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	0.12	0/1888	0.27	0/2516
2	B1	0.10	0/1971	0.25	0/2652
3	C1	0.11	0/1537	0.28	0/2065
4	D1	0.09	0/1728	0.24	0/2306
5	E1	0.10	0/1420	0.27	0/1899
6	F1	0.11	0/1707	0.26	0/2286
7	G1	0.11	0/1165	0.26	0/1558
8	H1	0.11	0/1746	0.26	0/2338
9	A2	0.13	0/86915	0.23	0/135538
10	B2	0.10	0/2858	0.22	0/4455
11	C2	0.13	0/3679	0.23	0/5732
12	D2	0.11	0/1959	0.27	0/2627
13	E2	0.10	0/3305	0.26	0/4422
14	F2	0.10	0/2971	0.24	0/3987
15	G2	0.09	0/2431	0.24	0/3256
16	H2	0.10	0/1822	0.25	0/2443
17	I2	0.12	0/1670	0.27	0/2232
18	J2	0.10	0/1268	0.27	0/1700
19	K2	0.09	0/1535	0.25	0/2048
20	L2	0.10	0/1558	0.22	0/2059
21	M2	0.11	0/1490	0.28	0/2000
22	N2	0.09	0/1326	0.21	0/1769
23	O2	0.10	0/839	0.27	0/1126
24	P2	0.09	0/983	0.24	0/1319
25	Q2	0.11	0/988	0.26	0/1306
26	R2	0.10	0/984	0.25	0/1323
27	S2	0.09	0/1132	0.23	0/1504
28	T2	0.09	0/1130	0.22	0/1507
29	U2	0.10	0/1193	0.23	0/1593
30	V2	0.11	0/954	0.30	0/1263
31	W2	0.11	0/742	0.26	0/996

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	X2	0.11	0/903	0.28	0/1216
33	Y2	0.09	0/1071	0.24	0/1429
34	Z2	0.10	0/895	0.23	0/1198
35	a2	0.09	0/916	0.23	0/1221
36	b2	0.10	0/1009	0.25	0/1332
37	c2	0.11	0/840	0.33	0/1114
38	d2	0.09	0/720	0.24	0/952
39	e2	0.08	0/574	0.23	0/760
40	f2	0.11	0/454	0.25	0/599
41	g2	0.09	0/425	0.25	0/561
42	h2	0.10	0/231	0.21	0/294
43	i2	0.09	0/855	0.23	0/1128
44	j2	0.11	0/704	0.24	0/935
45	k2	0.11	0/1016	0.28	0/1363
46	m2	0.12	0/40747	0.24	0/63507
47	n2	0.09	0/1795	0.20	0/2798
48	p2	0.09	0/1765	0.24	0/2362
49	q2	0.10	0/1784	0.27	0/2402
50	r2	0.08	0/2118	0.25	0/2849
51	w2	0.09	0/1268	0.25	0/1696
52	z2	0.09	0/1094	0.27	0/1469
53	o2	0.11	0/1731	0.25	0/2352
54	s2	0.09	0/1517	0.25	0/2038
55	v2	0.10	0/835	0.26	0/1126
56	x2	0.09	0/1094	0.26	0/1460
57	y2	0.11	0/1161	0.30	0/1553
58	A3	0.09	0/1208	0.27	0/1618
59	B3	0.08	0/1122	0.21	0/1503
60	C3	0.08	0/817	0.22	0/1097
61	D3	0.08	0/645	0.19	0/863
62	E3	0.10	0/1116	0.26	0/1490
63	F3	0.09	0/828	0.23	0/1109
64	G3	0.08	0/508	0.23	0/680
65	H3	0.10	0/466	0.29	0/618
66	I3	0.09	0/2493	0.29	0/3394
67	J3	0.10	0/1762	0.27	0/2382
68	K3	0.09	0/1863	0.27	0/2481
69	L3	0.09	0/1542	0.23	0/2058
70	M3	0.10	0/952	0.26	0/1278
71	N3	0.09	0/1232	0.23	0/1656
72	O3	0.10	0/1015	0.27	0/1361
73	P3	0.11	0/1051	0.26	0/1406
74	Q3	0.08	0/1066	0.23	0/1415

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	R3	0.10	0/604	0.26	0/810
76	S3	0.09	0/665	0.25	0/890
77	T3	0.08	0/443	0.25	0/582
78	U3	0.09	0/515	0.29	0/682
79	m	0.11	0/6538	0.29	0/8829
80	j	0.10	0/1530	0.28	0/2064
81	k	0.11	0/1173	0.32	0/1581
82	A	0.44	0/493	1.12	4/655 (0.6%)
83	t	0.11	0/1519	0.27	0/2033
84	u	0.09	0/1715	0.24	0/2287
85	L1	0.13	0/1686	0.35	0/2262
All	All	0.12	0/240983	0.25	4/352623 (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
82	A	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	A	226	THR	N-CA-C	-14.16	95.92	111.36
82	A	223	ASP	CB-CA-C	-13.28	90.28	111.39
82	A	223	ASP	CA-C-O	-5.53	115.09	120.89
82	A	225	LEU	N-CA-C	-5.34	106.76	113.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
82	A	222	LYS	Mainchain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	1851	0	1988	33	0
2	B1	1934	0	2081	21	0
3	C1	1519	0	1603	26	0
4	D1	1690	0	1745	24	0
5	E1	1397	0	1425	21	0
6	F1	1676	0	1777	28	0
7	G1	1143	0	1219	12	0
8	H1	1701	0	1749	42	0
9	A2	79546	0	40088	1170	0
10	B2	2558	0	1296	33	0
11	C2	3315	0	1685	49	0
12	D2	1921	0	2022	47	0
13	E2	3238	0	3380	57	0
14	F2	2928	0	3110	45	0
15	G2	2385	0	2409	36	0
16	H2	1789	0	1932	32	0
17	I2	1640	0	1792	26	0
18	J2	1242	0	1274	21	0
19	K2	1511	0	1636	28	0
20	L2	1542	0	1698	32	0
21	M2	1450	0	1488	24	0
22	N2	1298	0	1365	27	0
23	O2	825	0	850	9	0
24	P2	969	0	1031	20	0
25	Q2	974	0	1042	11	0
26	R2	967	0	1040	10	0
27	S2	1115	0	1205	20	0
28	T2	1107	0	1182	17	0
29	U2	1164	0	1213	21	0
30	V2	936	0	1029	16	0
31	W2	732	0	769	18	0
32	X2	888	0	930	20	0
33	Y2	1053	0	1147	19	0
34	Z2	876	0	912	11	0
35	a2	906	0	997	18	0
36	b2	1001	0	1138	14	0
37	c2	829	0	899	9	0
38	d2	705	0	737	31	0
39	e2	568	0	635	11	0
40	f2	444	0	483	7	0
41	g2	430	0	466	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	h2	230	0	276	3	0
43	i2	842	0	912	15	0
44	j2	694	0	738	15	0
45	k2	1001	0	1066	21	0
46	m2	36795	0	18588	626	0
47	n2	1604	0	816	27	0
48	p2	1738	0	1809	28	0
49	q2	1756	0	1851	38	0
50	r2	2076	0	2177	42	0
51	w2	1247	0	1323	21	0
52	z2	1080	0	1135	12	0
53	o2	1694	0	1696	38	0
54	s2	1496	0	1548	17	0
55	v2	811	0	831	11	0
56	x2	1073	0	1128	27	0
57	y2	1143	0	1213	20	0
58	A3	1190	0	1249	36	0
59	B3	1104	0	1139	19	0
60	C3	807	0	874	17	0
61	D3	638	0	635	11	0
62	E3	1098	0	1167	16	0
63	F3	811	0	864	18	0
64	G3	506	0	536	8	0
65	H3	455	0	445	8	0
66	I3	2436	0	2393	47	0
67	J3	1725	0	1815	40	0
68	K3	1840	0	1989	36	0
69	L3	1518	0	1632	37	0
70	M3	942	0	971	18	0
71	N3	1208	0	1294	17	0
72	O3	1002	0	1023	20	0
73	P3	1034	0	1080	18	0
74	Q3	1049	0	1122	15	0
75	R3	598	0	656	14	0
76	S3	652	0	676	18	0
77	T3	438	0	484	7	0
78	U3	505	0	507	7	0
79	m	6433	0	6501	102	0
80	j	1507	0	1564	29	0
81	k	1159	0	1216	24	0
82	A	486	0	441	39	0
83	t	1497	0	1590	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	u	1686	0	1772	32	0
85	L1	1660	0	1768	39	0
86	F3	1	0	0	0	0
86	H3	1	0	0	0	0
86	U3	1	0	0	0	0
86	d2	1	0	0	0	0
86	g2	1	0	0	0	0
86	i2	1	0	0	0	0
86	j2	1	0	0	0	0
87	H3	1	0	0	0	0
88	m	28	0	12	1	0
89	N3	1	0	0	0	0
89	m2	1	0	0	0	0
All	All	227065	0	170989	3141	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 3141 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:A:225:LEU:CD2	82:A:228:LEU:CD1	1.86	1.53
82:A:225:LEU:CD2	82:A:228:LEU:HD12	1.39	1.53
82:A:225:LEU:HD21	82:A:228:LEU:CD1	1.57	1.25
82:A:225:LEU:CD1	82:A:228:LEU:HD12	1.68	1.23
82:A:225:LEU:CG	82:A:228:LEU:HD12	1.75	1.15

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	221/270 (82%)	216 (98%)	5 (2%)	0	100	100
2	B1	240/266 (90%)	232 (97%)	8 (3%)	0	100	100
3	C1	188/192 (98%)	185 (98%)	3 (2%)	0	100	100
4	D1	204/214 (95%)	198 (97%)	6 (3%)	0	100	100
5	E1	172/178 (97%)	170 (99%)	2 (1%)	0	100	100
6	F1	205/211 (97%)	196 (96%)	9 (4%)	0	100	100
7	G1	137/217 (63%)	134 (98%)	3 (2%)	0	100	100
8	H1	201/204 (98%)	199 (99%)	2 (1%)	0	100	100
12	D2	249/257 (97%)	235 (94%)	14 (6%)	0	100	100
13	E2	400/403 (99%)	393 (98%)	7 (2%)	0	100	100
14	F2	364/419 (87%)	355 (98%)	9 (2%)	0	100	100
15	G2	291/297 (98%)	287 (99%)	4 (1%)	0	100	100
16	H2	215/296 (73%)	208 (97%)	7 (3%)	0	100	100
17	I2	199/203 (98%)	196 (98%)	3 (2%)	0	100	100
18	J2	151/184 (82%)	144 (95%)	7 (5%)	0	100	100
19	K2	184/188 (98%)	181 (98%)	3 (2%)	0	100	100
20	L2	182/196 (93%)	182 (100%)	0	0	100	100
21	M2	173/176 (98%)	166 (96%)	7 (4%)	0	100	100
22	N2	157/160 (98%)	156 (99%)	1 (1%)	0	100	100
23	O2	99/128 (77%)	99 (100%)	0	0	100	100
24	P2	127/140 (91%)	125 (98%)	2 (2%)	0	100	100
25	Q2	115/157 (73%)	109 (95%)	6 (5%)	0	100	100
26	R2	116/156 (74%)	113 (97%)	3 (3%)	0	100	100
27	S2	132/145 (91%)	131 (99%)	1 (1%)	0	100	100
28	T2	133/136 (98%)	133 (100%)	0	0	100	100
29	U2	145/148 (98%)	140 (97%)	5 (3%)	0	100	100
30	V2	114/160 (71%)	107 (94%)	7 (6%)	0	100	100
31	W2	92/115 (80%)	89 (97%)	3 (3%)	0	100	100
32	X2	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
33	Y2	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
34	Z2	107/110 (97%)	105 (98%)	2 (2%)	0	100	100
35	a2	112/117 (96%)	111 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	b2	118/123 (96%)	115 (98%)	3 (2%)	0	100	100
37	c2	100/105 (95%)	94 (94%)	5 (5%)	1 (1%)	12	40
38	d2	84/97 (87%)	84 (100%)	0	0	100	100
39	e2	67/70 (96%)	67 (100%)	0	0	100	100
40	f2	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	g2	49/128 (38%)	49 (100%)	0	0	100	100
42	h2	22/25 (88%)	22 (100%)	0	0	100	100
43	i2	101/106 (95%)	96 (95%)	5 (5%)	0	100	100
44	j2	87/92 (95%)	84 (97%)	3 (3%)	0	100	100
45	k2	123/137 (90%)	119 (97%)	4 (3%)	0	100	100
48	p2	212/264 (80%)	205 (97%)	7 (3%)	0	100	100
49	q2	224/243 (92%)	221 (99%)	3 (1%)	0	100	100
50	r2	260/263 (99%)	254 (98%)	6 (2%)	0	100	100
51	w2	151/158 (96%)	144 (95%)	7 (5%)	0	100	100
52	z2	132/135 (98%)	130 (98%)	2 (2%)	0	100	100
53	o2	212/295 (72%)	208 (98%)	4 (2%)	0	100	100
54	s2	187/204 (92%)	181 (97%)	6 (3%)	0	100	100
55	v2	94/165 (57%)	92 (98%)	2 (2%)	0	100	100
56	x2	128/145 (88%)	125 (98%)	3 (2%)	0	100	100
57	y2	142/146 (97%)	139 (98%)	3 (2%)	0	100	100
58	A3	142/152 (93%)	136 (96%)	6 (4%)	0	100	100
59	B3	139/145 (96%)	138 (99%)	1 (1%)	0	100	100
60	C3	100/119 (84%)	98 (98%)	2 (2%)	0	100	100
61	D3	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
62	E3	139/143 (97%)	137 (99%)	2 (1%)	0	100	100
63	F3	99/115 (86%)	97 (98%)	2 (2%)	0	100	100
64	G3	62/69 (90%)	60 (97%)	2 (3%)	0	100	100
65	H3	52/56 (93%)	49 (94%)	3 (6%)	0	100	100
66	I3	311/317 (98%)	297 (96%)	14 (4%)	0	100	100
67	J3	220/293 (75%)	215 (98%)	5 (2%)	0	100	100
68	K3	225/249 (90%)	219 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	L3	182/194 (94%)	175 (96%)	7 (4%)	0	100	100
70	M3	120/132 (91%)	119 (99%)	1 (1%)	0	100	100
71	N3	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
72	O3	132/151 (87%)	129 (98%)	3 (2%)	0	100	100
73	P3	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
74	Q3	127/133 (96%)	124 (98%)	3 (2%)	0	100	100
75	R3	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
76	S3	81/84 (96%)	74 (91%)	7 (9%)	0	100	100
77	T3	53/133 (40%)	53 (100%)	0	0	100	100
78	U3	60/156 (38%)	58 (97%)	2 (3%)	0	100	100
79	m	817/858 (95%)	796 (97%)	21 (3%)	0	100	100
80	j	194/317 (61%)	191 (98%)	3 (2%)	0	100	100
81	k	151/165 (92%)	143 (95%)	7 (5%)	1 (1%)	18	49
82	A	57/386 (15%)	56 (98%)	1 (2%)	0	100	100
83	t	182/194 (94%)	176 (97%)	6 (3%)	0	100	100
84	u	204/208 (98%)	196 (96%)	8 (4%)	0	100	100
85	L1	204/217 (94%)	187 (92%)	16 (8%)	1 (0%)	24	55
All	All	12679/14730 (86%)	12334 (97%)	342 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
37	c2	31	SER
81	k	86	LYS
85	L1	97	LYS

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	
1	A1	194/234 (83%)	194 (100%)	0	100	100
2	B1	204/223 (92%)	202 (99%)	2 (1%)	68	76
3	C1	169/171 (99%)	168 (99%)	1 (1%)	78	81
4	D1	177/180 (98%)	176 (99%)	1 (1%)	78	81
5	E1	147/149 (99%)	145 (99%)	2 (1%)	59	73
6	F1	174/178 (98%)	174 (100%)	0	100	100
7	G1	118/157 (75%)	118 (100%)	0	100	100
8	H1	171/172 (99%)	169 (99%)	2 (1%)	63	75
12	D2	193/199 (97%)	193 (100%)	0	100	100
13	E2	347/348 (100%)	346 (100%)	1 (0%)	86	86
14	F2	307/347 (88%)	303 (99%)	4 (1%)	61	74
15	G2	245/249 (98%)	243 (99%)	2 (1%)	73	79
16	H2	198/256 (77%)	196 (99%)	2 (1%)	68	76
17	I2	172/173 (99%)	172 (100%)	0	100	100
18	J2	134/164 (82%)	133 (99%)	1 (1%)	76	80
19	K2	164/165 (99%)	163 (99%)	1 (1%)	78	81
20	L2	163/175 (93%)	163 (100%)	0	100	100
21	M2	155/156 (99%)	154 (99%)	1 (1%)	78	81
22	N2	138/139 (99%)	137 (99%)	1 (1%)	76	80
23	O2	91/114 (80%)	91 (100%)	0	100	100
24	P2	100/107 (94%)	99 (99%)	1 (1%)	68	76
25	Q2	98/126 (78%)	97 (99%)	1 (1%)	68	76
26	R2	106/133 (80%)	105 (99%)	1 (1%)	70	78
27	S2	124/135 (92%)	124 (100%)	0	100	100
28	T2	117/118 (99%)	115 (98%)	2 (2%)	53	71
29	U2	120/121 (99%)	118 (98%)	2 (2%)	53	71
30	V2	97/124 (78%)	95 (98%)	2 (2%)	47	67
31	W2	79/97 (81%)	77 (98%)	2 (2%)	42	64
32	X2	98/110 (89%)	97 (99%)	1 (1%)	68	76
33	Y2	114/121 (94%)	114 (100%)	0	100	100
34	Z2	88/89 (99%)	88 (100%)	0	100	100
35	a2	98/100 (98%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	b2	108/110 (98%)	108 (100%)	0	100	100
37	c2	87/90 (97%)	86 (99%)	1 (1%)	65	76
38	d2	73/80 (91%)	73 (100%)	0	100	100
39	e2	64/65 (98%)	63 (98%)	1 (2%)	55	72
40	f2	47/48 (98%)	47 (100%)	0	100	100
41	g2	47/115 (41%)	47 (100%)	0	100	100
42	h2	23/24 (96%)	23 (100%)	0	100	100
43	i2	91/94 (97%)	90 (99%)	1 (1%)	65	76
44	j2	73/75 (97%)	72 (99%)	1 (1%)	59	73
45	k2	109/121 (90%)	109 (100%)	0	100	100
48	p2	195/229 (85%)	192 (98%)	3 (2%)	57	72
49	q2	189/202 (94%)	188 (100%)	1 (0%)	81	83
50	r2	224/225 (100%)	223 (100%)	1 (0%)	84	84
51	w2	137/142 (96%)	135 (98%)	2 (2%)	57	72
52	z2	120/121 (99%)	118 (98%)	2 (2%)	53	71
53	o2	179/242 (74%)	176 (98%)	3 (2%)	53	71
54	s2	159/170 (94%)	158 (99%)	1 (1%)	78	81
55	v2	87/136 (64%)	86 (99%)	1 (1%)	65	76
56	x2	116/130 (89%)	113 (97%)	3 (3%)	40	64
57	y2	119/121 (98%)	118 (99%)	1 (1%)	73	79
58	A3	125/132 (95%)	123 (98%)	2 (2%)	55	72
59	B3	112/115 (97%)	111 (99%)	1 (1%)	70	78
60	C3	93/107 (87%)	93 (100%)	0	100	100
61	D3	67/67 (100%)	67 (100%)	0	100	100
62	E3	113/115 (98%)	111 (98%)	2 (2%)	51	70
63	F3	88/98 (90%)	86 (98%)	2 (2%)	44	66
64	G3	57/62 (92%)	56 (98%)	1 (2%)	51	70
65	H3	48/49 (98%)	48 (100%)	0	100	100
66	I3	272/275 (99%)	268 (98%)	4 (2%)	57	72
67	J3	188/224 (84%)	185 (98%)	3 (2%)	55	72
68	K3	198/218 (91%)	195 (98%)	3 (2%)	57	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	L3	160/168 (95%)	160 (100%)	0	100	100
70	M3	102/108 (94%)	100 (98%)	2 (2%)	48	68
71	N3	130/131 (99%)	127 (98%)	3 (2%)	44	66
72	O3	104/119 (87%)	101 (97%)	3 (3%)	37	62
73	P3	112/113 (99%)	111 (99%)	1 (1%)	70	78
74	Q3	111/115 (96%)	108 (97%)	3 (3%)	39	63
75	R3	66/103 (64%)	65 (98%)	1 (2%)	57	72
76	S3	75/76 (99%)	73 (97%)	2 (3%)	39	63
77	T3	45/106 (42%)	44 (98%)	1 (2%)	45	66
78	U3	55/140 (39%)	54 (98%)	1 (2%)	51	70
79	m	702/729 (96%)	701 (100%)	1 (0%)	88	90
80	j	164/255 (64%)	160 (98%)	4 (2%)	43	65
81	k	126/137 (92%)	122 (97%)	4 (3%)	34	60
82	A	52/304 (17%)	48 (92%)	4 (8%)	12	37
83	t	166/174 (95%)	160 (96%)	6 (4%)	31	58
84	u	178/180 (99%)	173 (97%)	5 (3%)	38	62
85	L1	187/197 (95%)	181 (97%)	6 (3%)	34	60
All	All	11043/12487 (88%)	10923 (99%)	120 (1%)	63	76

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	B3	33	TRP
84	u	93	THR
68	K3	116	LYS
84	u	78	ILE
85	L1	201	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 88 such sidechains are listed below:

Mol	Chain	Res	Type
66	I3	117	ASN
79	m	719	GLN
68	K3	202	ASN
74	Q3	94	HIS

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Mol	Chain	Res	Type
80	j	105	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B2	119/121 (98%)	15 (12%)	0
11	C2	155/174 (89%)	32 (20%)	1 (0%)
46	m2	1716/1871 (91%)	448 (26%)	0
47	n2	74/75 (98%)	27 (36%)	0
9	A2	3693/4731 (78%)	815 (22%)	6 (0%)
All	All	5757/6972 (82%)	1337 (23%)	7 (0%)

5 of 1337 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A2	25	A
9	A2	39	A
9	A2	42	A
9	A2	48	G
9	A2	56	A

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A2	2430	G
9	A2	3771	G
11	C2	59	A
9	A2	4351	U
9	A2	1804	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	PSU	A2	1496	9	18,21,22	4.52	6 (33%)	21,30,33	3.02	6 (28%)
46	OMG	m2	685	46	23,26,27	2.48	9 (39%)	32,38,41	2.08	11 (34%)
9	UR3	A2	4249	9	19,22,23	3.23	9 (47%)	26,32,35	1.57	4 (15%)
9	I4U	A2	1472	9	20,24,25	3.54	8 (40%)	27,34,37	1.80	2 (7%)
9	PSU	A2	1490	9	18,21,22	4.56	6 (33%)	21,30,33	3.01	7 (33%)
9	A2M	A2	1140	9	22,25,26	2.66	11 (50%)	30,36,39	2.33	11 (36%)
9	A2M	A2	3379	9	22,25,26	2.66	11 (50%)	30,36,39	2.36	10 (33%)
9	A2M	A2	3374	9	22,25,26	2.65	11 (50%)	30,36,39	2.33	10 (33%)
9	PSU	A2	4288	9	18,21,22	4.54	6 (33%)	21,30,33	3.02	6 (28%)
9	B9B	A2	1387	9	25,28,29	1.78	6 (24%)	35,40,43	2.36	14 (40%)
9	B8Q	A2	1269	9	18,22,23	3.03	4 (22%)	21,32,35	1.88	6 (28%)
9	1MA	A2	4067	9	21,25,26	2.47	4 (19%)	30,37,40	1.92	7 (23%)
9	A2M	A2	4223	9	22,25,26	2.66	11 (50%)	30,36,39	2.31	9 (30%)
41	MLZ	g2	98	41	8,9,10	0.72	0	4,9,11	0.83	0
9	A2M	A2	1337	9	22,25,26	2.64	11 (50%)	30,36,39	2.35	9 (30%)
9	OMG	A2	1685	9	23,26,27	2.47	9 (39%)	32,38,41	2.11	11 (34%)
46	PSU	m2	614	46	18,21,22	4.57	6 (33%)	21,30,33	3.01	6 (28%)
9	A2M	A2	1673	9	22,25,26	2.65	11 (50%)	30,36,39	2.32	8 (26%)
9	OMG	A2	2119	9	23,26,27	2.46	9 (39%)	32,38,41	2.09	11 (34%)
9	B8W	A2	3837	9	23,26,27	2.19	6 (26%)	33,38,41	3.44	16 (48%)
9	P7G	A2	1711	9	24,28,29	3.60	10 (41%)	25,41,44	1.22	2 (8%)
9	PSU	A2	4152	9	18,21,22	4.56	7 (38%)	21,30,33	3.04	6 (28%)
9	6MZ	A2	3872	9	22,25,26	2.45	4 (18%)	29,36,39	2.22	10 (34%)
9	OMG	A2	1335	9	23,26,27	2.47	9 (39%)	32,38,41	2.08	11 (34%)
9	OMG	A2	4289	9	23,26,27	2.47	9 (39%)	32,38,41	2.13	11 (34%)
9	PSU	A2	4102	9	18,21,22	4.53	6 (33%)	21,30,33	2.96	5 (23%)
9	OMU	A2	3958	9	19,22,23	3.04	8 (42%)	25,31,34	1.82	5 (20%)
46	A2M	m2	670	46	22,25,26	2.71	11 (50%)	30,36,39	2.28	9 (30%)
9	G7M	A2	1418	9	23,26,27	3.53	11 (47%)	34,39,42	1.73	6 (17%)
9	A2M	A2	2118	9	22,25,26	2.65	11 (50%)	30,36,39	2.32	9 (30%)
9	PSU	A2	4280	9	18,21,22	4.53	6 (33%)	21,30,33	3.01	5 (23%)
9	A2M	A2	3481	9	22,25,26	2.64	11 (50%)	30,36,39	2.32	10 (33%)
46	A2M	m2	27	46	22,25,26	2.64	11 (50%)	30,36,39	2.21	7 (23%)
9	G7M	A2	4202	9	23,26,27	3.52	11 (47%)	34,39,42	1.73	7 (20%)
9	OMC	A2	3565	9	19,22,23	3.05	8 (42%)	25,31,34	0.76	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
79	DDE	m	714	79	18,20,21	2.13	5 (27%)	17,28,30	1.08	2 (11%)
9	OMG	A2	373	9	23,26,27	2.46	9 (39%)	32,38,41	2.02	11 (34%)
9	OMG	A2	4275	9	23,26,27	2.46	9 (39%)	32,38,41	2.08	11 (34%)
9	OMC	A2	4188	9	19,22,23	3.06	8 (42%)	25,31,34	0.78	0
9	OMG	A2	1438	9	23,26,27	2.48	9 (39%)	32,38,41	2.03	11 (34%)
46	OMC	m2	519	46	19,22,23	3.06	8 (42%)	25,31,34	0.73	0
9	OMC	A2	2559	9	19,22,23	3.04	8 (42%)	25,31,34	0.79	0
46	PSU	m2	1083	46	18,21,22	4.55	6 (33%)	21,30,33	2.99	6 (28%)
9	OMC	A2	2120	9	19,22,23	3.05	8 (42%)	25,31,34	0.76	0
9	G7M	A2	2277	9	23,26,27	3.53	11 (47%)	34,39,42	1.71	6 (17%)
9	A2M	A2	2156	9	22,25,26	2.65	11 (50%)	30,36,39	2.32	9 (30%)
9	OMG	A2	4146	9	23,26,27	2.46	9 (39%)	32,38,41	2.09	11 (34%)
9	E7G	A2	1599	9	24,27,28	3.35	11 (45%)	28,40,43	2.39	9 (32%)
9	B9B	A2	4007	9	24,27,29	1.79	6 (25%)	34,39,43	2.40	13 (38%)
46	4AC	m2	1844	46	21,24,25	3.65	9 (42%)	28,34,37	1.12	3 (10%)
9	OMC	A2	3543	9	19,22,23	3.05	8 (42%)	25,31,34	0.75	0
9	OMG	A2	1852	9	23,26,27	2.46	9 (39%)	32,38,41	2.08	11 (34%)
46	A2M	m2	1033	46	22,25,26	2.64	11 (50%)	30,36,39	2.34	9 (30%)
9	E7G	A2	2052	9	24,27,28	3.30	11 (45%)	28,40,43	2.29	8 (28%)
9	5MC	A2	3987	9	19,22,23	3.92	8 (42%)	26,32,35	1.02	1 (3%)
9	2MG	A2	4517	9	23,26,27	2.63	7 (30%)	33,38,41	2.30	13 (39%)
9	B9H	A2	2541	9	21,25,26	2.98	4 (19%)	22,35,38	1.85	6 (27%)
9	PSU	A2	3420	9	18,21,22	4.53	6 (33%)	21,30,33	2.84	5 (23%)
9	PSU	A2	4183	9	18,21,22	4.56	6 (33%)	21,30,33	2.88	5 (23%)
9	OMC	A2	2177	9	19,22,23	3.04	8 (42%)	25,31,34	0.94	2 (8%)
9	OMG	A2	3848	9	23,26,27	2.47	8 (34%)	32,38,41	2.10	11 (34%)
46	OMG	m2	646	46	23,26,27	2.50	8 (34%)	32,38,41	2.21	11 (34%)
9	A2M	A2	3523	9	22,25,26	2.66	11 (50%)	30,36,39	2.24	9 (30%)
9	A2M	A2	398	9	22,25,26	2.64	11 (50%)	30,36,39	2.34	10 (33%)
9	A2M	A2	3441	9	22,25,26	2.69	11 (50%)	30,36,39	2.44	11 (36%)
9	OMG	A2	4022	9	23,26,27	2.46	9 (39%)	32,38,41	2.06	11 (34%)
9	P7G	A2	3536	9	24,28,29	3.58	10 (41%)	25,41,44	1.28	2 (8%)
9	PSU	A2	2263	9	18,21,22	4.53	6 (33%)	21,30,33	2.98	6 (28%)
9	PSU	A2	3385	9	18,21,22	4.55	6 (33%)	21,30,33	2.94	5 (23%)
9	PSU	A2	4094	9	18,21,22	4.56	7 (38%)	21,30,33	3.00	6 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	PSU	A2	3371	9	18,21,22	4.51	6 (33%)	21,30,33	3.00	6 (28%)
9	OMC	A2	3525	9	19,22,23	3.04	8 (42%)	25,31,34	0.71	0
46	PSU	m2	825	46	18,21,22	4.55	6 (33%)	21,30,33	3.03	5 (23%)
9	2MG	A2	878	9	23,26,27	2.64	7 (30%)	33,38,41	2.31	11 (33%)
9	PSU	A2	4055	9	18,21,22	4.50	6 (33%)	21,30,33	2.95	5 (23%)
9	OMG	A2	4515	9	23,26,27	2.46	9 (39%)	32,38,41	2.07	11 (34%)
9	OMC	A2	2616	9	19,22,23	3.08	8 (42%)	25,31,34	0.98	2 (8%)
11	OMU	C2	14	11	19,22,23	3.06	8 (42%)	25,31,34	1.82	5 (20%)
46	PSU	m2	824	46	18,21,22	4.55	6 (33%)	21,30,33	3.03	5 (23%)
9	OMU	A2	4272	9	19,22,23	3.08	8 (42%)	25,31,34	1.80	4 (16%)
9	I4U	A2	3846	9	20,24,25	3.53	8 (40%)	27,34,37	1.45	2 (7%)
46	UR3	m2	1832	46	19,22,23	3.26	8 (42%)	26,32,35	1.70	4 (15%)
9	OMC	A2	3357	9	19,22,23	3.05	8 (42%)	25,31,34	0.73	0
9	UR3	A2	1668	9	19,22,23	3.28	8 (42%)	26,32,35	1.67	4 (15%)
9	PSU	A2	3945	9	18,21,22	4.51	7 (38%)	21,30,33	2.98	5 (23%)
9	OMG	A2	2528	9	23,26,27	2.49	9 (39%)	32,38,41	2.12	11 (34%)
9	2MG	A2	1330	9	23,26,27	2.62	8 (34%)	33,38,41	2.30	12 (36%)
14	MLZ	F2	333	14	8,9,10	0.73	0	4,9,11	0.96	0
9	5MC	A2	4099	9	19,22,23	3.86	8 (42%)	26,32,35	1.01	1 (3%)
9	B9B	A2	237	9	25,28,29	1.76	5 (20%)	35,40,43	2.36	13 (37%)
9	OMG	A2	2179	9	23,26,27	2.48	9 (39%)	32,38,41	2.05	10 (31%)
46	OMU	m2	116	46	19,22,23	3.11	8 (42%)	25,31,34	1.92	5 (20%)
46	A2M	m2	166	46	22,25,26	2.65	11 (50%)	30,36,39	2.33	8 (26%)
9	B8T	A2	4135	9	19,22,23	3.30	8 (42%)	25,31,34	0.85	1 (4%)
9	A2M	A2	1347	9	22,25,26	2.67	11 (50%)	30,36,39	2.32	9 (30%)
9	5MC	A2	3438	9	19,22,23	3.89	8 (42%)	26,32,35	1.04	2 (7%)
9	MHG	A2	4023	9	29,32,33	3.55	10 (34%)	34,46,49	2.54	9 (26%)
46	B8N	m2	1250	46	25,29,30	2.49	6 (24%)	28,42,45	2.05	8 (28%)
9	OMG	A2	3448	9	23,26,27	2.49	9 (39%)	32,38,41	2.15	11 (34%)
9	PSU	A2	1395	9	18,21,22	4.54	6 (33%)	21,30,33	2.90	5 (23%)
46	PSU	m2	1245	46	18,21,22	4.54	6 (33%)	21,30,33	3.01	5 (23%)

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
9	PSU	A2	1496	9	-	0/7/25/26	0/2/2/2
46	OMG	m2	685	46	-	2/9/27/28	0/3/3/3
9	UR3	A2	4249	9	-	0/7/25/26	0/2/2/2
9	I4U	A2	1472	9	-	0/9/29/30	0/2/2/2
9	PSU	A2	1490	9	-	1/7/25/26	0/2/2/2
9	A2M	A2	1140	9	-	1/9/27/28	0/3/3/3
9	A2M	A2	3379	9	-	1/9/27/28	0/3/3/3
9	A2M	A2	3374	9	-	1/9/27/28	0/3/3/3
9	PSU	A2	4288	9	-	4/7/25/26	0/2/2/2
9	B9B	A2	1387	9	-	4/11/29/30	0/3/3/3
9	B8Q	A2	1269	9	-	0/7/42/43	0/2/2/2
9	1MA	A2	4067	9	-	2/7/25/26	0/3/3/3
9	A2M	A2	4223	9	-	1/9/27/28	0/3/3/3
41	MLZ	g2	98	41	-	0/7/8/10	-
9	A2M	A2	1337	9	-	2/9/27/28	0/3/3/3
9	OMG	A2	1685	9	-	1/9/27/28	0/3/3/3
46	PSU	m2	614	46	-	1/7/25/26	0/2/2/2
9	A2M	A2	1673	9	-	1/9/27/28	0/3/3/3
9	OMG	A2	2119	9	-	3/9/27/28	0/3/3/3
9	B8W	A2	3837	9	-	2/9/27/28	0/3/3/3
9	P7G	A2	1711	9	-	3/10/40/41	0/3/3/3
9	PSU	A2	4152	9	-	4/7/25/26	0/2/2/2
9	6MZ	A2	3872	9	-	4/9/27/28	0/3/3/3
9	OMG	A2	1335	9	-	0/9/27/28	0/3/3/3
9	OMG	A2	4289	9	-	2/9/27/28	0/3/3/3
9	PSU	A2	4102	9	-	3/7/25/26	0/2/2/2
9	OMU	A2	3958	9	-	2/9/27/28	0/2/2/2
46	A2M	m2	670	46	-	3/9/27/28	0/3/3/3
9	G7M	A2	1418	9	-	0/7/25/26	0/3/3/3
9	A2M	A2	2118	9	-	0/9/27/28	0/3/3/3
9	PSU	A2	4280	9	-	0/7/25/26	0/2/2/2
9	A2M	A2	3481	9	-	1/9/27/28	0/3/3/3
46	A2M	m2	27	46	-	1/9/27/28	0/3/3/3
9	G7M	A2	4202	9	-	0/7/25/26	0/3/3/3
9	OMC	A2	3565	9	-	1/9/27/28	0/2/2/2
79	DDE	m	714	79	-	1/20/21/23	0/1/1/1
9	OMG	A2	373	9	-	2/9/27/28	0/3/3/3
9	OMG	A2	4275	9	-	0/9/27/28	0/3/3/3
9	OMC	A2	4188	9	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	OMG	A2	1438	9	-	5/9/27/28	0/3/3/3
46	OMC	m2	519	46	-	3/9/27/28	0/2/2/2
9	OMC	A2	2559	9	-	0/9/27/28	0/2/2/2
46	PSU	m2	1083	46	-	1/7/25/26	0/2/2/2
9	OMC	A2	2120	9	-	0/9/27/28	0/2/2/2
9	G7M	A2	2277	9	-	0/7/25/26	0/3/3/3
9	A2M	A2	2156	9	-	2/9/27/28	0/3/3/3
9	OMG	A2	4146	9	-	0/9/27/28	0/3/3/3
9	E7G	A2	1599	9	-	2/9/39/40	0/3/3/3
9	B9B	A2	4007	9	-	4/10/28/30	0/3/3/3
46	4AC	m2	1844	46	-	3/11/29/30	0/2/2/2
9	OMC	A2	3543	9	-	2/9/27/28	0/2/2/2
9	OMG	A2	1852	9	-	0/9/27/28	0/3/3/3
46	A2M	m2	1033	46	-	1/9/27/28	0/3/3/3
9	E7G	A2	2052	9	-	3/9/39/40	0/3/3/3
9	5MC	A2	3987	9	-	2/7/25/26	0/2/2/2
9	2MG	A2	4517	9	-	0/9/27/28	0/3/3/3
9	B9H	A2	2541	9	-	0/12/47/48	0/2/2/2
9	PSU	A2	3420	9	-	2/7/25/26	0/2/2/2
9	PSU	A2	4183	9	-	3/7/25/26	0/2/2/2
9	OMC	A2	2177	9	-	3/9/27/28	0/2/2/2
9	OMG	A2	3848	9	-	1/9/27/28	0/3/3/3
46	OMG	m2	646	46	-	4/9/27/28	0/3/3/3
9	A2M	A2	3523	9	-	3/9/27/28	0/3/3/3
9	A2M	A2	398	9	-	3/9/27/28	0/3/3/3
9	A2M	A2	3441	9	-	3/9/27/28	0/3/3/3
9	OMG	A2	4022	9	-	0/9/27/28	0/3/3/3
9	P7G	A2	3536	9	-	2/10/40/41	0/3/3/3
9	PSU	A2	2263	9	-	0/7/25/26	0/2/2/2
9	PSU	A2	3385	9	-	0/7/25/26	0/2/2/2
9	PSU	A2	4094	9	-	0/7/25/26	0/2/2/2
9	PSU	A2	3371	9	-	0/7/25/26	0/2/2/2
9	OMC	A2	3525	9	-	0/9/27/28	0/2/2/2
46	PSU	m2	825	46	-	1/7/25/26	0/2/2/2
9	2MG	A2	878	9	-	3/9/27/28	0/3/3/3
9	PSU	A2	4055	9	-	2/7/25/26	0/2/2/2
9	OMG	A2	4515	9	-	3/9/27/28	0/3/3/3
9	OMC	A2	2616	9	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	OMU	C2	14	11	-	3/9/27/28	0/2/2/2
46	PSU	m2	824	46	-	4/7/25/26	0/2/2/2
9	OMU	A2	4272	9	-	3/9/27/28	0/2/2/2
9	I4U	A2	3846	9	-	6/9/29/30	0/2/2/2
46	UR3	m2	1832	46	-	4/7/25/26	0/2/2/2
9	OMC	A2	3357	9	-	2/9/27/28	0/2/2/2
9	UR3	A2	1668	9	-	2/7/25/26	0/2/2/2
9	PSU	A2	3945	9	-	2/7/25/26	0/2/2/2
9	OMG	A2	2528	9	-	0/9/27/28	0/3/3/3
9	2MG	A2	1330	9	-	2/9/27/28	0/3/3/3
14	MLZ	F2	333	14	-	0/7/8/10	-
9	5MC	A2	4099	9	-	4/7/25/26	0/2/2/2
9	B9B	A2	237	9	-	2/11/29/30	0/3/3/3
9	OMG	A2	2179	9	-	3/9/27/28	0/3/3/3
46	OMU	m2	116	46	-	1/9/27/28	0/2/2/2
46	A2M	m2	166	46	-	3/9/27/28	0/3/3/3
9	B8T	A2	4135	9	-	0/7/27/28	0/2/2/2
9	A2M	A2	1347	9	-	2/9/27/28	0/3/3/3
9	5MC	A2	3438	9	-	2/7/25/26	0/2/2/2
9	MHG	A2	4023	9	-	3/16/46/47	0/3/3/3
46	B8N	m2	1250	46	-	5/16/34/35	0/2/2/2
9	OMG	A2	3448	9	-	0/9/27/28	0/3/3/3
9	PSU	A2	1395	9	-	2/7/25/26	0/2/2/2
46	PSU	m2	1245	46	-	2/7/25/26	0/2/2/2

The worst 5 of 812 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	m2	614	PSU	C6-C5	12.70	1.49	1.35
46	m2	824	PSU	C6-C5	12.66	1.49	1.35
9	A2	4094	PSU	C6-C5	12.62	1.49	1.35
9	A2	4183	PSU	C6-C5	12.61	1.49	1.35
46	m2	825	PSU	C6-C5	12.57	1.49	1.35

The worst 5 of 680 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A2	3837	B8W	O6-C6-N1	8.62	130.42	118.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A2	3837	B8W	N2-C2-N3	8.56	130.06	117.22
9	A2	4023	MHG	C2-N3-C4	7.96	121.96	112.00
9	A2	4094	PSU	N1-C2-N3	7.93	123.54	115.17
9	A2	3371	PSU	N1-C2-N3	7.89	123.49	115.17

There are no chirality outliers.

5 of 173 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
79	m	714	DDE	NAD-CBI-CBW-NCB
9	A2	237	B9B	C5-C6-O6-C61
9	A2	237	B9B	N1-C6-O6-C61
9	A2	878	2MG	C3'-C4'-C5'-O5'
9	A2	1140	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

44 monomers are involved in 67 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A2	1496	PSU	1	0
46	m2	685	OMG	1	0
9	A2	1140	A2M	2	0
9	A2	3379	A2M	3	0
9	A2	4288	PSU	1	0
9	A2	4067	1MA	1	0
9	A2	4223	A2M	1	0
9	A2	1337	A2M	1	0
9	A2	1685	OMG	1	0
9	A2	1673	A2M	2	0
9	A2	4152	PSU	2	0
9	A2	3872	6MZ	2	0
46	m2	670	A2M	3	0
9	A2	1418	G7M	1	0
9	A2	2118	A2M	1	0
9	A2	4280	PSU	1	0
46	m2	27	A2M	4	0
9	A2	3565	OMC	1	0
79	m	714	DDE	1	0
9	A2	373	OMG	3	0
9	A2	4275	OMG	2	0
46	m2	519	OMC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A2	2559	OMC	1	0
9	A2	1852	OMG	2	0
46	m2	1033	A2M	1	0
9	A2	4517	2MG	1	0
9	A2	3420	PSU	1	0
9	A2	4183	PSU	3	0
9	A2	2177	OMC	1	0
46	m2	646	OMG	1	0
9	A2	3523	A2M	2	0
9	A2	3441	A2M	1	0
9	A2	2263	PSU	1	0
9	A2	4094	PSU	1	0
9	A2	3371	PSU	1	0
9	A2	4055	PSU	2	0
9	A2	2616	OMC	1	0
11	C2	14	OMU	2	0
9	A2	4272	OMU	2	0
9	A2	2528	OMG	1	0
9	A2	4099	5MC	1	0
46	m2	116	OMU	1	0
46	m2	166	A2M	2	0
9	A2	1347	A2M	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 8 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
88	GDP	m	900	-	29,30,30	3.25	17 (58%)	45,47,47	2.08	11 (24%)

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
88	GDP	m	900	-	-	2/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	m	900	GDP	C4-N3	6.42	1.48	1.34
88	m	900	GDP	O4'-C4'	-6.33	1.30	1.45
88	m	900	GDP	C2-N3	5.49	1.46	1.33
88	m	900	GDP	C3'-C4'	5.47	1.66	1.53
88	m	900	GDP	PA-O3A	5.47	1.65	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	m	900	GDP	C1'-N9-C8	-6.29	108.86	126.73
88	m	900	GDP	N9-C8-N7	-4.98	104.17	113.40
88	m	900	GDP	C5-C4-N3	-4.24	121.65	128.39
88	m	900	GDP	C2-N3-C4	4.02	119.22	112.30
88	m	900	GDP	C1'-N9-C4	3.92	138.08	126.49

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
88	m	900	GDP	O4'-C4'-C5'-O5'
88	m	900	GDP	C3'-C4'-C5'-O5'

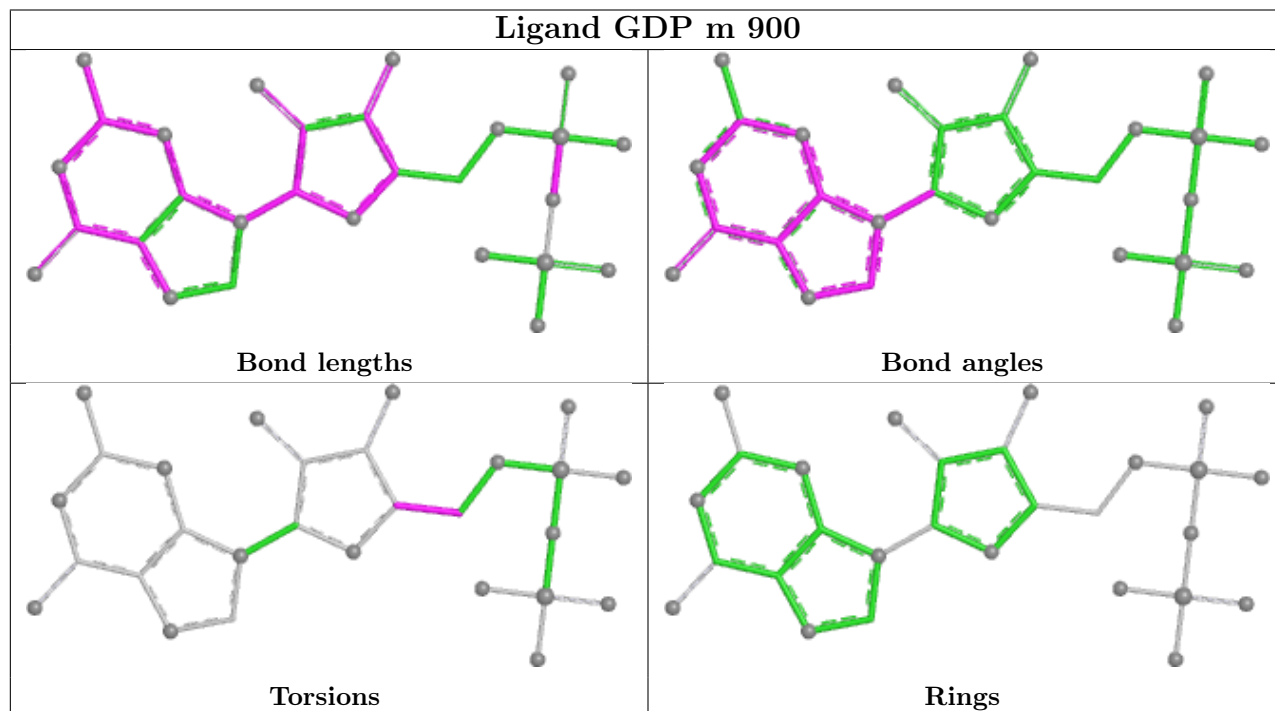
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	m	900	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

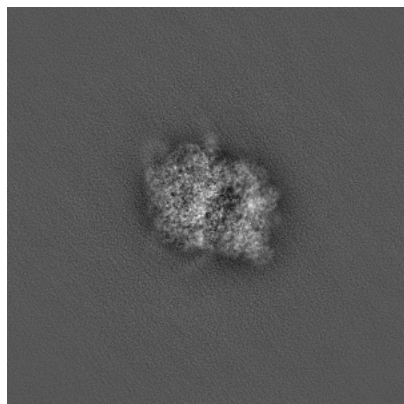
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23500. These allow visual inspection of the internal detail of the map and identification of artifacts.

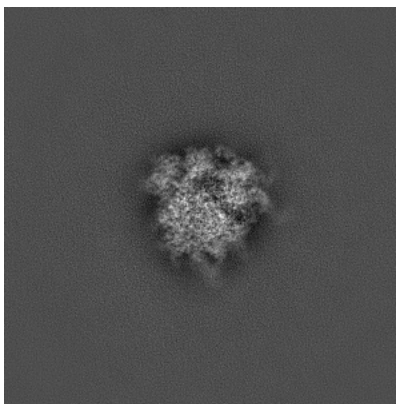
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

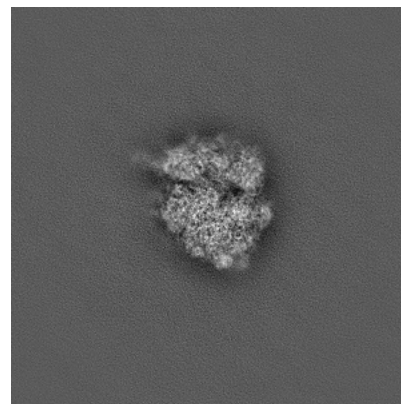
6.1.1 Primary map



X

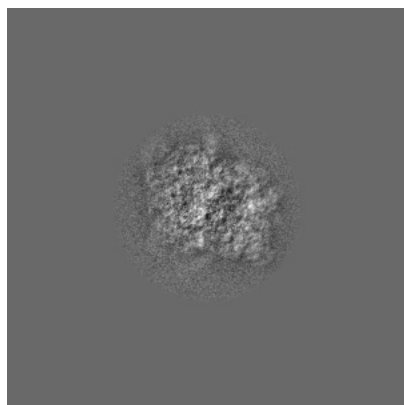


Y

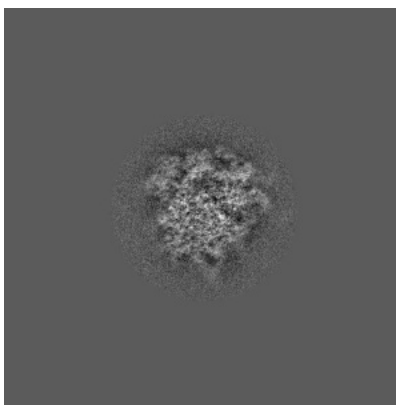


Z

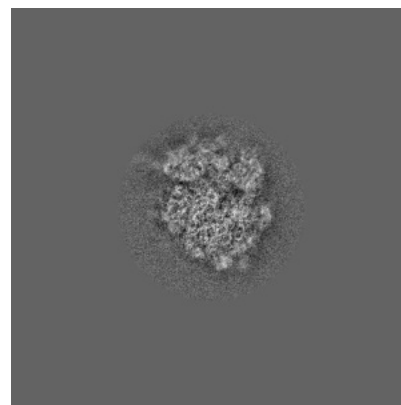
6.1.2 Raw map



X



Y

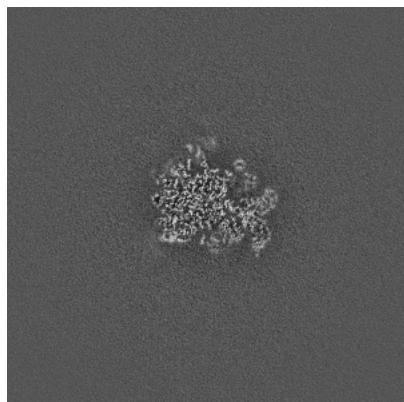


Z

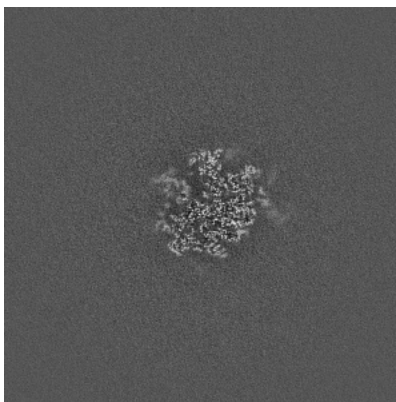
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

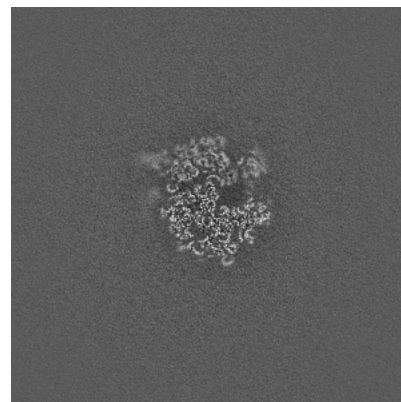
6.2.1 Primary map



X Index: 384

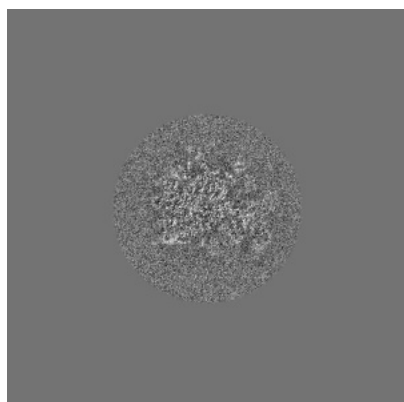


Y Index: 384

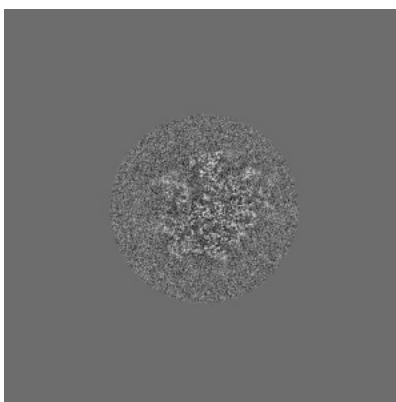


Z Index: 384

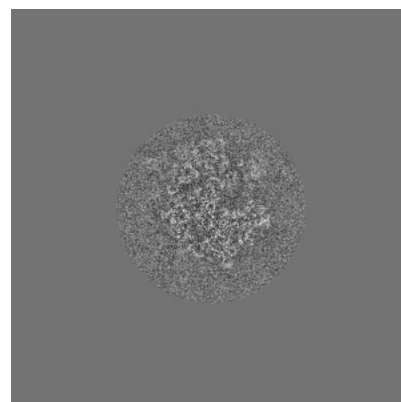
6.2.2 Raw map



X Index: 384



Y Index: 384

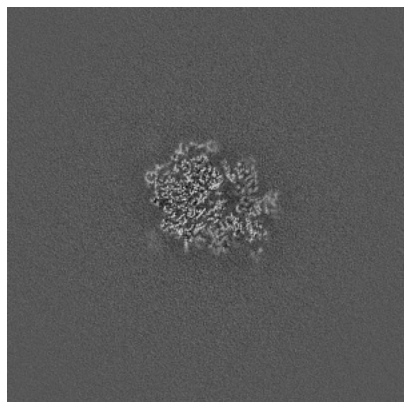


Z Index: 384

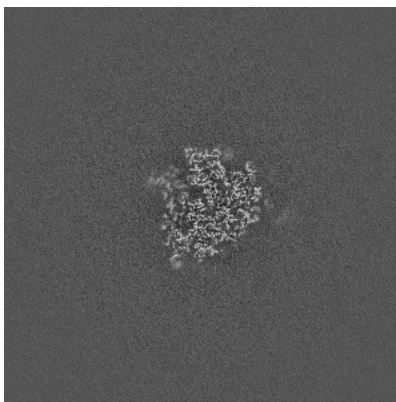
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

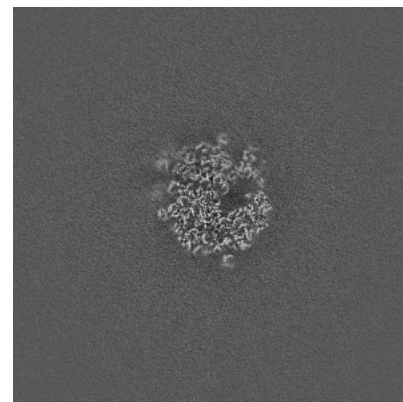
6.3.1 Primary map



X Index: 394

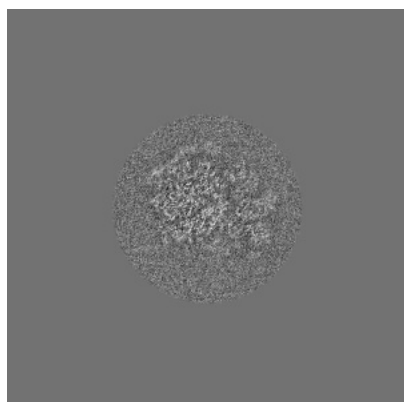


Y Index: 376

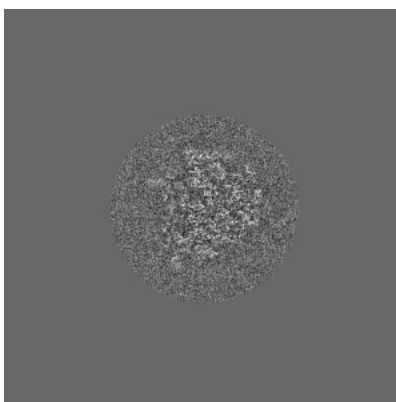


Z Index: 375

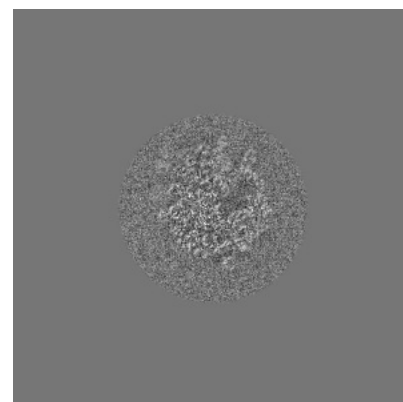
6.3.2 Raw map



X Index: 390



Y Index: 376

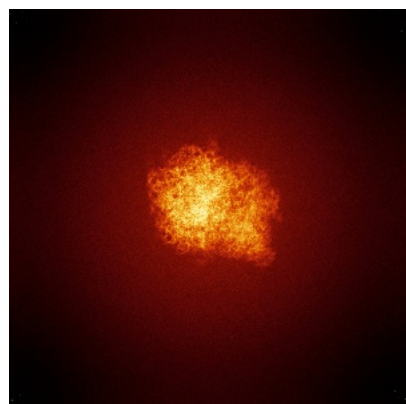


Z Index: 375

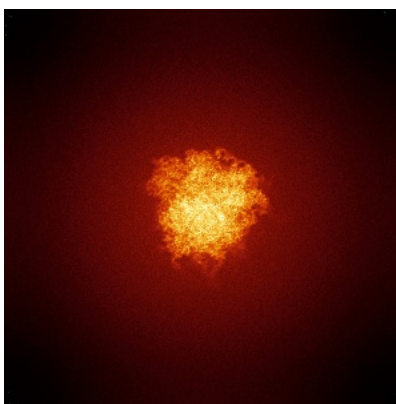
The images above show the largest variance slices of the map in three orthogonal directions.

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

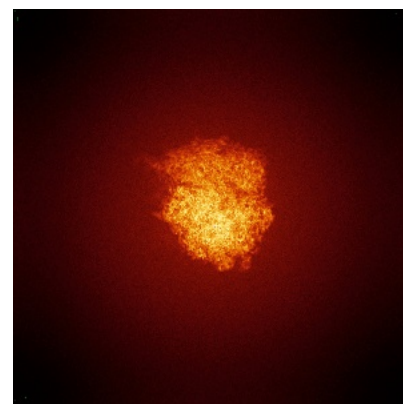
6.4.1 Primary map



X

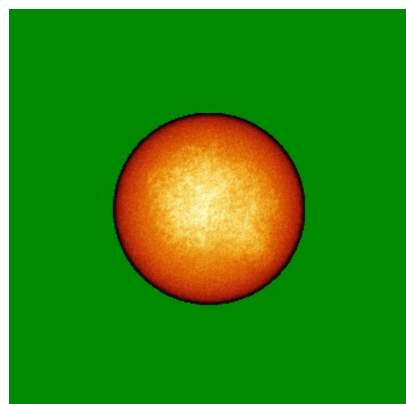


Y

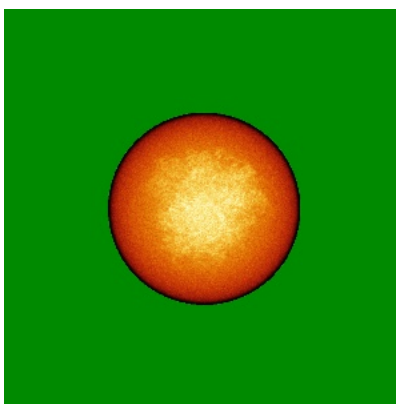


Z

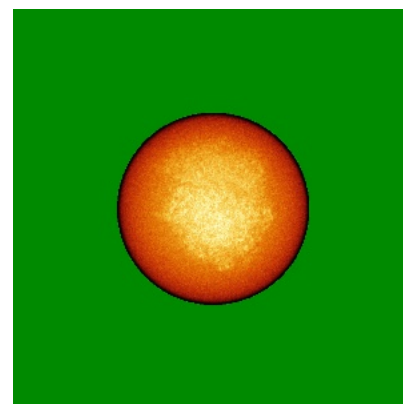
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



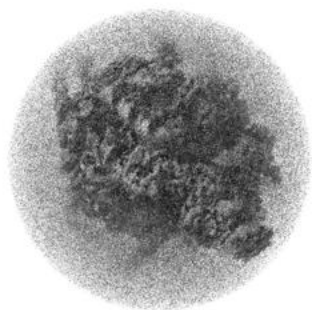
Y



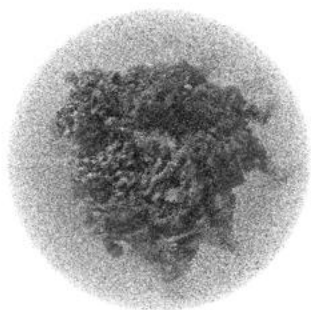
Z

The images above show the 3D surface view of the map at the recommended contour level 4.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

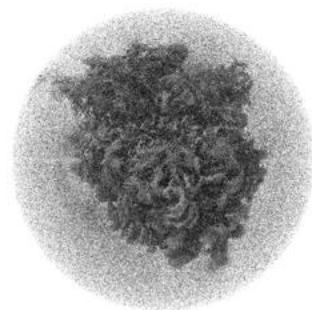
6.5.2 Raw map



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.

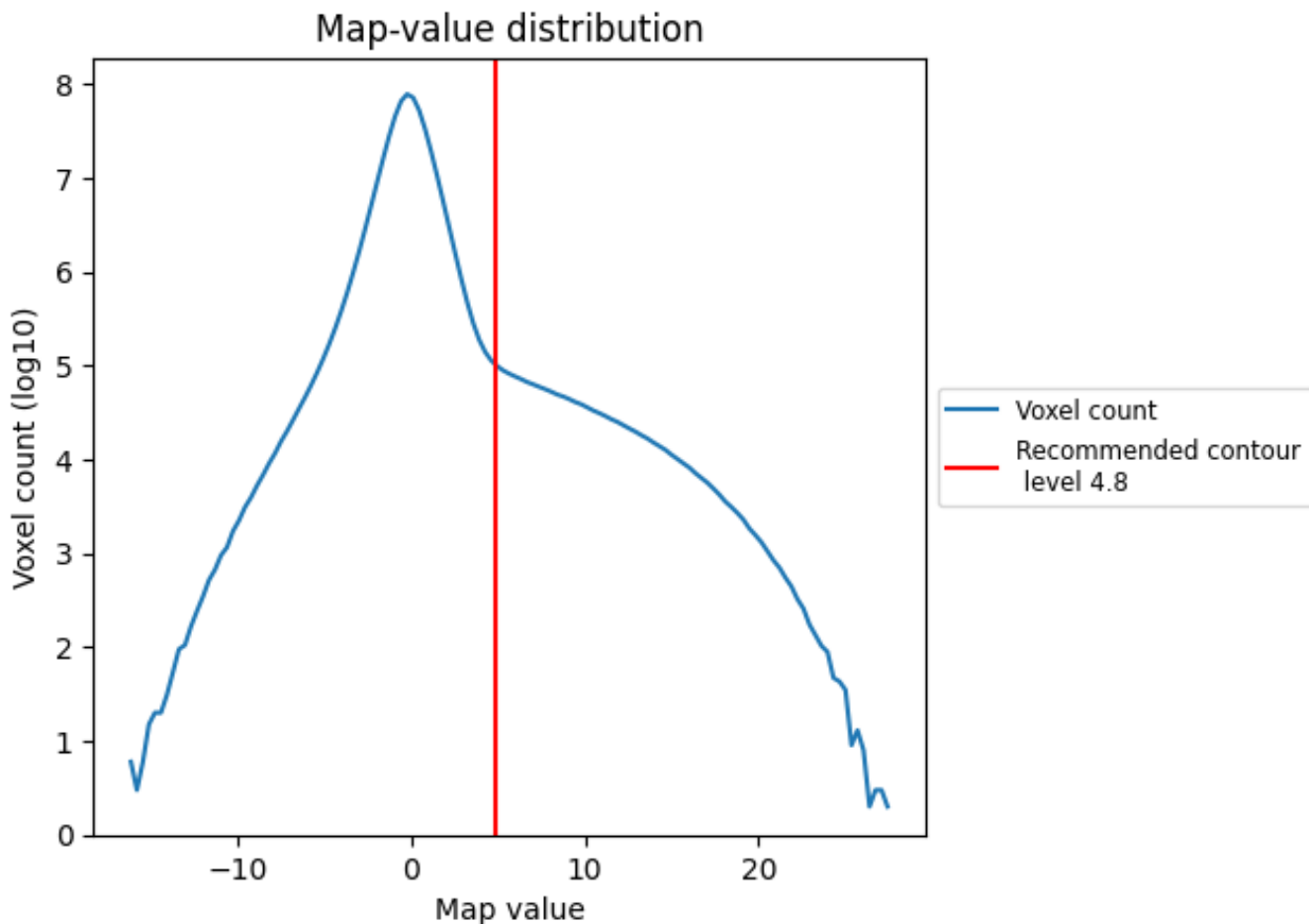
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

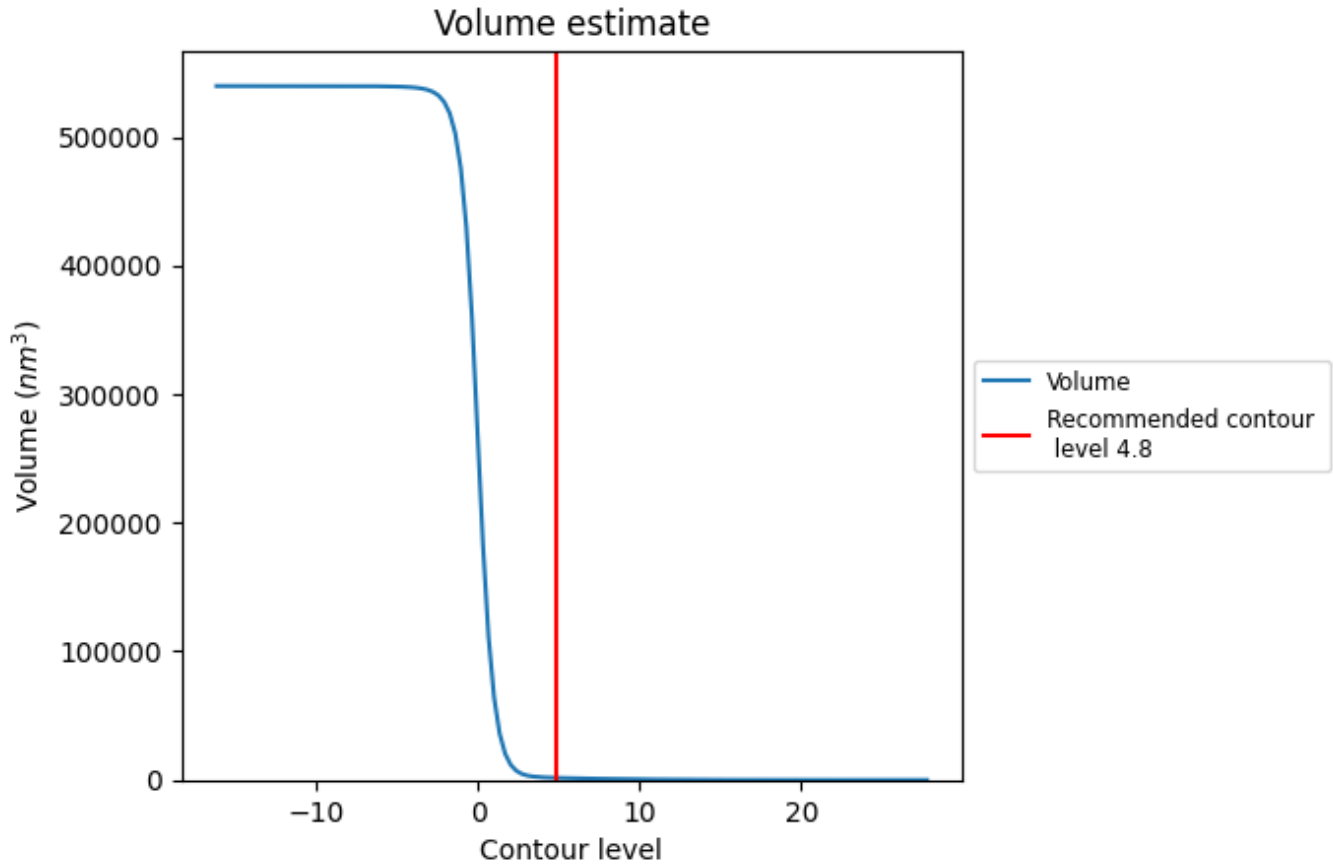
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

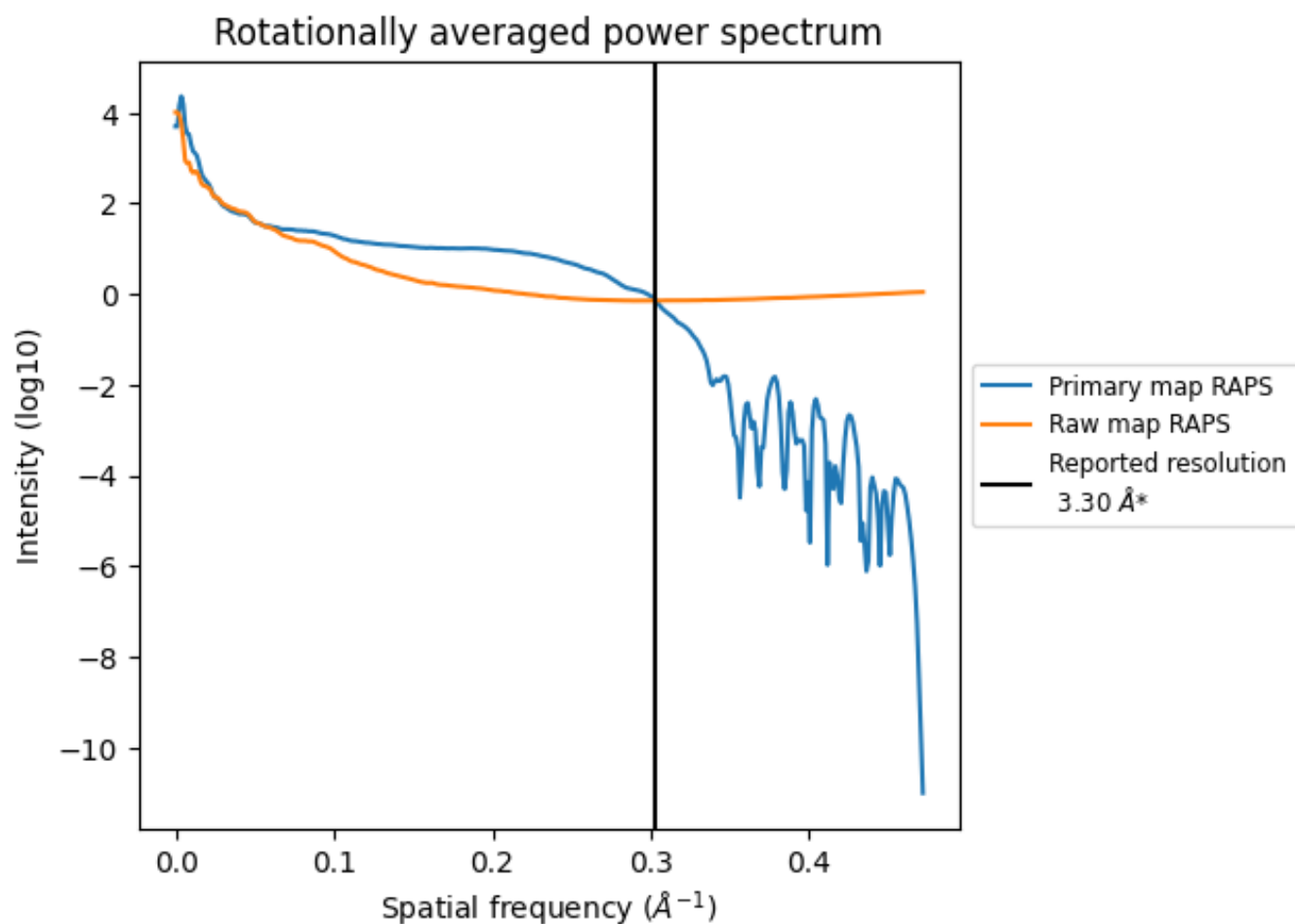
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1653 nm^3 ; this corresponds to an approximate mass of 1493 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](#)

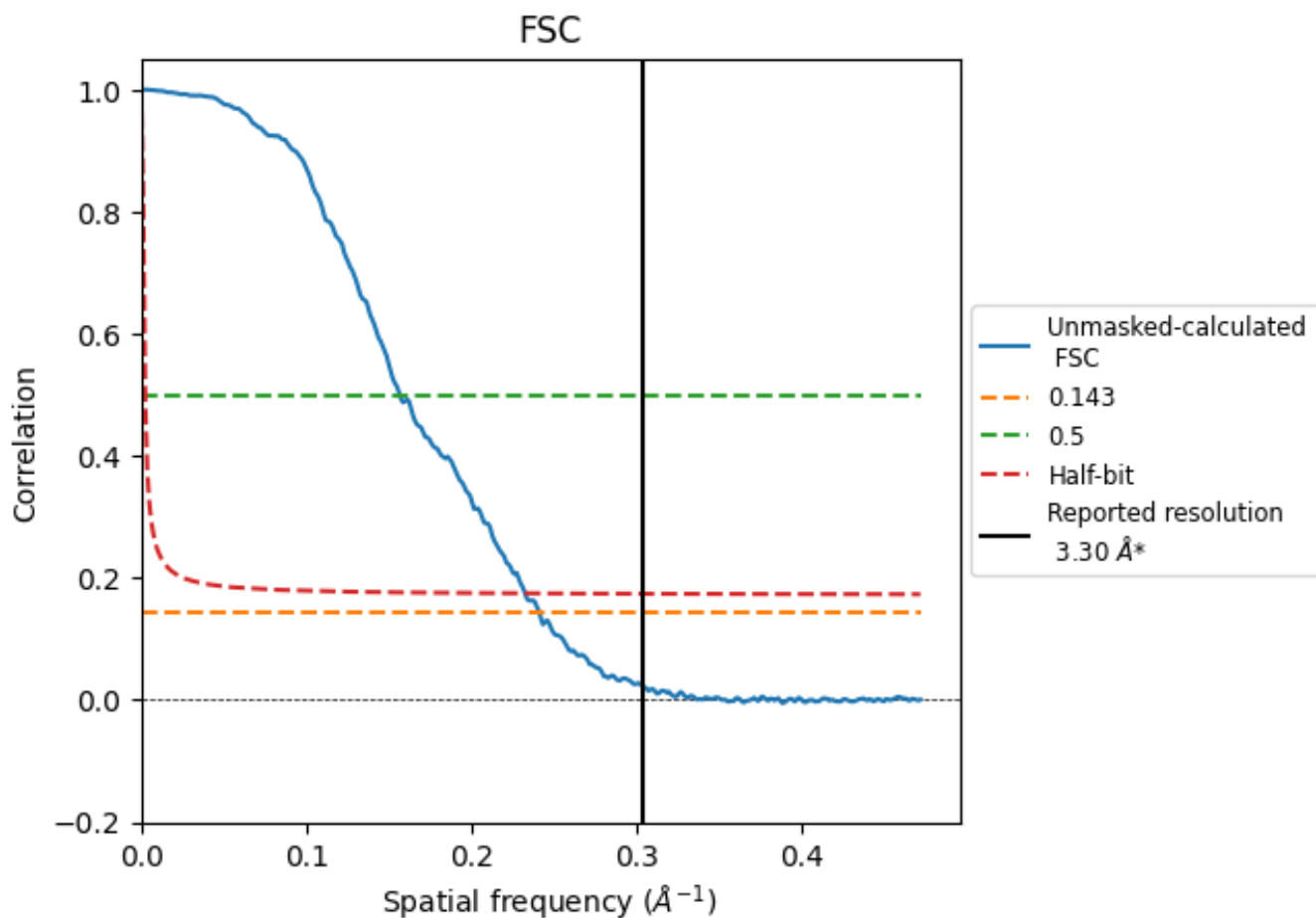


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

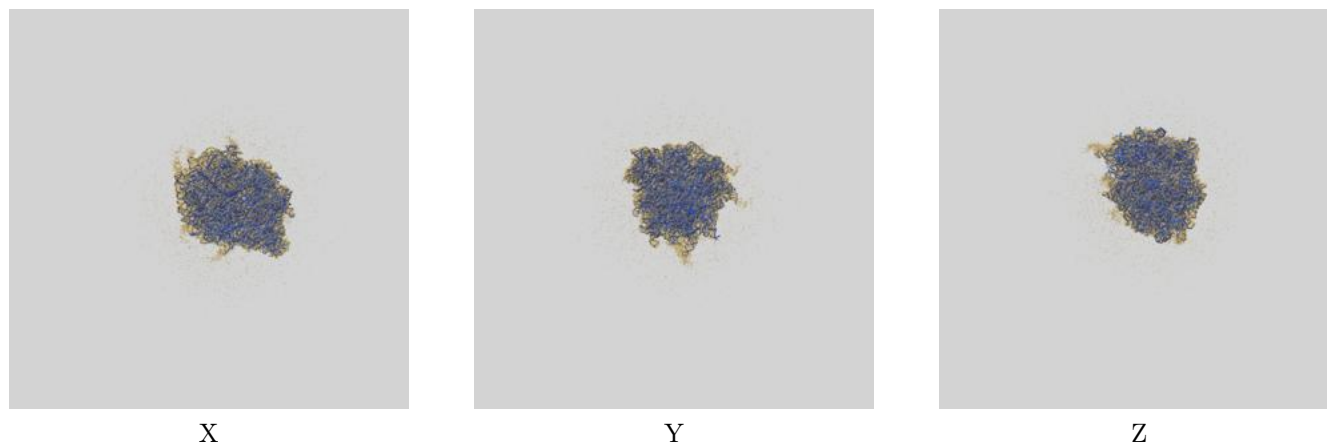
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.15	6.39	4.30

*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 4.15 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

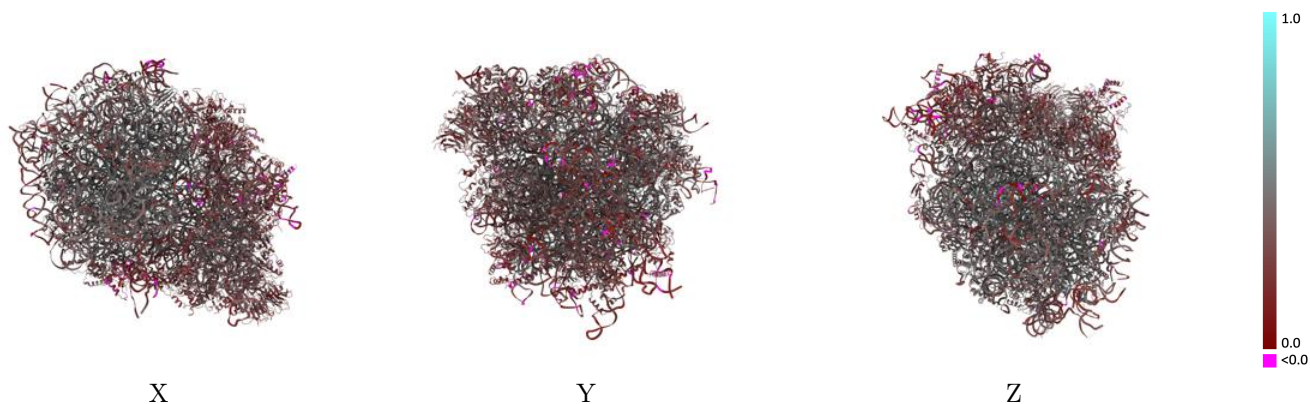
This section contains information regarding the fit between EMDB map EMD-23500 and PDB model 7LS1. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



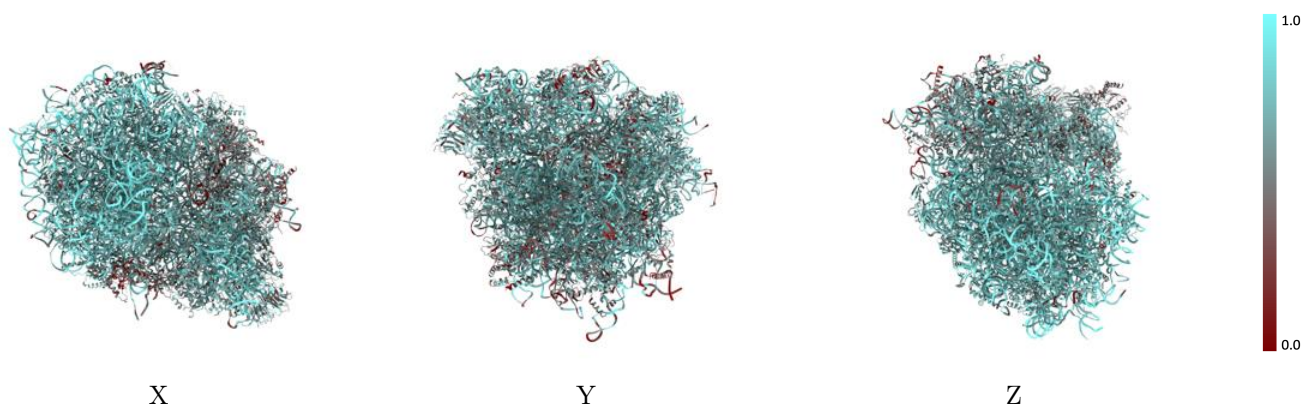
The images above show the 3D surface view of the map at the recommended contour level 4.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



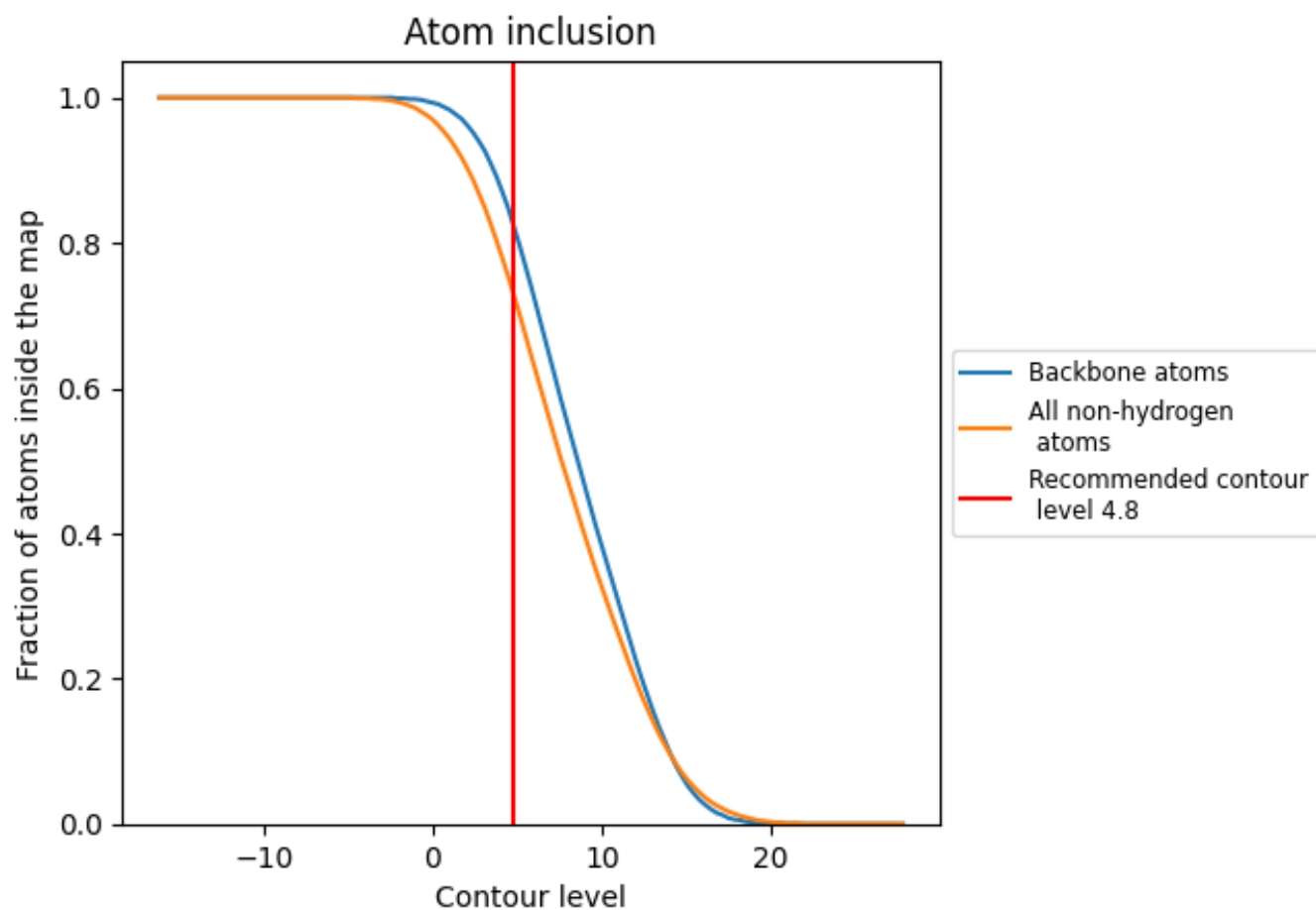
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (4.8).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 73% 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 (4.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7270	 0.3740
A	 0.1180	 0.2510
A1	 0.7010	 0.4300
A2	 0.8360	 0.3980
A3	 0.6120	 0.3230
B1	 0.6850	 0.3800
B2	 0.9140	 0.4390
B3	 0.6610	 0.3360
C1	 0.7100	 0.4280
C2	 0.8520	 0.4120
C3	 0.5900	 0.3270
D1	 0.6800	 0.4410
D2	 0.6710	 0.4510
D3	 0.6030	 0.3320
E1	 0.6750	 0.3810
E2	 0.7020	 0.4410
E3	 0.5100	 0.3530
F1	 0.7310	 0.4170
F2	 0.7020	 0.4390
F3	 0.6020	 0.3780
G1	 0.7310	 0.4160
G2	 0.7670	 0.4000
G3	 0.5290	 0.3380
H1	 0.7120	 0.4490
H2	 0.7190	 0.4200
H3	 0.6670	 0.3520
I2	 0.7230	 0.4300
I3	 0.6200	 0.3020
J2	 0.7120	 0.4500
J3	 0.6050	 0.3460
K2	 0.7020	 0.4430
K3	 0.5250	 0.2700
L1	 0.3110	 0.1850
L2	 0.6720	 0.3930
L3	 0.5280	 0.2780





















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Chain	Atom inclusion	Q-score
M2	 0.7330	 0.4460
M3	 0.4010	 0.2190
N2	 0.7090	 0.4460
N3	 0.5180	 0.3190
O2	 0.6720	 0.3740
O3	 0.5250	 0.3260
P2	 0.6600	 0.4580
P3	 0.5260	 0.3270
Q2	 0.5180	 0.3280
Q3	 0.4900	 0.2720
R2	 0.7010	 0.4240
R3	 0.5990	 0.3060
S2	 0.7290	 0.4250
S3	 0.4940	 0.3050
T2	 0.7260	 0.4160
T3	 0.4700	 0.2890
U2	 0.7390	 0.4630
U3	 0.5430	 0.2730
V2	 0.6570	 0.3950
W2	 0.7120	 0.4090
X2	 0.7110	 0.4320
Y2	 0.6830	 0.4530
Z2	 0.7190	 0.4580
a2	 0.6900	 0.4280
b2	 0.7220	 0.3890
c2	 0.7250	 0.4000
d2	 0.7440	 0.4490
e2	 0.6470	 0.3700
f2	 0.6600	 0.4370
g2	 0.7270	 0.4350
h2	 0.5310	 0.3970
i2	 0.6870	 0.4390
j	 0.6260	 0.3010
j2	 0.6610	 0.4210
k	 0.4190	 0.2240
k2	 0.7540	 0.4350
m	 0.5360	 0.3130
m2	 0.7750	 0.3350
n2	 0.6590	 0.2990
o2	 0.6200	 0.3320
p2	 0.5220	 0.3000
q2	 0.6180	 0.3500

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Chain	Atom inclusion	Q-score
r2	 0.4650	 0.3000
s2	 0.5880	 0.3200
t	 0.4880	 0.2660
u	 0.4890	 0.3190
v2	 0.6190	 0.3010
w2	 0.4580	 0.3230
x2	 0.6010	 0.3270
y2	 0.6180	 0.3450
z2	 0.5800	 0.3290