



Full wwPDB EM Validation Report ⓘ

Dec 11, 2022 – 07:59 pm GMT

PDB ID : 4UG0
EMDB ID : EMD-2938
Title : STRUCTURE OF THE HUMAN 80S RIBOSOME
Authors : Khatter, H.; Myasnikov, A.G.; Natchiar, S.K.; Klaholz, B.P.
Deposited on : 2015-03-20
Resolution : 3.60 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

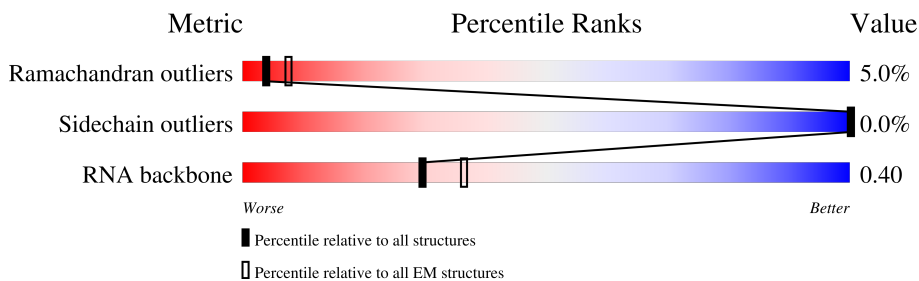
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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





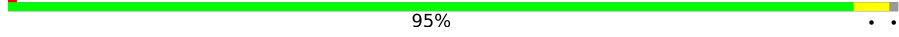
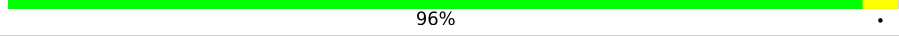
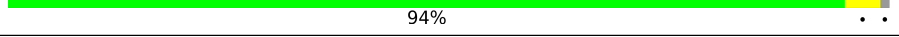
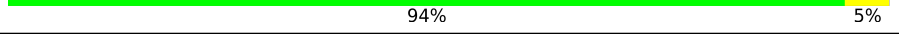

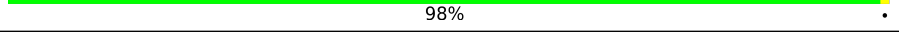
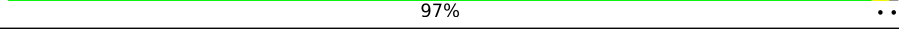

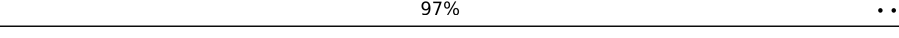
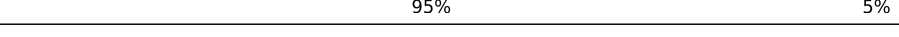
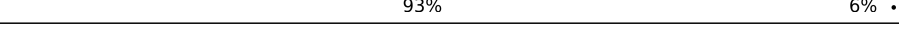
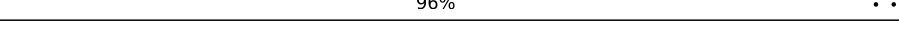


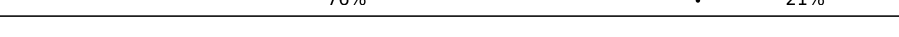

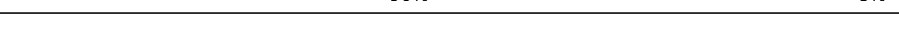






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	L5	5070	
2	L7	121	
3	L8	157	
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	

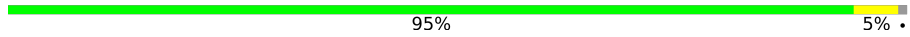
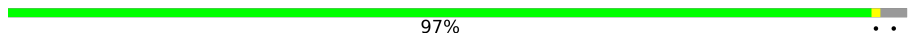
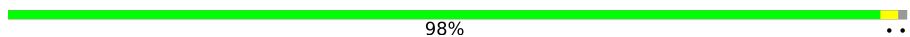
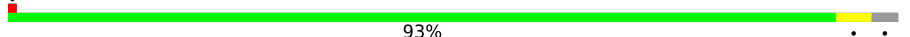


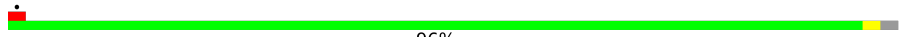



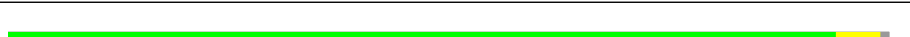


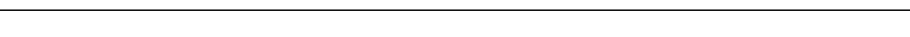
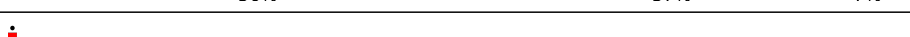
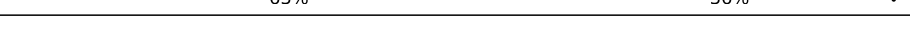



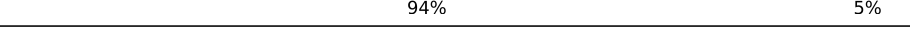


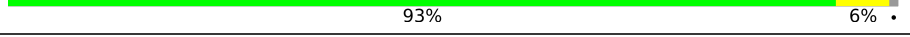


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Mol	Chain	Length	Quality of chain
9	LF	248	 89% 9%
10	LG	266	 85% 6% 9%
11	LH	192	 95%
12	LI	214	 96%
13	LJ	178	 94%
14	LL	211	 94% 5%
15	LM	215	 62% 35%
16	LN	204	 98%
17	LO	203	 97%
18	LP	184	 80% 17%
19	LQ	188	 97%
20	LR	196	 95% 5%
21	LS	176	 93% 6%
22	LT	160	 96%
23	LU	128	 78% 21%
24	LV	140	 89% 6%
25	LW	157	 76% 21%
26	LX	156	 76% 23%
27	LY	145	 90% 8%
28	LZ	136	 97%
29	La	148	 96%
30	Lb	159	 46% 53%
31	Lc	115	 80% 5% 15%
32	Ld	125	 82% 14%
33	Le	135	 91% 5%

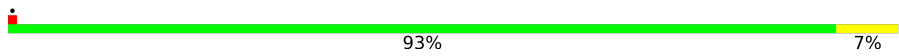
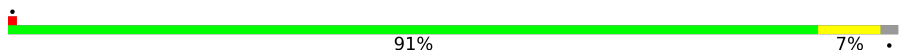

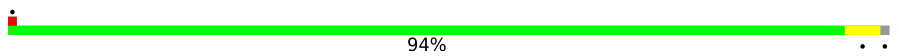

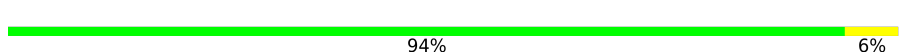
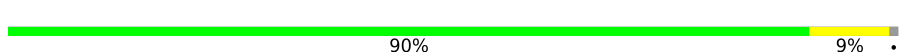


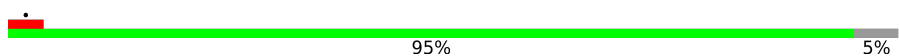

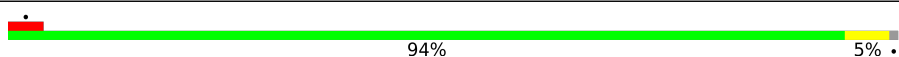
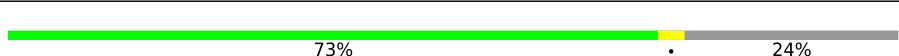
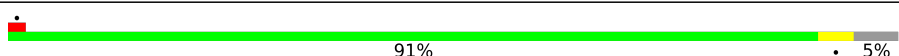
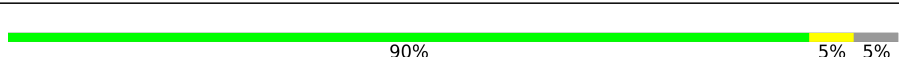

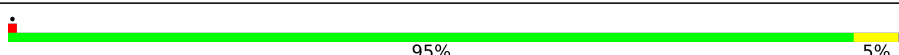
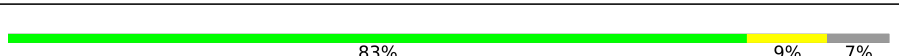
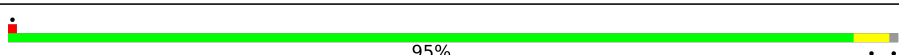
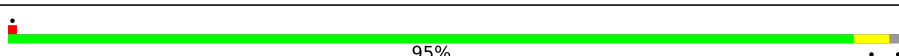
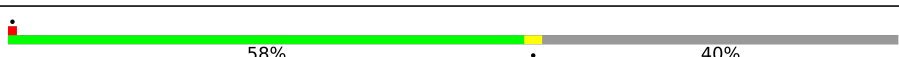
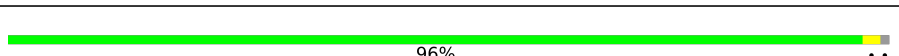
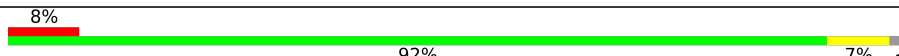
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Mol	Chain	Length	Quality of chain
34	Lf	110	 95% 5%
35	Lg	117	 97%
36	Lh	123	 98%
37	Li	105	 93%
38	Lj	97	 81% 7% 11%
39	Lk	70	 91% 7%
40	Ll	51	 96%
41	Lm	128	 39% 59%
42	Ln	25	 96%
43	Lo	106	 96%
44	Lp	92	 93% 5%
45	Lr	137	 87% 9%
46	Lz	217	 12% 93% 7%
47	S2	1869	 56% 37% 7%
48	S6	75	 63% 36%
49	SA	295	 73% 25%
50	SB	264	 78% 19%
51	SD	243	 86% 7% 7%
52	SE	263	 94% 5%
53	SF	204	 87% 7% 6%
54	SH	194	 90% 8%
55	SI	208	 93% 6%
56	SK	165	 57% 41%
57	SL	158	 91% 6%
58	SP	145	 57% 10% 33%

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Mol	Chain	Length	Quality of chain
59	SQ	146	 93% 7%
60	SR	135	 91% 7%
61	SS	152	 89% 9%
62	ST	145	 94%
63	SU	119	 83% 13%
64	SV	83	 94% 6%
65	SX	143	 90% 9%
66	Sa	115	 84% 9% 7%
67	Sc	69	 84% 9% 7%
68	Sd	56	 95% 5%
69	Sf	156	 12% 38% 8% 54%
70	Sg	317	 94% 5%
71	SC	293	 73% 24%
72	SG	249	 91% 5%
73	SJ	194	 90% 5% 5%
74	SM	132	 19% 83% 9% 8%
75	SN	151	 95% 5%
76	SO	151	 83% 9% 7%
77	SW	130	 95%
78	SY	133	 95%
79	SZ	125	 58% 40%
80	Sb	84	 96%
81	Se	59	 8% 92% 7%

2 Entry composition [i](#)

There are 83 unique types of molecules in this entry. The entry contains 218776 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	L5	3776	80184	35672	14597	26140	3775	0	0

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	LA	248	1898	1189	389	314	6	0	0

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LB	402	3238	2060	608	556	14	0	0

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	LC	367	2919	1835	582	488	14	0	0

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	LD	293	2382	1507	434	427	14	0	0

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	LE	242	1958	1257	372	325	4	0	0

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	LF	225	1870	1202	358	301	9	0	0

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LG	241	1927	1228	371	324	4	0	0

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LH	190	1518	956	284	272	6	0	0

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN L10-LIKE.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LI	213	1711	1082	329	285	15	0	0

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LJ	176	1410	888	263	253	6	0	0

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN L15.

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

- Molecule 17 is a protein called 60S RIBOSOMAL PROTEIN L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	LS	175	1453	925	283	235	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	LT	159	1298	823	252	217	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	LU	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	LV	131	979	618	184	172	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	LW	124	1015	634	207	170	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	LX	120	985	630	185	169	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	LY	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	LZ	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	La	147	1162	736	237	186	3	0	0

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Lb	75	610	378	130	99	3	0	0

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	Lc	98	764	485	135	138	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	Ld	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	Le	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	Lf	109	876	555	174	144	3	0	0

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Lg	114	906	566	187	147	6	0	0

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Lh	122	1015	641	205	168	1	0	0

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	Li	102	832	521	177	129	5	0	0

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L37.

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

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L38.

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

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L39.

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

- Molecule 41 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	Lm	52	429	266	90	67	6	0	0

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	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	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S2	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 48 is a RNA chain called HUMAN INITIATOR MET-TRNA-I.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 49 is a protein called 40S RIBOSOMAL PROTEIN SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SA	222	Total	C	N	O	S	0	0
			1747	1109	306	324	8		

- Molecule 50 is a protein called 40S RIBOSOMAL PROTEIN S3A.

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

- Molecule 51 is a protein called 40S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 52 is a protein called 40S RIBOSOMAL PROTEIN S4, X ISOFORM.

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

- Molecule 53 is a protein called 40S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 54 is a protein called 40S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 55 is a protein called 40S RIBOSOMAL PROTEIN S8.

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

- Molecule 56 is a protein called 40S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	SK	98	827	539	148	134	6	0	0

- Molecule 57 is a protein called 40S RIBOSOMAL PROTEIN S11.

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

- Molecule 58 is a protein called 40S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	SP	97	804	505	155	138	6	0	0

- Molecule 59 is a protein called 40S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	SQ	146	1158	736	218	200	4	0	0

- Molecule 60 is a protein called 40S RIBOSOMAL PROTEIN S17-LIKE.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	SR	132	1072	673	199	195	5	0	0

- Molecule 61 is a protein called 40S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	SS	150	1235	776	250	208	1	0	0

- Molecule 62 is a protein called 40S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	ST	143	1112	697	214	198	3	0	0

- Molecule 63 is a protein called 40S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	SU	104	821	514	155	148	4	0	0

- Molecule 64 is a protein called 40S RIBOSOMAL PROTEIN S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	SV	83	636	393	117	121	5	0	0

- Molecule 65 is a protein called 40S RIBOSOMAL PROTEIN S23.

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

- Molecule 66 is a protein called 40S RIBOSOMAL PROTEIN S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	Sa	107	847	528	176	138	5	0	0

- Molecule 67 is a protein called 40S RIBOSOMAL PROTEIN S28.

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

- Molecule 68 is a protein called 40S RIBOSOMAL PROTEIN S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	Sd	53	445	278	90	72	5	0	0

- Molecule 69 is a protein called UBIQUITIN-40S RIBOSOMAL PROTEIN S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Sf	71	581	367	109	98	7	0	0

- Molecule 70 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1.

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

- Molecule 71 is a protein called 40S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	SC	222	1725	1115	298	302	10	0	0

- Molecule 72 is a protein called 40S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	SG	237	1923	1200	387	329	7	0	0

- Molecule 73 is a protein called 40S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	SJ	185	1525	969	306	248	2	0	0

- Molecule 74 is a protein called 40S RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	SM	122	952	596	169	179	8	0	0

- Molecule 75 is a protein called 40S RIBOSOMAL PROTEIN S13.

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

- Molecule 76 is a protein called 40S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	SO	140	1049	642	204	197	6	0	0

- Molecule 77 is a protein called 40S RIBOSOMAL PROTEIN S15A.

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

- Molecule 78 is a protein called 40S RIBOSOMAL PROTEIN S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 79 is a protein called 40S RIBOSOMAL PROTEIN S25.

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

- Molecule 80 is a protein called 40S RIBOSOMAL PROTEIN S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 81 is a protein called 40S RIBOSOMAL PROTEIN S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 82 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	L5	149	Total	Mg	0
			149	149	
82	L7	5	Total	Mg	0
			5	5	
82	L8	2	Total	Mg	0
			2	2	
82	LA	1	Total	Mg	0
			1	1	
82	LB	1	Total	Mg	0
			1	1	
82	LH	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
82	LJ	1	Total 1	Mg 1	0
82	LN	1	Total 1	Mg 1	0
82	LP	1	Total 1	Mg 1	0
82	LQ	1	Total 1	Mg 1	0
82	La	1	Total 1	Mg 1	0
82	Le	1	Total 1	Mg 1	0
82	Ll	1	Total 1	Mg 1	0
82	S2	66	Total 66	Mg 66	0
82	S6	7	Total 7	Mg 7	0

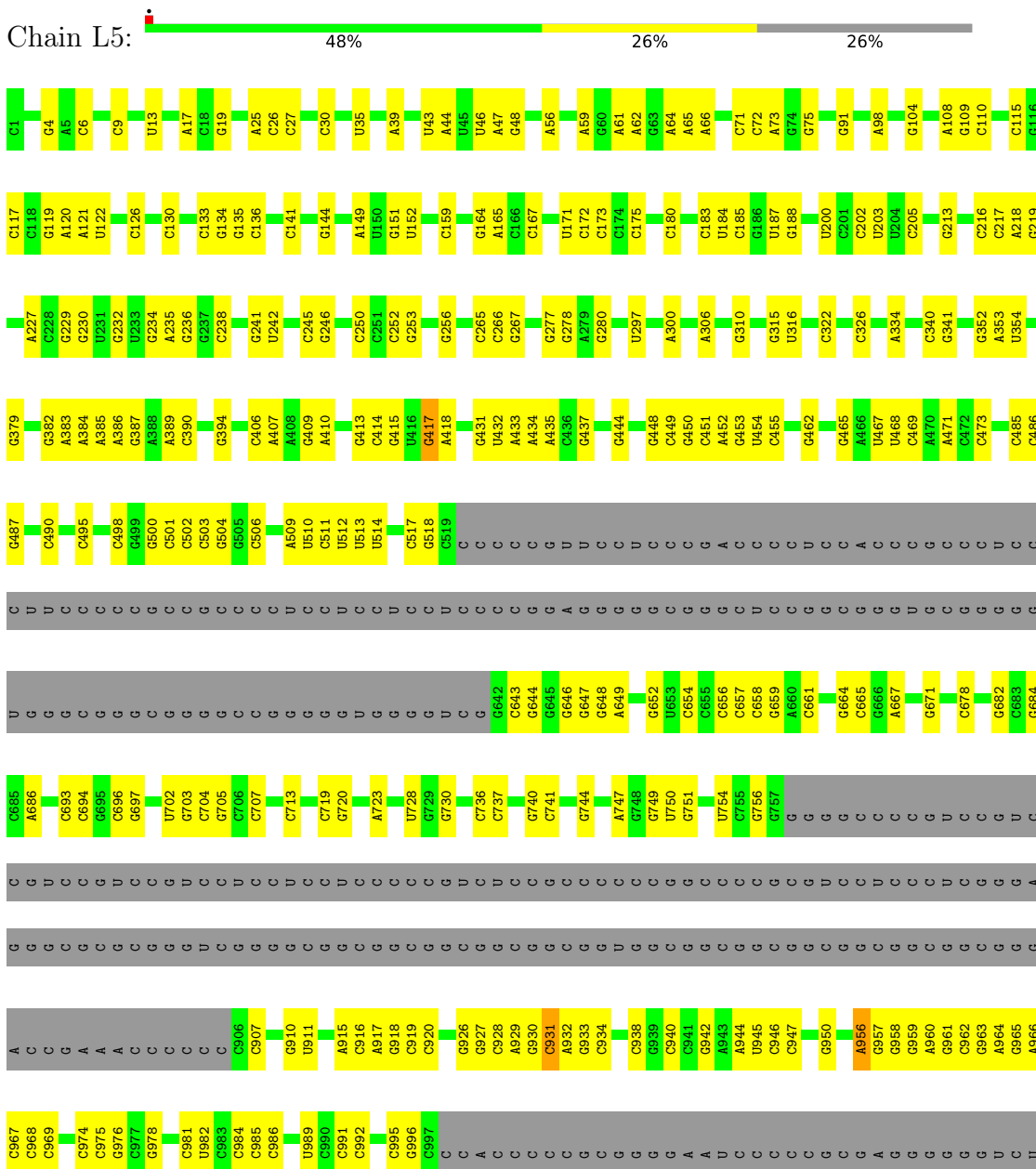
- Molecule 83 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	Lg	1	Total 1	Zn 1	0
83	Lj	1	Total 1	Zn 1	0
83	Lm	1	Total 1	Zn 1	0
83	Lo	1	Total 1	Zn 1	0
83	Lp	1	Total 1	Zn 1	0
83	Sa	1	Total 1	Zn 1	0

3 Residue-property plots i

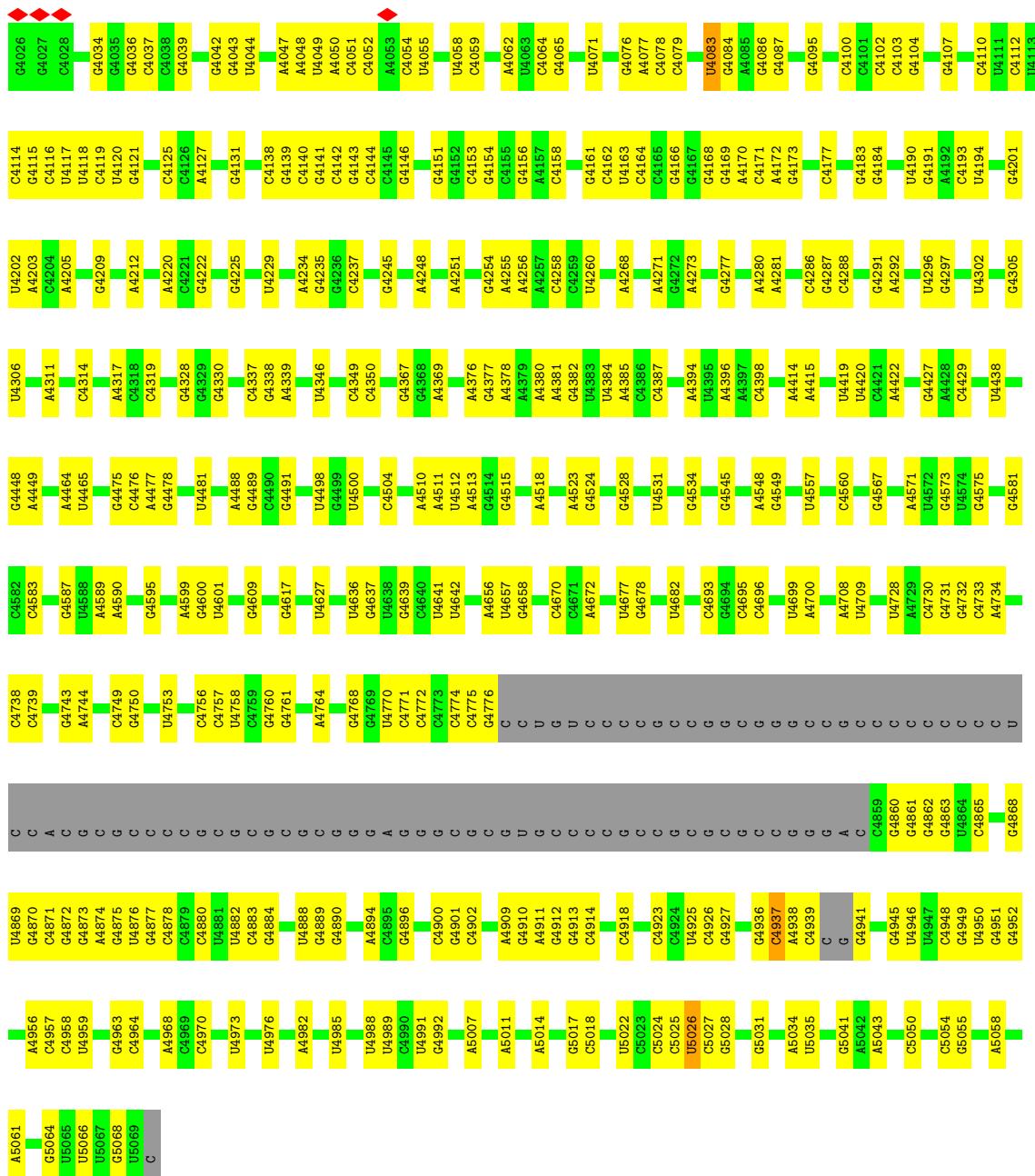
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 28S ribosomal RNA

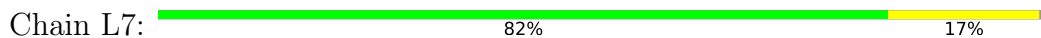


C2346	A2347	G2243	A2009	C1931	A1788	C1718	G1455	U1364	A1255	G1171	C
A2348	C2011	C2244	A2010	A1932	A1793	G1719	C1456	C1365	G1256	C1172	C
G2351	A2012	C2247	C2112	C1936	G1804	A1612	G1457	G1366	G1257	A1173	U
C2361	A2013	A2004	G2113	G1936	A1805	C1614	C1472	C1367	G1258	G1178	C
U2362	A2017	A2005	G2114	G1940	A1806	A1623	G1475	A1368	G1259	U1179	C
G2363	C2018	G2006	G2115	U1947	G1806	G1624	C1480	G1369	G1260	C1180	C
G2364	C2019	G2007	G2116	G1948	C1807	G1625	C1481	G1370	G1261	C1181	C
U2365	U2020	G2008	G2117	G1954	G1815	G1626	C1482	A1371	G1262	C1182	C
C2366	C2023	G2009	G2118	U1955	G1820	G1629	G1483	A1372	C1267	C1183	G
U2367	A2026	G2010	G2119	A1956	G1821	G1630	G1484	C1376	C1268	C1184	G
C2368	G2034	G2011	G2120	U1957	U1822	A1631	C1485	G1377	G1269	C1185	G
A2369	G2034	G2012	G2121	A1958	G	A1632	G1486	G1378	G1270	C1186	C
G2390	G2045	G2013	G2122	U1959	U1823	A1633	C1487	C1379	G1271	C1187	C
A2395	G2046	G2014	G2123	A1960	G1829	A1634	G1488	C1380	C1272	C1188	C
G2396	A2047	G2015	C2124	G1961	G1832	A1638	C1489	U1381	G1273	C1191	C
A2402	U2048	G2016	G2125	A1962	G1833	G1641	G1490	G1382	G1274	C1192	C
G2403	G2055	G2017	G2126	C1963	U1834	A1646	G1491	A1387	G1275	C1193	C
A2404	G2056	G2018	G2127	U1964	G1835	U1649	G1492	G1388	G1276	C1202	C
C2410	A2057	G2019	C2128	C1965	U1836	A1650	G1493	G1389	G1277	C1203	C
G2414	C2062	G2020	C2129	U1966	G1837	A1651	G1494	U1390	C1278	C1204	C
G2414	G2063	G2021	G2130	A1967	G1838	G1641	G1495	U1391	G1279	G1205	C
C2422	G2064	G2022	G2131	U1968	U1839	A1646	G1496	G1392	G1280	U1209	G
U2425	G2068	G2023	C	G1969	G1840	U1649	G1497	G1393	C1281	C1210	C
U2426	A2069	G2024	C	C1970	C	A1650	A1497	U1394	G1285	C1211	C
A2431	G2073	G2025	C	U1971	U1840	A1651	G1501	G1404	U1285	G1211	A
G2448	G2074	G2026	C	U1972	C	G1654	G1502	G1407	G1288	C1214	C
A2449	G2075	G2027	C	U1973	G1842	G1654	G1512	C1407	G1289	C1215	C
G2276	G2076	G2028	C	C1974	G1842	U1654	G1523	C1408	C1290	C1216	C
C2289	G2077	G2029	C	U1975	G1855	U1656	A1524	C1409	G1291	G1217	C
C2290	C2077	G2030	C	U1976	G1856	G1657	A1525	U1410	G1292	G1218	G
G2299	G2084	G2031	C	U1977	U1866	G1661	G1530	C1411	G1293	G1219	G
A2300	G2085	G2032	C	U1978	A1867	C1676	G1534	C1412	A1294	G1220	G
G2301	G2088	G2033	C	U1979	U1868	U1677	U1539	C1413	G1295	G1221	G
U2304	G2089	G2034	C	U1980	G1869	U1677	G1540	C1414	G1296	A1222	C
U2312	U2090	G2035	C	U1981	U1872	G1681	G1547	C1415	U1297	G	C
C2324	C2091	G2036	C	U1982	G1882	C1686	G1552	G1416	U1298	U	C
G2463	A2092	G2037	C	U1983	U1882	U1681	G1564	G1417	C1301	C1237	C
A2484	G2094	G2038	C	U1984	G1890	C1694	A1564	C1418	U1302	G1238	C
U2465	A2095	G2039	C	U1985	G1890	U1694	G1566	C1419	A1303	A1238	C
G2467	G2096	G2040	C	U1986	C1893	U1694	G1574	G1419	C1322	C1239	U
A2332	U2097	G2041	C	U1987	C1897	C1696	G1578	C1420	A1326	U	C
G2488	G2098	G2042	C	U1988	U1897	C1697	U1578	A1420	G1329	C1243	G
A2333	G2099	G2043	C	U1989	A1897	C1698	G1582	C1421	A1330	G1244	G
G2487	A2100	G2044	C	U1990	C1897	A1699	U1591	G1425	G1435	C1245	C
G2488	G2104	G2045	C	U1991	U1915	C1699	G1592	C1436	U1339	C1250	G
G2487	C2107	G2046	C	U1992	U1918	C1700	U1596	C1437	U1339	G1251	C
G2488	G2108	G2047	C	U1993	C1919	C1700	G1597	C1438	A1343	C1252	C
G2488	G2109	G2048	C	U1994	C1920	C1701	G1597	U1438	G1343	G1253	C
			C	U1995	C1921	C1702	U1597	C1439	A1343	G1167	C
			C	U1996	G1922	C1703	U1597	U1439	A1343	G1168	C
			C	U1997	G1925	C1704	U1597	C1441	G1353	G1169	C
			C	U1998	A1925	C1705	U1597	C1441	A1354	G1170	C
			C	U1999	A1929	C1706	U1597	C1446	G1358		
			C	U2000	U1930	C1707	U1597	G1453	G1359		
			C	U2001	U1930	C1708	U1597	G1454	G1360		
			C	U2002	U1930	C1709	U1597				
			C	U2003	U1930	C1710	U1597				
			C	U2004	U1930	C1711	U1597				
			C	U2005	U1930	C1712	U1597				
			C	U2006	U1930	C1713	U1597				
			C	U2007	U1930	C1714	U1597				
			C	U2008	U1930	C1715	U1597				

U3959	C3843	G3742	G3615	C2860	U2740	G2624	C2489
A3960	C3866	U3745	U3616	C2861	A2743	G2634	U2490
A3962	A3867	U3748	G3625	G2862	G2753	U2636	C2491
A3963	G3868	A3748	G3626	A2864	G2754	G2637	U2495
A3965	C3869	C3749	G3635	U2869	A2755	U2638	G2502
A3966	C3870	G3750	A3635	A2870	G2756	G2639	G2503
G3967	A3871	G3751	C3635	U2874	G2760	U2648	G2504
U3968	A3877	C3752	U3640	U2875	U2761	G2648	C2505
G3969	C3878	G3753	A3641	G2877	G2762	G2649	G2506
A3972	C3879	A3753	A3642	U2884	U2763	G2653	A2507
G3973	G3880	G3755	A3643	A2885	A2766	G2662	A2511
G3974	G3881	A3756	U3644	U2886	U2767	G2662	A2512
G3975	G3882	G3757	U3645	U2887	C2768	G2670	A2513
G3976	G3883	A3758	A3646	G2888	U2769	G2675	G2518
C3977	G3884	U3759	G3659	U2888	C2770	A2576	U2519
C3978	G3885	A3760	C3660	A2894	G2776	G2681	A2527
C3979	A3889	C3761	G3661	G2895	A2776	G2686	A2528
C3987	A3890	U3762	G3662	U2896	A2783	U2687	A2537
C3988	U3891	G3765	G3669	G2902	C2784	G2688	G2544
C3989	U3892	A3766	C3670	U2903	C2785	G2688	U2545
C3989	G3895	C3767	G3671	U2904	C2786	G2688	G2546
C3990	G3896	U3768	G3672	G2905	A2787	A2695	G2547
C3991	G3897	C3769	C3673	G2906	U2788	A2696	A2551
G3992	G3897	U3770	G3674	U2907	A2789	U2701	G2552
U3993	A3901	C3771	C3681	G2908	A2794	G2702	U2553
G3994	A3905	U3772	A3682	C2909	C2797	G2703	U2554
U3995	A3906	G3776	U3690	G2910	U2803	G2704	G2555
C3996	G3907	G3777	C3696	G	U2806	G2705	G2556
C3997	A3908	G3777	C3696	G	A2807	U2708	G2569
C3997	U3914	A3784	C3696	G	C2814	G2709	U2570
C3998	U3915	A3785	U3697	G	A2815	G2710	C2571
C3999	U3915	A3786	C3698	G	G2816	G2711	C2572
G4000	G3922	U3789	C3699	G	G2822	G2712	A2573
G4000	A3923	U3790	G3705	G	A2825	G2714	G2576
G4002	G3933	C3791	U3709	G	U2826	G2717	C2583
A4003	G3934	A3795	G3710	G	G2827	U2718	G2586
G4004	C3935	U3802	A3711	G	U2828	C2719	A2587
G4005	G3938	A3803	A3712	G	G2829	C2720	C2588
G4006	G3939	A3807	U3713	G	U2830	G2721	G2596
G4007	A3943	C3810	G3714	G	G2831	U2722	A2601
C4008	G3944	C3811	A3723	G	A2832	G2723	G2602
C4009	A3947	G3812	A3727	G	A2833	A2725	G2605
C4010	C3948	C3813	A3728	G	U2833	G2726	G2618
G4011	A3949	U3730	U3729	G	A2845	G2735	G2618
G4012	G4012	U3814	U3730	G	A2857	G2739	G2618
G4013	A3954	A3817	C3731	G	A2858	G2739	G2618
G4014	G3955	U3818	A3732	G	G2859	G2739	G2618
C4015	U3957	G3819	A3733	G	G2859	G2739	G2618
G4016	U3957	G3819	U3734	G	G2859	G2739	G2618
G4017	C3958	U3840	A3736	G	G2859	G2739	G2618
G4018	C3958	U3840	A3736	G	G2859	G2739	G2618
G4019	C3958	U3840	A3736	G	G2859	G2739	G2618
U4020	C3958	U3840	A3736	G	G2859	G2739	G2618
C4021	C3958	U3840	A3736	G	G2859	G2739	G2618
C4022	C3958	U3840	A3736	G	G2859	G2739	G2618
G4023	C3958	U3840	A3736	G	G2859	G2739	G2618
C4024	C3958	U3840	A3736	G	G2859	G2739	G2618



- Molecule 2: 5S ribosomal RNA



- Molecule 3: 5.8S ribosomal RNA





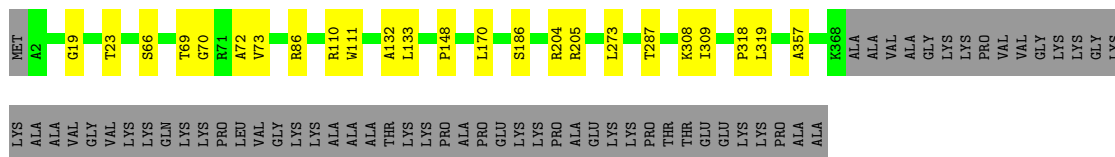
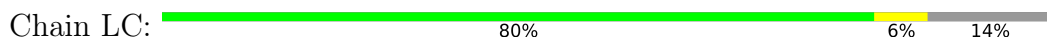
• Molecule 4: 60S RIBOSOMAL PROTEIN L8



• Molecule 5: 60S RIBOSOMAL PROTEIN L3



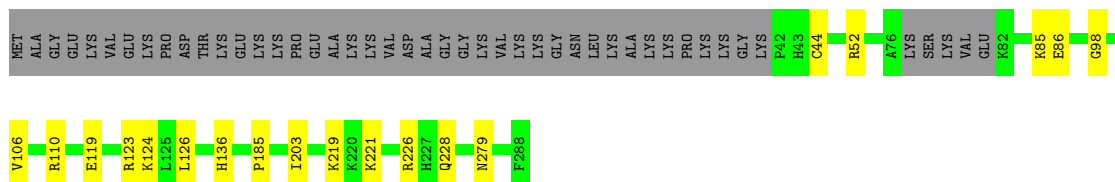
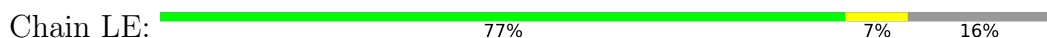
• Molecule 6: 60S RIBOSOMAL PROTEIN L4



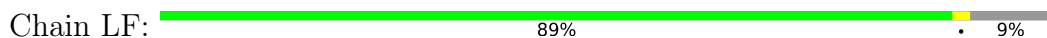
• Molecule 7: 60S RIBOSOMAL PROTEIN L5

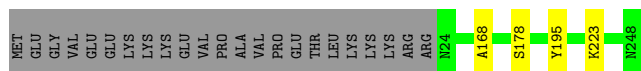


• Molecule 8: 60S RIBOSOMAL PROTEIN L6

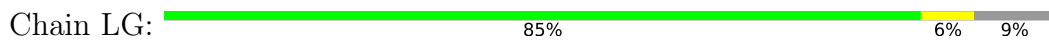


• Molecule 9: 60S RIBOSOMAL PROTEIN L7





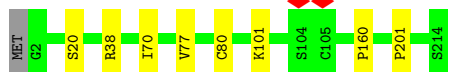
• Molecule 10: 60S RIBOSOMAL PROTEIN L7A



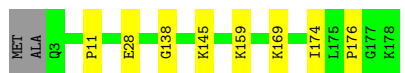
• Molecule 11: 60S RIBOSOMAL PROTEIN L9



• Molecule 12: 60S RIBOSOMAL PROTEIN L10-LIKE



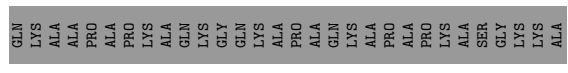
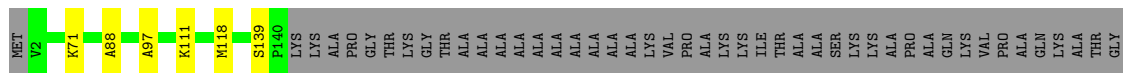
• Molecule 13: 60S RIBOSOMAL PROTEIN L11



• Molecule 14: 60S RIBOSOMAL PROTEIN L13



• Molecule 15: 60S RIBOSOMAL PROTEIN L14



• Molecule 16: 60S RIBOSOMAL PROTEIN L15

Chain LN:  98%




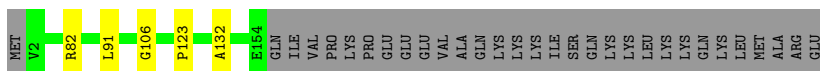
- Molecule 17: 60S RIBOSOMAL PROTEIN L13A

Chain LO:  97%



- Molecule 18: 60S RIBOSOMAL PROTEIN L17

Chain LP:  80% 17%



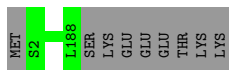
- Molecule 19: 60S RIBOSOMAL PROTEIN L18

Chain LQ:  97%



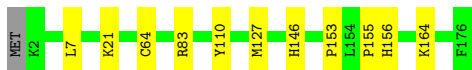
- Molecule 20: 60S RIBOSOMAL PROTEIN L19

Chain LR:  95% 5%



- Molecule 21: 60S RIBOSOMAL PROTEIN L18A

Chain LS:  93% 6%




- Molecule 22: 60S RIBOSOMAL PROTEIN L21

Chain LT:  96%



- Molecule 23: 60S RIBOSOMAL PROTEIN L22

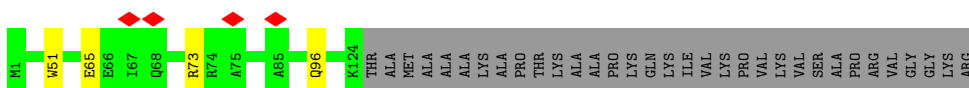
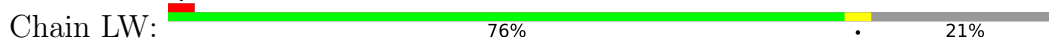
Chain LU:  78% 21%



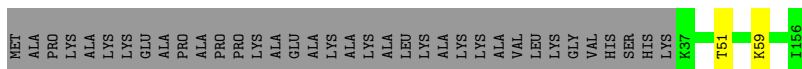
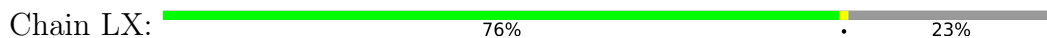
• Molecule 24: 60S RIBOSOMAL PROTEIN L23



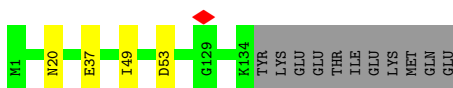
• Molecule 25: 60S RIBOSOMAL PROTEIN L24



• Molecule 26: 60S RIBOSOMAL PROTEIN L23A



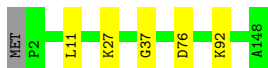
• Molecule 27: 60S RIBOSOMAL PROTEIN L26



• Molecule 28: 60S RIBOSOMAL PROTEIN L27

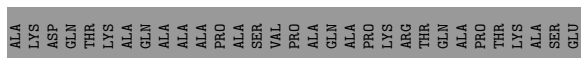
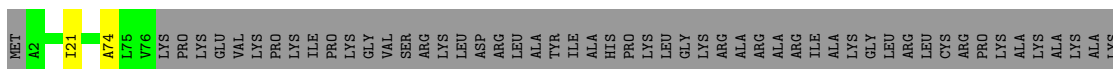


• Molecule 29: 60S RIBOSOMAL PROTEIN L27A

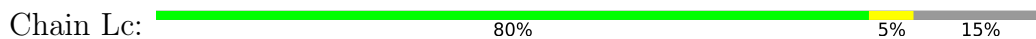


• Molecule 30: 60S RIBOSOMAL PROTEIN L29

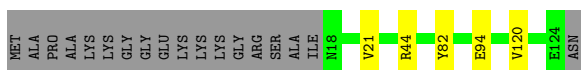
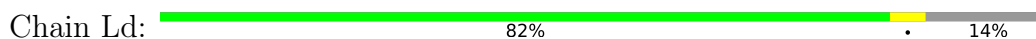




- Molecule 31: 60S RIBOSOMAL PROTEIN L30



- Molecule 32: 60S RIBOSOMAL PROTEIN L31



- Molecule 33: 60S RIBOSOMAL PROTEIN L32



- Molecule 34: 60S RIBOSOMAL PROTEIN L35A



- Molecule 35: 60S RIBOSOMAL PROTEIN L34

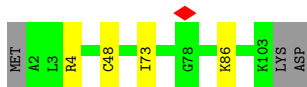


- Molecule 36: 60S RIBOSOMAL PROTEIN L35

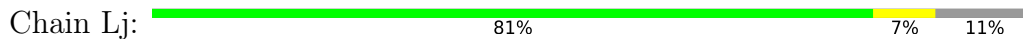


- Molecule 37: 60S RIBOSOMAL PROTEIN L36





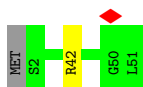
- Molecule 38: 60S RIBOSOMAL PROTEIN L37



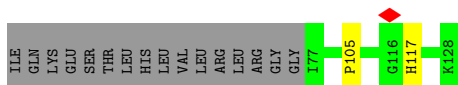
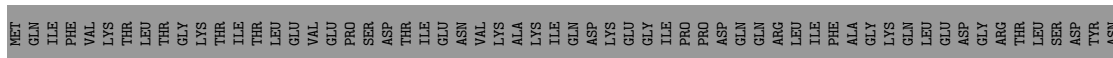
- Molecule 39: 60S RIBOSOMAL PROTEIN L38



- Molecule 40: 60S RIBOSOMAL PROTEIN L39



- Molecule 41: UBIQUITIN-60S RIBOSOMAL PROTEIN L40



- Molecule 42: 60S RIBOSOMAL PROTEIN L41



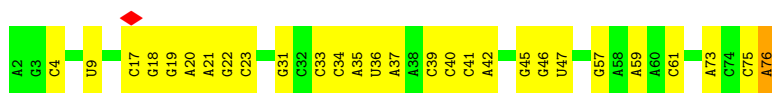
- Molecule 43: 60S RIBOSOMAL PROTEIN L36A



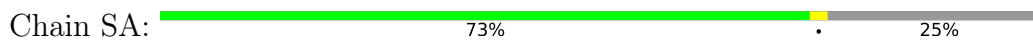
- Molecule 44: 60S RIBOSOMAL PROTEIN L37A

C750	C751	C752	C753	G	C	C	C	C	C	C	C	C	A	U	U	G	C	C	C	G	C785	G786	G787	G788	G789	G790	C791	A794	A795	G796	C797	A798	G799	U800	A810	A811	A812	A813	A814	U815	A818										
G821	U822	U823	A830	C833	C834	C835	G836	G837	G838	C839	C840	G841	C842	C843	A847	U848	C853	A854	A855	G868	A869	A870	G873	G874	A875	C876	C877	G878	C879	G880	G881	U882	U883	U887	U888	U889	G890	C891	U892	U893	G894	G895	U896	U897	U898	C900	C901	G902	A904		
G907	A908	C909	C912	A913	U914	U917	U918	A919	A920	C930	G933	G934	U939	U943	G952	C953	U954	A955	C956	A957	G958	G961	A962	A963	U965	G970	G971	C972	C973	G978	C979	A980	A981	A990	G991	A992	A996	C1138	C1139	U1002	A1008	U1016									
U1017	U1022	A1023	A1027	A1028	G1029	G1041	A1042	G1043	G1044	A1052	C1057	A1058	G1059	A1060	A1062	G1068	G1076	U1081	A1082	A1083	A1084	C1085	G1086	C1087	A1088	G1110	A1113	U1114	U1115	C1116	C1117	C1118	A1119	U1120	G1126	G1134	U1137	C1138	C1139	A1148	A1149	A1150	C1153								
U1154	U1155	U1156	G1166	A1170	G1171	U1172	G1175	C1180	A1181	U1186	U1288	U1289	A1194	A1195	G1198	A1208	G1211	G1212	A1214	C1215	C1216	A1217	G1224	C1231	U1238	U1239	A1240	A1241	U1242	U1248	C1249	A1250	A1251	A1253	G1256	G1257	A1258	A1259	A1260	C1284	A1285	C1288									
G1269	G1270	C1271	G1274	G1275	A1276	C1277	G1280	A1281	C1282	C1283	A1284	A1287	U1288	U1289	U1290	A1291	C1292	G1293	G1294	A1295	U1296	U1297	G1298	A1299	U1300	A1301	C1302	C1303	U1304	C1305	A1306	U1307	U1308	C1309	U1310	C1311	G1312	A1313	U1314	U1315	C1316	G1318	G1321	C1322	U1323	G1324	G1330	C1331	A1332	C1337	C1341
U1342	U1343	C1363	U1364	U1371	U1372	C1373	A1378	A1383	G1383	U1389	A1396	U1397	G1398	U1400	A1405	G1406	U1407	U1408	A1409	C1410	G1411	C1412	C1413	A1414	C1415	C1416	C1417	C1418	C1419	G1420	C1423	G1424	G1425	U1426	G1427	G1428	U1431	U1432	C1433	C1435	C1436	A1438	U1442	A1448	G1449	C1453					
A1454	A1455	G1456	U1457	G1458	U1463	C1464	C1468	C1471	A1472	G1473	A1474	U1475	A1476	U1477	A1480	G1481	A1484	U1487	C1488	A1489	C1490	G1493	U1494	G1495	U1496	C1497	A1498	U1505	A1506	U1507	A1508	U1509	G1510	U1511	C1512	C1513	G1514	G1515	G1520	A1521	C1522	C1523	G1524	U1525	A1526	C1527	A1531	C1532	A1533		
C1534	U1535	G1536	A1537	C1538	U1539	G1540	U1543	C1544	A1545	G1546	G1550	U1551	U1552	C1553	C1554	U1555	A1556	C1557	C1558	G1567	C1568	A1569	G1570	G1573	C1574	G1575	U1579	A1580	C1581	U1585	U1586	G1587	A1588	A1589	U1598	U1599	G1600	G1603	A1614	U1621	U1622	A1623	U1624	U1625	C1626	G1636	A1637	G1638			
G1639	A1640	C1644	G1648	A1651	G1652	U1653	A1654	C1655	C1660	A1661	U1662	C1663	A1664	G1665	A1679	G1680	G1686	C1687	C1688	U1694	A1695	C1696	A1697	C1698	C1701	U1714	A1719	U1720	U1721	G1722	U1729	U1730	A1735	G1736	G1737	G1742	G1743	G1744	A1745	U1746	G1747	G1748	C1751	C1752	C1753						
G1754	C1755	C1756	G1757	G1758	C1772	C1773	C1774	U1775	G1776	G1777	A1781	G1782	C1783	G1784	C1785	U1786	G1805	U1812	G1813	G1814	A1823	A1824	A1825	G1826	A1831	A1835	U1838	U1839	G1849	A1850	A1851	C1852	G1857	G1858	A1859	A1860	G1861	G1862	A1863	U1864	C1865	U1868	A1869								

● Molecule 48: HUMAN INITIATOR MET-TRNA-I



● Molecule 49: 40S RIBOSOMAL PROTEIN SA



MET	S2	G3	A4	E13	D31	P98	T125	S170	T223	LVS	GLU	GLU	GLU	PHE	GLN	GLY	TRP	THR	ALA	PRO	ALA	ALA	PRO	TRP	GLU	GLY	GLN	PRO	GLY	VAL	ALA	ASP	TRP	SER	GLY	GLY	VAL	GLN	VAL	PRO	SER	VAL	PRO	ILE	GLN	GLN	PHE	PRO	THR	GLU	ASP	TRP
-----	----	----	----	-----	-----	-----	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

SER
ALA
GLN
PRO
GLY
ALA
THR
THR
GLU
ASP
TRP
LEU
SER
ALA
ALA
ALA
PRO
THR
ALA
GLN
ALA
ALA
THR
GLU
TRP
VAL
GLY
ALA
THR
THR
ASP
TRP
SER

- Molecule 50: 40S RIBOSOMAL PROTEIN S3A

Chain SB: 78% 19%

MET
ALA
VAL
GLY
LYS
ASN
LYS
ARG
LEU
THR
SER
LYS
GLY
GLY
LYS
LYS
GLN
GLN
ALA
ALA
LYS
LYS
LYS
V21
V22
A37
N76
K83
L86
N147
P190
F223
E234
GLY
SER
SER
SER
GLY
LYS
LYS
ALA
THR
THR
GLY
GLY
ASP
GLU
THR
GLY
GLY
ALA
ALA
LYS
VAL
GLU
ARG
ALA
ASP
GLY
TYR

GLU
PRO
PRO
VAL
GLN
GLU
SER
VAL

- Molecule 51: 40S RIBOSOMAL PROTEIN S3

Chain SD: 86% 7% 7%

K1
A2
V3
E38
V41
T44
T55
E68
E81
E82
S83
T93
E135
S149
V163
D164
I198
G199
P200
D206
D215
E216
T220
T221
P222
I223
K227
GLY
GLY
LYS
PRO
PRO
GLU
PRO
PRO
ALA
ALA
MET
PRO
GLN
PRO
VAL
VAL
PRO
THR
ALA

- Molecule 52: 40S RIBOSOMAL PROTEIN S4, X ISOFORM

Chain SE: 94% 5%

MET
A2
P15
R30
R68
F69
V76
R77
D88
D93
V131
A144
L164
K168
T196
N214
M232
R245
G263

- Molecule 53: 40S RIBOSOMAL PROTEIN S5

Chain SF: 87% 7% 6%

MET
THR
GLU
TRP
GLU
THR
ALA
ALA
PRO
ALA
ALA
VAL
ALA
GLU
T14
P16
D16
I17
F20
D32
I33
V41
K42
K47
Y48
A57
R81
K85
K86
L87
T126
G129
R130
V139
S202
H203
R204

- Molecule 54: 40S RIBOSOMAL PROTEIN S7

Chain SH: 90% 8%

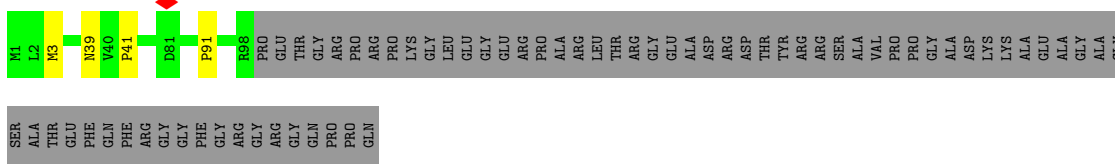
MET
PHE
SER
SER
S5
M12
S34
A38
V66
G69
R99
I100
K107
M112
K113
Q114
K115
E138
L148
Q162
P190
Q193
LEU

- Molecule 55: 40S RIBOSOMAL PROTEIN S8

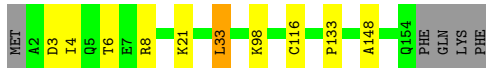
Chain SI: 93% 6%

MET
G2
K75
S86
V97
V102
G122
T130
F131
E132
K140
K143
M155
G180
D186
G207
LYS

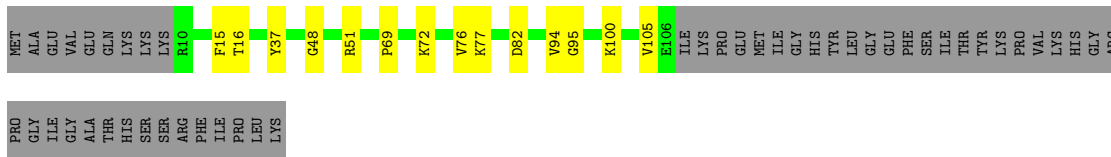
- Molecule 56: 40S RIBOSOMAL PROTEIN S10



- Molecule 57: 40S RIBOSOMAL PROTEIN S11



- Molecule 58: 40S RIBOSOMAL PROTEIN S15



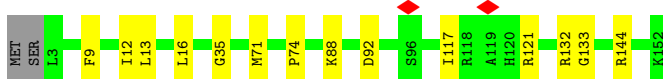
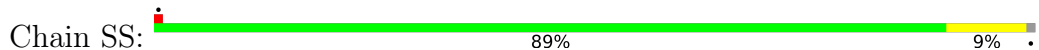
- Molecule 59: 40S RIBOSOMAL PROTEIN S16



- Molecule 60: 40S RIBOSOMAL PROTEIN S17-LIKE



- Molecule 61: 40S RIBOSOMAL PROTEIN S18

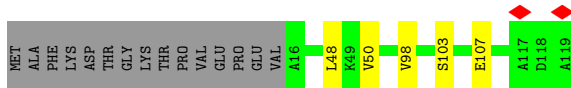
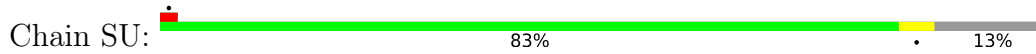


- Molecule 62: 40S RIBOSOMAL PROTEIN S19





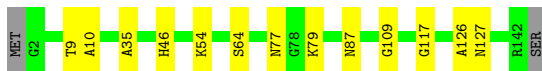
- Molecule 63: 40S RIBOSOMAL PROTEIN S20



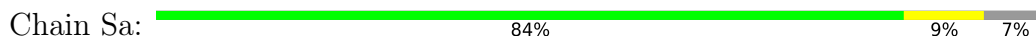
- Molecule 64: 40S RIBOSOMAL PROTEIN S21



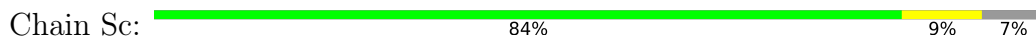
- Molecule 65: 40S RIBOSOMAL PROTEIN S23



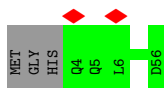
- Molecule 66: 40S RIBOSOMAL PROTEIN S26



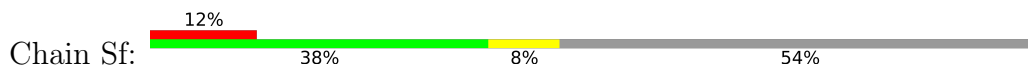
- Molecule 67: 40S RIBOSOMAL PROTEIN S28

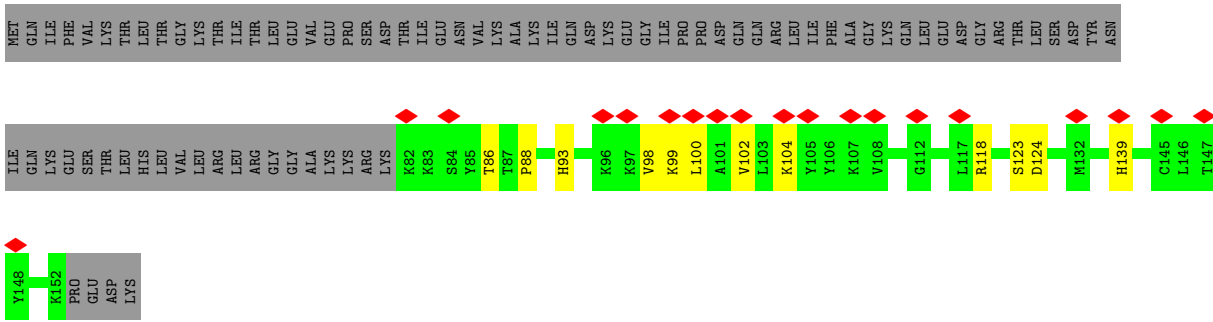


- Molecule 68: 40S RIBOSOMAL PROTEIN S29

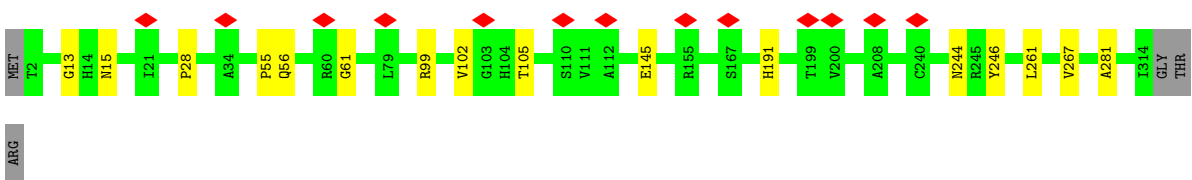


- Molecule 69: UBIQUITIN-40S RIBOSOMAL PROTEIN S27A

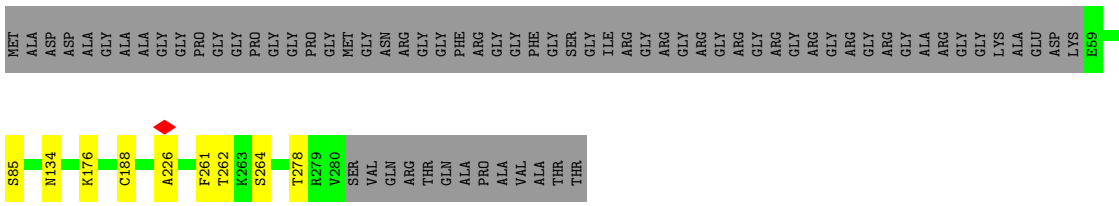




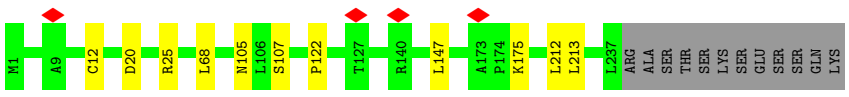
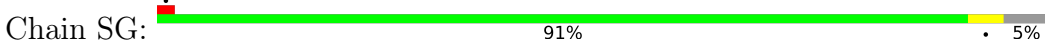
• Molecule 70: GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1



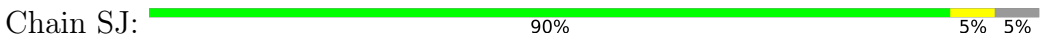
• Molecule 71: 40S RIBOSOMAL PROTEIN S2



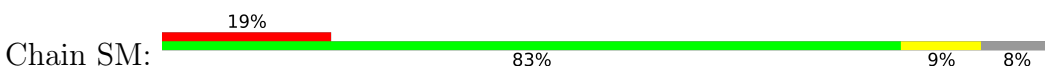
• Molecule 72: 40S RIBOSOMAL PROTEIN S6

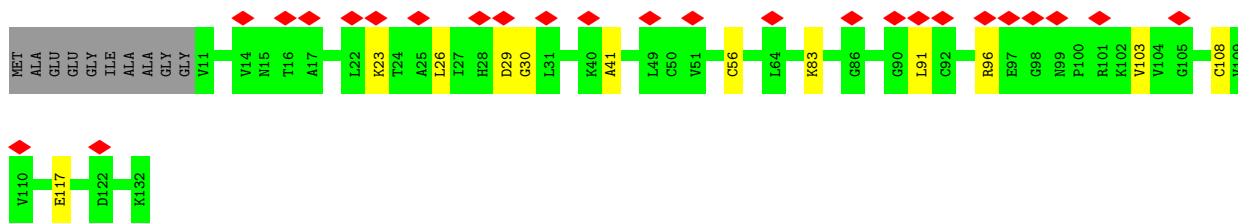


• Molecule 73: 40S RIBOSOMAL PROTEIN S9



• Molecule 74: 40S RIBOSOMAL PROTEIN

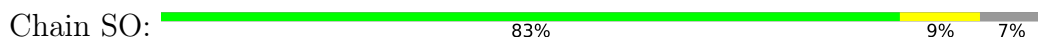




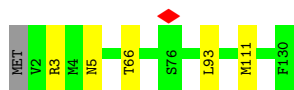
• Molecule 75: 40S RIBOSOMAL PROTEIN S13



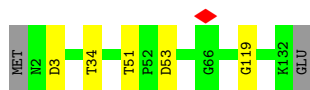
• Molecule 76: 40S RIBOSOMAL PROTEIN S14



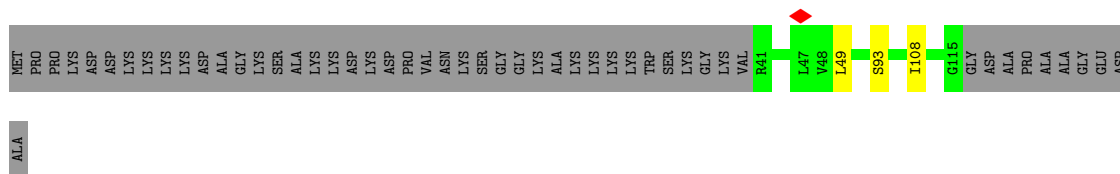
• Molecule 77: 40S RIBOSOMAL PROTEIN S15A



• Molecule 78: 40S RIBOSOMAL PROTEIN S24



• Molecule 79: 40S RIBOSOMAL PROTEIN S25

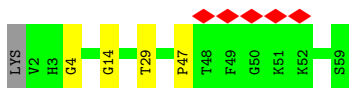
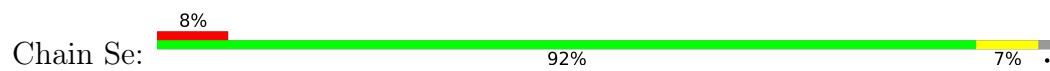


• Molecule 80: 40S RIBOSOMAL PROTEIN S27





- Molecule 81: 40S RIBOSOMAL PROTEIN S30



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.362	Depositor
Minimum map value	-0.237	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.01	Depositor
Map size (\AA)	330.0, 330.0, 330.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

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

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	L5	0.42	0/89645	0.79	26/139764 (0.0%)
2	L7	0.37	0/2858	0.73	0/4455
3	L8	0.40	0/3701	0.76	0/5766
4	LA	0.34	0/1936	0.56	1/2596 (0.0%)
5	LB	0.30	0/3306	0.52	1/4424 (0.0%)
6	LC	0.29	0/2973	0.50	0/3992
7	LD	0.29	0/2428	0.47	0/3252
8	LE	0.27	0/1996	0.59	0/2673
9	LF	0.31	0/1905	0.49	0/2539
10	LG	0.27	0/1960	0.50	0/2637
11	LH	0.26	0/1537	0.48	0/2066
12	LI	0.30	0/1751	0.50	0/2340
13	LJ	0.26	0/1433	0.49	0/1915
14	LL	0.30	0/1732	0.53	0/2315
15	LM	0.28	0/1161	0.46	0/1554
16	LN	0.33	0/1746	0.51	0/2338
17	LO	0.31	0/1682	0.47	0/2250
18	LP	0.31	0/1268	0.49	0/1701
19	LQ	0.30	0/1537	0.49	0/2052
20	LR	0.28	0/1582	0.49	0/2091
21	LS	0.31	0/1493	0.48	0/2003
22	LT	0.32	0/1326	0.52	0/1770
23	LU	0.27	0/839	0.47	0/1126
24	LV	0.31	0/993	0.49	0/1332
25	LW	0.29	0/1030	0.57	0/1364
26	LX	0.29	0/1002	0.49	0/1345
27	LY	0.28	0/1132	0.47	0/1504
28	LZ	0.29	0/1130	0.47	0/1507
29	La	0.31	0/1191	0.50	0/1591
30	Lb	0.26	0/620	0.44	0/819
31	Lc	0.29	0/774	0.48	0/1038
32	Ld	0.29	0/903	0.50	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.33	0/1071	0.53	0/1429
34	Lf	0.30	0/895	0.51	0/1198
35	Lg	0.28	0/916	0.49	0/1220
36	Lh	0.28	0/1023	0.46	0/1351
37	Li	0.28	0/843	0.47	0/1115
38	Lj	0.35	0/720	0.55	0/952
39	Lk	0.28	0/575	0.54	0/761
40	Ll	0.28	0/454	0.48	0/599
41	Lm	0.29	0/435	0.47	0/575
42	Ln	0.29	0/231	0.53	0/294
43	Lo	0.31	0/875	0.49	0/1153
44	Lp	0.36	0/718	0.51	0/953
45	Lr	0.27	0/1017	0.50	0/1364
46	Lz	0.24	0/1769	0.49	0/2371
47	S2	0.35	0/41243	0.77	11/64257 (0.0%)
48	S6	0.32	1/1795 (0.1%)	0.80	1/2798 (0.0%)
49	SA	0.26	0/1784	0.49	0/2424
50	SB	0.28	0/1765	0.52	0/2362
51	SD	0.26	0/1793	0.49	0/2414
52	SE	0.26	0/2118	0.53	1/2849 (0.0%)
53	SF	0.27	0/1531	0.52	0/2059
54	SH	0.26	0/1544	0.50	0/2068
55	SI	0.27	0/1715	0.48	0/2287
56	SK	0.27	0/851	0.50	0/1147
57	SL	0.29	0/1268	0.51	1/1696 (0.1%)
58	SP	0.26	0/815	0.56	0/1087
59	SQ	0.26	0/1177	0.48	0/1575
60	SR	0.27	0/1086	0.57	0/1457
61	SS	0.25	0/1253	0.52	0/1676
62	ST	0.25	0/1131	0.48	0/1515
63	SU	0.26	0/831	0.56	0/1115
64	SV	0.26	0/643	0.44	0/860
65	SX	0.29	0/1116	0.47	0/1490
66	Sa	0.31	0/862	0.52	0/1156
67	Sc	0.25	0/508	0.51	0/680
68	Sd	0.26	0/455	0.42	0/603
69	Sf	0.25	0/593	0.47	0/786
70	Sg	0.24	0/2493	0.50	0/3394
71	SC	0.29	0/1762	0.49	0/2381
72	SG	0.25	0/1946	0.52	0/2590
73	SJ	0.26	0/1550	0.47	0/2069
74	SM	0.23	0/962	0.53	0/1290
75	SN	0.28	0/1232	0.48	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SO	0.29	0/1062	0.57	1/1425 (0.1%)
77	SW	0.30	0/1051	0.52	0/1406
78	SY	0.26	0/1083	0.47	0/1438
79	SZ	0.26	0/604	0.57	0/810
80	Sb	0.27	0/665	0.51	0/891
81	Se	0.24	0/465	0.43	0/612
All	All	0.36	1/234864 (0.0%)	0.69	43/344993 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
34	Lf	0	1
58	SP	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	S6	76	A	C4'-O4'	-5.87	1.38	1.45

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	S6	76	A	C5'-C4'-O4'	13.26	125.02	109.10
1	L5	4083	U	N1-C2-O2	8.35	128.64	122.80
1	L5	4083	U	C2-N1-C1'	8.04	127.35	117.70
1	L5	4937	C	C2-N1-C1'	7.68	127.25	118.80
1	L5	1367	C	N1-C2-O2	7.38	123.33	118.90
47	S2	1453	C	C2-N1-C1'	7.27	126.80	118.80
47	S2	1016	U	C2-N1-C1'	6.95	126.03	117.70
1	L5	4083	U	N3-C2-O2	-6.89	117.38	122.20
47	S2	1453	C	N1-C2-O2	6.86	123.02	118.90
1	L5	1367	C	C2-N1-C1'	6.84	126.32	118.80
1	L5	4937	C	N1-C2-O2	6.69	122.92	118.90
5	LB	360	LEU	CA-CB-CG	6.22	129.61	115.30
47	S2	1016	U	N1-C2-O2	6.19	127.14	122.80
1	L5	1367	C	N3-C2-O2	-6.10	117.63	121.90
1	L5	3771	C	C6-N1-C2	-6.07	117.87	120.30
1	L5	115	C	C2-N1-C1'	6.05	125.45	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	3771	C	C2-N1-C1'	5.99	125.39	118.80
1	L5	931	C	C2-N1-C1'	5.93	125.33	118.80
4	LA	150	LEU	CA-CB-CG	5.85	128.76	115.30
1	L5	5026	U	C2-N1-C1'	5.83	124.69	117.70
1	L5	3956	G	P-O3'-C3'	5.80	126.66	119.70
1	L5	1238	A	OP1-P-O3'	5.80	117.95	105.20
1	L5	956	A	OP2-P-O3'	5.75	117.86	105.20
1	L5	115	C	N1-C2-O2	5.75	122.35	118.90
1	L5	4083	U	C6-N1-C1'	-5.59	113.38	121.20
57	SL	33	LEU	CA-CB-CG	5.56	128.09	115.30
76	SO	17	LEU	CA-CB-CG	5.47	127.89	115.30
1	L5	4937	C	C6-N1-C1'	-5.43	114.28	120.80
1	L5	2362	U	C2-N1-C1'	5.41	124.19	117.70
47	S2	1016	U	N3-C2-O2	-5.40	118.42	122.20
1	L5	931	C	N1-C2-O2	5.34	122.11	118.90
47	S2	1453	C	C6-N1-C1'	-5.31	114.43	120.80
1	L5	3968	U	C2-N1-C1'	5.28	124.04	117.70
47	S2	1118	C	C2-N1-C1'	5.20	124.52	118.80
1	L5	5026	U	N1-C2-O2	5.17	126.42	122.80
47	S2	1057	C	N1-C2-O2	5.15	121.99	118.90
47	S2	1453	C	N3-C2-O2	-5.10	118.33	121.90
52	SE	164	LEU	CA-CB-CG	5.08	126.98	115.30
1	L5	115	C	N3-C2-O2	-5.06	118.36	121.90
47	S2	1057	C	C2-N1-C1'	5.05	124.35	118.80
1	L5	417	G	P-O3'-C3'	5.01	125.72	119.70
1	L5	1612	G	N3-C4-N9	5.00	129.00	126.00
47	S2	1624	U	C2-N1-C1'	5.00	123.71	117.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	Lf	105	LEU	Peptide
58	SP	72	LYS	Peptide

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	246/257 (96%)	207 (84%)	25 (10%)	14 (6%)	1	18
5	LB	400/403 (99%)	344 (86%)	42 (10%)	14 (4%)	3	30
6	LC	365/427 (86%)	311 (85%)	30 (8%)	24 (7%)	1	16
7	LD	291/297 (98%)	258 (89%)	22 (8%)	11 (4%)	3	27
8	LE	238/288 (83%)	182 (76%)	37 (16%)	19 (8%)	1	11
9	LF	223/248 (90%)	201 (90%)	18 (8%)	4 (2%)	8	43
10	LG	239/266 (90%)	205 (86%)	19 (8%)	15 (6%)	1	17
11	LH	188/192 (98%)	162 (86%)	18 (10%)	8 (4%)	2	24
12	LI	211/214 (99%)	177 (84%)	26 (12%)	8 (4%)	3	27
13	LJ	174/178 (98%)	147 (84%)	19 (11%)	8 (5%)	2	23
14	LL	208/211 (99%)	179 (86%)	18 (9%)	11 (5%)	2	19
15	LM	137/215 (64%)	115 (84%)	16 (12%)	6 (4%)	2	23
16	LN	201/204 (98%)	180 (90%)	18 (9%)	3 (2%)	10	47
17	LO	199/203 (98%)	180 (90%)	15 (8%)	4 (2%)	7	41
18	LP	151/184 (82%)	130 (86%)	16 (11%)	5 (3%)	4	31
19	LQ	185/188 (98%)	159 (86%)	22 (12%)	4 (2%)	6	39
20	LR	185/196 (94%)	168 (91%)	17 (9%)	0	100	100
21	LS	173/176 (98%)	141 (82%)	21 (12%)	11 (6%)	1	17
22	LT	157/160 (98%)	134 (85%)	18 (12%)	5 (3%)	4	31
23	LU	99/128 (77%)	81 (82%)	17 (17%)	1 (1%)	15	55
24	LV	129/140 (92%)	105 (81%)	18 (14%)	6 (5%)	2	22
25	LW	122/157 (78%)	96 (79%)	22 (18%)	4 (3%)	4	31
26	LX	118/156 (76%)	103 (87%)	13 (11%)	2 (2%)	9	45
27	LY	132/145 (91%)	118 (89%)	10 (8%)	4 (3%)	4	33
28	LZ	133/136 (98%)	118 (89%)	12 (9%)	3 (2%)	6	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	145/148 (98%)	122 (84%)	18 (12%)	5 (3%)	3	31
30	Lb	73/159 (46%)	62 (85%)	9 (12%)	2 (3%)	5	35
31	Lc	96/115 (84%)	81 (84%)	9 (9%)	6 (6%)	1	17
32	Ld	105/125 (84%)	85 (81%)	15 (14%)	5 (5%)	2	22
33	Le	126/135 (93%)	107 (85%)	14 (11%)	5 (4%)	3	26
34	Lf	107/110 (97%)	87 (81%)	16 (15%)	4 (4%)	3	28
35	Lg	112/117 (96%)	103 (92%)	8 (7%)	1 (1%)	17	57
36	Lh	120/123 (98%)	110 (92%)	8 (7%)	2 (2%)	9	45
37	Li	100/105 (95%)	92 (92%)	4 (4%)	4 (4%)	3	26
38	Lj	84/97 (87%)	67 (80%)	10 (12%)	7 (8%)	1	10
39	Lk	67/70 (96%)	50 (75%)	12 (18%)	5 (8%)	1	12
40	Ll	48/51 (94%)	44 (92%)	3 (6%)	1 (2%)	7	40
41	Lm	50/128 (39%)	43 (86%)	5 (10%)	2 (4%)	3	26
42	Ln	22/25 (88%)	20 (91%)	2 (9%)	0	100	100
43	Lo	102/106 (96%)	85 (83%)	15 (15%)	2 (2%)	7	41
44	Lp	89/92 (97%)	71 (80%)	13 (15%)	5 (6%)	2	19
45	Lr	123/137 (90%)	102 (83%)	15 (12%)	6 (5%)	2	21
46	Lz	215/217 (99%)	168 (78%)	31 (14%)	16 (7%)	1	13
49	SA	220/295 (75%)	187 (85%)	27 (12%)	6 (3%)	5	35
50	SB	212/264 (80%)	174 (82%)	30 (14%)	8 (4%)	3	27
51	SD	225/243 (93%)	183 (81%)	24 (11%)	18 (8%)	1	11
52	SE	260/263 (99%)	215 (83%)	30 (12%)	15 (6%)	1	18
53	SF	189/204 (93%)	144 (76%)	31 (16%)	14 (7%)	1	13
54	SH	187/194 (96%)	145 (78%)	27 (14%)	15 (8%)	1	11
55	SI	204/208 (98%)	168 (82%)	24 (12%)	12 (6%)	1	18
56	SK	96/165 (58%)	76 (79%)	16 (17%)	4 (4%)	3	25
57	SL	151/158 (96%)	130 (86%)	11 (7%)	10 (7%)	1	16
58	SP	95/145 (66%)	61 (64%)	21 (22%)	13 (14%)	0	4
59	SQ	144/146 (99%)	114 (79%)	20 (14%)	10 (7%)	1	14
60	SR	130/135 (96%)	104 (80%)	17 (13%)	9 (7%)	1	14
61	SS	148/152 (97%)	121 (82%)	13 (9%)	14 (10%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	ST	141/145 (97%)	119 (84%)	16 (11%)	6 (4%)	2	24
63	SU	102/119 (86%)	86 (84%)	11 (11%)	5 (5%)	2	21
64	SV	81/83 (98%)	65 (80%)	11 (14%)	5 (6%)	1	17
65	SX	139/143 (97%)	114 (82%)	12 (9%)	13 (9%)	0	8
66	Sa	103/115 (90%)	77 (75%)	16 (16%)	10 (10%)	0	8
67	Sc	62/69 (90%)	47 (76%)	9 (14%)	6 (10%)	0	8
68	Sd	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
69	Sf	69/156 (44%)	47 (68%)	10 (14%)	12 (17%)	0	2
70	Sg	311/317 (98%)	237 (76%)	58 (19%)	16 (5%)	2	20
71	SC	220/293 (75%)	188 (86%)	23 (10%)	9 (4%)	3	26
72	SG	235/249 (94%)	198 (84%)	26 (11%)	11 (5%)	2	22
73	SJ	183/194 (94%)	157 (86%)	16 (9%)	10 (6%)	2	19
74	SM	120/132 (91%)	79 (66%)	29 (24%)	12 (10%)	0	8
75	SN	148/151 (98%)	133 (90%)	8 (5%)	7 (5%)	2	22
76	SO	138/151 (91%)	101 (73%)	24 (17%)	13 (9%)	0	8
77	SW	127/130 (98%)	109 (86%)	13 (10%)	5 (4%)	3	27
78	SY	129/133 (97%)	108 (84%)	16 (12%)	5 (4%)	3	27
79	SZ	73/125 (58%)	59 (81%)	11 (15%)	3 (4%)	3	26
80	Sb	81/84 (96%)	67 (83%)	12 (15%)	2 (2%)	5	36
81	Se	56/59 (95%)	41 (73%)	11 (20%)	4 (7%)	1	14
All	All	11518/12905 (89%)	9598 (83%)	1346 (12%)	574 (5%)	4	21

All (574) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	LA	118	GLU
5	LB	360	LEU
6	LC	23	THR
6	LC	148	PRO
6	LC	186	SER
6	LC	204	ARG
7	LD	4	VAL
8	LE	110	ARG
8	LE	123	ARG
8	LE	226	ARG

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Mol	Chain	Res	Type
10	LG	195	HIS
11	LH	139	ALA
11	LH	141	LYS
12	LI	77	VAL
12	LI	101	LYS
12	LI	160	PRO
21	LS	21	LYS
21	LS	127	MET
22	LT	53	PRO
22	LT	81	LYS
23	LU	115	PHE
32	Ld	82	TYR
33	Le	62	SER
33	Le	104	SER
36	Lh	39	GLY
37	Li	73	ILE
45	Lr	46	ARG
46	Lz	17	VAL
46	Lz	122	ARG
49	SA	125	THR
50	SB	147	ASN
51	SD	3	VAL
51	SD	55	THR
51	SD	81	GLU
52	SE	76	VAL
52	SE	164	LEU
53	SF	15	PRO
53	SF	33	ILE
54	SH	66	VAL
54	SH	107	LYS
55	SI	130	THR
56	SK	3	MET
57	SL	8	ARG
57	SL	116	CYS
58	SP	37	TYR
58	SP	76	VAL
59	SQ	42	ILE
59	SQ	117	ARG
60	SR	42	PRO
60	SR	94	GLU
61	SS	117	ILE
62	ST	4	VAL

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Mol	Chain	Res	Type
63	SU	50	VAL
63	SU	103	SER
63	SU	107	GLU
65	SX	35	ALA
66	Sa	3	LYS
66	Sa	18	VAL
66	Sa	106	ALA
67	Sc	67	ARG
69	Sf	93	HIS
70	Sg	55	PRO
70	Sg	99	ARG
70	Sg	102	VAL
70	Sg	281	ALA
71	SC	262	THR
72	SG	107	SER
72	SG	122	PRO
73	SJ	3	VAL
73	SJ	8	VAL
73	SJ	17	ARG
74	SM	108	CYS
74	SM	117	GLU
75	SN	24	THR
77	SW	66	THR
4	LA	172	GLY
4	LA	195	CYS
5	LB	113	GLU
6	LC	69	THR
6	LC	73	VAL
6	LC	86	ARG
6	LC	273	LEU
6	LC	308	LYS
6	LC	319	LEU
6	LC	357	ALA
7	LD	21	ARG
7	LD	89	LYS
7	LD	119	TYR
7	LD	177	THR
8	LE	106	VAL
8	LE	124	LYS
8	LE	185	PRO
8	LE	279	ASN
9	LF	168	ALA

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Mol	Chain	Res	Type
9	LF	178	SER
9	LF	223	LYS
10	LG	200	THR
10	LG	202	VAL
11	LH	63	ASN
11	LH	189	GLN
12	LI	70	ILE
12	LI	80	CYS
13	LJ	11	PRO
13	LJ	28	GLU
14	LL	62	PRO
14	LL	90	VAL
14	LL	100	PRO
14	LL	165	LYS
15	LM	71	LYS
16	LN	16	SER
17	LO	123	ALA
17	LO	143	HIS
18	LP	91	LEU
18	LP	132	ALA
19	LQ	77	ASN
19	LQ	103	LEU
21	LS	110	TYR
22	LT	136	ARG
24	LV	21	PRO
24	LV	125	CYS
24	LV	127	ASP
25	LW	51	TRP
25	LW	96	GLN
26	LX	51	THR
26	LX	59	LYS
27	LY	20	ASN
27	LY	49	ILE
28	LZ	33	THR
29	La	11	LEU
29	La	76	ASP
29	La	92	LYS
31	Lc	23	LYS
31	Lc	51	ASN
31	Lc	54	ALA
31	Lc	101	ASP
32	Ld	44	ARG

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Mol	Chain	Res	Type
32	Ld	94	GLU
33	Le	125	PRO
34	Lf	54	LYS
34	Lf	83	MET
36	Lh	97	LYS
39	Lk	9	LYS
44	Lp	64	VAL
45	Lr	22	LYS
45	Lr	67	ARG
46	Lz	93	LEU
49	SA	13	GLU
49	SA	31	ASP
49	SA	170	SER
50	SB	22	VAL
50	SB	37	ALA
50	SB	83	LYS
50	SB	190	PRO
51	SD	93	THR
51	SD	198	ILE
52	SE	144	ALA
52	SE	214	ASN
53	SF	17	ILE
53	SF	48	TYR
53	SF	57	ALA
53	SF	130	ARG
53	SF	139	VAL
53	SF	202	SER
54	SH	34	SER
54	SH	115	LYS
55	SI	75	LYS
55	SI	122	GLY
55	SI	140	LYS
55	SI	143	LYS
55	SI	155	ASN
55	SI	186	ASP
58	SP	15	PHE
58	SP	94	VAL
58	SP	100	LYS
58	SP	105	VAL
59	SQ	100	VAL
60	SR	72	LYS
60	SR	119	VAL

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Mol	Chain	Res	Type
60	SR	131	PRO
61	SS	12	ILE
61	SS	71	MET
61	SS	74	PRO
61	SS	88	LYS
61	SS	121	ARG
61	SS	133	GLY
62	ST	5	THR
62	ST	132	ASP
64	SV	9	VAL
64	SV	10	ASP
64	SV	78	ILE
65	SX	10	ALA
66	Sa	13	LYS
66	Sa	46	GLU
66	Sa	89	ARG
67	Sc	59	LEU
69	Sf	102	VAL
69	Sf	139	HIS
70	Sg	15	ASN
70	Sg	28	PRO
70	Sg	56	GLN
70	Sg	145	GLU
70	Sg	261	LEU
71	SC	261	PHE
71	SC	278	THR
72	SG	12	CYS
72	SG	20	ASP
72	SG	25	ARG
72	SG	147	LEU
73	SJ	37	LEU
73	SJ	147	PHE
74	SM	41	ALA
74	SM	91	LEU
74	SM	96	ARG
75	SN	3	ARG
75	SN	102	LEU
76	SO	48	SER
76	SO	126	ILE
76	SO	128	ARG
77	SW	5	ASN
78	SY	34	THR

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Mol	Chain	Res	Type
78	SY	119	GLY
79	SZ	93	SER
80	Sb	10	PRO
80	Sb	75	GLU
81	Se	29	THR
81	Se	47	PRO
4	LA	144	LYS
4	LA	180	LEU
4	LA	239	ALA
4	LA	240	ALA
5	LB	291	TYR
5	LB	295	ASP
5	LB	314	ILE
6	LC	110	ARG
6	LC	111	TRP
6	LC	132	ALA
6	LC	170	LEU
6	LC	287	THR
6	LC	309	ILE
6	LC	318	PRO
7	LD	20	PHE
7	LD	130	TYR
7	LD	178	LYS
7	LD	182	GLY
7	LD	255	LYS
8	LE	52	ARG
8	LE	86	GLU
8	LE	136	HIS
8	LE	228	GLN
10	LG	58	PRO
10	LG	264	LYS
11	LH	98	HIS
12	LI	38	ARG
13	LJ	169	LYS
14	LL	91	ALA
15	LM	111	LYS
15	LM	118	MET
17	LO	37	ARG
17	LO	202	LEU
19	LQ	96	PRO
21	LS	7	LEU
21	LS	64	CYS

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Mol	Chain	Res	Type
21	LS	83	ARG
21	LS	146	HIS
22	LT	69	GLN
24	LV	130	PRO
25	LW	65	GLU
25	LW	73	ARG
27	LY	37	GLU
28	LZ	8	GLY
29	La	37	GLY
31	Lc	75	SER
32	Ld	21	VAL
35	Lg	57	ARG
37	Li	48	CYS
38	Lj	21	ARG
38	Lj	63	ARG
39	Lk	38	CYS
39	Lk	68	GLU
41	Lm	117	HIS
44	Lp	71	TYR
45	Lr	68	SER
46	Lz	27	LYS
46	Lz	86	ASP
46	Lz	129	ASN
49	SA	98	PRO
51	SD	44	THR
51	SD	215	ASP
51	SD	216	GLU
52	SE	77	ARG
52	SE	93	ASP
52	SE	196	THR
52	SE	232	ASN
53	SF	42	LYS
53	SF	47	LYS
53	SF	85	LYS
54	SH	112	ASN
54	SH	148	LEU
55	SI	86	SER
55	SI	132	GLU
55	SI	180	GLY
57	SL	3	ASP
57	SL	21	LYS
57	SL	33	LEU

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Mol	Chain	Res	Type
57	SL	133	PRO
57	SL	148	ALA
58	SP	16	THR
58	SP	51	ARG
58	SP	95	GLY
59	SQ	4	LYS
59	SQ	48	GLN
59	SQ	56	LEU
59	SQ	101	ASP
59	SQ	145	TYR
61	SS	16	LEU
61	SS	92	ASP
61	SS	132	ARG
61	SS	144	ARG
62	ST	34	VAL
64	SV	36	VAL
65	SX	46	HIS
65	SX	64	SER
65	SX	77	ASN
65	SX	79	LYS
65	SX	109	GLY
65	SX	126	ALA
66	Sa	5	ARG
66	Sa	61	ALA
67	Sc	36	ASP
69	Sf	99	LYS
69	Sf	100	LEU
69	Sf	104	LYS
69	Sf	118	ARG
69	Sf	124	ASP
70	Sg	105	THR
70	Sg	244	ASN
70	Sg	246	TYR
71	SC	188	CYS
71	SC	226	ALA
72	SG	175	LYS
72	SG	212	LEU
72	SG	213	LEU
73	SJ	119	LEU
73	SJ	122	SER
74	SM	23	LYS
74	SM	29	ASP

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Mol	Chain	Res	Type
74	SM	56	CYS
74	SM	83	LYS
75	SN	12	SER
76	SO	65	ASP
76	SO	67	ASP
76	SO	68	GLU
76	SO	138	ASP
76	SO	140	THR
77	SW	93	LEU
78	SY	3	ASP
4	LA	28	ARG
4	LA	80	GLU
4	LA	115	CYS
5	LB	5	LYS
5	LB	10	ARG
5	LB	294	LYS
5	LB	310	SER
6	LC	66	SER
6	LC	205	ARG
8	LE	219	LYS
8	LE	221	LYS
10	LG	59	ARG
10	LG	121	LYS
10	LG	128	VAL
10	LG	165	GLU
12	LI	20	SER
13	LJ	138	GLY
13	LJ	174	ILE
14	LL	151	THR
14	LL	169	ILE
15	LM	88	ALA
16	LN	188	ARG
21	LS	153	PRO
21	LS	155	PRO
24	LV	108	ASN
24	LV	110	GLY
27	LY	53	ASP
29	La	27	LYS
30	Lb	74	ALA
33	Le	8	VAL
34	Lf	5	LEU
37	Li	4	ARG

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Mol	Chain	Res	Type
38	Lj	15	THR
38	Lj	36	LYS
39	Lk	62	PRO
40	Ll	42	ARG
41	Lm	105	PRO
44	Lp	65	ALA
44	Lp	91	ASP
45	Lr	86	ALA
46	Lz	153	SER
46	Lz	195	LYS
46	Lz	203	ALA
49	SA	4	ALA
50	SB	76	ASN
50	SB	86	LEU
50	SB	223	PHE
51	SD	83	SER
51	SD	153	VAL
51	SD	206	ASP
51	SD	222	PRO
51	SD	223	ILE
52	SE	68	ARG
52	SE	131	VAL
54	SH	12	ASN
54	SH	38	ALA
54	SH	138	GLU
54	SH	162	GLN
56	SK	39	ASN
56	SK	41	PRO
56	SK	91	PRO
57	SL	4	ILE
57	SL	6	THR
59	SQ	144	SER
60	SR	110	ASP
62	ST	6	VAL
63	SU	48	LEU
65	SX	9	THR
65	SX	87	ASN
65	SX	117	GLY
66	Sa	62	TYR
66	Sa	64	LEU
69	Sf	86	THR
69	Sf	88	PRO

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Mol	Chain	Res	Type
69	Sf	98	VAL
70	Sg	191	HIS
71	SC	85	SER
71	SC	134	ASN
71	SC	264	SER
73	SJ	138	ARG
74	SM	26	LEU
75	SN	143	SER
76	SO	47	LEU
76	SO	129	ILE
77	SW	111	MET
78	SY	51	THR
78	SY	53	ASP
79	SZ	49	LEU
4	LA	21	LYS
4	LA	26	ALA
4	LA	177	LYS
5	LB	159	VAL
6	LC	72	ALA
6	LC	133	LEU
8	LE	85	LYS
8	LE	126	LEU
9	LF	195	TYR
10	LG	31	LEU
10	LG	51	LEU
10	LG	158	ALA
11	LH	22	GLY
11	LH	51	LYS
12	LI	201	PRO
13	LJ	145	LYS
14	LL	51	ALA
14	LL	55	ILE
14	LL	60	ARG
15	LM	97	ALA
18	LP	106	GLY
18	LP	123	PRO
21	LS	164	LYS
30	Lb	21	ILE
31	Lc	52	CYS
33	Le	71	PRO
37	Li	86	LYS
38	Lj	14	LYS

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Mol	Chain	Res	Type
38	Lj	27	TYR
39	Lk	32	VAL
43	Lo	99	ARG
44	Lp	20	ALA
46	Lz	81	ASP
46	Lz	113	SER
46	Lz	125	GLY
46	Lz	137	LEU
51	SD	68	GLU
51	SD	220	THR
52	SE	30	ARG
52	SE	69	PHE
52	SE	168	LYS
52	SE	245	ARG
53	SF	20	PHE
53	SF	32	ASP
54	SH	89	GLY
54	SH	99	ARG
54	SH	100	ILE
58	SP	77	LYS
58	SP	82	ASP
60	SR	69	ILE
61	SS	9	PHE
61	SS	35	GLY
63	SU	98	VAL
64	SV	45	ARG
65	SX	54	LYS
65	SX	127	ASN
69	Sf	123	SER
71	SC	176	LYS
72	SG	105	ASN
75	SN	8	GLY
76	SO	56	VAL
76	SO	112	ALA
76	SO	134	PRO
77	SW	3	ARG
79	SZ	108	ILE
81	Se	4	GLY
81	Se	14	GLY
7	LD	269	PRO
8	LE	44	CYS
8	LE	119	GLU

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Mol	Chain	Res	Type
10	LG	125	LYS
10	LG	163	PRO
11	LH	109	GLY
13	LJ	159	LYS
18	LP	82	ARG
21	LS	156	HIS
28	LZ	56	ALA
34	Lf	107	PRO
38	Lj	85	LYS
43	Lo	62	THR
51	SD	154	ASP
53	SF	41	VAL
54	SH	113	LYS
54	SH	190	PRO
55	SI	97	VAL
57	SL	98	LYS
60	SR	97	GLU
61	SS	13	LEU
62	ST	142	ASN
67	Sc	38	THR
72	SG	68	LEU
73	SJ	76	ALA
74	SM	30	GLY
5	LB	375	GLY
16	LN	89	VAL
58	SP	48	GLY
67	Sc	8	PRO
70	Sg	13	GLY
73	SJ	171	GLY
75	SN	68	GLY
14	LL	48	PRO
45	Lr	103	ARG
51	SD	41	VAL
52	SE	15	PRO
59	SQ	6	PRO
5	LB	18	PRO
5	LB	299	ILE
10	LG	164	ILE
13	LJ	176	PRO
46	Lz	201	VAL
51	SD	200	PRO
55	SI	102	VAL

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Mol	Chain	Res	Type
60	SR	121	GLN
70	Sg	61	GLY
70	Sg	267	VAL
4	LA	43	GLY
5	LB	110	ILE
6	LC	19	GLY
6	LC	70	GLY
8	LE	203	ILE
22	LT	37	GLY
32	Ld	120	VAL
46	Lz	100	VAL
46	Lz	162	VAL
58	SP	69	PRO
8	LE	98	GLY
15	LM	139	SER
19	LQ	171	GLY
67	Sc	22	GLY
74	SM	103	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LA	190/199 (96%)	189 (100%)	1 (0%)	88	95
5	LB	348/349 (100%)	348 (100%)	0	100	100
6	LC	305/348 (88%)	305 (100%)	0	100	100
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	215/252 (85%)	215 (100%)	0	100	100
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	180/181 (99%)	180 (100%)	0	100	100
13	LJ	148/149 (99%)	148 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	LL	176/177 (99%)	176 (100%)	0	100	100
15	LM	118/161 (73%)	118 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	173 (100%)	0	100	100
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	164 (100%)	0	100	100
20	LR	166/175 (95%)	166 (100%)	0	100	100
21	LS	156/157 (99%)	156 (100%)	0	100	100
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	101 (100%)	0	100	100
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	124 (100%)	0	100	100
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	120 (100%)	0	100	100
30	Lb	63/126 (50%)	63 (100%)	0	100	100
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	98 (100%)	0	100	100
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	98/100 (98%)	98 (100%)	0	100	100
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	48/116 (41%)	48 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	92 (99%)	1 (1%)	73	88
44	Lp	74/75 (99%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	Lr	109/121 (90%)	109 (100%)	0	100	100
46	Lz	195/196 (100%)	195 (100%)	0	100	100
49	SA	184/243 (76%)	184 (100%)	0	100	100
50	SB	195/231 (84%)	195 (100%)	0	100	100
51	SD	190/202 (94%)	190 (100%)	0	100	100
52	SE	224/225 (100%)	224 (100%)	0	100	100
53	SF	161/170 (95%)	161 (100%)	0	100	100
54	SH	169/174 (97%)	169 (100%)	0	100	100
55	SI	178/180 (99%)	178 (100%)	0	100	100
56	SK	89/136 (65%)	89 (100%)	0	100	100
57	SL	137/142 (96%)	137 (100%)	0	100	100
58	SP	87/130 (67%)	87 (100%)	0	100	100
59	SQ	121/121 (100%)	121 (100%)	0	100	100
60	SR	120/122 (98%)	120 (100%)	0	100	100
61	SS	130/132 (98%)	130 (100%)	0	100	100
62	ST	113/115 (98%)	113 (100%)	0	100	100
63	SU	94/107 (88%)	94 (100%)	0	100	100
64	SV	67/67 (100%)	67 (100%)	0	100	100
65	SX	113/115 (98%)	113 (100%)	0	100	100
66	Sa	90/98 (92%)	90 (100%)	0	100	100
67	Sc	57/62 (92%)	57 (100%)	0	100	100
68	Sd	47/49 (96%)	47 (100%)	0	100	100
69	Sf	64/140 (46%)	64 (100%)	0	100	100
70	Sg	272/275 (99%)	272 (100%)	0	100	100
71	SC	188/225 (84%)	188 (100%)	0	100	100
72	SG	207/218 (95%)	207 (100%)	0	100	100
73	SJ	161/168 (96%)	161 (100%)	0	100	100
74	SM	104/108 (96%)	104 (100%)	0	100	100
75	SN	130/131 (99%)	130 (100%)	0	100	100
76	SO	110/119 (92%)	110 (100%)	0	100	100
77	SW	112/113 (99%)	112 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	SY	113/115 (98%)	113 (100%)	0	100	100
79	SZ	66/103 (64%)	66 (100%)	0	100	100
80	Sb	75/76 (99%)	75 (100%)	0	100	100
81	Se	47/48 (98%)	47 (100%)	0	100	100
All	All	10039/10997 (91%)	10037 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	215	ASN
43	Lo	31	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	22	HIS
4	LA	215	ASN
5	LB	11	HIS
5	LB	175	GLN
5	LB	179	HIS
5	LB	258	HIS
5	LB	354	GLN
6	LC	47	ASN
6	LC	119	GLN
6	LC	142	HIS
6	LC	215	ASN
6	LC	317	ASN
7	LD	111	ASN
8	LE	101	ASN
8	LE	191	GLN
8	LE	228	GLN
8	LE	284	HIS
9	LF	116	GLN
9	LF	119	ASN
9	LF	239	GLN
10	LG	100	HIS
11	LH	79	ASN
11	LH	149	ASN
11	LH	188	GLN
12	LI	213	HIS

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Mol	Chain	Res	Type
13	LJ	98	ASN
14	LL	15	HIS
14	LL	113	ASN
15	LM	20	HIS
15	LM	131	GLN
17	LO	26	GLN
17	LO	150	GLN
17	LO	184	ASN
18	LP	80	GLN
18	LP	116	HIS
18	LP	137	ASN
19	LQ	7	HIS
21	LS	117	HIS
21	LS	146	HIS
25	LW	17	HIS
25	LW	63	GLN
25	LW	68	GLN
25	LW	96	GLN
27	LY	24	HIS
29	La	41	HIS
29	La	44	ASN
29	La	85	GLN
30	Lb	60	ASN
33	Le	117	GLN
35	Lg	112	GLN
36	Lh	68	ASN
40	Li	17	GLN
44	Lp	56	HIS
45	Lr	6	GLN
45	Lr	70	GLN
45	Lr	100	ASN
46	Lz	35	GLN
46	Lz	143	ASN
49	SA	36	GLN
50	SB	202	GLN
51	SD	57	ASN
51	SD	226	GLN
52	SE	67	GLN
53	SF	83	ASN
53	SF	118	ASN
54	SH	33	ASN
54	SH	76	GLN

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Mol	Chain	Res	Type
54	SH	163	GLN
55	SI	88	ASN
56	SK	50	GLN
56	SK	73	ASN
57	SL	13	GLN
57	SL	141	ASN
59	SQ	8	GLN
59	SQ	35	ASN
63	SU	81	GLN
65	SX	63	ASN
65	SX	110	HIS
69	Sf	151	ASN
70	Sg	62	HIS
70	Sg	187	ASN
70	Sg	188	HIS
70	Sg	285	GLN
71	SC	115	GLN
72	SG	4	ASN
73	SJ	156	HIS
74	SM	52	GLN
75	SN	58	HIS
75	SN	105	ASN
76	SO	13	GLN
76	SO	26	ASN
76	SO	103	ASN
77	SW	15	ASN
79	SZ	89	GLN
81	Se	44	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3707/5070 (73%)	1303 (35%)	56 (1%)
2	L7	119/121 (98%)	21 (17%)	0
3	L8	155/157 (98%)	44 (28%)	2 (1%)
47	S2	1716/1869 (91%)	677 (39%)	22 (1%)
48	S6	74/75 (98%)	28 (37%)	2 (2%)
All	All	5771/7292 (79%)	2073 (35%)	82 (1%)

All (2073) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	4	G
1	L5	6	C
1	L5	9	C
1	L5	13	U
1	L5	17	A
1	L5	19	G
1	L5	25	A
1	L5	26	C
1	L5	27	C
1	L5	30	C
1	L5	35	U
1	L5	39	A
1	L5	43	U
1	L5	44	A
1	L5	46	U
1	L5	47	A
1	L5	48	G
1	L5	56	A
1	L5	59	A
1	L5	61	A
1	L5	62	A
1	L5	64	A
1	L5	65	A
1	L5	66	A
1	L5	71	C
1	L5	72	C
1	L5	73	A
1	L5	75	G
1	L5	91	G
1	L5	98	A
1	L5	104	G
1	L5	108	A
1	L5	109	G
1	L5	110	C
1	L5	117	C
1	L5	119	G
1	L5	120	A
1	L5	121	A
1	L5	122	U
1	L5	126	C
1	L5	130	C
1	L5	133	C
1	L5	134	G

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Mol	Chain	Res	Type
1	L5	135	G
1	L5	136	C
1	L5	141	C
1	L5	144	G
1	L5	149	A
1	L5	151	G
1	L5	152	U
1	L5	159	C
1	L5	164	G
1	L5	165	A
1	L5	167	C
1	L5	171	U
1	L5	172	C
1	L5	173	C
1	L5	175	C
1	L5	180	C
1	L5	183	C
1	L5	184	U
1	L5	185	C
1	L5	187	U
1	L5	188	G
1	L5	200	U
1	L5	202	C
1	L5	203	U
1	L5	205	C
1	L5	213	G
1	L5	216	C
1	L5	217	C
1	L5	218	A
1	L5	219	G
1	L5	227	A
1	L5	229	G
1	L5	230	G
1	L5	232	G
1	L5	234	G
1	L5	235	A
1	L5	236	G
1	L5	238	C
1	L5	241	G
1	L5	242	U
1	L5	245	C
1	L5	246	G

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Mol	Chain	Res	Type
1	L5	250	C
1	L5	252	C
1	L5	253	G
1	L5	256	G
1	L5	265	C
1	L5	266	C
1	L5	267	G
1	L5	277	G
1	L5	278	G
1	L5	280	G
1	L5	297	U
1	L5	300	A
1	L5	306	A
1	L5	310	G
1	L5	315	G
1	L5	316	U
1	L5	322	C
1	L5	326	C
1	L5	334	A
1	L5	340	C
1	L5	341	G
1	L5	352	G
1	L5	353	A
1	L5	354	U
1	L5	379	G
1	L5	382	G
1	L5	383	A
1	L5	384	A
1	L5	386	A
1	L5	387	G
1	L5	389	A
1	L5	390	C
1	L5	394	G
1	L5	406	C
1	L5	407	A
1	L5	409	G
1	L5	410	A
1	L5	413	G
1	L5	414	C
1	L5	415	G
1	L5	418	A
1	L5	431	G

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Mol	Chain	Res	Type
1	L5	432	U
1	L5	433	A
1	L5	434	A
1	L5	435	A
1	L5	437	G
1	L5	444	G
1	L5	448	G
1	L5	449	C
1	L5	450	G
1	L5	451	C
1	L5	452	A
1	L5	453	G
1	L5	454	U
1	L5	455	C
1	L5	462	G
1	L5	465	G
1	L5	467	U
1	L5	468	U
1	L5	469	C
1	L5	471	A
1	L5	473	C
1	L5	485	C
1	L5	486	C
1	L5	487	G
1	L5	490	C
1	L5	495	C
1	L5	498	C
1	L5	500	G
1	L5	501	C
1	L5	502	C
1	L5	503	C
1	L5	504	G
1	L5	506	C
1	L5	509	A
1	L5	510	U
1	L5	511	C
1	L5	512	U
1	L5	513	U
1	L5	514	U
1	L5	517	C
1	L5	518	G
1	L5	643	C

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Mol	Chain	Res	Type
1	L5	644	G
1	L5	646	G
1	L5	647	G
1	L5	648	G
1	L5	649	A
1	L5	652	G
1	L5	654	C
1	L5	656	C
1	L5	657	C
1	L5	658	C
1	L5	659	G
1	L5	661	C
1	L5	664	G
1	L5	665	C
1	L5	667	A
1	L5	671	G
1	L5	678	C
1	L5	682	G
1	L5	684	G
1	L5	686	A
1	L5	694	C
1	L5	696	C
1	L5	697	G
1	L5	702	U
1	L5	703	G
1	L5	704	C
1	L5	705	G
1	L5	707	C
1	L5	713	C
1	L5	719	C
1	L5	720	G
1	L5	723	A
1	L5	728	U
1	L5	730	G
1	L5	736	C
1	L5	737	C
1	L5	740	G
1	L5	741	C
1	L5	744	G
1	L5	747	A
1	L5	749	G
1	L5	750	U

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Mol	Chain	Res	Type
1	L5	751	G
1	L5	754	U
1	L5	756	G
1	L5	907	C
1	L5	910	G
1	L5	911	U
1	L5	915	A
1	L5	916	C
1	L5	917	A
1	L5	918	G
1	L5	919	C
1	L5	920	C
1	L5	926	G
1	L5	927	G
1	L5	928	C
1	L5	929	A
1	L5	930	G
1	L5	931	C
1	L5	932	A
1	L5	933	G
1	L5	934	C
1	L5	938	C
1	L5	940	C
1	L5	942	G
1	L5	944	A
1	L5	945	U
1	L5	946	C
1	L5	947	C
1	L5	950	G
1	L5	956	A
1	L5	957	G
1	L5	958	G
1	L5	959	G
1	L5	960	A
1	L5	961	G
1	L5	962	C
1	L5	963	G
1	L5	964	A
1	L5	965	G
1	L5	966	A
1	L5	967	C
1	L5	968	C

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Mol	Chain	Res	Type
1	L5	969	C
1	L5	975	C
1	L5	976	G
1	L5	978	G
1	L5	981	C
1	L5	982	U
1	L5	984	C
1	L5	985	C
1	L5	986	C
1	L5	989	U
1	L5	991	C
1	L5	992	C
1	L5	995	C
1	L5	996	G
1	L5	1049	C
1	L5	1051	G
1	L5	1065	G
1	L5	1071	C
1	L5	1072	C
1	L5	1073	G
1	L5	1076	C
1	L5	1078	A
1	L5	1079	C
1	L5	1080	C
1	L5	1081	C
1	L5	1083	U
1	L5	1096	C
1	L5	1100	U
1	L5	1169	G
1	L5	1170	G
1	L5	1172	C
1	L5	1173	G
1	L5	1178	G
1	L5	1179	U
1	L5	1180	C
1	L5	1181	C
1	L5	1182	C
1	L5	1183	C
1	L5	1184	A
1	L5	1188	C
1	L5	1191	C
1	L5	1193	C

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Mol	Chain	Res	Type
1	L5	1202	C
1	L5	1203	G
1	L5	1205	G
1	L5	1210	C
1	L5	1211	G
1	L5	1214	C
1	L5	1215	C
1	L5	1216	C
1	L5	1217	G
1	L5	1219	G
1	L5	1221	G
1	L5	1222	A
1	L5	1233	G
1	L5	1237	C
1	L5	1238	A
1	L5	1239	C
1	L5	1243	C
1	L5	1244	G
1	L5	1245	C
1	L5	1250	C
1	L5	1252	C
1	L5	1254	A
1	L5	1256	G
1	L5	1257	A
1	L5	1259	G
1	L5	1260	G
1	L5	1262	G
1	L5	1267	C
1	L5	1268	G
1	L5	1269	G
1	L5	1270	A
1	L5	1271	G
1	L5	1272	C
1	L5	1273	G
1	L5	1274	A
1	L5	1275	G
1	L5	1276	C
1	L5	1277	G
1	L5	1279	A
1	L5	1280	C
1	L5	1281	G
1	L5	1285	U

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Mol	Chain	Res	Type
1	L5	1288	G
1	L5	1289	C
1	L5	1290	G
1	L5	1293	G
1	L5	1295	C
1	L5	1296	G
1	L5	1297	U
1	L5	1298	C
1	L5	1301	C
1	L5	1303	A
1	L5	1322	A
1	L5	1326	A
1	L5	1330	A
1	L5	1339	U
1	L5	1343	A
1	L5	1353	G
1	L5	1354	A
1	L5	1358	G
1	L5	1359	G
1	L5	1360	G
1	L5	1364	U
1	L5	1365	C
1	L5	1366	G
1	L5	1367	C
1	L5	1368	A
1	L5	1369	C
1	L5	1370	G
1	L5	1371	A
1	L5	1372	A
1	L5	1376	C
1	L5	1377	G
1	L5	1378	C
1	L5	1379	C
1	L5	1381	U
1	L5	1387	A
1	L5	1394	G
1	L5	1396	G
1	L5	1399	G
1	L5	1404	G
1	L5	1407	C
1	L5	1409	C
1	L5	1410	U

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Mol	Chain	Res	Type
1	L5	1411	C
1	L5	1413	C
1	L5	1415	G
1	L5	1416	G
1	L5	1417	C
1	L5	1418	C
1	L5	1420	A
1	L5	1421	G
1	L5	1425	G
1	L5	1428	U
1	L5	1434	G
1	L5	1435	G
1	L5	1437	C
1	L5	1438	U
1	L5	1440	U
1	L5	1441	C
1	L5	1446	C
1	L5	1453	G
1	L5	1456	C
1	L5	1457	G
1	L5	1472	C
1	L5	1475	G
1	L5	1480	C
1	L5	1481	C
1	L5	1482	G
1	L5	1483	C
1	L5	1485	C
1	L5	1486	C
1	L5	1493	G
1	L5	1495	G
1	L5	1497	A
1	L5	1498	G
1	L5	1501	C
1	L5	1502	G
1	L5	1503	A
1	L5	1512	G
1	L5	1523	A
1	L5	1525	A
1	L5	1530	G
1	L5	1534	A
1	L5	1539	G
1	L5	1540	C

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Mol	Chain	Res	Type
1	L5	1547	A
1	L5	1552	G
1	L5	1563	A
1	L5	1564	A
1	L5	1566	C
1	L5	1574	G
1	L5	1578	U
1	L5	1582	U
1	L5	1591	U
1	L5	1592	G
1	L5	1596	U
1	L5	1597	G
1	L5	1611	C
1	L5	1612	G
1	L5	1613	A
1	L5	1614	C
1	L5	1623	A
1	L5	1624	G
1	L5	1625	G
1	L5	1626	G
1	L5	1629	G
1	L5	1631	A
1	L5	1633	G
1	L5	1634	A
1	L5	1638	A
1	L5	1641	G
1	L5	1646	A
1	L5	1650	A
1	L5	1651	G
1	L5	1654	G
1	L5	1656	U
1	L5	1657	G
1	L5	1661	C
1	L5	1676	C
1	L5	1677	U
1	L5	1681	G
1	L5	1686	C
1	L5	1694	C
1	L5	1696	C
1	L5	1697	G
1	L5	1698	C
1	L5	1699	A

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Mol	Chain	Res	Type
1	L5	1719	A
1	L5	1721	G
1	L5	1723	A
1	L5	1725	U
1	L5	1727	U
1	L5	1728	U
1	L5	1729	A
1	L5	1731	C
1	L5	1734	G
1	L5	1735	U
1	L5	1741	G
1	L5	1742	A
1	L5	1748	U
1	L5	1750	G
1	L5	1751	A
1	L5	1753	G
1	L5	1754	U
1	L5	1755	C
1	L5	1756	U
1	L5	1757	U
1	L5	1758	G
1	L5	1759	G
1	L5	1760	G
1	L5	1761	G
1	L5	1762	C
1	L5	1763	C
1	L5	1764	G
1	L5	1765	A
1	L5	1766	A
1	L5	1767	A
1	L5	1768	C
1	L5	1771	U
1	L5	1772	C
1	L5	1775	A
1	L5	1777	C
1	L5	1778	C
1	L5	1781	U
1	L5	1787	A
1	L5	1788	A
1	L5	1793	A
1	L5	1804	A
1	L5	1805	A

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Mol	Chain	Res	Type
1	L5	1806	G
1	L5	1807	C
1	L5	1815	G
1	L5	1820	C
1	L5	1821	G
1	L5	1822	U
1	L5	1829	G
1	L5	1832	C
1	L5	1833	G
1	L5	1834	U
1	L5	1835	G
1	L5	1836	G
1	L5	1837	A
1	L5	1842	G
1	L5	1855	G
1	L5	1856	C
1	L5	1866	U
1	L5	1867	A
1	L5	1869	G
1	L5	1882	U
1	L5	1890	G
1	L5	1893	C
1	L5	1897	A
1	L5	1910	G
1	L5	1915	C
1	L5	1918	U
1	L5	1919	G
1	L5	1920	C
1	L5	1921	C
1	L5	1922	G
1	L5	1925	G
1	L5	1929	A
1	L5	1930	U
1	L5	1932	A
1	L5	1936	C
1	L5	1940	G
1	L5	1948	G
1	L5	1954	U
1	L5	1956	A
1	L5	1958	A
1	L5	1959	U
1	L5	1960	A

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Mol	Chain	Res	Type
1	L5	1961	G
1	L5	1963	C
1	L5	1966	C
1	L5	1968	G
1	L5	1971	C
1	L5	1974	U
1	L5	1975	G
1	L5	1976	G
1	L5	1977	C
1	L5	1978	C
1	L5	1981	G
1	L5	1982	G
1	L5	1983	A
1	L5	1984	A
1	L5	1985	G
1	L5	1987	C
1	L5	1989	G
1	L5	1990	A
1	L5	1991	A
1	L5	1993	C
1	L5	1994	C
1	L5	1997	U
1	L5	1998	A
1	L5	1999	A
1	L5	2001	G
1	L5	2002	A
1	L5	2003	G
1	L5	2005	G
1	L5	2006	U
1	L5	2007	G
1	L5	2008	U
1	L5	2009	A
1	L5	2010	A
1	L5	2011	C
1	L5	2012	A
1	L5	2013	A
1	L5	2017	A
1	L5	2018	C
1	L5	2020	U
1	L5	2023	C
1	L5	2026	A
1	L5	2034	G

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Mol	Chain	Res	Type
1	L5	2045	G
1	L5	2046	G
1	L5	2048	U
1	L5	2055	G
1	L5	2056	G
1	L5	2057	A
1	L5	2062	C
1	L5	2063	G
1	L5	2064	G
1	L5	2068	C
1	L5	2069	A
1	L5	2073	C
1	L5	2075	G
1	L5	2077	C
1	L5	2084	C
1	L5	2085	G
1	L5	2089	G
1	L5	2090	U
1	L5	2091	C
1	L5	2092	G
1	L5	2093	A
1	L5	2094	G
1	L5	2095	A
1	L5	2097	U
1	L5	2099	G
1	L5	2100	A
1	L5	2104	G
1	L5	2107	C
1	L5	2108	G
1	L5	2109	G
1	L5	2110	C
1	L5	2111	G
1	L5	2112	G
1	L5	2113	G
1	L5	2114	G
1	L5	2115	G
1	L5	2116	C
1	L5	2117	G
1	L5	2118	G
1	L5	2119	C
1	L5	2120	G
1	L5	2121	C

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Mol	Chain	Res	Type
1	L5	2122	G
1	L5	2123	C
1	L5	2124	G
1	L5	2125	C
1	L5	2126	G
1	L5	2128	G
1	L5	2130	G
1	L5	2244	C
1	L5	2247	C
1	L5	2250	C
1	L5	2251	G
1	L5	2252	G
1	L5	2254	G
1	L5	2255	C
1	L5	2256	C
1	L5	2257	C
1	L5	2259	G
1	L5	2260	C
1	L5	2262	G
1	L5	2263	A
1	L5	2264	C
1	L5	2265	G
1	L5	2268	A
1	L5	2270	G
1	L5	2278	G
1	L5	2289	C
1	L5	2290	C
1	L5	2299	G
1	L5	2300	A
1	L5	2301	G
1	L5	2304	U
1	L5	2312	U
1	L5	2324	C
1	L5	2327	G
1	L5	2331	G
1	L5	2332	A
1	L5	2333	G
1	L5	2346	C
1	L5	2347	A
1	L5	2348	G
1	L5	2351	C
1	L5	2361	G

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Mol	Chain	Res	Type
1	L5	2362	U
1	L5	2364	G
1	L5	2379	A
1	L5	2382	A
1	L5	2390	G
1	L5	2395	A
1	L5	2396	A
1	L5	2397	G
1	L5	2402	G
1	L5	2404	A
1	L5	2410	C
1	L5	2414	G
1	L5	2422	C
1	L5	2425	U
1	L5	2426	U
1	L5	2431	A
1	L5	2448	G
1	L5	2450	G
1	L5	2454	U
1	L5	2465	C
1	L5	2468	U
1	L5	2471	G
1	L5	2474	G
1	L5	2475	G
1	L5	2482	C
1	L5	2483	G
1	L5	2484	A
1	L5	2486	G
1	L5	2487	G
1	L5	2488	C
1	L5	2489	C
1	L5	2490	U
1	L5	2491	C
1	L5	2495	U
1	L5	2502	G
1	L5	2503	G
1	L5	2504	C
1	L5	2505	C
1	L5	2506	G
1	L5	2507	A
1	L5	2511	A
1	L5	2513	A

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Mol	Chain	Res	Type
1	L5	2518	G
1	L5	2519	U
1	L5	2527	A
1	L5	2529	A
1	L5	2537	A
1	L5	2544	G
1	L5	2546	G
1	L5	2547	G
1	L5	2551	A
1	L5	2553	A
1	L5	2554	U
1	L5	2556	G
1	L5	2569	G
1	L5	2570	U
1	L5	2572	C
1	L5	2573	A
1	L5	2576	G
1	L5	2583	C
1	L5	2586	G
1	L5	2587	A
1	L5	2588	C
1	L5	2596	G
1	L5	2601	A
1	L5	2602	G
1	L5	2605	G
1	L5	2618	G
1	L5	2624	G
1	L5	2634	C
1	L5	2636	U
1	L5	2638	G
1	L5	2639	U
1	L5	2648	G
1	L5	2649	G
1	L5	2653	C
1	L5	2662	G
1	L5	2670	C
1	L5	2675	G
1	L5	2676	A
1	L5	2681	G
1	L5	2686	G
1	L5	2687	U
1	L5	2689	C

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Mol	Chain	Res	Type
1	L5	2695	A
1	L5	2696	A
1	L5	2701	U
1	L5	2702	C
1	L5	2703	G
1	L5	2704	C
1	L5	2705	G
1	L5	2708	U
1	L5	2710	C
1	L5	2712	G
1	L5	2714	G
1	L5	2717	G
1	L5	2719	C
1	L5	2721	G
1	L5	2723	U
1	L5	2725	A
1	L5	2726	G
1	L5	2735	G
1	L5	2739	C
1	L5	2740	U
1	L5	2743	A
1	L5	2753	G
1	L5	2754	G
1	L5	2756	G
1	L5	2760	G
1	L5	2761	U
1	L5	2762	G
1	L5	2763	U
1	L5	2766	A
1	L5	2768	C
1	L5	2769	U
1	L5	2770	C
1	L5	2776	G
1	L5	2783	A
1	L5	2786	C
1	L5	2787	A
1	L5	2788	U
1	L5	2789	A
1	L5	2794	C
1	L5	2797	C
1	L5	2803	U
1	L5	2807	A

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Mol	Chain	Res	Type
1	L5	2814	C
1	L5	2815	A
1	L5	2816	G
1	L5	2822	G
1	L5	2825	A
1	L5	2826	U
1	L5	2827	G
1	L5	2828	U
1	L5	2829	U
1	L5	2830	G
1	L5	2831	G
1	L5	2833	A
1	L5	2845	A
1	L5	2857	A
1	L5	2859	G
1	L5	2860	C
1	L5	2862	G
1	L5	2864	A
1	L5	2869	U
1	L5	2870	A
1	L5	2874	U
1	L5	2877	G
1	L5	2884	G
1	L5	2885	A
1	L5	2887	U
1	L5	2888	G
1	L5	2894	A
1	L5	2896	G
1	L5	2902	G
1	L5	2903	G
1	L5	2904	U
1	L5	2905	C
1	L5	2906	G
1	L5	2907	G
1	L5	2909	C
1	L5	3587	C
1	L5	3589	G
1	L5	3593	C
1	L5	3596	A
1	L5	3597	G
1	L5	3600	G
1	L5	3606	U

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Mol	Chain	Res	Type
1	L5	3608	A
1	L5	3615	G
1	L5	3616	U
1	L5	3625	G
1	L5	3626	G
1	L5	3635	A
1	L5	3640	U
1	L5	3642	A
1	L5	3644	U
1	L5	3646	A
1	L5	3659	G
1	L5	3661	G
1	L5	3662	A
1	L5	3669	G
1	L5	3670	C
1	L5	3671	G
1	L5	3672	G
1	L5	3673	C
1	L5	3674	G
1	L5	3681	G
1	L5	3682	A
1	L5	3690	U
1	L5	3696	C
1	L5	3697	U
1	L5	3699	C
1	L5	3705	G
1	L5	3709	U
1	L5	3710	G
1	L5	3711	A
1	L5	3713	U
1	L5	3714	G
1	L5	3723	A
1	L5	3727	A
1	L5	3728	A
1	L5	3729	U
1	L5	3730	U
1	L5	3732	A
1	L5	3734	U
1	L5	3735	G
1	L5	3736	A
1	L5	3742	G
1	L5	3745	U

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Mol	Chain	Res	Type
1	L5	3748	A
1	L5	3750	G
1	L5	3751	G
1	L5	3753	G
1	L5	3755	G
1	L5	3756	A
1	L5	3757	G
1	L5	3758	U
1	L5	3759	A
1	L5	3760	A
1	L5	3761	C
1	L5	3762	U
1	L5	3764	U
1	L5	3766	A
1	L5	3767	C
1	L5	3768	U
1	L5	3769	C
1	L5	3770	U
1	L5	3772	U
1	L5	3776	G
1	L5	3777	G
1	L5	3785	A
1	L5	3786	U
1	L5	3789	C
1	L5	3790	U
1	L5	3791	C
1	L5	3795	A
1	L5	3802	U
1	L5	3803	A
1	L5	3807	A
1	L5	3811	G
1	L5	3813	A
1	L5	3814	U
1	L5	3817	A
1	L5	3818	U
1	L5	3819	G
1	L5	3840	U
1	L5	3843	C
1	L5	3866	C
1	L5	3867	A
1	L5	3868	G
1	L5	3869	C

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Mol	Chain	Res	Type
1	L5	3870	C
1	L5	3871	A
1	L5	3877	A
1	L5	3878	C
1	L5	3879	G
1	L5	3881	G
1	L5	3885	G
1	L5	3888	G
1	L5	3889	G
1	L5	3890	A
1	L5	3892	U
1	L5	3895	G
1	L5	3897	G
1	L5	3901	A
1	L5	3905	A
1	L5	3906	A
1	L5	3907	G
1	L5	3908	A
1	L5	3914	U
1	L5	3915	U
1	L5	3922	G
1	L5	3923	A
1	L5	3933	G
1	L5	3935	C
1	L5	3938	G
1	L5	3939	G
1	L5	3943	A
1	L5	3944	G
1	L5	3947	A
1	L5	3948	C
1	L5	3949	A
1	L5	3954	A
1	L5	3956	G
1	L5	3957	U
1	L5	3958	G
1	L5	3959	U
1	L5	3960	A
1	L5	3961	G
1	L5	3962	A
1	L5	3963	A
1	L5	3965	A
1	L5	3966	A

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Mol	Chain	Res	Type
1	L5	3968	U
1	L5	3969	G
1	L5	3972	A
1	L5	3973	G
1	L5	3975	C
1	L5	3977	C
1	L5	4034	G
1	L5	4036	G
1	L5	4037	C
1	L5	4039	G
1	L5	4042	G
1	L5	4043	G
1	L5	4044	U
1	L5	4047	A
1	L5	4048	A
1	L5	4049	U
1	L5	4050	A
1	L5	4051	C
1	L5	4052	C
1	L5	4054	C
1	L5	4055	U
1	L5	4058	U
1	L5	4059	C
1	L5	4062	A
1	L5	4064	C
1	L5	4065	G
1	L5	4071	U
1	L5	4076	G
1	L5	4077	A
1	L5	4078	C
1	L5	4079	C
1	L5	4083	U
1	L5	4084	G
1	L5	4086	G
1	L5	4087	G
1	L5	4095	G
1	L5	4100	C
1	L5	4102	C
1	L5	4103	C
1	L5	4104	G
1	L5	4107	G
1	L5	4110	C

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Mol	Chain	Res	Type
1	L5	4112	C
1	L5	4114	C
1	L5	4115	G
1	L5	4116	C
1	L5	4117	U
1	L5	4118	U
1	L5	4119	C
1	L5	4120	U
1	L5	4121	G
1	L5	4125	C
1	L5	4127	A
1	L5	4131	G
1	L5	4138	C
1	L5	4139	G
1	L5	4140	C
1	L5	4141	G
1	L5	4142	C
1	L5	4143	G
1	L5	4144	C
1	L5	4146	G
1	L5	4151	G
1	L5	4153	C
1	L5	4154	G
1	L5	4156	G
1	L5	4158	C
1	L5	4161	G
1	L5	4162	C
1	L5	4163	U
1	L5	4164	C
1	L5	4166	G
1	L5	4168	G
1	L5	4169	G
1	L5	4170	A
1	L5	4171	C
1	L5	4172	A
1	L5	4173	G
1	L5	4177	C
1	L5	4183	G
1	L5	4184	G
1	L5	4190	U
1	L5	4191	G
1	L5	4193	C

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Mol	Chain	Res	Type
1	L5	4194	U
1	L5	4201	G
1	L5	4202	U
1	L5	4203	A
1	L5	4205	A
1	L5	4209	G
1	L5	4212	A
1	L5	4220	A
1	L5	4222	G
1	L5	4225	G
1	L5	4229	U
1	L5	4234	A
1	L5	4235	G
1	L5	4237	C
1	L5	4245	G
1	L5	4248	A
1	L5	4251	A
1	L5	4254	G
1	L5	4255	A
1	L5	4256	A
1	L5	4258	C
1	L5	4260	U
1	L5	4268	A
1	L5	4271	A
1	L5	4273	A
1	L5	4277	G
1	L5	4280	A
1	L5	4281	A
1	L5	4286	C
1	L5	4287	G
1	L5	4288	C
1	L5	4291	G
1	L5	4292	A
1	L5	4296	U
1	L5	4297	G
1	L5	4302	U
1	L5	4305	G
1	L5	4306	U
1	L5	4311	A
1	L5	4314	C
1	L5	4317	A
1	L5	4319	C

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Mol	Chain	Res	Type
1	L5	4328	G
1	L5	4330	G
1	L5	4337	C
1	L5	4338	G
1	L5	4339	A
1	L5	4346	U
1	L5	4349	C
1	L5	4350	C
1	L5	4367	G
1	L5	4369	A
1	L5	4376	A
1	L5	4377	G
1	L5	4378	A
1	L5	4380	A
1	L5	4381	A
1	L5	4382	G
1	L5	4384	U
1	L5	4385	A
1	L5	4387	C
1	L5	4394	A
1	L5	4396	A
1	L5	4398	C
1	L5	4414	A
1	L5	4415	A
1	L5	4419	U
1	L5	4420	U
1	L5	4422	A
1	L5	4427	G
1	L5	4429	C
1	L5	4438	U
1	L5	4448	G
1	L5	4449	A
1	L5	4464	A
1	L5	4465	U
1	L5	4475	G
1	L5	4476	C
1	L5	4477	A
1	L5	4478	G
1	L5	4481	U
1	L5	4488	A
1	L5	4489	G
1	L5	4491	G

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Mol	Chain	Res	Type
1	L5	4498	U
1	L5	4500	U
1	L5	4504	C
1	L5	4510	A
1	L5	4511	A
1	L5	4512	U
1	L5	4513	A
1	L5	4515	G
1	L5	4518	A
1	L5	4523	A
1	L5	4524	G
1	L5	4528	G
1	L5	4531	U
1	L5	4534	G
1	L5	4545	G
1	L5	4548	A
1	L5	4549	G
1	L5	4557	U
1	L5	4560	C
1	L5	4567	G
1	L5	4571	A
1	L5	4573	G
1	L5	4575	G
1	L5	4581	G
1	L5	4583	C
1	L5	4587	G
1	L5	4589	A
1	L5	4590	A
1	L5	4595	G
1	L5	4599	A
1	L5	4600	G
1	L5	4601	U
1	L5	4609	G
1	L5	4617	G
1	L5	4627	U
1	L5	4636	U
1	L5	4637	G
1	L5	4639	G
1	L5	4641	U
1	L5	4642	U
1	L5	4656	A
1	L5	4657	U

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Mol	Chain	Res	Type
1	L5	4658	G
1	L5	4670	C
1	L5	4672	A
1	L5	4677	U
1	L5	4678	G
1	L5	4682	U
1	L5	4693	C
1	L5	4695	C
1	L5	4696	C
1	L5	4699	U
1	L5	4700	A
1	L5	4708	A
1	L5	4709	U
1	L5	4728	U
1	L5	4730	C
1	L5	4731	G
1	L5	4732	G
1	L5	4733	C
1	L5	4734	A
1	L5	4738	C
1	L5	4739	C
1	L5	4743	G
1	L5	4744	A
1	L5	4749	C
1	L5	4750	G
1	L5	4753	U
1	L5	4756	C
1	L5	4757	C
1	L5	4758	U
1	L5	4760	G
1	L5	4761	G
1	L5	4764	A
1	L5	4768	G
1	L5	4770	U
1	L5	4771	C
1	L5	4772	C
1	L5	4774	C
1	L5	4775	C
1	L5	4776	G
1	L5	4860	G
1	L5	4861	G
1	L5	4862	G

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Mol	Chain	Res	Type
1	L5	4863	G
1	L5	4865	C
1	L5	4868	G
1	L5	4869	U
1	L5	4870	G
1	L5	4871	C
1	L5	4872	G
1	L5	4873	G
1	L5	4874	A
1	L5	4875	G
1	L5	4876	U
1	L5	4877	G
1	L5	4878	C
1	L5	4880	C
1	L5	4882	U
1	L5	4883	C
1	L5	4884	G
1	L5	4888	U
1	L5	4890	G
1	L5	4894	A
1	L5	4896	G
1	L5	4900	C
1	L5	4901	G
1	L5	4902	C
1	L5	4910	G
1	L5	4911	A
1	L5	4912	G
1	L5	4913	G
1	L5	4914	C
1	L5	4918	C
1	L5	4923	C
1	L5	4925	U
1	L5	4926	C
1	L5	4927	G
1	L5	4936	G
1	L5	4938	A
1	L5	4939	C
1	L5	4941	G
1	L5	4945	G
1	L5	4946	U
1	L5	4949	G
1	L5	4950	U

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Mol	Chain	Res	Type
1	L5	4951	G
1	L5	4952	G
1	L5	4956	A
1	L5	4957	C
1	L5	4958	C
1	L5	4959	U
1	L5	4963	G
1	L5	4964	C
1	L5	4968	A
1	L5	4970	C
1	L5	4973	U
1	L5	4976	U
1	L5	4982	A
1	L5	4985	U
1	L5	4988	U
1	L5	4989	U
1	L5	4991	U
1	L5	4992	G
1	L5	5007	A
1	L5	5011	A
1	L5	5014	A
1	L5	5017	G
1	L5	5018	C
1	L5	5022	U
1	L5	5024	C
1	L5	5025	C
1	L5	5026	U
1	L5	5027	C
1	L5	5028	G
1	L5	5031	G
1	L5	5034	A
1	L5	5035	U
1	L5	5041	G
1	L5	5043	A
1	L5	5050	C
1	L5	5054	C
1	L5	5055	G
1	L5	5058	A
1	L5	5061	A
1	L5	5064	G
1	L5	5066	U
1	L5	5068	G

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Mol	Chain	Res	Type
2	L7	7	G
2	L7	20	U
2	L7	22	A
2	L7	24	C
2	L7	25	G
2	L7	26	C
2	L7	36	C
2	L7	40	U
2	L7	49	A
2	L7	54	A
2	L7	60	G
2	L7	63	C
2	L7	64	G
2	L7	73	U
2	L7	84	U
2	L7	97	G
2	L7	100	A
2	L7	109	U
2	L7	110	G
2	L7	111	C
2	L7	120	U
3	L8	2	G
3	L8	8	U
3	L8	17	A
3	L8	22	U
3	L8	23	C
3	L8	27	U
3	L8	34	U
3	L8	35	C
3	L8	48	A
3	L8	50	C
3	L8	52	A
3	L8	56	G
3	L8	59	A
3	L8	63	U
3	L8	76	C
3	L8	80	A
3	L8	82	A
3	L8	83	C
3	L8	84	A
3	L8	86	U
3	L8	87	G

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Mol	Chain	Res	Type
3	L8	88	A
3	L8	89	U
3	L8	93	C
3	L8	95	A
3	L8	98	C
3	L8	103	A
3	L8	104	A
3	L8	105	C
3	L8	109	C
3	L8	110	U
3	L8	114	G
3	L8	118	C
3	L8	122	G
3	L8	123	U
3	L8	124	U
3	L8	125	C
3	L8	126	C
3	L8	127	U
3	L8	128	C
3	L8	129	C
3	L8	146	U
3	L8	149	G
3	L8	150	C
47	S2	2	A
47	S2	3	C
47	S2	4	C
47	S2	9	U
47	S2	17	C
47	S2	18	C
47	S2	25	A
47	S2	27	A
47	S2	31	U
47	S2	33	G
47	S2	41	G
47	S2	42	A
47	S2	44	U
47	S2	45	A
47	S2	46	A
47	S2	52	G
47	S2	56	G
47	S2	62	G
47	S2	64	A

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Mol	Chain	Res	Type
47	S2	67	C
47	S2	68	A
47	S2	69	C
47	S2	70	G
47	S2	72	C
47	S2	73	C
47	S2	74	G
47	S2	76	U
47	S2	77	A
47	S2	78	C
47	S2	79	A
47	S2	83	A
47	S2	84	A
47	S2	98	C
47	S2	99	A
47	S2	103	A
47	S2	113	G
47	S2	114	G
47	S2	126	G
47	S2	127	C
47	S2	139	C
47	S2	140	C
47	S2	141	A
47	S2	142	C
47	S2	144	U
47	S2	148	U
47	S2	153	G
47	S2	154	U
47	S2	155	G
47	S2	156	G
47	S2	160	U
47	S2	161	U
47	S2	162	C
47	S2	163	U
47	S2	167	G
47	S2	168	C
47	S2	171	A
47	S2	172	U
47	S2	175	A
47	S2	177	G
47	S2	178	C
47	S2	180	G

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Mol	Chain	Res	Type
47	S2	181	A
47	S2	184	G
47	S2	185	G
47	S2	188	C
47	S2	190	G
47	S2	191	A
47	S2	192	C
47	S2	198	U
47	S2	201	C
47	S2	202	G
47	S2	208	G
47	S2	209	A
47	S2	210	U
47	S2	211	G
47	S2	214	U
47	S2	215	G
47	S2	219	U
47	S2	291	G
47	S2	292	A
47	S2	293	C
47	S2	295	C
47	S2	299	A
47	S2	304	C
47	S2	305	U
47	S2	306	C
47	S2	307	G
47	S2	308	G
47	S2	309	G
47	S2	312	G
47	S2	313	A
47	S2	314	U
47	S2	316	G
47	S2	319	C
47	S2	320	G
47	S2	323	C
47	S2	324	C
47	S2	325	C
47	S2	326	C
47	S2	328	U
47	S2	329	G
47	S2	330	G
47	S2	334	C

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Mol	Chain	Res	Type
47	S2	338	G
47	S2	339	A
47	S2	340	C
47	S2	341	C
47	S2	342	C
47	S2	343	A
47	S2	347	G
47	S2	351	G
47	S2	354	U
47	S2	360	A
47	S2	361	U
47	S2	362	C
47	S2	364	A
47	S2	369	C
47	S2	370	G
47	S2	371	A
47	S2	385	G
47	S2	386	C
47	S2	388	U
47	S2	391	C
47	S2	400	C
47	S2	401	A
47	S2	402	C
47	S2	407	G
47	S2	408	A
47	S2	409	C
47	S2	411	G
47	S2	413	G
47	S2	417	C
47	S2	418	A
47	S2	423	U
47	S2	426	A
47	S2	429	C
47	S2	434	G
47	S2	435	A
47	S2	436	G
47	S2	438	G
47	S2	441	C
47	S2	448	A
47	S2	449	A
47	S2	450	C
47	S2	452	G

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Mol	Chain	Res	Type
47	S2	459	C
47	S2	464	A
47	S2	465	A
47	S2	466	G
47	S2	467	G
47	S2	469	A
47	S2	472	C
47	S2	473	A
47	S2	474	G
47	S2	482	G
47	S2	487	U
47	S2	488	U
47	S2	489	A
47	S2	492	C
47	S2	493	A
47	S2	495	U
47	S2	502	C
47	S2	503	C
47	S2	505	G
47	S2	507	G
47	S2	516	A
47	S2	517	C
47	S2	530	U
47	S2	532	C
47	S2	533	A
47	S2	534	G
47	S2	535	G
47	S2	537	C
47	S2	538	U
47	S2	539	C
47	S2	540	U
47	S2	542	U
47	S2	544	G
47	S2	545	A
47	S2	547	G
47	S2	549	C
47	S2	550	C
47	S2	551	U
47	S2	556	U
47	S2	557	U
47	S2	559	G
47	S2	560	A

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Mol	Chain	Res	Type
47	S2	563	G
47	S2	566	U
47	S2	574	A
47	S2	575	A
47	S2	576	A
47	S2	581	U
47	S2	582	C
47	S2	584	G
47	S2	585	C
47	S2	587	A
47	S2	588	G
47	S2	589	G
47	S2	590	A
47	S2	591	U
47	S2	592	C
47	S2	593	C
47	S2	596	U
47	S2	604	A
47	S2	605	A
47	S2	606	G
47	S2	607	U
47	S2	608	C
47	S2	613	G
47	S2	621	C
47	S2	627	U
47	S2	628	A
47	S2	629	A
47	S2	631	U
47	S2	634	A
47	S2	643	A
47	S2	644	G
47	S2	651	U
47	S2	655	A
47	S2	656	G
47	S2	657	U
47	S2	660	C
47	S2	666	U
47	S2	669	A
47	S2	670	A
47	S2	671	A
47	S2	672	A
47	S2	673	G

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Mol	Chain	Res	Type
47	S2	675	U
47	S2	679	A
47	S2	683	G
47	S2	685	A
47	S2	686	U
47	S2	687	C
47	S2	688	U
47	S2	689	U
47	S2	690	G
47	S2	691	G
47	S2	692	G
47	S2	693	A
47	S2	694	G
47	S2	695	C
47	S2	696	G
47	S2	697	G
47	S2	698	G
47	S2	731	G
47	S2	733	C
47	S2	734	C
47	S2	735	C
47	S2	736	C
47	S2	738	C
47	S2	739	C
47	S2	746	C
47	S2	747	U
47	S2	749	U
47	S2	750	C
47	S2	751	G
47	S2	752	G
47	S2	753	C
47	S2	787	G
47	S2	788	G
47	S2	789	G
47	S2	790	C
47	S2	791	C
47	S2	794	A
47	S2	795	A
47	S2	796	G
47	S2	797	C
47	S2	798	A
47	S2	800	U

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Mol	Chain	Res	Type
47	S2	810	A
47	S2	811	A
47	S2	812	A
47	S2	813	A
47	S2	815	U
47	S2	818	A
47	S2	821	G
47	S2	822	U
47	S2	823	U
47	S2	830	A
47	S2	834	C
47	S2	835	C
47	S2	837	A
47	S2	838	G
47	S2	839	C
47	S2	840	C
47	S2	841	G
47	S2	842	C
47	S2	843	C
47	S2	847	A
47	S2	848	U
47	S2	853	C
47	S2	864	A
47	S2	865	A
47	S2	869	A
47	S2	870	A
47	S2	873	G
47	S2	874	G
47	S2	876	C
47	S2	877	C
47	S2	878	G
47	S2	879	C
47	S2	881	G
47	S2	883	U
47	S2	887	U
47	S2	888	U
47	S2	889	U
47	S2	890	U
47	S2	891	G
47	S2	892	U
47	S2	893	U
47	S2	894	G

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Mol	Chain	Res	Type
47	S2	896	U
47	S2	897	U
47	S2	899	U
47	S2	900	C
47	S2	901	G
47	S2	902	G
47	S2	903	A
47	S2	904	A
47	S2	907	G
47	S2	908	A
47	S2	909	G
47	S2	913	A
47	S2	914	U
47	S2	917	U
47	S2	919	A
47	S2	920	A
47	S2	930	C
47	S2	933	G
47	S2	934	G
47	S2	939	U
47	S2	943	U
47	S2	952	G
47	S2	954	U
47	S2	955	A
47	S2	956	G
47	S2	958	G
47	S2	961	G
47	S2	963	A
47	S2	964	A
47	S2	965	U
47	S2	970	G
47	S2	971	G
47	S2	972	A
47	S2	973	C
47	S2	978	G
47	S2	979	C
47	S2	981	A
47	S2	990	A
47	S2	992	A
47	S2	996	A
47	S2	999	G
47	S2	1002	U

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Mol	Chain	Res	Type
47	S2	1008	A
47	S2	1017	U
47	S2	1022	U
47	S2	1023	A
47	S2	1027	A
47	S2	1028	A
47	S2	1029	G
47	S2	1041	G
47	S2	1042	A
47	S2	1044	G
47	S2	1052	A
47	S2	1059	G
47	S2	1060	A
47	S2	1061	U
47	S2	1062	A
47	S2	1068	G
47	S2	1076	G
47	S2	1081	U
47	S2	1083	A
47	S2	1084	A
47	S2	1085	C
47	S2	1087	A
47	S2	1088	U
47	S2	1110	G
47	S2	1113	A
47	S2	1114	U
47	S2	1115	U
47	S2	1116	C
47	S2	1118	C
47	S2	1119	A
47	S2	1120	U
47	S2	1126	G
47	S2	1134	G
47	S2	1138	C
47	S2	1139	C
47	S2	1148	A
47	S2	1149	A
47	S2	1150	A
47	S2	1153	C
47	S2	1154	U
47	S2	1155	U
47	S2	1157	G

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Mol	Chain	Res	Type
47	S2	1166	G
47	S2	1170	A
47	S2	1171	G
47	S2	1172	U
47	S2	1175	G
47	S2	1180	C
47	S2	1181	A
47	S2	1186	U
47	S2	1194	A
47	S2	1195	A
47	S2	1198	G
47	S2	1208	A
47	S2	1211	G
47	S2	1212	G
47	S2	1213	C
47	S2	1214	A
47	S2	1215	C
47	S2	1216	C
47	S2	1217	A
47	S2	1224	G
47	S2	1231	C
47	S2	1238	U
47	S2	1240	A
47	S2	1241	A
47	S2	1242	U
47	S2	1248	U
47	S2	1250	A
47	S2	1251	A
47	S2	1253	A
47	S2	1256	G
47	S2	1257	G
47	S2	1258	A
47	S2	1259	A
47	S2	1260	A
47	S2	1264	C
47	S2	1265	A
47	S2	1268	C
47	S2	1269	G
47	S2	1271	C
47	S2	1274	G
47	S2	1275	G
47	S2	1276	A

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Mol	Chain	Res	Type
47	S2	1277	C
47	S2	1280	G
47	S2	1281	G
47	S2	1283	C
47	S2	1284	A
47	S2	1287	A
47	S2	1288	U
47	S2	1289	U
47	S2	1290	G
47	S2	1292	C
47	S2	1294	G
47	S2	1295	A
47	S2	1296	U
47	S2	1297	U
47	S2	1298	G
47	S2	1299	A
47	S2	1300	U
47	S2	1301	A
47	S2	1302	G
47	S2	1303	C
47	S2	1305	C
47	S2	1306	U
47	S2	1307	U
47	S2	1308	U
47	S2	1310	U
47	S2	1311	C
47	S2	1313	A
47	S2	1315	U
47	S2	1317	C
47	S2	1318	G
47	S2	1321	G
47	S2	1323	U
47	S2	1324	G
47	S2	1330	G
47	S2	1331	C
47	S2	1332	A
47	S2	1337	C
47	S2	1341	C
47	S2	1342	U
47	S2	1343	U
47	S2	1363	C
47	S2	1364	U

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Mol	Chain	Res	Type
47	S2	1371	U
47	S2	1372	U
47	S2	1373	C
47	S2	1378	A
47	S2	1383	A
47	S2	1393	G
47	S2	1396	A
47	S2	1397	U
47	S2	1398	G
47	S2	1404	U
47	S2	1405	A
47	S2	1407	U
47	S2	1409	A
47	S2	1410	C
47	S2	1412	C
47	S2	1413	G
47	S2	1414	A
47	S2	1415	C
47	S2	1416	C
47	S2	1418	C
47	S2	1419	C
47	S2	1420	G
47	S2	1423	C
47	S2	1424	G
47	S2	1425	G
47	S2	1427	C
47	S2	1428	G
47	S2	1431	G
47	S2	1432	U
47	S2	1434	C
47	S2	1436	C
47	S2	1437	C
47	S2	1438	A
47	S2	1442	U
47	S2	1448	A
47	S2	1449	G
47	S2	1454	A
47	S2	1455	A
47	S2	1456	G
47	S2	1457	U
47	S2	1458	G
47	S2	1463	U

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Mol	Chain	Res	Type
47	S2	1464	C
47	S2	1468	C
47	S2	1471	C
47	S2	1472	C
47	S2	1473	G
47	S2	1475	G
47	S2	1476	A
47	S2	1477	U
47	S2	1480	A
47	S2	1481	G
47	S2	1484	A
47	S2	1487	A
47	S2	1489	A
47	S2	1490	G
47	S2	1493	C
47	S2	1494	U
47	S2	1495	G
47	S2	1497	G
47	S2	1498	A
47	S2	1505	U
47	S2	1506	A
47	S2	1507	G
47	S2	1508	A
47	S2	1509	U
47	S2	1510	G
47	S2	1512	C
47	S2	1513	C
47	S2	1515	G
47	S2	1520	G
47	S2	1521	C
47	S2	1522	A
47	S2	1523	C
47	S2	1525	C
47	S2	1526	G
47	S2	1527	C
47	S2	1531	A
47	S2	1533	A
47	S2	1535	U
47	S2	1536	G
47	S2	1538	C
47	S2	1540	G
47	S2	1543	U

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Mol	Chain	Res	Type
47	S2	1545	A
47	S2	1546	G
47	S2	1550	G
47	S2	1551	U
47	S2	1552	G
47	S2	1553	C
47	S2	1554	C
47	S2	1555	U
47	S2	1556	A
47	S2	1557	C
47	S2	1558	C
47	S2	1567	G
47	S2	1568	C
47	S2	1569	A
47	S2	1570	G
47	S2	1573	G
47	S2	1574	C
47	S2	1575	G
47	S2	1579	A
47	S2	1580	A
47	S2	1581	C
47	S2	1585	U
47	S2	1586	U
47	S2	1587	G
47	S2	1588	A
47	S2	1589	A
47	S2	1598	G
47	S2	1599	U
47	S2	1600	G
47	S2	1603	G
47	S2	1614	A
47	S2	1621	U
47	S2	1623	A
47	S2	1626	C
47	S2	1636	G
47	S2	1637	A
47	S2	1638	G
47	S2	1639	G
47	S2	1640	A
47	S2	1644	C
47	S2	1648	G
47	S2	1651	A

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Mol	Chain	Res	Type
47	S2	1653	U
47	S2	1654	G
47	S2	1655	C
47	S2	1660	C
47	S2	1661	A
47	S2	1662	U
47	S2	1663	A
47	S2	1664	A
47	S2	1665	G
47	S2	1679	A
47	S2	1680	G
47	S2	1686	G
47	S2	1688	C
47	S2	1694	U
47	S2	1695	A
47	S2	1697	A
47	S2	1698	C
47	S2	1701	C
47	S2	1714	U
47	S2	1719	A
47	S2	1721	U
47	S2	1722	G
47	S2	1729	U
47	S2	1730	U
47	S2	1735	A
47	S2	1737	G
47	S2	1742	C
47	S2	1743	G
47	S2	1744	G
47	S2	1745	A
47	S2	1746	U
47	S2	1748	G
47	S2	1751	C
47	S2	1752	C
47	S2	1754	G
47	S2	1755	C
47	S2	1757	G
47	S2	1758	G
47	S2	1772	C
47	S2	1773	C
47	S2	1775	U
47	S2	1777	G

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Mol	Chain	Res	Type
47	S2	1781	A
47	S2	1783	C
47	S2	1784	G
47	S2	1786	U
47	S2	1805	G
47	S2	1812	U
47	S2	1813	A
47	S2	1814	G
47	S2	1823	A
47	S2	1824	A
47	S2	1825	A
47	S2	1826	G
47	S2	1831	A
47	S2	1835	A
47	S2	1838	U
47	S2	1839	U
47	S2	1849	G
47	S2	1850	A
47	S2	1851	A
47	S2	1852	C
47	S2	1857	G
47	S2	1858	G
47	S2	1861	G
47	S2	1862	G
47	S2	1863	A
47	S2	1865	C
47	S2	1868	U
47	S2	1869	A
48	S6	4	C
48	S6	9	U
48	S6	17	C
48	S6	18	G
48	S6	19	G
48	S6	20	A
48	S6	21	A
48	S6	22	G
48	S6	23	C
48	S6	31	G
48	S6	33	C
48	S6	34	C
48	S6	35	A
48	S6	36	U

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Mol	Chain	Res	Type
48	S6	37	A
48	S6	39	C
48	S6	40	C
48	S6	41	C
48	S6	42	A
48	S6	45	G
48	S6	46	G
48	S6	47	U
48	S6	57	G
48	S6	59	A
48	S6	61	C
48	S6	73	A
48	S6	75	C
48	S6	76	A

All (82) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	172	C
1	L5	385	A
1	L5	406	C
1	L5	417	G
1	L5	648	G
1	L5	693	C
1	L5	918	G
1	L5	930	G
1	L5	931	C
1	L5	956	A
1	L5	958	G
1	L5	974	C
1	L5	1072	C
1	L5	1238	A
1	L5	1329	G
1	L5	1359	G
1	L5	1410	U
1	L5	1455	G
1	L5	1633	G
1	L5	1649	U
1	L5	1821	G
1	L5	1947	U
1	L5	2019	C
1	L5	2068	C

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Mol	Chain	Res	Type
1	L5	2096	G
1	L5	2116	C
1	L5	2119	C
1	L5	2120	G
1	L5	2124	G
1	L5	2256	C
1	L5	2389	A
1	L5	2467	U
1	L5	2505	C
1	L5	2695	A
1	L5	2785	C
1	L5	2806	A
1	L5	2828	U
1	L5	3625	G
1	L5	3673	C
1	L5	3713	U
1	L5	3767	C
1	L5	3784	A
1	L5	3810	C
1	L5	3888	G
1	L5	3956	G
1	L5	4600	G
1	L5	4730	C
1	L5	4731	G
1	L5	4889	G
1	L5	4909	A
1	L5	4913	G
1	L5	4937	C
1	L5	4948	C
1	L5	4958	C
1	L5	4991	U
1	L5	5027	C
3	L8	16	G
3	L8	87	G
47	S2	24	C
47	S2	213	G
47	S2	339	A
47	S2	370	G
47	S2	417	C
47	S2	465	A
47	S2	604	A
47	S2	606	G

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Mol	Chain	Res	Type
47	S2	668	A
47	S2	688	U
47	S2	795	A
47	S2	833	C
47	S2	868	G
47	S2	912	C
47	S2	980	A
47	S2	1061	U
47	S2	1137	U
47	S2	1404	U
47	S2	1419	C
47	S2	1664	A
47	S2	1823	A
47	S2	1860	A
48	S6	33	C
48	S6	34	C

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 245 ligands modelled in this entry, 245 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
43	Lo	1
66	Sa	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lo	105:GLN	C	106:PHE	N	3.21
1	Sa	99:PRO	C	100:ARG	N	3.14

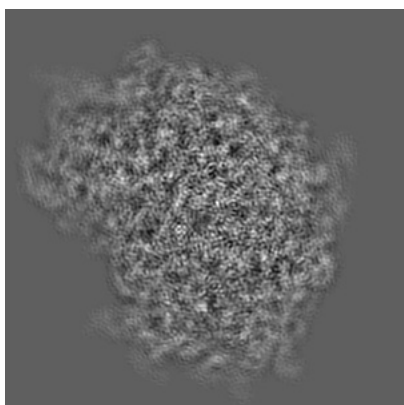
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2938. These allow visual inspection of the internal detail of the map and identification of artifacts.

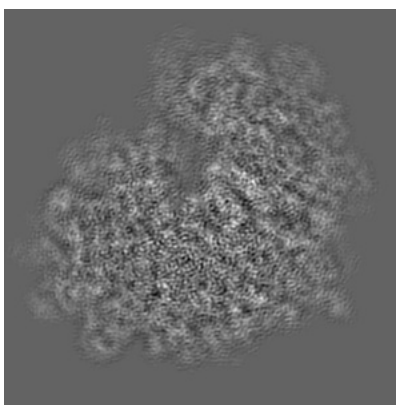
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

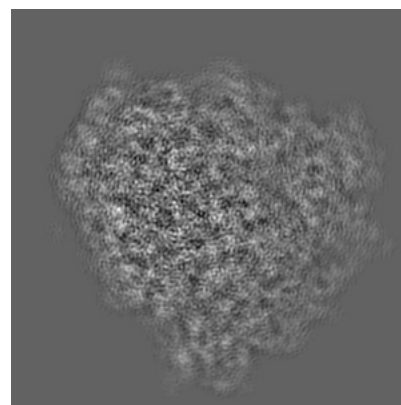
6.1.1 Primary map



X



Y

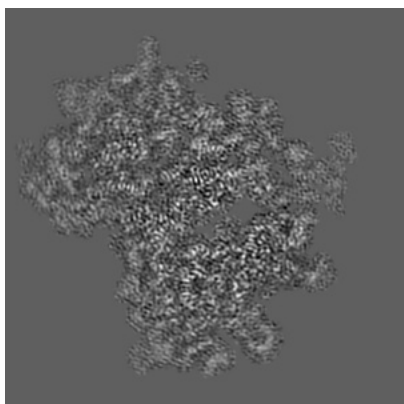


Z

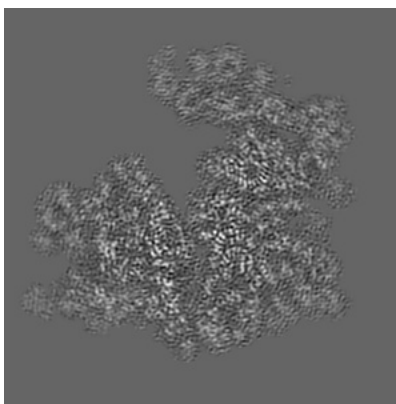
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

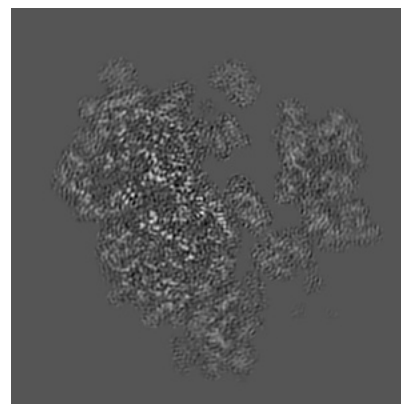
6.2.1 Primary map



X Index: 150



Y Index: 150

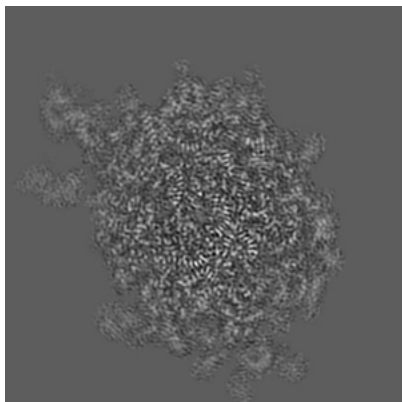


Z Index: 150

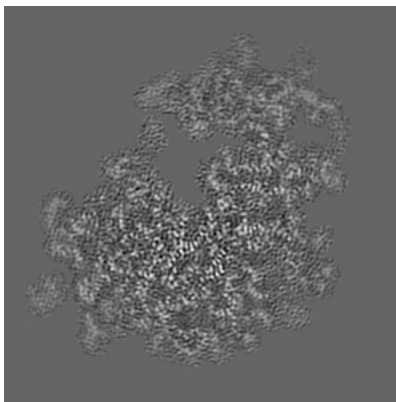
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

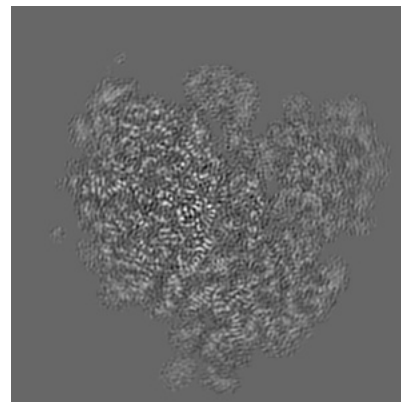
6.3.1 Primary map



X Index: 123



Y Index: 162

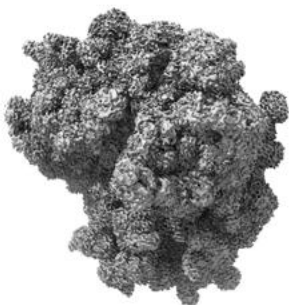


Z Index: 172

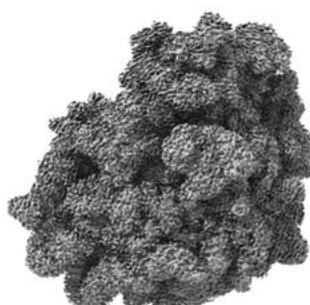
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

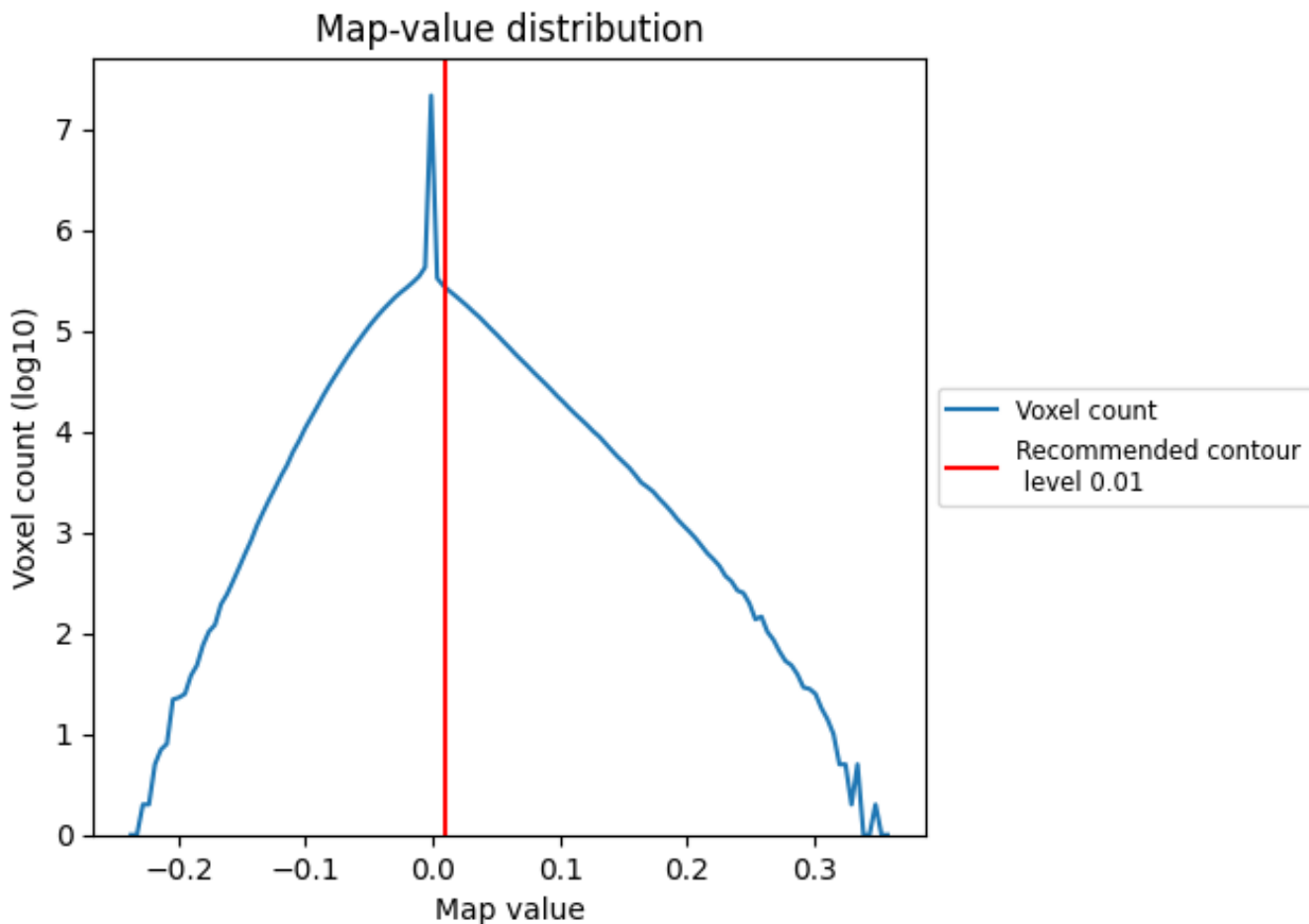
6.5 Mask visualisation

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

7 Map analysis [i](#)

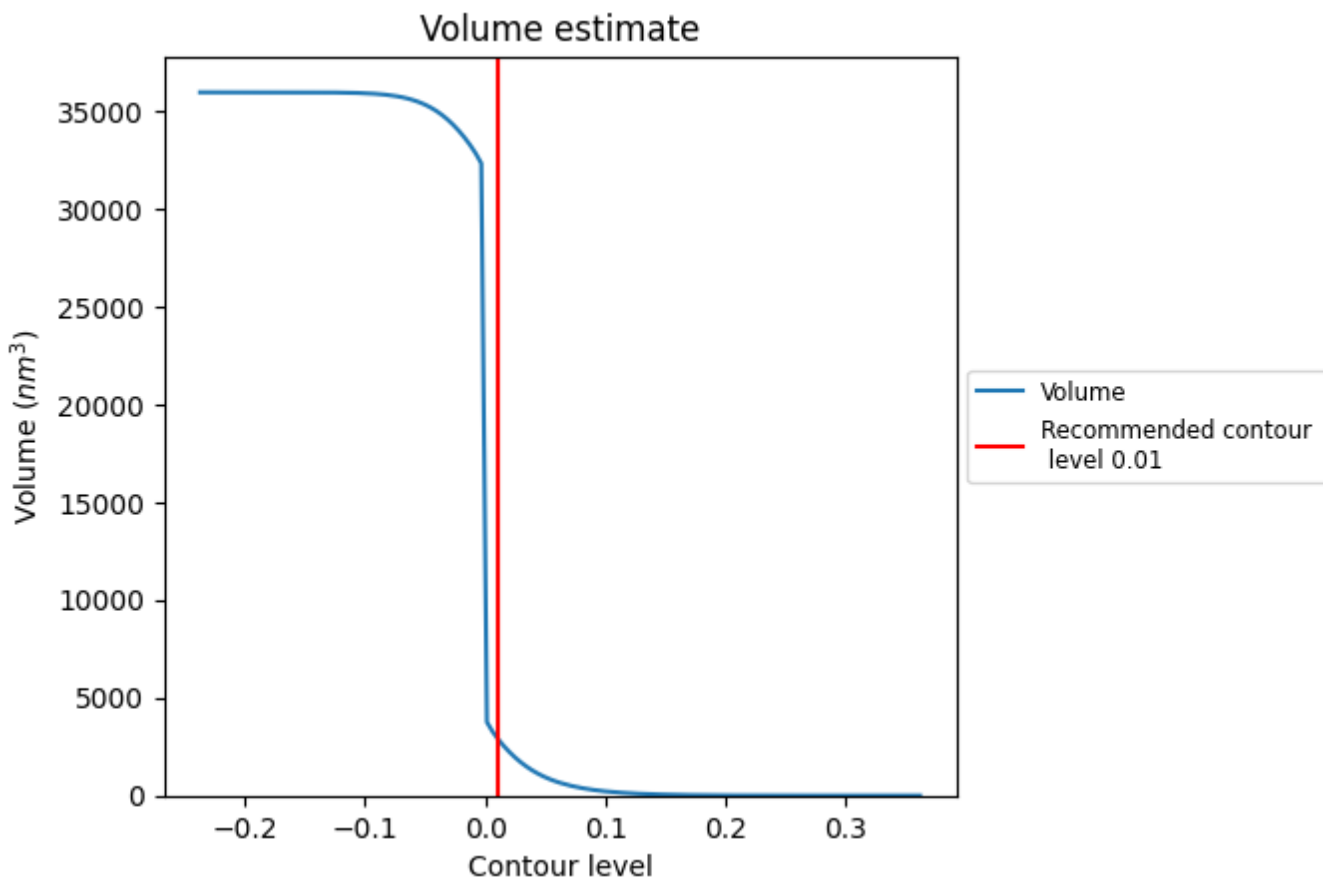
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

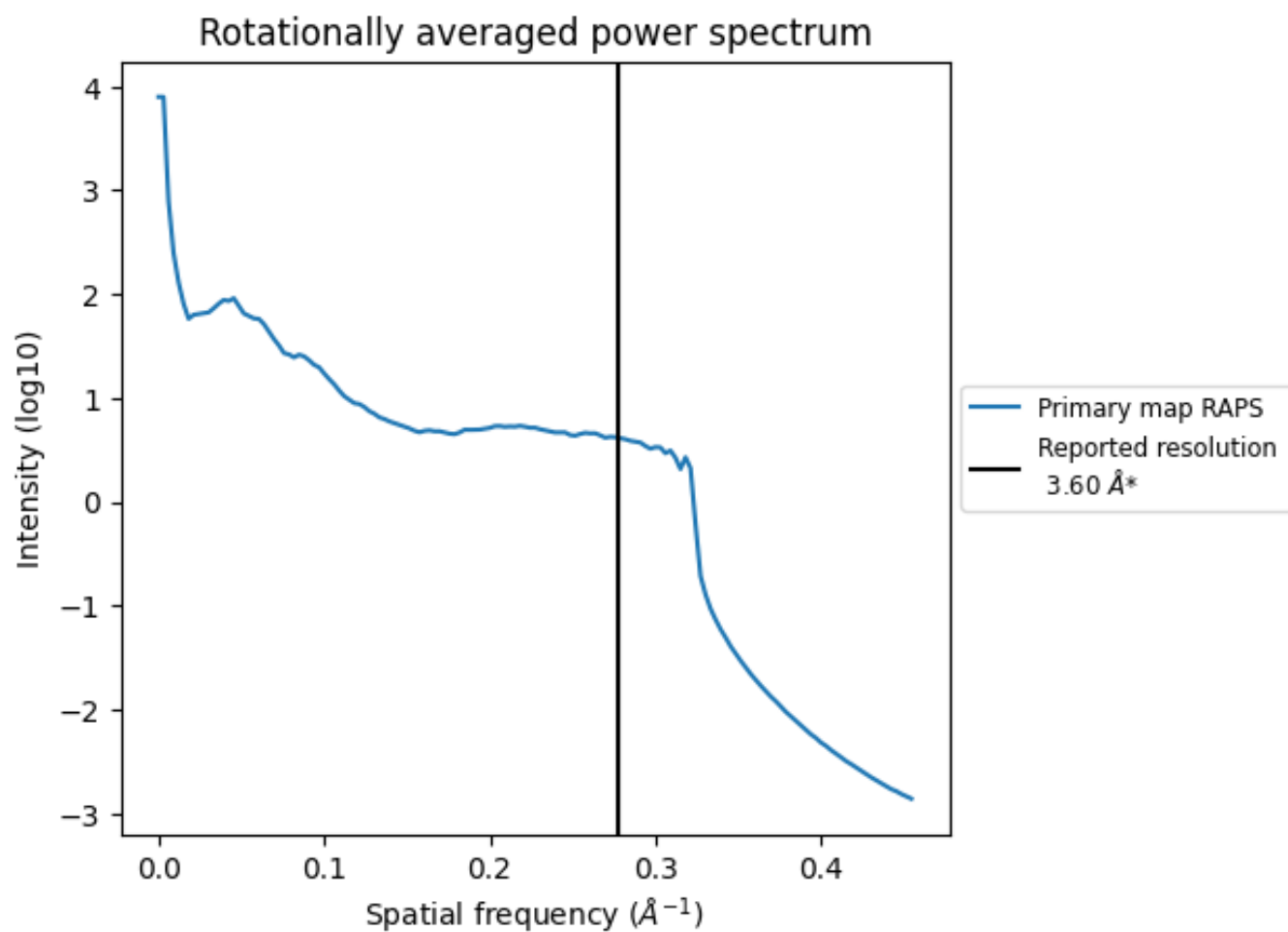
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2951 nm³; this corresponds to an approximate mass of 2666 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 0.278\AA^{-1}

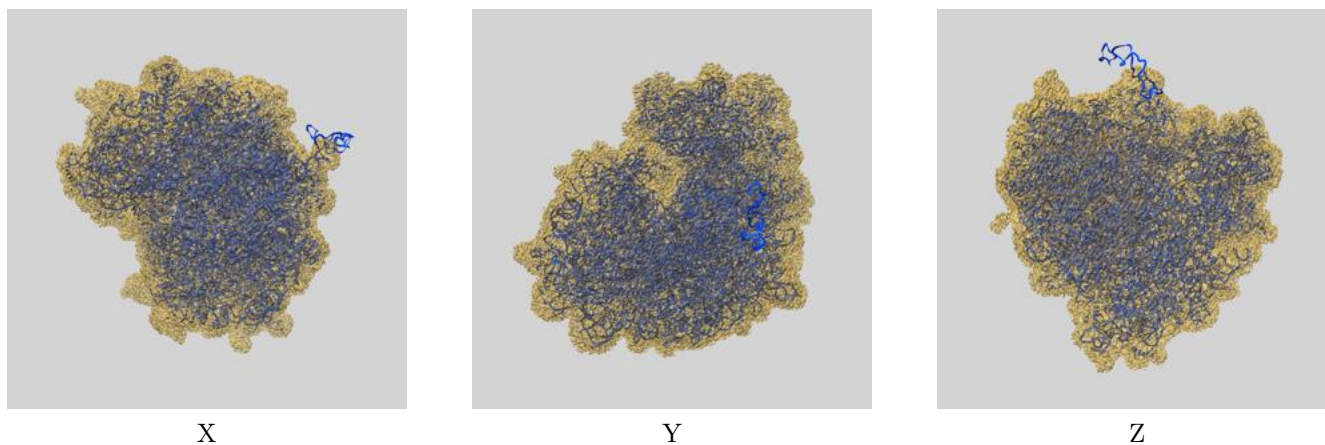
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

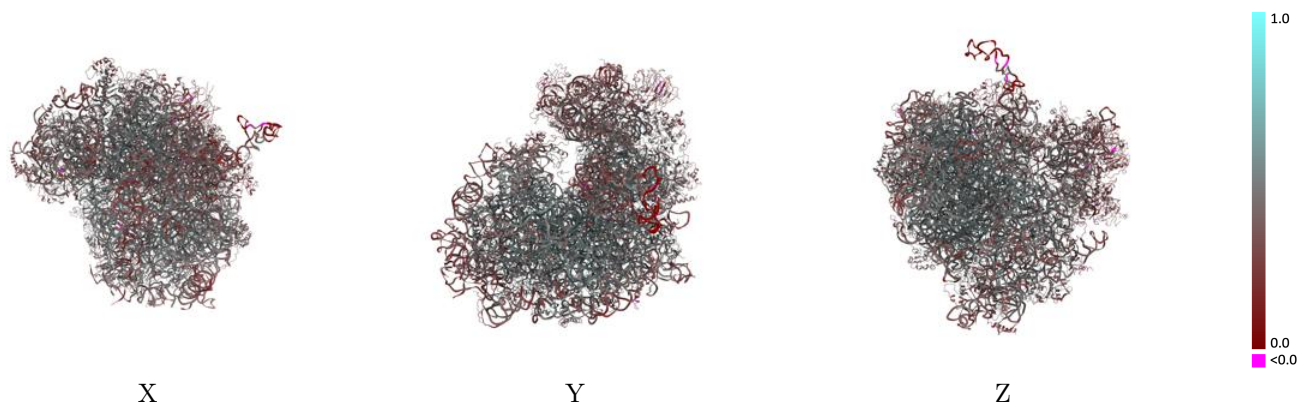
This section contains information regarding the fit between EMDB map EMD-2938 and PDB model 4UG0. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



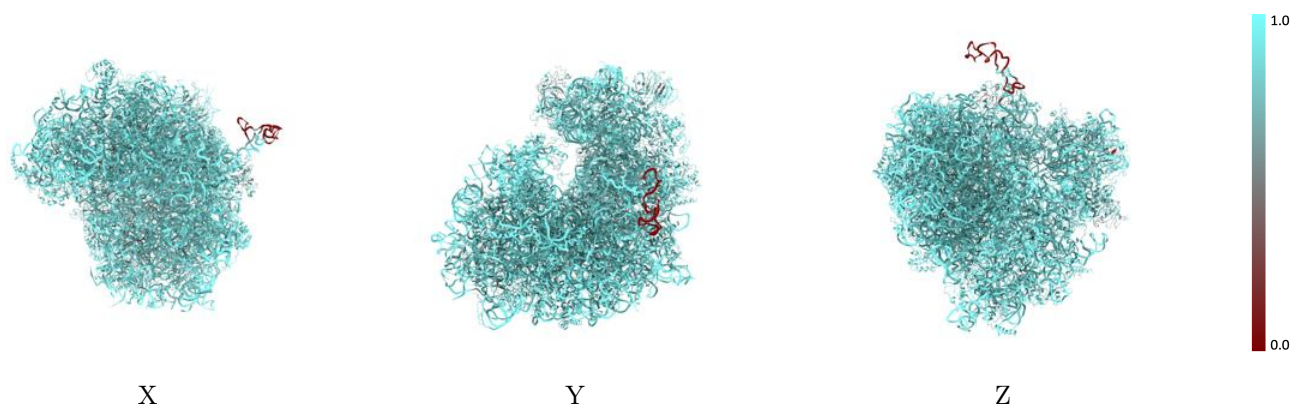
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



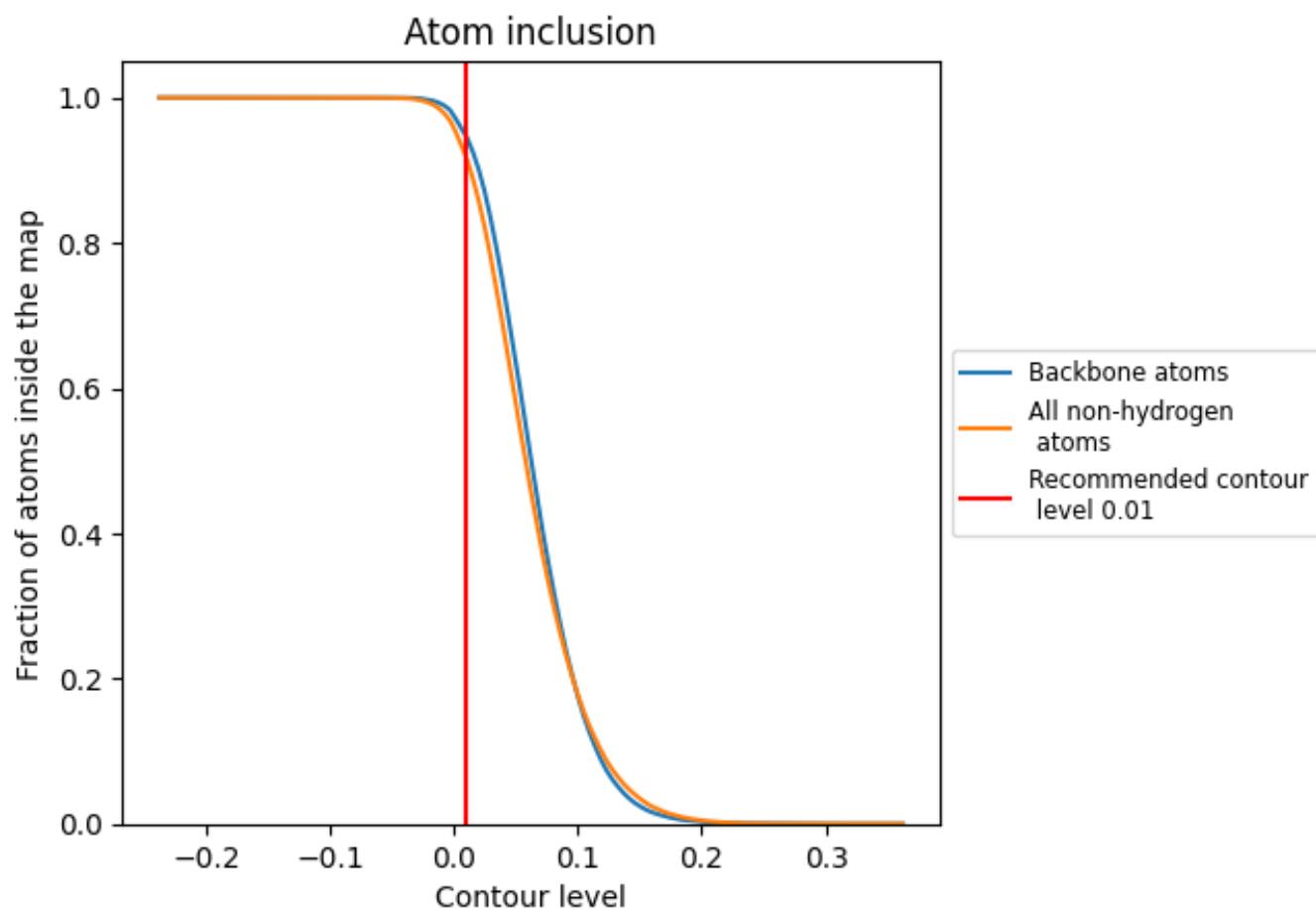
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9183	 0.4400
L5	 0.9449	 0.4620
L7	 0.9727	 0.4890
L8	 0.9587	 0.4900
LA	 0.9161	 0.5040
LB	 0.9118	 0.4670
LC	 0.9043	 0.4700
LD	 0.8975	 0.4170
LE	 0.8792	 0.4070
LF	 0.8921	 0.4770
LG	 0.8959	 0.4090
LH	 0.9034	 0.4300
LI	 0.8928	 0.4370
LJ	 0.8883	 0.3890
LL	 0.9247	 0.4550
LM	 0.9088	 0.4410
LN	 0.8951	 0.5010
LO	 0.9179	 0.4750
LP	 0.9072	 0.4790
LQ	 0.8999	 0.4750
LR	 0.9113	 0.4530
LS	 0.9129	 0.4730
LT	 0.9089	 0.4690
LU	 0.9108	 0.4010
LV	 0.9248	 0.4790
LW	 0.8724	 0.3930
LX	 0.8914	 0.4510
LY	 0.9128	 0.4350
LZ	 0.9021	 0.4380
La	 0.9195	 0.4960
Lb	 0.8805	 0.4310
Lc	 0.9143	 0.4480
Ld	 0.9218	 0.4620
Le	 0.9047	 0.4980
Lf	 0.9240	 0.5010













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Chain	Atom inclusion	Q-score
Lg	 0.9000	 0.4660
Lh	 0.9032	 0.4350
Li	 0.9060	 0.4380
Lj	 0.9153	 0.4900
Lk	 0.9138	 0.4010
Ll	 0.9009	 0.4850
Lm	 0.9087	 0.4620
Ln	 0.9330	 0.5140
Lo	 0.9200	 0.4800
Lp	 0.9245	 0.4920
Lr	 0.9211	 0.4720
Lz	 0.7025	 0.2650
S2	 0.9427	 0.4350
S6	 0.8864	 0.3390
SA	 0.8921	 0.4110
SB	 0.9040	 0.4260
SC	 0.8888	 0.4200
SD	 0.8438	 0.3480
SE	 0.8785	 0.4290
SF	 0.8399	 0.3670
SG	 0.8728	 0.3710
SH	 0.8901	 0.3800
SI	 0.8875	 0.4320
SJ	 0.8799	 0.4030
SK	 0.8211	 0.3020
SL	 0.8944	 0.4650
SM	 0.6631	 0.2750
SN	 0.8916	 0.4370
SO	 0.8873	 0.4430
SP	 0.8592	 0.3280
SQ	 0.8209	 0.3530
SR	 0.8618	 0.3650
SS	 0.8563	 0.3290
ST	 0.8364	 0.3470
SU	 0.8337	 0.3320
SV	 0.9019	 0.4270
SW	 0.8772	 0.4560
SX	 0.8889	 0.4620
SY	 0.8821	 0.3870
SZ	 0.8834	 0.3340
Sa	 0.9067	 0.4620
Sb	 0.9218	 0.4170

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Chain	Atom inclusion	Q-score
Sc	 0.8745	 0.3650
Sd	 0.7939	 0.3770
Se	 0.8063	 0.3550
Sf	 0.5795	 0.2200
Sg	 0.8156	 0.3010