



Full wwPDB EM Validation Report ⓘ

Dec 17, 2022 – 01:55 pm GMT

PDB ID : 6Z6N
EMDB ID : EMD-11100
Title : Cryo-EM structure of human EBP1-80S ribosomes (focus on EBP1)
Authors : Wells, J.N.; Buschauer, R.; Mackens-Kiani, T.; Best, K.; Kratzat, H.; Berninghausen, O.; Becker, T.; Cheng, J.; Beckmann, R.
Deposited on : 2020-05-28
Resolution : 2.90 Å(reported)
Based on initial model : 6EK0

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

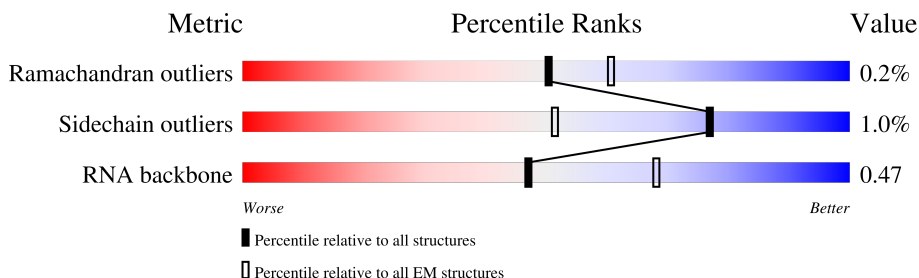
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.





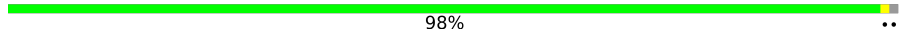
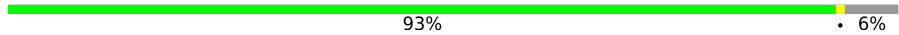
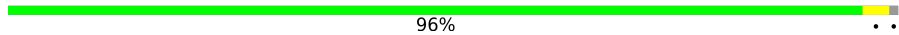
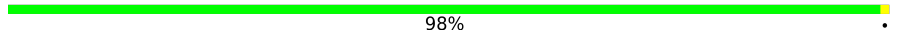

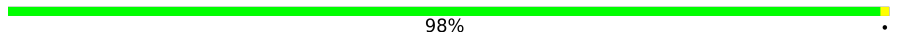
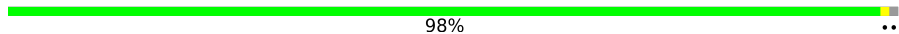

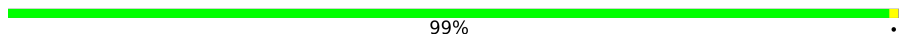
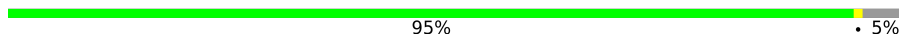
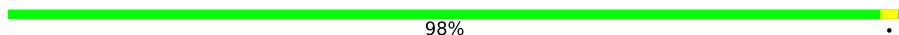
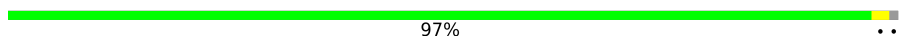





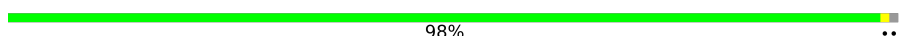
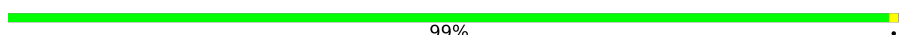



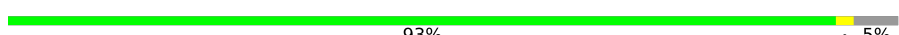
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	 90% 9%
10	LG	266	 89% 9%
11	LH	192	 98% ..
12	LI	214	 93% 6%
13	LJ	178	 96% ..
14	LL	211	 98% .
15	LM	215	 63% 35%
16	LN	204	 98% .
17	LO	203	 98% ..
18	LP	184	 83% 17%
19	LQ	188	 99% ..
20	LR	196	 95% 5%
21	LS	176	 98% ..
22	LT	160	 97% ..
23	LU	128	 77% 21%
24	LV	140	 93% 6%
25	LW	157	 78% 21%
26	LX	156	 77% 23%
27	LY	145	 91% 8%
28	LZ	136	 98% ..
29	La	148	 99% ..
30	Lb	159	 69% 31%
31	Lc	115	 83% 15%
32	Ld	125	 84% 14%
33	Le	135	 93% 5%

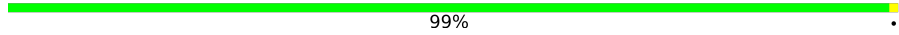
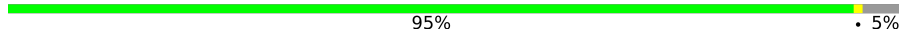
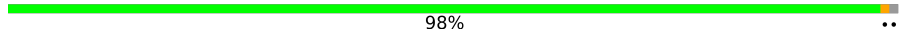

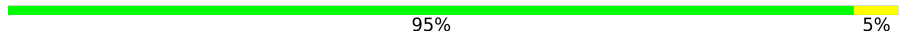
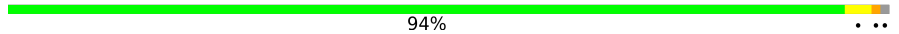


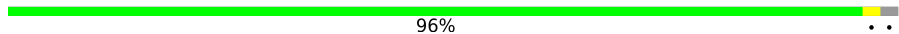
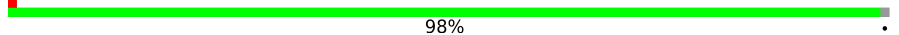

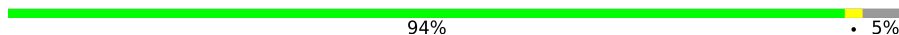
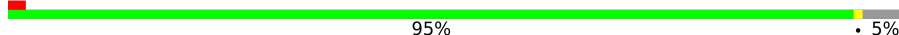



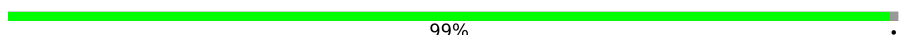
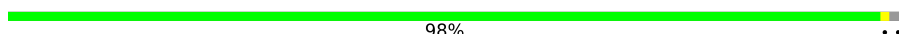

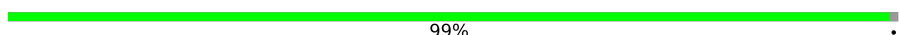
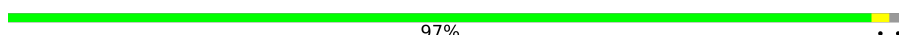




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Mol	Chain	Length	Quality of chain
34	Lf	110	95%
35	Lg	117	96%
36	Lh	123	98%
37	Li	105	97%
38	Lj	97	86%
39	Lk	70	99%
40	Ll	51	96%
41	Lm	128	40%
42	Ln	25	96%
43	Lo	106	99%
44	Lp	92	99%
45	Lr	137	90%
46	Lz	217	10%
47	S2	1869	65%
48	SA	295	74%
49	SB	264	79%
50	SD	243	91%
51	SE	263	99%
52	SF	204	92%
53	SH	194	93%
54	SI	208	99%
55	SK	165	58%
56	SL	158	6%
57	SP	145	88%
58	SQ	146	95%


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Mol	Chain	Length	Quality of chain
59	SR	135	 99%
60	SS	152	 95% 5%
61	ST	145	 98%
62	SU	119	 87% 13%
63	SV	83	 95% 5%
64	SX	143	 94%
65	Sa	115	 88% 11%
66	Sc	69	 91% 7%
67	Sd	56	 96%
68	Sg	317	 98%
69	SC	293	 75% 24%
70	SG	249	 94% 5%
71	SJ	194	 95% 5%
72	SM	132	 87% 5% 8%
73	SN	151	 99%
74	SO	151	 91% 7%
75	SW	130	 99%
76	SY	133	 98%
77	SZ	125	 58% 40%
78	Sb	84	 99%
79	Se	59	 97%
80	Sf	156	 42% 57%
81	CA	394	 90% 10%
82	CB	858	 97%
83	CC	75	 57% 36% 7%

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Mol	Chain	Length	Quality of chain
84	CD	408	 7% 92%

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 228566 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	L5	3772	80116	35645	14585	26115	3771	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	L7	120	2561	1141	456	844	120	0	0

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

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	368	2927	1840	583	489	15	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	236	1904	1222	361	317	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	202	1634	1037	314	269	14	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	109	876	546	189	137	4	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
35	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

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

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

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

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

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

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

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

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

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

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

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

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

- 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 49 is a protein called 40S ribosomal protein S3a.

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

- Molecule 50 is a protein called 40S ribosomal protein S3.

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

- Molecule 51 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	SF	189	1495	934	284	270	7	0	0

- Molecule 53 is a protein called 40S ribosomal protein S7.

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

- Molecule 54 is a protein called 40S ribosomal protein S8.

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

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

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

- Molecule 56 is a protein called 40S ribosomal protein S11.

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

- Molecule 57 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	SP	127	1045	663	198	177	7	0	0

- Molecule 58 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	SQ	144	1142	726	216	197	3	0	0

- Molecule 59 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	SR	135	1090	685	202	198	5	0	0

- Molecule 60 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	SS	145	1198	751	242	203	2	0	0

- Molecule 61 is a protein called 40S ribosomal protein S19.

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

- Molecule 62 is a protein called 40S ribosomal protein S20.

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

- Molecule 63 is a protein called 40S ribosomal protein S21.

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

- Molecule 64 is a protein called 40S ribosomal protein S23.

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

- Molecule 65 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	Sa	102	821	512	171	133	5	0	0

- Molecule 66 is a protein called 40S ribosomal protein S28.

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

- Molecule 67 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Sd	55	459	286	94	74	5	0	0

- Molecule 68 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 69 is a protein called 40S ribosomal protein S2.

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

- Molecule 70 is a protein called 40S ribosomal protein S6.

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

- Molecule 71 is a protein called 40S ribosomal protein S9.

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

- Molecule 72 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 73 is a protein called 40S ribosomal protein S13.

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

- Molecule 74 is a protein called 40S ribosomal protein S14.

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

- Molecule 75 is a protein called 40S ribosomal protein S15a.

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

- Molecule 76 is a protein called 40S ribosomal protein S24.

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

- Molecule 77 is a protein called 40S ribosomal protein S25.

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

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

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

- Molecule 79 is a protein called 40S ribosomal protein S30.

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

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 81 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	17		

- Molecule 82 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CB	846	Total	C	N	O	S	0	0
			6609	4195	1136	1234	44		

- Molecule 83 is a RNA chain called tRNA.

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

- Molecule 84 is a protein called Plasminogen activator inhibitor 1 RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CD	32	Total	C	N	O	S	0	0
			232	135	59	37	1		

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

Mol	Chain	Residues	Atoms		AltConf
85	L5	211	Total	Mg	0
			211	211	
85	L7	3	Total	Mg	0
			3	3	
85	L8	4	Total	Mg	0
			4	4	
85	LA	1	Total	Mg	0
			1	1	
85	LI	1	Total	Mg	0
			1	1	
85	LP	1	Total	Mg	0
			1	1	
85	LV	1	Total	Mg	0
			1	1	
85	Le	2	Total	Mg	0
			2	2	
85	Lg	1	Total	Mg	0
			1	1	
85	S2	30	Total	Mg	0
			30	30	
85	SG	1	Total	Mg	0
			1	1	

- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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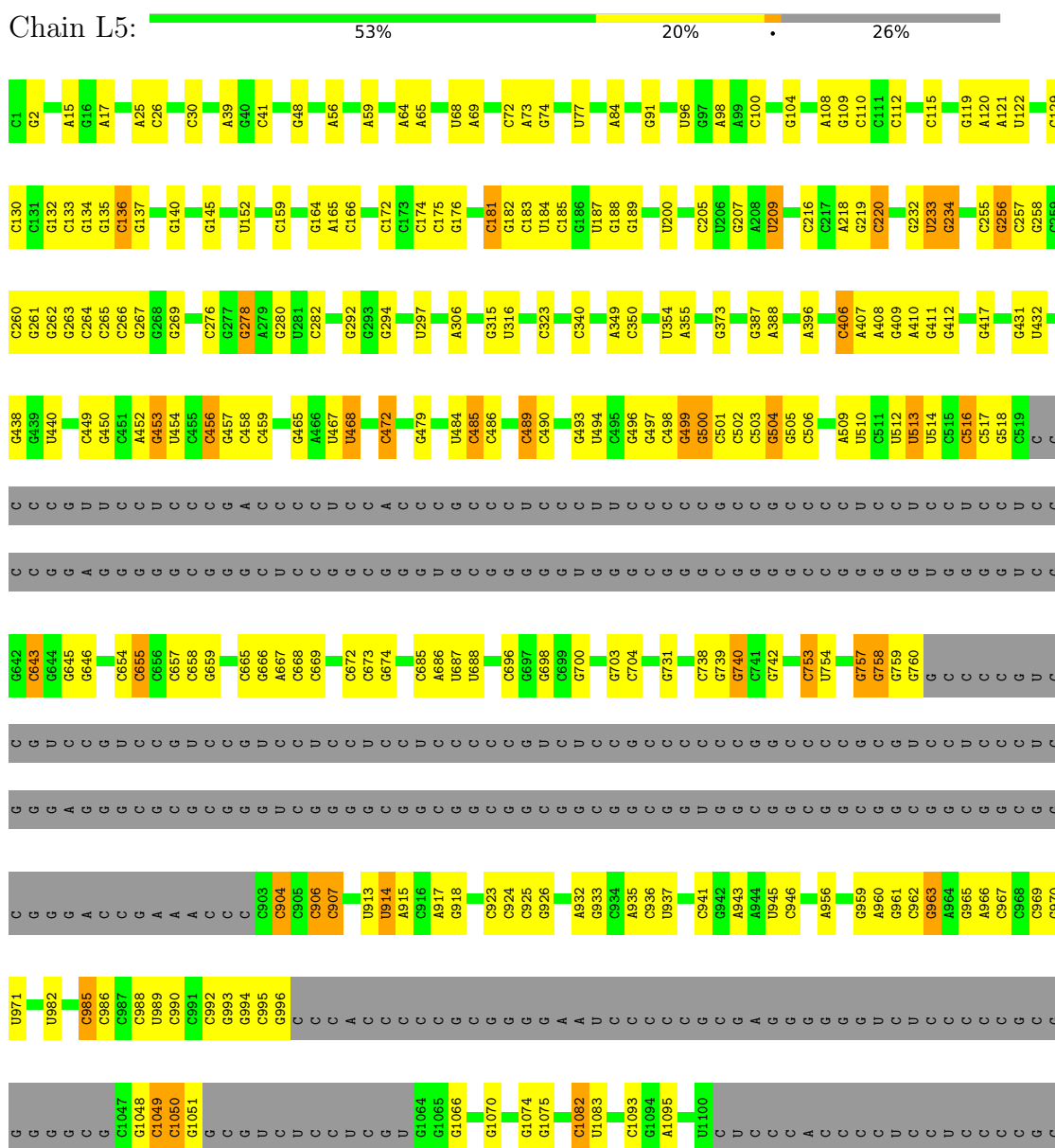
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Mol	Chain	Residues	Atoms		AltConf
86	Sd	1	Total 1	Zn 1	0
86	Sf	1	Total 1	Zn 1	0

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 rRNA



U2763	A1184	G1275	C1413	U1620	G1842	U1974	U2048	C2465	C2466	A2601	U2763
A2764	C1191	C1276	C1414	G1734	A1843	G1975	U2054	G2466	G2467	A2606	A2764
U2769	G1199	G1277	G1415	C1740	G1853	G1976	G2054	U2467	U2468	G2606	U2769
C2770	C1202	G1280	G1416	G1741	G1854	G2055	C2056	C2474	C2475	G2618	C2770
A2783	G1204	C1284	C1417	A1631	G1855	C1977	G2056	G2475	G2476	G2618	A2783
C2786	C1210	G1287	A1420	A1632	A1868	U1980	A2069	C2476	C2477	C2627	C2786
A2787	G1211	G1287	A1433	G1633	G1869	G1981	C2084	G2477	G2478	G2638	A2787
U2788	C1214	A1294	C1437	A1634	G1878	G1982	G2085	C2478	C2479	U2638	U2788
A2789	G1215	C1295	U1438	C1755	U1754	A1983	G2089	G2483	G2484	U2638	A2789
U2790	C1216	G1296	C1439	U1756	U1757	U1984	U2090	U2484	U2485	G2652	U2790
U2803	G1218	C1301	U1440	U1757	C1887	U1985	G2091	G2485	G2486	C2653	U2803
A2806	G1219	A1324	A1443	G1758	G1888	G1986	G2092	G2486	G2487	U2661	A2806
C2814	G1222	C1325	A1444	G1759	G1889	U1987	G2093	G2487	G2488	C2662	C2814
A2815	G	A1326	C1446	G1760	C1893	A1990	G2094	G2488	C2489	G2663	A2815
C2820	G	C1327	C1447	C1762	U1662	U1991	A2095	G2489	U2490	G2664	C2820
A2825	G	U1337	C1472	C1763	C1663	U1992	G2096	G2490	C2492	G2669	A2825
U2826	G	U	G	C1764	C1663	C1994	G2098	G2491	U2494	C2675	U2826
G2827	G	U	G	A1765	C1663	G1995	G2099	G2492	U2494	A2676	G2827
A2835	G	U	G	A1766	C1663	G1996	A2100	G2493	U2494	A2676	A2835
G2838	G	U	G	A1767	C1663	C1997	A2101	G2494	U2494	G2695	G2838
U2848	G	U	G	A1768	C1663	U1997	G2102	G2495	U2494	G2695	U2848
A2849	G	U	G	G1769	C1663	U1998	C2107	G2496	U2494	U2697	A2849
A2850	G	U	G	A1770	C1663	U1999	G2108	G2497	U2494	U2697	A2850
G2855	G	U	G	C1771	C1663	G1999	G2109	G2498	U2494	G2695	G2855
U2856	G	U	G	C1772	C1663	C1999	G2111	G2499	U2494	G2695	U2856
A2857	G	U	G	C1773	C1663	U1999	G2112	G2500	U2494	G2695	A2857
A2858	G	U	G	C1774	C1663	U1999	G	G2501	U2494	G2695	A2858
C2867	G	U	G	A1775	C1663	G2000	G	G2502	U2494	G2695	C2867
G2877	G	U	G	C1776	C1663	G2001	G	G2503	U2494	G2695	G2877
C2892	G	U	G	A1777	C1663	A2002	G	G2504	U2494	G2695	C2892
A2895	G	U	G	C1778	C1663	G2003	G	G2505	U2494	G2695	A2895
G2896	G	U	G	C1779	C1663	U2004	G	G2506	U2494	G2695	G2896
G2897	G	U	G	A1804	C1663	U2005	G	G2507	U2494	G2695	G2897
G2898	G	U	G	C1805	C1663	G2007	G	G2508	U2494	G2695	G2898
C2899	G	U	G	G1806	C1663	U2008	G	G2509	U2494	G2695	C2899
G2901	G	U	G	C1807	C1663	A2010	G	G2510	U2494	G2695	G2901
G2902	G	U	G	C1808	C1663	C2011	G	G2511	U2494	G2695	G2902
G2903	G	U	G	C1809	C1663	A2012	G	G2512	U2494	G2695	G2903
U2904	G	U	G	G1810	C1663	C2013	G	G2513	U2494	G2695	U2904
C2905	G	U	G	A1804	C1663	C2014	G	G2514	U2494	G2695	C2905
G2906	G	U	G	C1805	C1663	U2015	G	G2515	U2494	G2695	G2906
G2907	G	U	G	C1806	C1663	G2018	G	G2516	U2494	G2695	G2907
U2908	G	U	G	G1807	C1663	C2019	G	G2517	U2494	G2695	U2908
	G	U	G	C1808	C1663	U2020	G	G2518	U2494	G2695	
	G	U	G	G1809	C1663	G2021	G	G2519	U2494	G2695	
	G	U	G	C1810	C1663	C2022	G	G2520	U2494	G2695	
	G	U	G	A1815	C1663	G2023	G	G2521	U2494	G2695	
	G	U	G	C1816	C1663	G2024	G	G2522	U2494	G2695	
	G	U	G	C1816	C1663	A2025	G	G2523	U2494	G2695	
	G	U	G	C1820	C1663	A2026	G	G2524	U2494	G2695	
	G	U	G	G1821	C1663	G2033	G	G2525	U2494	G2695	
	G	U	G	C1715	C1663	G2034	G	G2526	U2494	G2695	
	G	U	G	C1717	C1663	G1961	G	G2527	U2494	G2695	
	G	U	G	G1831	C1663	A1962	G	G2528	U2494	G2695	
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	G	U	G	A1837	C1663	C1971	G	G2530	U2494	G2695	
	G	U	G	C1731	C1663	U1972	G	G2531	U2494	G2695	
	G	U	G	C1731	C1663	A1973	G	G2532	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2533	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2534	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2535	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2536	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2537	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2538	U2494	G2695	
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	G	U	G	C1731	C1663	C1973	G	G2542	U2494	G2695	
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	G	U	G	C1731	C1663	C1973	G	G2554	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2555	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2556	U2494	G2695	
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	G	U	G	C1731	C1663	C1973	G	G2568	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2569	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2570	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2571	U2494	G2695	
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	G	U	G	C1731	C1663	C1973	G	G2574	U2494	G2695	
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	G	U	G	C1731	C1663	C1973	G	G2576	U2494	G2695	
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	G	U	G	C1731	C1663	C1973	G	G2578	U2494	G2695	
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	G	U	G	C1731	C1663	C1973	G	G2580	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2581	U2494	G2695	
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	G	U	G	C1731	C1663	C1973	G	G2583	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2584	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2585	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2586	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2587	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2588	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2589	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2590	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2591	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2592	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2593	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2594	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2595	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2596	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2597	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2598	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2599	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2600	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2601	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2602	U2494	G2695	
	G	U	G	C1731	C1663	C1973	G	G2603	U2494	G2695	

A4513	A4518	A4524	G4527	U4531	G4545	A4548	G4549	U4551	U4555	U4556	U4557	C4560	G4567	A4568	U4569	G4573	A4574	G4575	A4584	A4589	A4590	U4594	G4600	G4617	A4626	A4635	U4636	G4637	G4647	G4652	A4656	U4657	G4658	G4659	C4670	G4671																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
U4005	A4056	C4057	U4058	C4059	A4062	U4063	C4064	G4065	U4069	G4076	G4084	A4085	G4086	G4097	A4098	G4099	C4100	C4101	C4102	G4103	G4104	G4107	C4108	G4109	C4110	U4111	C4112	U4113	C4114	G4115	C4116	U4117	U4118	C4119	U4120	G4121	A4127	C4133	C4138	G4139	C4140	G4141	C4142	C4143	C4144	G4145	G4146	G4147	C4162																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
U4163	G4168	U4169	A4170	G4183	G4191	G4196	G4197	A4203	G4222	G4228	U4229	U4232	A4233	C4241	U4242	G4249	G4250	A4251	G4254	A4255	A4256	A4257	U4265	A4268	A4273	A4281	G4291	C4303	A4304	G4305	U4306	C4314	C4318	C4319	G4329	G4330	G4331	C4332	C4339	C4340	C4341	C4342	C4343	C4344	C4345	C4346	C4347	C4350	C4351	C4352	C4353	C4354	C4355	C4356	C4357	C4358	C4359	C4360	C4361	C4362	C4363	C4364	C4365	C4366	C4367	C4368	C4369	C4370	C4371	C4372	C4373	C4374	C4375	C4376	C4377	C4378	C4379	C4380	C4381	C4382	C4383	C4384	C4385	C4386	C4387	C4388	C4389	C4390	C4391	C4392	C4393	C4394	C4395	C4396	C4397	C4398	C4399	C4400	C4401	C4402	C4403	C4404	C4405	C4406	C4407	C4408	C4409	C4410	C4411	C4412	C4413	C4414	C4415	C4416	C4417	C4418	C4419	C4420	C4421	C4422	C4423	C4424	C4425	C4426	C4427	C4428	C4429	C4430	C4431	C4432	C4433	C4434	C4435	C4436	C4437	C4438	C4439	C4440	C4441	C4442	C4443	C4444	C4445	C4446	C4447	C4448	C4449	C4450	C4451	C4452	C4453	C4454	C4455	C4456	C4457	C4458	C4459	C4460	C4461	C4462	C4463	C4464	C4465	C4466	C4467	C4468	C4469	C4470	C4471	C4472	C4473	C4474	C4475	C4476	C4477	C4478	C4479	C4480	C4481	C4482	C4483	C4484	C4485	C4486	C4487	C4488	C4489	C4490	C4491	C4492	C4493	C4494	C4495	C4496	C4497	C4498	C4499	C4500	C4501	C4502	C4503	C4504	C4505	C4506	C4507	C4508	C4509	C4510	C4511	C4512	C4513	C4514	C4515	C4516	C4517	C4518	C4519	C4520	C4521	C4522	C4523	C4524	C4525	C4526	C4527	C4528	C4529	C4530	C4531	C4532	C4533	C4534	C4535	C4536	C4537	C4538	C4539	C4540	C4541	C4542	C4543	C4544	C4545	C4546	C4547	C4548	C4549	C4550	C4551	C4552	C4553	C4554	C4555	C4556	C4557	C4558	C4559	C4560	C4561	C4562	C4563	C4564	C4565	C4566	C4567	C4568	C4569	C4570	C4571	C4572	C4573	C4574	C4575	C4576	C4577	C4578	C4579	C4580	C4581	C4582	C4583	C4584	C4585	C4586	C4587	C4588	C4589	C4590	C4591	C4592	C4593	C4594	C4595	C4596	C4597	C4598	C4599	C4600	C4601	C4602	C4603	C4604	C4605	C4606	C4607	C4608	C4609	C4610	C4611	C4612	C4613	C4614	C4615	C4616	C4617	C4618	C4619	C4620	C4621	C4622	C4623	C4624	C4625	C4626	C4627	C4628	C4629	C4630	C4631	C4632	C4633	C4634	C4635	C4636	C4637	C4638	C4639	C4640	C4641	C4642	C4643	C4644	C4645	C4646	C4647	C4648	C4649	C4650	C4651	C4652	C4653	C4654	C4655	C4656	C4657	C4658	C4659	C4660	C4661	C4662	C4663	C4664	C4665	C4666	C4667	C4668	C4669	C4670	C4671	C4672	C4673	C4674	C4675	C4676	C4677	C4678	C4679	C4680	C4681	C4682	C4683	C4684	C4685	C4686	C4687	C4688	C4689	C4690	C4691	C4692	C4693	C4694	C4695	C4696	C4697	C4698	C4699	C4700	C4701	C4702	C4703	C4704	C4705	C4706	C4707	C4708	C4709	C4710	C4711	C4712	C4713	C4714	C4715	C4716	C4717	C4718	C4719	C4720	C4721	C4722	C4723	C4724	C4725	C4726	C4727	C4728	C4729	C4730	C4731	C4732	C4733	C4734	C4735	C4736	C4737	C4738	C4739	C4740	C4741	C4742	C4743	C4744	C4745	C4746	C4747	C4748	C4749	C4750	C4751	C4752	C4753	C4754	C4755	C4756	C4757	C4758	C4759	C4760	C4761	C4762	C4763	C4764	C4765	C4766	C4767	C4768	C4769	C4770	C4771	C4772	C4773	C4774	C4775	C4776	C4777	C4778	C4779	C4780	C4781	C4782	C4783	C4784	C4785	C4786	C4787	C4788	C4789	C4790	C4791	C4792	C4793	C4794	C4795	C4796	C4797	C4798	C4799	C4800	C4801	C4802	C4803	C4804	C4805	C4806	C4807	C4808	C4809	C4810	C4811	C4812	C4813	C4814	C4815	C4816	C4817	C4818	C4819	C4820	C4821	C4822	C4823	C4824	C4825	C4826	C4827	C4828	C4829	C4830	C4831	C4832	C4833	C4834	C4835	C4836	C4837	C4838	C4839	C4840	C4841	C4842	C4843	C4844	C4845	C4846	C4847	C4848	C4849	C4850	C4851	C4852	C4853	C4854	C4855	C4856	C4857	C4858	C4859	C4860	C4861	C4862	C4863	C4864	C4865	C4866	C4867	C4868	C4869	C4870	C4871	C4872	C4873	C4874	C4875	C4876	C4877	C4878	C4879	C4880	C4881	C4882	C4883	C4884	C4885	C4886	C4887	C4888	C4889	C4890	C4891	C4892	C4893	C4894	C4895	C4896	C4897	C4898	C4899	C4900	C4901	C4902	C4903	C4904	C4905	C4906	C4907	C4908	C4909	C4910	C4911	C4912	C4913	C4914	C4915	C4916	C4917	C4918	C4919	C4920	C4921	C4922	C4923	C4924	C4925	C4926	C4927	C4928	C4929	C4930	C4931	C4932	C4933	C4934	C4935	C4936	C4937	C4938	C4939	C4940	C4941	C4942	C4943	C4944	C4945	C4946	C4947	C4948	C4949	C4950	C4951	C4952	C4953	C4954	C4955	C4956	C4957	C4958	C4959	C4960	C4961	C4962	C4963	C4964	C4965	C4966	C4967	C4968	C4969	C4970	C4971	C4972	C4973	C4974	C4975	C4976	C4977	C4978	C4979	C4980	C4981	C4982	C4983	C4984	C4985	C4986	C4987	C4988	C4989	C4990	C4991	C4992	C4993	C4994	C4995	C4996	C4997	C4998	C4999	C5000	C5001	C5002	C5003	C5004	C5005	C5006	C5007	C5008	C5009	C5010	C5011	C5012	C5013	C5014	C5015	C5016	C5017	C5018	C5019	C5020	C5021	C5022	C5023	C5024	C5025	C5026	C5027	C5028	C5029	C5030	C5031	C5032	C5033	C5034	C5035	C5036	C5037	C5038	C5039	C5040	C5041	C5042	C5043	C5044	C5045	C5046	C5047	C5048	C5049	C5050	C5051	C5052	C5053	C5054	C5055	C5056	C5057	C5058	C5059	C5060	C5061	C5062	C5063	C5064	C5065	C5066	C5067	C5068	C5069	C5070	C5071	C5072	C5073	C5074	C5075	C5076	C5077	C5078	C5079	C5080	C5081	C5082	C5083	C5084	C5085	C5086	C5087	C5088	C5089	C5090	C5091	C5092	C5093	C5094	C5095	C5096	C5097	C5098	C5099	C5100	C5101	C5102	C5103	C5104	C5105	C5106	C5107	C5108	C5109	C5110	C5111	C5112	C5113	C5114	C5115	C5116	C5117	C5118	C5119	C5120	C5121	C5122	C5123	C5124	C5125	C5126	C5127	C5128	C5129	C5130	C5131	C5132	C5133	C5134	C5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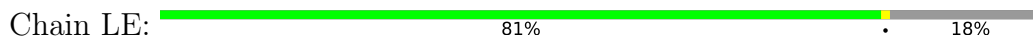
LYS
PRO
ALA
ALA

- Molecule 7: 60S ribosomal protein L5



MET
G2
K85
A294
ALA
GLU
SER

- Molecule 8: 60S ribosomal protein L6



MET
ALA
GLY
GLU
LYS
VAL
GLU
LYS
PRO
ASP
THR
LYS
GLU
LYS
LYS
PRO
GLU
ALA
LYS
LYS
VAL
ASP
ALA
GLY
GLY
LYS
VAL
LYS
P42
B56
A76
LYS
SER
LYS
VAL
GLU
LYS
LYS
LYS
LYS
LYS
Y88
G129

T176
F288

- Molecule 9: 60S ribosomal protein L7



MET
GLU
GLY
VAL
GLU
GLU
LYS
LYS
LYS
VAL
VAL
PRO
ALA
VAL
PRO
GLU
THR
LEU
LYS
LYS
LYS
ARG
ARG
N24
K29
N248

- Molecule 10: 60S ribosomal protein L7a



MET
PRO
LYS
GLY
LYS
LYS
ALA
LYS
GLY
LYS
LYS
VAL
VAL
PRO
ALA
PRO
GLU
ALA
VAL
VAL
LYS
LYS
GLN
GLU
LYS
K26
K111
R175
L193
K259
G266

- Molecule 11: 60S ribosomal protein L9



H1
Q106
R173
A180
ASP
GLU

- Molecule 12: 60S ribosomal protein L10-like

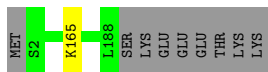


MET
G2
N14
K78
N102
LEU
SER
SER
CYS
ALA
GLY
ALA
ASP
ARG
LEU
GLN
THR
G114
S214

- Molecule 13: 60S ribosomal protein L11

- Molecule 20: 60S ribosomal protein L19

Chain LR:  95% • 5%



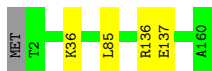
- Molecule 21: 60S ribosomal protein L18a

Chain LS:  98% ••




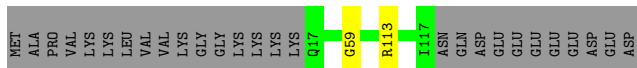
- Molecule 22: 60S ribosomal protein L21

Chain LT:  97% ••



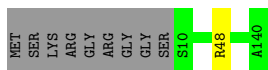
- Molecule 23: 60S ribosomal protein L22

Chain LU:  77% • 21%




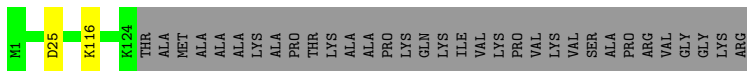
- Molecule 24: 60S ribosomal protein L23

Chain LV:  93% • 6%




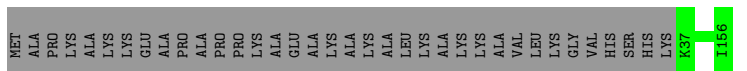
- Molecule 25: 60S ribosomal protein L24

Chain LW:  78% • 21%



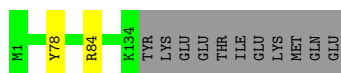
- Molecule 26: 60S ribosomal protein L23a

Chain LX:  77% 23%



- Molecule 27: 60S ribosomal protein L26

Chain LY:  91% 8%



- Molecule 28: 60S ribosomal protein L27

Chain LZ:  98%



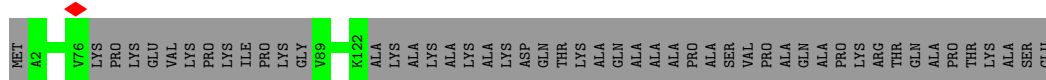
- Molecule 29: 60S ribosomal protein L27a

Chain La:  99%




- Molecule 30: 60S ribosomal protein L29

Chain Lb:  69% 31%




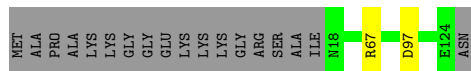
- Molecule 31: 60S ribosomal protein L30

Chain Lc:  83% 15%



- Molecule 32: 60S ribosomal protein L31

Chain Ld:  84% 14%



- Molecule 33: 60S ribosomal protein L32

Chain Le:  93% 5%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf:  95% ..



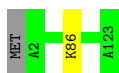
- Molecule 35: 60S ribosomal protein L34

Chain Lg:  96% ..



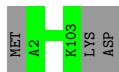
- Molecule 36: 60S ribosomal protein L35

Chain Lh:  98% ..




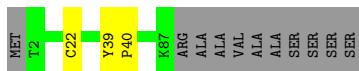
- Molecule 37: 60S ribosomal protein L36

Chain Li:  97% .



- Molecule 38: 60S ribosomal protein L37

Chain Lj:  86% . 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk:  99% .

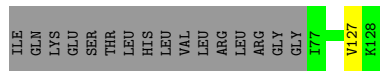
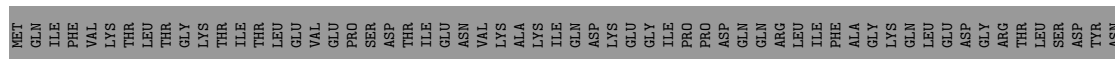


- Molecule 40: 60S ribosomal protein L39

Chain Ll:  96% ..



- Molecule 41: Ubiquitin-60S ribosomal protein L40



• Molecule 42: 60S ribosomal protein L41



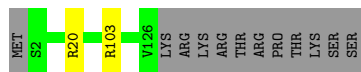
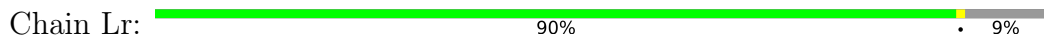
• Molecule 43: 60S ribosomal protein L36a



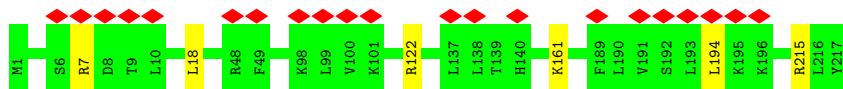
• Molecule 44: 60S ribosomal protein L37a



• Molecule 45: 60S ribosomal protein L28



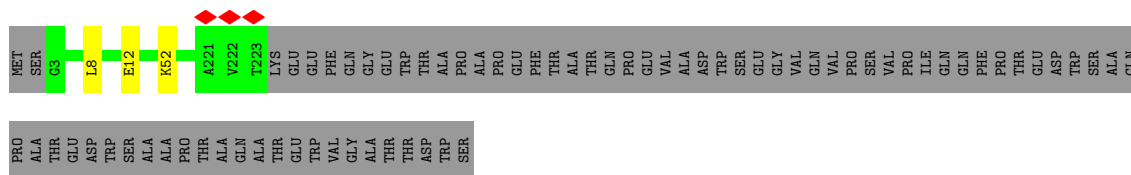
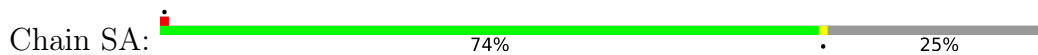
• Molecule 46: 60S ribosomal protein L10a



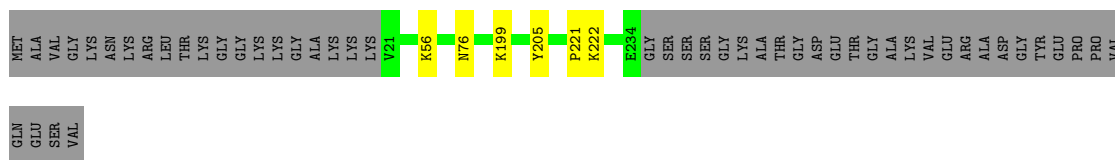
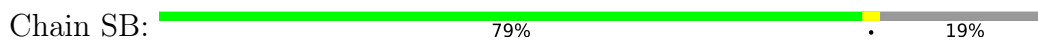
• Molecule 47: 18S rRNA



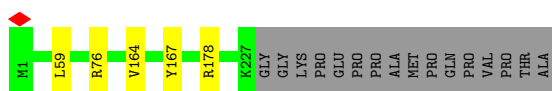
A149	C	C317	G436	G547	G644	G730	G793	G901	C1078	C1234	U1372	G1497	G1632	G1776
A154	C	A316	G437	C548	G659	G731	A794	G902	C1079	A1234	A1378	A1496	A1633	G1777
A158	U	C319	G438	U551	G660	U732	G798	A903	A1080	A1241	A1505	A1498	A1634	G1778
A159	U	G320	C321	G552	C663	C733	U801	G909	A1083	U1242	A1506	U1506	A1637	G1783
U160	U	C322	A448	U553	A664	C734	U810	G910	A1084	U1243	A1507	A1507	A1638	G1784
U161	C	C323	A449	A554	A665	C735	A810	G919	A1085	U1244	A1508	U1509	A1639	C1785
C162	C	C324	G450	A555	A666	C736	A811	U914	C1085	A1251	A1401	U1509	A1640	U1786
U163	G	C325	G451	U556	U666	C737	A811	U914	U1088	C1252	A1402	A1519	G1648	C1802
A175	G	C326	G452	U557	U667	C738	U814	A919	U1089	A1253	A1403	A1520	G1654	G1805
C178	C	G327	C456	U558	A668	C739	U814	A920	U1090	A1254	U1407	C1521	G1660	A1806
C179	C	U328	U464	G559	A671	C	G821	A920	C1109	A1255	U1408	A1533	C1660	U1821
G184	C	C329	A464	U560	A672	U749	U822	C930	G1110	A1256	U1409	A1537	A1663	A1822
U188	C	G330	A465	U561	A673	G750	U823	G933	G1111	A1257	A1410	A1540	A1664	A1823
U189	G	G331	G467	U562	G673	G751	U823	G934	U1114	A1258	A1411	G1546	G1665	A1824
G190	G	G332	G471	U563	G684	C746	A827	G934	U1115	A1259	G1412	C1547	G1671	A1825
C196	G	C340	A472	U564	U688	U749	A830	U939	U1116	A1260	C1415	G1552	G1686	U1831
U197	G	C340	A473	U565	U689	G750	C834	U943	U1117	A1261	C1416	C1553	G1687	U1832
U198	G	C340	A474	U566	U690	G751	C835	U943	U1118	A1262	C1417	C1554	G1688	U1833
C199	G	C340	A475	U567	U691	G752	C836	U943	U1119	A1263	C1418	C1555	G1689	U1834
G200	G	C340	A476	U568	U692	G753	C837	U943	U1120	A1264	C1419	C1556	G1690	U1835
G203	G	C340	A477	U569	U693	C	C838	U943	U1121	A1265	C1420	C1557	G1691	U1836
G204	G	C340	A478	U570	U694	C	C839	U943	U1122	A1266	C1421	C1558	G1692	U1837
G205	C	C340	A479	U571	U695	C	C840	U943	U1123	A1267	C1422	C1559	G1693	U1838
G206	C	C340	A480	U572	U696	C	C841	U943	U1124	A1268	C1423	C1560	G1694	U1839
G207	G	C340	A481	U573	U697	C	C842	U943	U1125	A1269	C1424	G1570	G1702	U1840
G208	G	C340	A482	U574	U698	C	C843	U943	U1126	A1270	C1425	G1571	G1715	C1852
G213	G	C340	A483	U575	U699	C	C844	U943	U1127	A1271	C1426	G1572	G1716	G1861
U214	G	C340	A484	U576	U700	C	C845	U943	U1128	A1272	C1427	G1573	G1717	G1862
G225	C	C340	A485	U577	U701	C	C846	U943	U1129	A1273	C1428	G1574	G1718	G1863
A	U	C340	A486	U578	U702	C	C847	U943	U1130	A1274	C1429	G1575	G1719	G1864
U	U	C340	A487	U579	U703	C	C848	U943	U1131	A1275	C1430	G1576	G1720	C1865
C	U	C340	A488	U580	U704	C	C849	U943	U1132	A1276	C1431	G1577	G1721	A1869
U287	U	C340	A489	U581	U705	C	C850	U943	U1133	A1277	C1432	G1578	G1722	
G291	U	C340	A490	U582	U706	C	C851	U943	U1134	A1278	C1433	G1579	G1723	
A292	U	C340	A491	U583	U707	C	C852	U943	U1135	A1279	C1434	G1580	G1724	
C293	U	C340	A492	U584	U708	C	C853	U943	U1136	A1280	C1435	G1581	G1725	
U294	U	C340	A493	U585	U709	C	C854	U943	U1137	A1281	C1436	G1582	G1726	
C295	U	C340	A494	U586	U710	C	C855	U943	U1138	A1282	C1437	G1583	G1727	
A302	U	C340	A495	U587	U711	C	C856	U943	U1139	A1283	C1438	G1584	G1728	
C306	U	C340	A496	U588	U712	C	C857	U943	U1140	A1284	C1439	G1585	G1729	
G307	U	C340	A497	U589	U713	C	C858	U943	U1141	A1285	C1440	G1586	G1730	
G308	U	C340	A498	U590	U714	C	C859	U943	U1142	A1286	C1441	G1587	G1731	
G309	U	C340	A499	U591	U715	C	C860	U943	U1143	A1287	C1442	G1588	G1732	
C310	U	C340	A500	U592	U716	C	C861	U943	U1144	A1288	C1443	G1589	G1733	
U311	U	C340	A501	U593	U717	C	C862	U943	U1145	A1289	C1444	G1590	G1734	
C312	U	C340	A502	U594	U718	C	C863	U943	U1146	A1290	C1445	G1591	G1735	
A313	U	C340	A503	U595	U719	C	C864	U943	U1147	A1291	C1446	G1592	G1736	
G316	U	C340	A504	U596	U720	C	C865	U943	U1148	A1292	C1447	G1593	G1737	
		C340	A505	U597	U721	C	C866	U943	U1149	A1293	C1448	G1594	G1738	
		C340	A506	U598	U722	C	C867	U943	U1150	A1294	C1449	G1595	G1739	
		C340	A507	U599	U723	C	C868	U943	U1151	A1295	C1450	G1596	G1740	
		C340	A508	U600	U724	C	C869	U943	U1152	A1296	C1451	G1597	G1741	
		C340	A509	U601	U725	C	C870	U943	U1153	A1297	C1452	G1598	G1742	
		C340	A510	U602	U726	C	C871	U943	U1154	A1298	C1453	G1599	G1743	
		C340	A511	U603	U727	C	C872	U943	U1155	A1299	C1454	G1600	G1744	
		C340	A512	U604	U728	C	C873	U943	U1156	A1300	C1455	G1601	G1745	
		C340	A513	U605	U729	C	C874	U943	U1157	A1301	C1456	G1602	G1746	
		C340	A514	U606	U730	C	C875	U943	U1158	A1302	C1457	G1603	G1747	
		C340	A515	U607	U731	C	C876	U943	U1159	A1303	C1458	G1604	G1748	
		C340	A516	U608	U732	C	C877	U943	U1160	A1304	C1459	G1605	G1749	
		C340	A517	U609	U733	C	C878	U943	U1161	A1305	C1460	G1606	G1750	
		C340	A518	U610	U734	C	C879	U943	U1162	A1306	C1461	G1607	G1751	
		C340	A519	U611	U735	C	C880	U943	U1163	A1307	C1462	G1608	G1752	
		C340	A520	U612	U736	C	C881	U943	U1164	A1308	C1463	G1609	G1753	
		C340	A521	U613	U737	C	C882	U943	U1165	A1309	C1464	G1610	G1754	
		C340	A522	U614	U738	C	C883	U943	U1166	A1310	C1465	G1611	G1755	
		C340	A523	U615	U739	C	C884	U943	U1167	A1311	C1466	G1612	G1756	
		C340	A524	U616	U740	C	C885	U943	U1168	A1312	C1467	G1613	G1757	
		C340	A525	U617	U741	C	C886	U943	U1169	A1313	C1468	G1614	G1758	
		C340	A526	U618	U742	C	C887	U943	U1170	A1314	C1469	G1615	G1759	
		C340	A527	U619	U743	C	C888	U943	U1171	A1315	C1470	G1616	G1760	
		C340	A528	U620	U744	C	C889	U943	U1172	A1316	C1471	G1617	G1761	
		C340	A529	U621	U745	C	C890	U943	U1173	A1317	C1472	G1618	G1762	
		C340	A530	U622	U746	C	C891	U943	U1174	A1318	C1473	G1619	G1763	
		C340	A531	U623	U747	C	C892	U943	U1175	A1319	C1474	G1620	G1764	
		C340	A532	U624	U748	C	C893	U943	U1176	A1320	C1475	G1621	G1765	
		C340	A533	U625	U749	C	C894	U943	U1177	A1321	C1476	G1622	G1766	
		C340	A534	U626	U750	C	C895	U943	U1178	A1322	C1477	G1623	G1767	
		C340	A535	U627	U751	C	C896	U943	U1179	A1323	C1478	G1624	G1768	
		C340	A536	U628	U752	C	C897	U943	U1180	A1324	C1479	G1625	G1769	
		C340	A537	U629	U753	C	C898	U943	U1181	A1325	C1480	G1626	G1770	
		C340	A538	U630	U754	C	C899	U943	U1182	A1326	C1481	G1627	G1771	
		C340	A539	U631	U755	C	C900	U943	U1183	A1327	C1482	G1628	G1772	
		C340	A540	U632	U756	C	C901	U943	U1184	A1328	C1483	G1629	G1773	
		C340	A541	U633	U757	C	C902	U943	U1185	A1329	C1484	G1630	G1774	
		C340	A542	U634	U758	C	C903	U943	U1186	A1330	C1485	G1631	G1775	
		C340	A543	U635	U759	C	C904	U943	U1187	A1331	C1486	G1632	G1776	
		C340	A544	U636	U760	C	C905	U943	U1188	A1332	C1487	G1633	G1777	
		C340	A545	U637	U761	C	C906	U943	U1189	A1333	C1488	G1634	G1778	
		C340	A546	U638	U762	C	C907	U943	U1190	A1334	C1489	G1635	G1779	
		C340	A547	U639	U763	C	C908	U943	U1191	A1335	C1490	G1636	G1780	
		C340	A548	U640	U764	C	C909	U943	U1192	A1336	C1491	G1637	G1781	
		C340	A549	U641	U765	C	C910	U943	U1193	A1337	C1492	G1638	G1782	
		C340	A550	U642	U766	C	C911	U943	U1194	A1338	C1493	G1639	G1783	
		C340	A551	U643	U767	C	C912	U943	U1195	A1339	C1494	G1640	G1784	
		C340	A552	U644	U768	C	C913	U943	U1196	A1340	C1495	G1641	G1785	
		C340	A553	U645	U769	C	C914	U943	U1197	A1341	C1496	G1642	G1786	
		C340	A554	U646	U770	C	C915	U943	U1198	A1342	C1497	G1643	G1787	
		C340	A555	U647	U771	C	C916	U943	U1199	A1343	C			



• Molecule 49: 40S ribosomal protein S3a



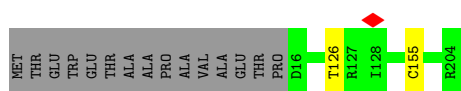
• Molecule 50: 40S ribosomal protein S3



• Molecule 51: 40S ribosomal protein S4, X isoform



• Molecule 52: 40S ribosomal protein S5

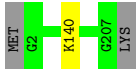


• Molecule 53: 40S ribosomal protein S7



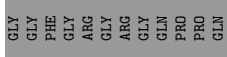
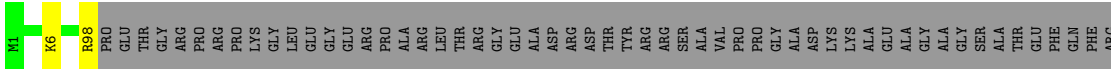
• Molecule 54: 40S ribosomal protein S8





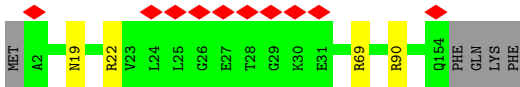
- Molecule 55: 40S ribosomal protein S10

Chain SK: 58% 41%



- Molecule 56: 40S ribosomal protein S11

Chain SL: 6% 94%



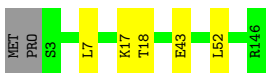
- Molecule 57: 40S ribosomal protein S15

Chain SP: 88% 12%



- Molecule 58: 40S ribosomal protein S16

Chain SQ: 95%



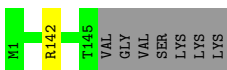
- Molecule 59: 40S ribosomal protein S17

Chain SR: 99%



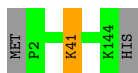
- Molecule 60: 40S ribosomal protein S18

Chain SS: 95% 5%




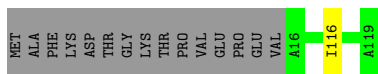
- Molecule 61: 40S ribosomal protein S19

Chain ST:  98% ..



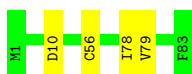
- Molecule 62: 40S ribosomal protein S20

Chain SU:  87% 13%



- Molecule 63: 40S ribosomal protein S21

Chain SV:  95% 5%



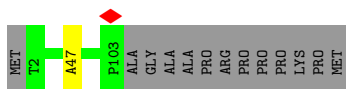
- Molecule 64: 40S ribosomal protein S23

Chain SX:  94% ..



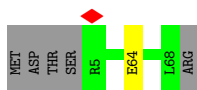
- Molecule 65: 40S ribosomal protein S26

Chain Sa:  88% 11%



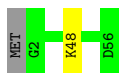
- Molecule 66: 40S ribosomal protein S28

Chain Sc:  91% 7%



- Molecule 67: 40S ribosomal protein S29

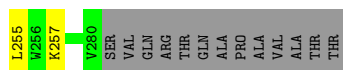
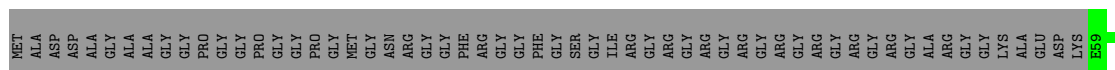
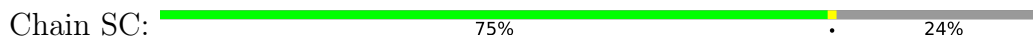
Chain Sd:  96% ..



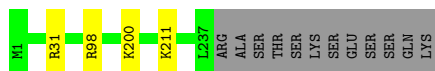
- Molecule 68: Receptor of activated protein C kinase 1



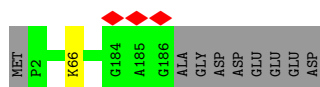
- Molecule 69: 40S ribosomal protein S2



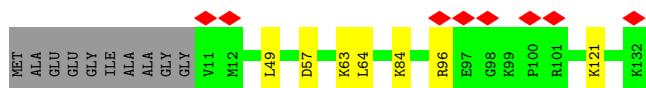
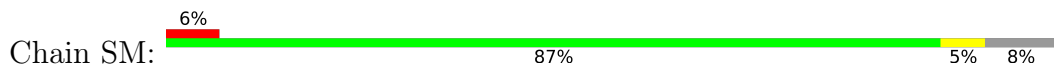
- Molecule 70: 40S ribosomal protein S6



- Molecule 71: 40S ribosomal protein S9



- Molecule 72: 40S ribosomal protein S12



- Molecule 73: 40S ribosomal protein S13



- Molecule 74: 40S ribosomal protein S14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	127706	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.277	Depositor
Minimum map value	-0.092	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	477.44998, 477.44998, 477.44998	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.061, 1.061, 1.061	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 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	1.18	10/89570 (0.0%)	1.10	478/139647 (0.3%)
2	L7	1.17	0/2861	0.97	1/4459 (0.0%)
3	L8	1.18	0/3701	1.00	9/5766 (0.2%)
4	LA	0.60	1/1936 (0.1%)	0.65	1/2596 (0.0%)
5	LB	0.55	0/3306	0.62	2/4424 (0.0%)
6	LC	0.53	0/2981	0.60	0/4002
7	LD	0.49	0/2428	0.54	0/3252
8	LE	0.45	0/1942	0.56	0/2606
9	LF	0.59	0/1905	0.57	0/2539
10	LG	0.47	0/1960	0.56	1/2637 (0.0%)
11	LH	0.52	0/1537	0.58	0/2066
12	LI	0.54	0/1673	0.57	0/2233
13	LJ	0.42	0/1433	0.65	0/1915
14	LL	0.47	0/1732	0.56	0/2315
15	LM	0.50	0/1161	0.57	1/1554 (0.1%)
16	LN	0.61	0/1746	0.60	1/2338 (0.0%)
17	LO	0.56	0/1682	0.52	0/2250
18	LP	0.55	0/1268	0.56	0/1701
19	LQ	0.57	0/1537	0.57	0/2052
20	LR	0.47	0/1582	0.55	0/2091
21	LS	0.59	0/1493	0.53	0/2003
22	LT	0.57	0/1326	0.59	0/1770
23	LU	0.47	0/839	0.64	0/1126
24	LV	0.56	0/993	0.59	0/1332
25	LW	0.47	0/1030	0.52	0/1364
26	LX	0.49	0/1002	0.54	0/1345
27	LY	0.52	0/1132	0.54	0/1504
28	LZ	0.53	0/1130	0.56	0/1507
29	La	0.56	0/1191	0.55	0/1591
30	Lb	0.43	0/889	0.57	0/1175
31	Lc	0.53	0/774	0.57	0/1038
32	Ld	0.55	0/903	0.60	1/1216 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.59	1/1071 (0.1%)	0.59	0/1429
34	Lf	0.61	0/895	0.62	0/1198
35	Lg	0.55	0/916	0.58	0/1220
36	Lh	0.45	0/1023	0.53	0/1351
37	Li	0.42	0/843	0.51	0/1115
38	Lj	0.60	0/720	0.61	0/952
39	Lk	0.43	0/575	0.56	0/761
40	Ll	0.53	0/454	0.52	0/599
41	Lm	0.53	0/435	0.57	0/575
42	Ln	0.42	0/231	0.54	0/294
43	Lo	0.54	0/876	0.55	0/1156
44	Lp	0.55	0/718	0.55	0/953
45	Lr	0.52	0/1017	0.57	0/1364
46	Lz	0.31	0/1769	0.63	1/2371 (0.0%)
47	S2	0.67	1/41244 (0.0%)	1.08	186/64263 (0.3%)
48	SA	0.38	0/1778	0.60	1/2416 (0.0%)
49	SB	0.35	0/1765	0.56	0/2362
50	SD	0.33	0/1793	0.62	1/2414 (0.0%)
51	SE	0.33	0/2118	0.57	1/2849 (0.0%)
52	SF	0.31	0/1516	0.54	0/2037
53	SH	0.34	0/1519	0.63	2/2033 (0.1%)
54	SI	0.36	0/1715	0.58	0/2287
55	SK	0.28	0/851	0.53	0/1147
56	SL	0.40	0/1268	0.55	0/1696
57	SP	0.29	0/1065	0.54	0/1423
58	SQ	0.29	0/1160	0.58	2/1553 (0.1%)
59	SR	0.31	0/1105	0.56	0/1484
60	SS	0.29	0/1216	0.56	0/1628
61	ST	0.30	0/1131	0.53	0/1515
62	SU	0.29	0/831	0.59	0/1115
63	SV	0.36	0/643	0.61	0/860
64	SX	0.40	0/1116	0.63	0/1490
65	Sa	0.39	0/836	0.58	0/1121
66	Sc	0.33	0/508	0.63	0/680
67	Sd	0.34	0/470	0.52	0/623
68	Sg	0.29	0/2493	0.59	0/3394
69	SC	0.42	0/1762	0.58	1/2381 (0.0%)
70	SG	0.29	0/1946	0.53	0/2590
71	SJ	0.34	0/1550	0.57	0/2069
72	SM	0.31	0/950	0.72	3/1275 (0.2%)
73	SN	0.36	0/1232	0.52	0/1656
74	SO	0.36	0/1062	0.62	0/1425
75	SW	0.38	0/1051	0.53	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SY	0.32	0/1083	0.53	0/1438
77	SZ	0.30	0/604	0.67	1/810 (0.1%)
78	Sb	0.34	0/665	0.54	0/891
79	Se	0.35	0/465	0.56	0/612
80	Sf	0.30	0/560	0.63	0/745
81	CA	0.34	0/2810	0.58	0/3780
82	CB	0.32	0/6738	0.61	1/9099 (0.0%)
83	CC	0.55	0/1773	1.15	12/2759 (0.4%)
84	CD	0.30	0/233	0.73	0/302
All	All	0.84	13/244811 (0.0%)	0.93	707/358380 (0.2%)

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
4	LA	0	2
5	LB	0	3
8	LE	0	2
11	LH	0	2
12	LI	0	1
13	LJ	0	1
14	LL	0	1
15	LM	0	2
16	LN	0	1
17	LO	0	1
21	LS	0	1
22	LT	0	1
33	Le	0	1
34	Lf	0	2
36	Lh	0	1
38	Lj	0	1
45	Lr	0	1
49	SB	0	1
50	SD	0	1
52	SF	0	1
53	SH	0	1
58	SQ	0	3
63	SV	0	1
64	SX	0	3
66	Sc	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
82	CB	0	2
84	CD	0	1
All	All	0	39

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	3646	A	N7-C5	-5.98	1.35	1.39
1	L5	4764	A	N9-C4	-5.94	1.34	1.37
47	S2	1422	G	C6-N1	-5.87	1.35	1.39
1	L5	4355	G	C2-N3	-5.82	1.28	1.32
33	Le	72	SER	CA-CB	-5.82	1.44	1.52
1	L5	4355	G	C2-N2	-5.80	1.28	1.34
1	L5	4355	G	N3-C4	-5.77	1.31	1.35
1	L5	2465	C	N1-C6	-5.55	1.33	1.37
1	L5	121	A	N9-C4	-5.51	1.34	1.37
1	L5	1612	G	C6-N1	-5.42	1.35	1.39
1	L5	4281	A	N3-C4	-5.35	1.31	1.34
4	LA	169	VAL	CB-CG1	-5.28	1.41	1.52
1	L5	4242	U	C2-N3	-5.18	1.34	1.37

All (707) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	S2	1417	C	N3-C4-N4	-27.49	98.76	118.00
47	S2	1422	G	N1-C6-O6	-24.74	105.05	119.90
47	S2	1417	C	C5-C4-N4	21.24	135.07	120.20
47	S2	1422	G	C5-C6-O6	21.20	141.32	128.60
47	S2	1772	C	N1-C2-O2	14.69	127.71	118.90
47	S2	1772	C	N3-C2-O2	-14.07	112.05	121.90
1	L5	2710	C	N1-C2-O2	13.98	127.29	118.90
1	L5	969	C	N1-C2-O2	13.80	127.18	118.90
1	L5	485	C	C2-N1-C1'	12.67	132.74	118.80
47	S2	293	C	N1-C2-O2	12.50	126.40	118.90
1	L5	969	C	C2-N1-C1'	11.60	131.56	118.80
47	S2	1772	C	C2-N1-C1'	11.36	131.29	118.80
1	L5	2710	C	N3-C2-O2	-11.33	113.97	121.90
1	L5	2019	C	N3-C2-O2	-11.14	114.10	121.90
1	L5	906	C	N3-C2-O2	-11.00	114.20	121.90
1	L5	2019	C	N1-C2-O2	10.70	125.32	118.90
47	S2	322	C	N3-C2-O2	-10.65	114.45	121.90
1	L5	181	C	N1-C2-O2	10.32	125.09	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	969	C	N3-C2-O2	-10.31	114.68	121.90
47	S2	1772	C	C6-N1-C2	-10.20	116.22	120.30
1	L5	323	C	N3-C2-O2	-10.16	114.78	121.90
47	S2	1417	C	N3-C4-C5	10.06	125.92	121.90
47	S2	1453	C	C2-N1-C1'	10.05	129.85	118.80
1	L5	485	C	C6-N1-C1'	-10.04	108.75	120.80
47	S2	1417	C	C4-C5-C6	-10.04	112.38	117.40
47	S2	49	C	N3-C2-O2	-9.85	115.00	121.90
1	L5	2710	C	C2-N1-C1'	9.81	129.59	118.80
1	L5	655	C	N3-C2-O2	-9.77	115.06	121.90
1	L5	417	G	O4'-C1'-N9	9.72	115.97	108.20
1	L5	1447	C	N3-C2-O2	-9.70	115.11	121.90
47	S2	882	U	N1-C2-O2	9.69	129.58	122.80
1	L5	485	C	N1-C2-O2	9.67	124.70	118.90
47	S2	293	C	C2-N1-C1'	9.50	129.25	118.80
1	L5	4355	G	C5-C6-O6	9.43	134.26	128.60
1	L5	4303	C	N3-C2-O2	-9.37	115.34	121.90
47	S2	501	C	C2-N1-C1'	9.30	129.03	118.80
3	L8	126	C	N3-C4-N4	-9.13	111.61	118.00
1	L5	4355	G	N3-C4-N9	-9.12	120.53	126.00
1	L5	1050	C	N3-C2-O2	-9.10	115.53	121.90
1	L5	234	G	N9-C4-C5	-9.07	101.77	105.40
1	L5	234	G	C6-C5-N7	-9.03	124.98	130.40
1	L5	2544	G	N1-C6-O6	-9.01	114.50	119.90
1	L5	1082	C	O4'-C1'-N1	8.99	115.39	108.20
1	L5	753	C	N3-C2-O2	-8.99	115.61	121.90
3	L8	126	C	C5-C4-N4	8.90	126.43	120.20
47	S2	501	C	N1-C2-O2	8.89	124.23	118.90
47	S2	293	C	N3-C2-O2	-8.88	115.69	121.90
1	L5	4921	C	N3-C2-O2	-8.83	115.72	121.90
1	L5	4921	C	C6-N1-C2	-8.82	116.77	120.30
47	S2	322	C	N1-C2-O2	8.79	124.17	118.90
1	L5	4355	G	N9-C4-C5	8.73	108.89	105.40
1	L5	2260	C	N1-C2-O2	8.72	124.13	118.90
1	L5	1762	C	N1-C2-O2	8.72	124.13	118.90
1	L5	174	C	N3-C2-O2	-8.68	115.82	121.90
1	L5	1367	C	N1-C2-O2	8.66	124.09	118.90
1	L5	753	C	N1-C2-O2	8.64	124.09	118.90
1	L5	4138	C	N3-C2-O2	-8.64	115.85	121.90
83	CC	33	U	C5-C6-N1	8.63	127.02	122.70
47	S2	1453	C	N1-C2-O2	8.60	124.06	118.90
1	L5	3948	C	C2-N1-C1'	8.59	128.25	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	925	C	C6-N1-C2	-8.48	116.91	120.30
1	L5	234	G	C4-C5-N7	8.45	114.18	110.80
1	L5	4945	G	C5-C6-O6	-8.41	123.55	128.60
1	L5	3647	A	C6-N1-C2	-8.40	113.56	118.60
1	L5	181	C	N3-C2-O2	-8.39	116.03	121.90
1	L5	234	G	C8-N9-C1'	-8.37	116.12	127.00
1	L5	986	C	C6-N1-C2	-8.36	116.95	120.30
1	L5	1367	C	C2-N1-C1'	8.34	127.97	118.80
1	L5	969	C	C6-N1-C1'	-8.30	110.83	120.80
47	S2	877	C	N3-C2-O2	-8.28	116.10	121.90
47	S2	118	C	N1-C2-O2	8.27	123.86	118.90
1	L5	456	C	O4'-C1'-N1	8.26	114.81	108.20
1	L5	1762	C	C2-N1-C1'	8.26	127.89	118.80
1	L5	907	C	N3-C2-O2	-8.25	116.12	121.90
1	L5	3647	A	C5-C6-N1	8.25	121.83	117.70
47	S2	1453	C	C5-C6-N1	8.18	125.09	121.00
47	S2	882	U	C2-N1-C1'	8.18	127.51	117.70
1	L5	3948	C	N1-C2-O2	8.15	123.79	118.90
1	L5	456	C	N3-C2-O2	-8.15	116.20	121.90
1	L5	1216	C	C2-N1-C1'	8.11	127.72	118.80
3	L8	51	U	N3-C2-O2	-8.11	116.53	122.20
1	L5	4926	C	N1-C2-O2	8.10	123.76	118.90
1	L5	100	C	N3-C2-O2	-8.09	116.24	121.90
1	L5	1447	C	C6-N1-C2	-8.08	117.07	120.30
1	L5	459	C	N3-C2-O2	-8.07	116.25	121.90
1	L5	100	C	C2-N1-C1'	8.06	127.66	118.80
1	L5	985	C	N1-C2-O2	8.04	123.73	118.90
1	L5	1968	G	N3-C4-N9	8.03	130.82	126.00
1	L5	4709	U	C2-N1-C1'	8.02	127.32	117.70
1	L5	4303	C	N1-C2-O2	8.01	123.71	118.90
1	L5	4928	C	C2-N1-C1'	7.97	127.57	118.80
1	L5	5022	U	N1-C2-O2	7.97	128.38	122.80
1	L5	654	C	N1-C2-O2	7.95	123.67	118.90
1	L5	1191	C	N3-C2-O2	-7.91	116.36	121.90
1	L5	3757	G	O4'-C1'-N9	7.88	114.50	108.20
47	S2	118	C	C2-N1-C1'	7.87	127.45	118.80
47	S2	1139	C	N3-C2-O2	-7.86	116.40	121.90
1	L5	2709	C	C6-N1-C2	7.85	123.44	120.30
47	S2	356	C	C2-N1-C1'	7.84	127.43	118.80
1	L5	4355	G	N3-C2-N2	-7.83	114.42	119.90
3	L8	51	U	N1-C2-O2	7.80	128.26	122.80
47	S2	570	C	C2-N1-C1'	7.80	127.38	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	2260	C	C2-N1-C1'	7.76	127.34	118.80
1	L5	233	U	N3-C2-O2	-7.73	116.79	122.20
1	L5	234	G	C4-N9-C1'	7.73	136.55	126.50
1	L5	2709	C	N3-C4-C5	7.71	124.98	121.90
1	L5	181	C	C2-N1-C1'	7.71	127.28	118.80
47	S2	1424	G	N3-C4-N9	7.71	130.62	126.00
1	L5	175	C	N3-C2-O2	-7.69	116.51	121.90
47	S2	1139	C	N1-C2-O2	7.69	123.51	118.90
1	L5	2544	G	C5-C6-O6	7.68	133.21	128.60
1	L5	234	G	N3-C2-N2	7.66	125.26	119.90
1	L5	2303	C	N1-C2-O2	7.65	123.49	118.90
47	S2	501	C	N3-C2-O2	-7.65	116.55	121.90
1	L5	3909	C	C6-N1-C2	-7.61	117.26	120.30
1	L5	4557	U	N3-C2-O2	-7.61	116.87	122.20
1	L5	4281	A	O4'-C1'-N9	7.61	114.28	108.20
47	S2	1416	C	N3-C2-O2	-7.57	116.60	121.90
1	L5	516	C	N1-C2-O2	7.57	123.44	118.90
47	S2	402	C	C5-C6-N1	7.55	124.77	121.00
1	L5	77	U	N3-C2-O2	-7.54	116.92	122.20
1	L5	985	C	C2-N1-C1'	7.52	127.07	118.80
1	L5	1050	C	N1-C2-O2	7.50	123.40	118.90
47	S2	1078	C	C2-N1-C1'	7.49	127.04	118.80
1	L5	209	U	C2-N1-C1'	7.48	126.68	117.70
1	L5	4926	C	C2-N1-C1'	7.48	127.03	118.80
1	L5	1082	C	N3-C2-O2	-7.48	116.67	121.90
47	S2	570	C	N1-C2-O2	7.47	123.39	118.90
1	L5	5022	U	C2-N1-C1'	7.47	126.67	117.70
47	S2	882	U	N3-C2-O2	-7.43	117.00	122.20
47	S2	417	C	OP1-P-O3'	7.42	121.51	105.20
46	Lz	194	LEU	CA-CB-CG	7.40	132.32	115.30
1	L5	234	G	N3-C4-N9	7.40	130.44	126.00
1	L5	4557	U	C2-N1-C1'	7.38	126.55	117.70
1	L5	468	U	C5-C4-O4	-7.37	121.48	125.90
47	S2	1273	C	C6-N1-C2	-7.37	117.35	120.30
47	S2	527	C	N3-C2-O2	-7.35	116.76	121.90
47	S2	1453	C	C6-N1-C2	-7.33	117.37	120.30
1	L5	925	C	C5-C6-N1	7.32	124.66	121.00
47	S2	293	C	C6-N1-C1'	-7.32	112.02	120.80
1	L5	234	G	O4'-C1'-N9	7.31	114.05	108.20
1	L5	234	G	N1-C2-N2	-7.31	109.62	116.20
1	L5	4355	G	C4-C5-N7	-7.28	107.89	110.80
1	L5	489	C	C2-N1-C1'	7.24	126.76	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	S2	537	C	C2-N1-C1'	7.24	126.76	118.80
1	L5	468	U	N3-C4-O4	7.24	124.46	119.40
1	L5	2786	C	C6-N1-C2	-7.23	117.41	120.30
1	L5	4281	A	N1-C2-N3	7.22	132.91	129.30
1	L5	4355	G	N1-C6-O6	-7.21	115.57	119.90
1	L5	3641	U	C4-C5-C6	7.14	123.98	119.70
1	L5	4945	G	C4-C5-N7	7.14	113.65	110.80
47	S2	1139	C	C2-N1-C1'	7.12	126.64	118.80
1	L5	2627	C	C2-N1-C1'	7.12	126.63	118.80
1	L5	986	C	N3-C2-O2	-7.11	116.92	121.90
47	S2	427	U	C2-N1-C1'	7.10	126.22	117.70
1	L5	323	C	N3-C4-N4	-7.09	113.03	118.00
1	L5	4758	U	C2-N1-C1'	7.09	126.21	117.70
1	L5	2260	C	N3-C2-O2	-7.09	116.94	121.90
47	S2	1701	C	C6-N1-C2	-7.09	117.46	120.30
47	S2	356	C	N1-C2-O2	7.08	123.15	118.90
1	L5	4928	C	N1-C2-O2	7.08	123.15	118.90
47	S2	427	U	N1-C2-O2	7.07	127.75	122.80
1	L5	654	C	C2-N1-C1'	7.05	126.56	118.80
47	S2	1231	C	C6-N1-C2	-7.02	117.49	120.30
47	S2	179	C	N1-C2-O2	7.00	123.10	118.90
1	L5	2814	C	N1-C2-O2	6.98	123.09	118.90
1	L5	4557	U	N1-C2-O2	6.98	127.69	122.80
47	S2	1772	C	C6-N1-C1'	-6.97	112.44	120.80
1	L5	130	C	N3-C2-O2	-6.96	117.03	121.90
1	L5	4147	G	C5-C6-O6	6.95	132.77	128.60
47	S2	427	U	N3-C2-O2	-6.95	117.33	122.20
1	L5	2710	C	C6-N1-C1'	-6.94	112.47	120.80
47	S2	1078	C	C6-N1-C2	-6.93	117.53	120.30
1	L5	100	C	N1-C2-O2	6.93	123.06	118.90
1	L5	2410	C	C2-N1-C1'	6.92	126.42	118.80
1	L5	2303	C	N3-C2-O2	-6.92	117.06	121.90
47	S2	1701	C	C5-C6-N1	6.91	124.45	121.00
1	L5	2262	G	C4-N9-C1'	6.91	135.48	126.50
47	S2	1022	U	C2-N1-C1'	6.90	125.98	117.70
1	L5	233	U	N1-C2-O2	6.89	127.62	122.80
1	L5	1367	C	N3-C2-O2	-6.89	117.08	121.90
1	L5	129	C	N3-C2-O2	-6.89	117.08	121.90
1	L5	1552	G	O4'-C1'-N9	6.88	113.70	108.20
1	L5	115	C	C2-N1-C1'	6.88	126.36	118.80
1	L5	1216	C	N1-C2-O2	6.87	123.02	118.90
1	L5	456	C	C6-N1-C2	-6.86	117.56	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	1969	G	N1-C2-N2	-6.85	110.03	116.20
1	L5	4742	G	C4-N9-C1'	-6.84	117.60	126.50
47	S2	118	C	N3-C2-O2	-6.84	117.11	121.90
1	L5	115	C	N1-C2-O2	6.83	123.00	118.90
1	L5	969	C	C6-N1-C2	-6.81	117.58	120.30
47	S2	1520	G	C4-N9-C1'	6.80	135.34	126.50
47	S2	909	G	N3-C4-N9	6.80	130.08	126.00
1	L5	4758	U	N3-C2-O2	-6.79	117.45	122.20
1	L5	1245	C	C2-N1-C1'	6.79	126.27	118.80
1	L5	4758	U	N1-C2-O2	6.78	127.54	122.80
1	L5	4742	G	C8-N9-C1'	6.76	135.79	127.00
1	L5	4926	C	N3-C2-O2	-6.76	117.17	121.90
47	S2	1205	C	C6-N1-C2	-6.76	117.60	120.30
1	L5	4303	C	C2-N1-C1'	6.75	126.23	118.80
1	L5	4229	U	N3-C2-O2	-6.75	117.47	122.20
1	L5	3948	C	N3-C2-O2	-6.75	117.18	121.90
1	L5	490	C	C6-N1-C2	-6.75	117.60	120.30
1	L5	5022	U	N3-C2-O2	-6.73	117.49	122.20
1	L5	257	C	C6-N1-C2	-6.71	117.61	120.30
1	L5	489	C	N1-C2-O2	6.71	122.93	118.90
1	L5	1915	C	N3-C2-O2	-6.70	117.21	121.90
1	L5	4281	A	C2-N3-C4	-6.70	107.25	110.60
47	S2	1314	U	C2-N1-C1'	6.70	125.74	117.70
1	L5	175	C	C6-N1-C2	-6.68	117.63	120.30
47	S2	1453	C	C6-N1-C1'	-6.68	112.78	120.80
1	L5	4138	C	C6-N1-C2	-6.67	117.63	120.30
72	SM	57	ASP	C-N-CA	-6.67	105.03	121.70
1	L5	906	C	N1-C2-O2	6.67	122.90	118.90
1	L5	4709	U	C5-C4-O4	-6.67	121.90	125.90
47	S2	688	U	P-O3'-C3'	6.67	127.70	119.70
1	L5	2257	C	N1-C2-O2	6.64	122.89	118.90
47	S2	501	C	C6-N1-C2	-6.64	117.64	120.30
1	L5	4945	G	N9-C4-C5	-6.64	102.75	105.40
1	L5	925	C	N3-C2-O2	-6.63	117.25	121.90
1	L5	3892	U	N3-C2-O2	-6.63	117.56	122.20
1	L5	4450	U	N3-C2-O2	-6.63	117.56	122.20
1	L5	2021	G	N3-C4-N9	6.62	129.97	126.00
1	L5	1082	C	P-O3'-C3'	6.62	127.64	119.70
1	L5	2528	G	C4-N9-C1'	6.61	135.10	126.50
1	L5	1082	C	OP1-P-O3'	6.59	119.69	105.20
47	S2	1231	C	C5-C6-N1	6.59	124.29	121.00
1	L5	1446	C	N1-C2-O2	6.58	122.85	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	1241	C	N1-C2-O2	6.57	122.84	118.90
1	L5	1821	G	N3-C4-C5	-6.57	125.32	128.60
1	L5	4355	G	N1-C2-N3	6.56	127.84	123.90
1	L5	3948	C	C6-N1-C2	-6.56	117.68	120.30
1	L5	4747	C	C2-N1-C1'	6.56	126.01	118.80
1	L5	3775	A	N7-C8-N9	6.55	117.07	113.80
1	L5	1049	C	N1-C2-O2	6.54	122.83	118.90
1	L5	925	C	N1-C2-O2	6.53	122.82	118.90
1	L5	1216	C	N3-C2-O2	-6.52	117.33	121.90
1	L5	1882	U	C5-C4-O4	-6.52	121.99	125.90
83	CC	55	C	N3-C2-O2	-6.52	117.33	121.90
47	S2	1424	G	C4-N9-C1'	6.52	134.98	126.50
1	L5	4147	G	N1-C6-O6	-6.50	116.00	119.90
1	L5	1720	C	C6-N1-C2	-6.49	117.71	120.30
47	S2	417	C	P-O3'-C3'	6.49	127.48	119.70
1	L5	3775	A	C5-N7-C8	-6.48	100.66	103.90
1	L5	3772	U	C2-N1-C1'	6.47	125.47	117.70
1	L5	1715	C	C2-N1-C1'	6.46	125.91	118.80
83	CC	74	C	C6-N1-C2	-6.46	117.71	120.30
47	S2	1304	U	C2-N1-C1'	6.46	125.45	117.70
1	L5	1378	C	N1-C2-O2	6.45	122.77	118.90
1	L5	1968	G	N9-C4-C5	-6.45	102.82	105.40
1	L5	100	C	C6-N1-C2	-6.44	117.72	120.30
47	S2	1261	C	C2-N1-C1'	6.43	125.88	118.80
1	L5	4773	C	N1-C2-O2	6.43	122.76	118.90
1	L5	516	C	N3-C2-O2	-6.42	117.41	121.90
1	L5	4447	C	C6-N1-C1'	6.41	128.49	120.80
47	S2	1234	C	C2-N1-C1'	6.40	125.84	118.80
1	L5	4447	C	C2-N1-C1'	-6.39	111.77	118.80
83	CC	55	C	N1-C2-O2	6.39	122.73	118.90
47	S2	1273	C	N3-C2-O2	-6.38	117.43	121.90
1	L5	1241	C	C2-N1-C1'	6.38	125.82	118.80
3	L8	64	U	N3-C2-O2	-6.38	117.74	122.20
1	L5	490	C	N3-C2-O2	-6.37	117.44	121.90
47	S2	882	U	C5-C6-N1	6.37	125.89	122.70
1	L5	1762	C	N3-C2-O2	-6.37	117.44	121.90
1	L5	2257	C	C2-N1-C1'	6.37	125.80	118.80
1	L5	4891	G	C5-C6-O6	6.35	132.41	128.60
1	L5	969	C	C5-C6-N1	6.35	124.17	121.00
53	SH	30	LEU	CA-CB-CG	6.34	129.88	115.30
47	S2	1701	C	C2-N1-C1'	6.33	125.77	118.80
1	L5	1968	G	C8-N9-C1'	-6.33	118.77	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	S2	402	C	C6-N1-C2	-6.32	117.77	120.30
47	S2	478	G	C5-C6-O6	6.32	132.39	128.60
47	S2	1772	C	C5-C6-N1	6.31	124.16	121.00
1	L5	654	C	C6-N1-C1'	-6.31	113.22	120.80
1	L5	2803	U	N1-C2-O2	6.30	127.21	122.80
47	S2	501	C	C6-N1-C1'	-6.29	113.26	120.80
1	L5	1755	C	C2-N1-C1'	6.28	125.71	118.80
1	L5	2260	C	C6-N1-C2	-6.27	117.79	120.30
47	S2	130	G	N3-C4-C5	-6.27	125.47	128.60
1	L5	2675	G	P-O3'-C3'	6.26	127.21	119.70
47	S2	130	G	C4-N9-C1'	6.26	134.64	126.50
1	L5	1663	C	C5-C6-N1	6.25	124.13	121.00
47	S2	1738	C	C5-C6-N1	6.25	124.13	121.00
77	SZ	44	LEU	CA-CB-CG	6.24	129.64	115.30
47	S2	659	G	C4-N9-C1'	6.23	134.60	126.50
1	L5	2760	G	P-O3'-C3'	6.23	127.17	119.70
47	S2	570	C	N3-C2-O2	-6.23	117.54	121.90
47	S2	1424	G	C8-N9-C1'	-6.22	118.92	127.00
1	L5	4360	U	N3-C2-O2	-6.21	117.85	122.20
3	L8	51	U	C2-N1-C1'	6.21	125.15	117.70
1	L5	1968	G	C4-N9-C1'	6.21	134.57	126.50
1	L5	453	G	N3-C4-C5	-6.19	125.50	128.60
1	L5	4742	G	O4'-C1'-N9	6.19	113.15	108.20
48	SA	8	LEU	CA-CB-CG	6.18	129.52	115.30
47	S2	1272	C	N1-C2-O2	6.18	122.61	118.90
1	L5	1182	C	N1-C2-O2	6.18	122.61	118.90
1	L5	1853	G	C4-N9-C1'	6.17	134.53	126.50
1	L5	2627	C	N1-C2-O2	6.17	122.60	118.90
1	L5	499	G	C4-N9-C1'	6.17	134.51	126.50
47	S2	1453	C	N3-C2-O2	-6.16	117.59	121.90
1	L5	4355	G	C2-N3-C4	-6.16	108.82	111.90
1	L5	1808	C	N3-C2-O2	-6.16	117.59	121.90
1	L5	453	G	N3-C4-N9	6.15	129.69	126.00
1	L5	1405	C	N1-C2-O2	6.15	122.59	118.90
1	L5	4746	C	C2-N1-C1'	6.14	125.56	118.80
1	L5	3911	C	C6-N1-C2	-6.14	117.84	120.30
47	S2	663	C	C5-C6-N1	6.14	124.07	121.00
1	L5	4709	U	C6-N1-C1'	-6.14	112.61	121.20
1	L5	655	C	C6-N1-C2	-6.13	117.85	120.30
1	L5	2409	U	C5-C6-N1	-6.13	119.63	122.70
1	L5	4097	G	N3-C4-N9	-6.13	122.32	126.00
1	L5	904	C	N3-C2-O2	-6.13	117.61	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	3930	U	N3-C2-O2	-6.13	117.91	122.20
1	L5	4775	C	N1-C2-O2	6.12	122.58	118.90
47	S2	329	G	N1-C2-N2	-6.12	110.69	116.20
1	L5	209	U	C6-N1-C1'	-6.12	112.63	121.20
1	L5	1367	C	C6-N1-C1'	-6.12	113.45	120.80
1	L5	504	G	C4-N9-C1'	6.12	134.45	126.50
47	S2	1424	G	C6-C5-N7	-6.10	126.74	130.40
1	L5	914	U	P-O3'-C3'	6.09	127.01	119.70
1	L5	1968	G	C4-C5-N7	6.09	113.24	110.80
47	S2	930	C	N1-C2-O2	6.07	122.54	118.90
82	CB	329	ASP	CB-CG-OD1	6.07	123.76	118.30
1	L5	4112	C	N3-C2-O2	-6.07	117.65	121.90
47	S2	1139	C	C6-N1-C2	-6.07	117.87	120.30
47	S2	1417	C	N1-C2-N3	-6.07	114.95	119.20
1	L5	4929	C	N3-C2-O2	-6.06	117.66	121.90
47	S2	1520	G	N3-C4-N9	6.05	129.63	126.00
1	L5	3641	U	C2-N3-C4	-6.05	123.37	127.00
1	L5	907	C	C6-N1-C1'	6.05	128.06	120.80
1	L5	1893	C	C2-N1-C1'	6.05	125.46	118.80
1	L5	1915	C	N1-C2-O2	6.05	122.53	118.90
1	L5	698	G	C5-C6-O6	6.04	132.23	128.60
1	L5	2262	G	N3-C4-C5	-6.04	125.58	128.60
1	L5	1182	C	C2-N1-C1'	6.04	125.44	118.80
1	L5	2710	C	C6-N1-C2	-6.04	117.89	120.30
1	L5	2708	U	C2-N1-C1'	6.03	124.94	117.70
47	S2	322	C	C6-N1-C2	-6.03	117.89	120.30
1	L5	256	G	N3-C4-N9	-6.03	122.38	126.00
1	L5	758	G	C5-C6-O6	6.02	132.21	128.60
1	L5	1762	C	C6-N1-C1'	-6.02	113.58	120.80
47	S2	1047	C	C6-N1-C2	-6.02	117.89	120.30
1	L5	2409	U	C4-C5-C6	6.01	123.31	119.70
47	S2	130	G	N3-C4-N9	6.01	129.60	126.00
47	S2	1304	U	N1-C2-O2	5.99	126.99	122.80
1	L5	904	C	N1-C2-O2	5.97	122.48	118.90
1	L5	2560	C	C2-N1-C1'	5.97	125.37	118.80
1	L5	115	C	N3-C2-O2	-5.97	117.72	121.90
32	Ld	97	ASP	C-N-CA	5.97	136.62	121.70
1	L5	2362	U	N3-C2-O2	-5.96	118.03	122.20
1	L5	2505	C	N1-C2-O2	5.95	122.47	118.90
58	SQ	7	LEU	CA-CB-CG	5.95	128.99	115.30
1	L5	2528	G	C8-N9-C1'	-5.95	119.27	127.00
47	S2	1271	C	C2-N1-C1'	5.95	125.34	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	LB	17	LEU	CA-CB-CG	5.94	128.96	115.30
1	L5	1663	C	C2-N1-C1'	5.94	125.33	118.80
1	L5	2858	A	N1-C6-N6	-5.92	115.05	118.60
1	L5	994	G	N3-C2-N2	5.92	124.05	119.90
47	S2	456	C	C6-N1-C2	-5.91	117.94	120.30
47	S2	1261	C	N1-C2-O2	5.91	122.45	118.90
83	CC	35	U	P-O3'-C3'	5.90	126.78	119.70
1	L5	3778	U	N3-C2-O2	-5.90	118.07	122.20
3	L8	126	C	C2-N1-C1'	-5.88	112.33	118.80
1	L5	485	C	N3-C2-O2	-5.87	117.79	121.90
1	L5	1969	G	C5-C6-O6	5.87	132.12	128.60
47	S2	478	G	N1-C6-O6	-5.87	116.38	119.90
1	L5	1171	G	C5-C6-O6	5.87	132.12	128.60
47	S2	356	C	N3-C2-O2	-5.87	117.79	121.90
47	S2	1590	C	N1-C2-O2	5.86	122.42	118.90
47	S2	877	C	C6-N1-C2	-5.86	117.95	120.30
69	SC	255	LEU	CA-CB-CG	5.86	128.77	115.30
47	S2	527	C	N1-C2-O2	5.85	122.41	118.90
47	S2	1547	C	N1-C2-O2	5.85	122.41	118.90
1	L5	323	C	C5-C4-N4	5.85	124.30	120.20
1	L5	758	G	C8-N9-C4	-5.85	104.06	106.40
58	SQ	52	LEU	CA-CB-CG	5.85	128.75	115.30
1	L5	2409	U	N1-C2-N3	5.84	118.40	114.90
47	S2	537	C	N1-C2-O2	5.83	122.40	118.90
1	L5	459	C	C6-N1-C2	-5.83	117.97	120.30
1	L5	323	C	N1-C2-N3	5.82	123.28	119.20
1	L5	2262	G	N3-C4-N9	5.82	129.49	126.00
47	S2	578	C	N1-C2-O2	5.82	122.39	118.90
1	L5	1821	G	N3-C4-N9	5.81	129.49	126.00
1	L5	4742	G	N3-C4-N9	-5.81	122.51	126.00
1	L5	907	C	N1-C2-N3	5.81	123.27	119.20
1	L5	1663	C	C6-N1-C2	-5.80	117.98	120.30
2	L7	39	C	N1-C2-O2	5.79	122.37	118.90
47	S2	179	C	C2-N1-C1'	5.79	125.17	118.80
47	S2	910	G	N1-C6-O6	-5.79	116.43	119.90
47	S2	1219	C	N3-C2-O2	-5.79	117.85	121.90
1	L5	1808	C	C6-N1-C1'	5.78	127.74	120.80
1	L5	4913	G	P-O3'-C3'	5.78	126.63	119.70
1	L5	1808	C	N1-C2-N3	5.77	123.24	119.20
1	L5	500	G	N1-C2-N2	-5.77	111.01	116.20
1	L5	2021	G	N9-C4-C5	-5.76	103.09	105.40
1	L5	489	C	C6-N1-C1'	-5.76	113.89	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	LN	134	LEU	CA-CB-CG	5.76	128.54	115.30
1	L5	282	C	N3-C2-O2	-5.76	117.87	121.90
1	L5	512	U	N1-C2-O2	5.75	126.83	122.80
1	L5	4281	A	N7-C8-N9	5.75	116.68	113.80
47	S2	325	C	C2-N1-C1'	5.75	125.13	118.80
1	L5	3930	U	N1-C2-O2	5.74	126.82	122.80
1	L5	4891	G	N1-C6-O6	-5.74	116.45	119.90
1	L5	757	G	N1-C2-N2	-5.74	111.04	116.20
1	L5	4928	C	N3-C2-O2	-5.73	117.89	121.90
1	L5	4945	G	N3-C4-N9	5.73	129.44	126.00
1	L5	2506	G	C4-N9-C1'	5.72	133.94	126.50
1	L5	1969	G	N3-C2-N2	5.72	123.90	119.90
1	L5	4551	U	N3-C2-O2	-5.72	118.20	122.20
1	L5	1327	C	C6-N1-C2	-5.72	118.01	120.30
47	S2	1520	G	C8-N9-C1'	-5.71	119.57	127.00
1	L5	2506	G	C6-C5-N7	-5.71	126.97	130.40
1	L5	1968	G	N3-C2-N2	5.70	123.89	119.90
1	L5	3778	U	N1-C2-O2	5.70	126.79	122.80
1	L5	234	G	N9-C1'-C2'	5.70	121.41	114.00
1	L5	472	C	N1-C2-O2	5.69	122.32	118.90
1	L5	485	C	C5-C6-N1	5.69	123.84	121.00
1	L5	4682	U	N3-C2-O2	-5.68	118.22	122.20
1	L5	1821	G	C4-N9-C1'	5.68	133.88	126.50
47	S2	1219	C	N1-C2-O2	5.68	122.31	118.90
3	L8	126	C	C6-N1-C1'	5.67	127.61	120.80
1	L5	2022	C	C2-N1-C1'	5.67	125.03	118.80
47	S2	329	G	N3-C2-N2	5.67	123.87	119.90
1	L5	4392	G	N1-C6-O6	-5.66	116.50	119.90
47	S2	876	C	N1-C2-O2	5.66	122.30	118.90
1	L5	2262	G	C8-N9-C1'	-5.66	119.64	127.00
1	L5	453	G	C4-N9-C1'	5.66	133.85	126.50
1	L5	758	G	N7-C8-N9	5.65	115.93	113.10
47	S2	325	C	N1-C2-O2	5.65	122.29	118.90
47	S2	814	U	N3-C2-O2	-5.65	118.25	122.20
47	S2	909	G	C8-N9-C1'	-5.64	119.66	127.00
1	L5	3948	C	C5-C6-N1	5.64	123.82	121.00
1	L5	2033	A	P-O3'-C3'	5.63	126.46	119.70
1	L5	985	C	C6-N1-C1'	-5.63	114.05	120.80
83	CC	31	G	N3-C2-N2	-5.63	115.96	119.90
1	L5	994	G	N1-C2-N2	-5.62	111.14	116.20
1	L5	1620	U	N3-C2-O2	-5.62	118.27	122.20
47	S2	971	G	C4-N9-C1'	-5.62	119.19	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	513	U	N1-C2-O2	5.62	126.73	122.80
1	L5	3948	C	C6-N1-C1'	-5.62	114.06	120.80
47	S2	1437	C	N1-C2-O2	5.62	122.27	118.90
1	L5	4097	G	C5-C6-O6	5.62	131.97	128.60
1	L5	4928	C	C6-N1-C1'	-5.62	114.06	120.80
1	L5	2394	G	O4'-C1'-N9	5.61	112.69	108.20
1	L5	3646	A	C5-N7-C8	5.61	106.70	103.90
47	S2	494	C	C6-N1-C2	-5.61	118.06	120.30
1	L5	499	G	N3-C4-N9	5.60	129.36	126.00
1	L5	3584	C	N1-C2-O2	5.60	122.26	118.90
1	L5	2018	C	C2-N1-C1'	-5.60	112.64	118.80
1	L5	2786	C	P-O3'-C3'	5.60	126.42	119.70
47	S2	118	C	C6-N1-C1'	-5.59	114.09	120.80
1	L5	985	C	C5-C6-N1	5.58	123.79	121.00
1	L5	1968	G	C6-C5-N7	-5.57	127.06	130.40
1	L5	4920	C	N1-C2-O2	5.57	122.24	118.90
1	L5	4945	G	N1-C6-O6	5.57	123.24	119.90
1	L5	4864	U	N1-C2-O2	5.56	126.69	122.80
1	L5	1216	C	C6-N1-C1'	-5.56	114.13	120.80
1	L5	4945	G	C6-C5-N7	-5.56	127.07	130.40
1	L5	1882	U	N3-C4-O4	5.55	123.29	119.40
1	L5	3598	C	C2-N1-C1'	5.55	124.91	118.80
47	S2	570	C	C6-N1-C2	-5.55	118.08	120.30
72	SM	64	LEU	CA-CB-CG	5.55	128.08	115.30
1	L5	655	C	N1-C2-N3	5.55	123.09	119.20
47	S2	1424	G	N3-C4-C5	-5.55	125.82	128.60
1	L5	2005	G	C4-N9-C1'	5.55	133.71	126.50
47	S2	666	U	C2-N1-C1'	5.55	124.36	117.70
1	L5	963	G	N3-C4-C5	-5.54	125.83	128.60
47	S2	1520	G	N3-C4-C5	-5.54	125.83	128.60
1	L5	907	C	C5-C4-N4	5.54	124.08	120.20
1	L5	740	G	N3-C4-N9	-5.54	122.68	126.00
1	L5	1447	C	N1-C2-O2	5.54	122.22	118.90
47	S2	1591	C	N1-C2-O2	5.54	122.22	118.90
47	S2	950	C	C5-C6-N1	5.54	123.77	121.00
1	L5	3646	A	N7-C8-N9	-5.53	111.03	113.80
1	L5	1632	A	C2-N3-C4	5.53	113.37	110.60
1	L5	220	C	C2-N1-C1'	5.52	124.87	118.80
1	L5	4420	U	C2-N1-C1'	5.52	124.32	117.70
1	L5	1816	C	C6-N1-C2	-5.51	118.09	120.30
47	S2	1271	C	N1-C2-O2	5.51	122.21	118.90
1	L5	205	C	N1-C2-O2	5.51	122.21	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	S2	632	C	C2-N1-C1'	5.51	124.86	118.80
1	L5	4594	U	N3-C2-O2	-5.51	118.34	122.20
1	L5	2255	C	C2-N1-C1'	5.50	124.85	118.80
1	L5	96	U	N3-C2-O2	-5.50	118.35	122.20
1	L5	2856	C	C6-N1-C2	-5.50	118.10	120.30
1	L5	4364	G	N1-C6-O6	-5.50	116.60	119.90
1	L5	278	G	O4'-C1'-N9	-5.49	103.80	108.20
47	S2	1205	C	C5-C6-N1	5.49	123.75	121.00
1	L5	4694	G	O4'-C1'-N9	5.49	112.59	108.20
1	L5	516	C	C2-N1-C1'	5.49	124.84	118.80
1	L5	129	C	C6-N1-C2	-5.49	118.11	120.30
1	L5	2528	G	N3-C4-N9	5.48	129.29	126.00
1	L5	499	G	C8-N9-C1'	-5.47	119.89	127.00
1	L5	1398	A	N1-C2-N3	5.47	132.04	129.30
47	S2	1701	C	N1-C2-O2	5.47	122.18	118.90
1	L5	2820	C	N1-C2-O2	5.47	122.18	118.90
1	L5	1620	U	N1-C2-O2	5.47	126.63	122.80
1	L5	4555	U	C2-N1-C1'	-5.47	111.14	117.70
47	S2	663	C	C6-N1-C2	-5.47	118.11	120.30
1	L5	4773	C	C2-N1-C1'	5.46	124.81	118.80
1	L5	181	C	C6-N1-C1'	-5.46	114.25	120.80
1	L5	1807	C	N1-C2-O2	5.46	122.17	118.90
1	L5	3909	C	N3-C2-O2	-5.46	118.08	121.90
1	L5	2820	C	N3-C2-O2	-5.46	118.08	121.90
1	L5	499	G	N3-C4-C5	-5.45	125.87	128.60
1	L5	906	C	N3-C4-N4	-5.45	114.19	118.00
47	S2	1865	C	N3-C2-O2	-5.45	118.08	121.90
1	L5	757	G	N1-C6-O6	-5.44	116.63	119.90
47	S2	494	C	N3-C2-O2	-5.44	118.09	121.90
1	L5	1050	C	C6-N1-C2	-5.44	118.12	120.30
1	L5	3767	C	N1-C2-O2	5.44	122.17	118.90
47	S2	1309	C	C2-N1-C1'	5.44	124.78	118.80
47	S2	1434	C	P-O3'-C3'	5.44	126.23	119.70
1	L5	1093	C	C5-C6-N1	5.44	123.72	121.00
1	L5	2494	U	N3-C2-O2	-5.44	118.39	122.20
47	S2	478	G	N1-C2-N3	5.43	127.16	123.90
47	S2	356	C	C6-N1-C1'	-5.43	114.28	120.80
47	S2	632	C	C6-N1-C2	-5.43	118.13	120.30
1	L5	963	G	C4-N9-C1'	5.43	133.56	126.50
1	L5	112	C	C2-N1-C1'	5.42	124.77	118.80
47	S2	638	C	C2-N1-C1'	5.42	124.77	118.80
47	S2	801	U	N3-C2-O2	-5.42	118.40	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	CC	61	C	C5-C6-N1	5.42	123.71	121.00
47	S2	48	C	N3-C2-O2	-5.42	118.11	121.90
83	CC	33	U	C6-N1-C2	-5.42	117.75	121.00
1	L5	2560	C	N1-C2-O2	5.42	122.15	118.90
1	L5	1217	G	N3-C4-N9	5.41	129.25	126.00
1	L5	1809	C	C2-N1-C1'	5.41	124.75	118.80
47	S2	1660	C	C2-N1-C1'	5.41	124.75	118.80
1	L5	643	C	N1-C2-O2	5.40	122.14	118.90
1	L5	2899	C	C2-N1-C1'	5.39	124.73	118.80
1	L5	4355	G	C6-C5-N7	5.39	133.63	130.40
1	L5	1216	C	C6-N1-C2	-5.39	118.14	120.30
1	L5	1808	C	C6-N1-C2	-5.38	118.15	120.30
47	S2	950	C	C2-N1-C1'	5.38	124.71	118.80
1	L5	504	G	OP1-P-O3'	5.37	117.02	105.20
47	S2	1219	C	C6-N1-C2	-5.37	118.15	120.30
1	L5	3775	A	O4'-C1'-N9	5.37	112.50	108.20
1	L5	262	G	N1-C6-O6	-5.37	116.68	119.90
1	L5	4775	C	N3-C2-O2	-5.37	118.14	121.90
1	L5	3648	A	O4'-C1'-N9	5.36	112.48	108.20
1	L5	2260	C	C5-C6-N1	5.35	123.68	121.00
1	L5	963	G	N3-C4-N9	5.35	129.21	126.00
47	S2	409	C	C5-C6-N1	5.35	123.67	121.00
1	L5	323	C	C6-N1-C1'	5.35	127.22	120.80
47	S2	178	C	N1-C2-O2	5.34	122.10	118.90
1	L5	1831	G	N3-C4-N9	-5.33	122.80	126.00
1	L5	3680	U	N3-C2-O2	-5.32	118.47	122.20
1	L5	740	G	N3-C4-C5	5.31	131.26	128.60
1	L5	1241	C	N3-C2-O2	-5.31	118.18	121.90
1	L5	1633	G	P-O3'-C3'	5.31	126.07	119.70
1	L5	740	G	C4-N9-C1'	-5.30	119.60	126.50
1	L5	753	C	N3-C4-N4	-5.30	114.29	118.00
1	L5	490	C	C6-N1-C1'	5.30	127.16	120.80
1	L5	504	G	C8-N9-C1'	-5.30	120.11	127.00
47	S2	687	C	N3-C2-O2	-5.30	118.19	121.90
83	CC	39	C	C6-N1-C2	-5.30	118.18	120.30
5	LB	360	LEU	CA-CB-CG	5.30	127.49	115.30
1	L5	1472	C	C2-N1-C1'	5.30	124.63	118.80
47	S2	1738	C	C6-N1-C2	-5.30	118.18	120.30
1	L5	136	C	N1-C2-O2	5.30	122.08	118.90
1	L5	3770	U	N1-C2-O2	5.30	126.51	122.80
47	S2	291	G	P-O3'-C3'	5.30	126.06	119.70
51	SE	38	LEU	CA-CB-CG	5.29	127.46	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	1632	A	N1-C6-N6	-5.28	115.43	118.60
1	L5	2478	C	C6-N1-C2	-5.28	118.19	120.30
1	L5	5035	U	N3-C2-O2	-5.28	118.51	122.20
1	L5	1715	C	C6-N1-C2	-5.28	118.19	120.30
47	S2	570	C	C6-N1-C1'	-5.28	114.47	120.80
1	L5	2899	C	N1-C2-O2	5.26	122.06	118.90
47	S2	537	C	C6-N1-C1'	-5.26	114.49	120.80
1	L5	5028	G	N3-C4-N9	5.26	129.15	126.00
1	L5	2900	U	N1-C2-O2	5.25	126.48	122.80
1	L5	1715	C	N1-C2-O2	5.25	122.05	118.90
47	S2	882	U	C6-N1-C1'	-5.25	113.84	121.20
1	L5	4926	C	C6-N1-C2	-5.25	118.20	120.30
4	LA	204	MET	C-N-CA	5.25	134.83	121.70
47	S2	1865	C	N1-C2-O2	5.25	122.05	118.90
1	L5	1582	U	N1-C2-O2	5.25	126.47	122.80
47	S2	1437	C	C2-N1-C1'	5.24	124.57	118.80
1	L5	4112	C	C6-N1-C2	-5.24	118.20	120.30
1	L5	294	G	C4-N9-C1'	5.24	133.31	126.50
1	L5	1755	C	C5-C6-N1	5.24	123.62	121.00
1	L5	3680	U	N1-C2-O2	5.23	126.46	122.80
1	L5	220	C	C6-N1-C2	-5.23	118.21	120.30
1	L5	4557	U	C6-N1-C1'	-5.23	113.88	121.20
47	S2	909	G	N9-C4-C5	-5.23	103.31	105.40
47	S2	659	G	C8-N9-C1'	-5.23	120.20	127.00
1	L5	458	C	N1-C2-O2	5.23	122.04	118.90
47	S2	420	G	P-O3'-C3'	5.23	125.97	119.70
1	L5	4241	C	C2-N1-C1'	5.22	124.55	118.80
47	S2	321	C	N1-C2-O2	5.22	122.03	118.90
47	S2	1304	U	C5-C6-N1	5.22	125.31	122.70
1	L5	3840	U	N3-C2-O2	-5.22	118.55	122.20
47	S2	1304	U	N3-C2-O2	-5.22	118.55	122.20
47	S2	585	C	C2-N1-C1'	5.22	124.54	118.80
1	L5	906	C	C5-C4-N4	5.22	123.85	120.20
1	L5	2494	U	N1-C2-O2	5.21	126.45	122.80
47	S2	494	C	N1-C2-O2	5.21	122.03	118.90
1	L5	1182	C	N3-C2-O2	-5.21	118.25	121.90
47	S2	909	G	C4-N9-C1'	5.21	133.27	126.50
1	L5	4773	C	N3-C2-O2	-5.21	118.26	121.90
1	L5	4742	G	C6-C5-N7	5.20	133.52	130.40
1	L5	4766	C	C6-N1-C2	-5.20	118.22	120.30
47	S2	1218	C	C5-C6-N1	5.20	123.60	121.00
47	S2	130	G	C8-N9-C1'	-5.20	120.24	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	CC	35	U	OP1-P-O3'	5.20	116.64	105.20
47	S2	559	G	N1-C6-O6	-5.19	116.78	119.90
1	L5	4229	U	N1-C2-O2	5.19	126.43	122.80
1	L5	496	G	N3-C4-N9	-5.19	122.89	126.00
1	L5	698	G	N1-C6-O6	-5.19	116.79	119.90
1	L5	2814	C	N3-C2-O2	-5.19	118.27	121.90
83	CC	33	U	O5'-P-OP2	-5.19	101.03	105.70
47	S2	841	G	O4'-C1'-N9	5.18	112.35	108.20
72	SM	49	LEU	CA-CB-CG	5.18	127.22	115.30
47	S2	1416	C	C6-N1-C2	-5.18	118.23	120.30
1	L5	209	U	N1-C2-O2	5.18	126.42	122.80
1	L5	757	G	C5-C6-O6	5.18	131.71	128.60
47	S2	179	C	N3-C2-O2	-5.18	118.28	121.90
1	L5	2814	C	C2-N1-C1'	5.18	124.50	118.80
1	L5	4043	G	N3-C4-N9	5.18	129.11	126.00
1	L5	2255	C	N1-C2-O2	5.17	122.00	118.90
1	L5	4318	C	N3-C4-C5	5.17	123.97	121.90
50	SD	59	LEU	CA-CB-CG	5.17	127.20	115.30
1	L5	406	C	P-O3'-C3'	5.17	125.91	119.70
1	L5	2303	C	N3-C4-C5	5.17	123.97	121.90
47	S2	559	G	C5-C6-O6	5.16	131.70	128.60
1	L5	1808	C	C5-C4-N4	5.16	123.81	120.20
47	S2	632	C	C5-C6-N1	5.16	123.58	121.00
1	L5	205	C	N3-C2-O2	-5.16	118.29	121.90
1	L5	100	C	C6-N1-C1'	-5.16	114.61	120.80
1	L5	3772	U	N3-C2-O2	-5.15	118.59	122.20
1	L5	4281	A	C5-N7-C8	-5.15	101.33	103.90
47	S2	49	C	N1-C2-O2	5.15	121.99	118.90
1	L5	4303	C	C6-N1-C2	-5.15	118.24	120.30
1	L5	323	C	C2-N3-C4	-5.15	117.33	119.90
47	S2	910	G	C5-C6-O6	5.15	131.69	128.60
1	L5	2018	C	N3-C4-N4	-5.14	114.40	118.00
1	L5	2257	C	N3-C2-O2	-5.14	118.30	121.90
1	L5	4694	G	C4-N9-C1'	5.14	133.19	126.50
1	L5	1217	G	C8-N9-C1'	-5.14	120.31	127.00
47	S2	592	C	N1-C2-O2	5.14	121.98	118.90
1	L5	3693	U	N1-C2-O2	5.14	126.40	122.80
1	L5	3778	U	C2-N1-C1'	5.14	123.86	117.70
1	L5	4682	U	N1-C2-O2	5.13	126.39	122.80
47	S2	1219	C	C2-N1-C1'	5.13	124.45	118.80
10	LG	193	LEU	CA-CB-CG	5.13	127.10	115.30
47	S2	1865	C	C2-N1-C1'	5.13	124.44	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	S2	1261	C	C6-N1-C2	-5.13	118.25	120.30
1	L5	68	U	N3-C2-O2	-5.12	118.61	122.20
1	L5	176	G	C5-C6-N1	5.12	114.06	111.50
1	L5	1821	G	C2-N3-C4	5.12	114.46	111.90
3	L8	111	U	C2-N1-C1'	5.12	123.85	117.70
47	S2	939	U	N1-C2-O2	5.12	126.39	122.80
1	L5	504	G	N3-C4-N9	5.12	129.07	126.00
1	L5	2729	C	C2-N1-C1'	5.12	124.43	118.80
1	L5	4133	C	C2-N1-C1'	5.12	124.43	118.80
1	L5	140	G	C5-C6-O6	5.11	131.67	128.60
1	L5	1702	C	C2-N1-C1'	5.10	124.42	118.80
47	S2	112	U	P-O3'-C3'	5.10	125.82	119.70
1	L5	2783	A	C6-N1-C2	5.10	121.66	118.60
1	L5	4398	C	C6-N1-C2	-5.10	118.26	120.30
1	L5	1612	G	C6-C5-N7	-5.10	127.34	130.40
47	S2	1117	C	N1-C2-O2	5.08	121.95	118.90
1	L5	655	C	C6-N1-C1'	5.08	126.90	120.80
1	L5	458	C	N3-C2-O2	-5.08	118.34	121.90
1	L5	1929	A	C4-N9-C1'	5.07	135.43	126.30
53	SH	127	ASP	CB-CG-OD2	5.07	122.86	118.30
47	S2	356	C	C6-N1-C2	-5.07	118.27	120.30
47	S2	1547	C	N3-C2-O2	-5.07	118.35	121.90
47	S2	478	G	N3-C4-N9	-5.06	122.96	126.00
1	L5	2850	A	C8-N9-C4	-5.06	103.78	105.80
1	L5	2856	C	N3-C2-O2	-5.06	118.36	121.90
1	L5	1853	G	C8-N9-C1'	-5.05	120.43	127.00
1	L5	4926	C	C6-N1-C1'	-5.05	114.74	120.80
1	L5	4714	C	N3-C2-O2	-5.05	118.36	121.90
47	S2	877	C	N1-C2-O2	5.05	121.93	118.90
1	L5	4921	C	N1-C2-O2	5.05	121.93	118.90
1	L5	4973	U	N3-C2-O2	-5.05	118.67	122.20
1	L5	2492	C	C6-N1-C2	-5.04	118.28	120.30
1	L5	4527	G	O4'-C1'-N9	5.04	112.23	108.20
15	LM	87	ALA	C-N-CA	5.04	134.29	121.70
1	L5	740	G	C8-N9-C1'	5.04	133.55	127.00
1	L5	1340	C	C5-C6-N1	5.04	123.52	121.00
1	L5	3673	C	P-O3'-C3'	5.04	125.74	119.70
1	L5	2627	C	C5-C6-N1	5.03	123.52	121.00
1	L5	4885	U	N1-C2-O2	5.03	126.32	122.80
83	CC	33	U	O5'-P-OP1	5.03	116.74	110.70
1	L5	1831	G	C5-C6-O6	5.03	131.62	128.60
1	L5	2410	C	C6-N1-C2	-5.03	118.29	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	41	C	C6-N1-C2	-5.03	118.29	120.30
1	L5	2506	G	N7-C8-N9	5.03	115.61	113.10
1	L5	2709	C	N3-C4-N4	-5.02	114.48	118.00
1	L5	4396	A	C6-N1-C2	5.02	121.61	118.60
1	L5	1868	A	N1-C6-N6	5.02	121.61	118.60
1	L5	3775	A	C2-N3-C4	-5.02	108.09	110.60
47	S2	563	G	P-O3'-C3'	5.02	125.72	119.70
1	L5	2099	G	C5-C6-O6	5.01	131.61	128.60
1	L5	3675	G	N1-C6-O6	-5.01	116.89	119.90
1	L5	4463	U	O4'-C1'-N1	5.01	112.21	108.20
1	L5	2712	G	C6-C5-N7	-5.01	127.39	130.40
1	L5	2560	C	C5-C6-N1	5.01	123.50	121.00
1	L5	4594	U	C2-N1-C1'	5.01	123.71	117.70
1	L5	2506	G	N1-C2-N3	5.00	126.90	123.90
1	L5	3841	C	C2-N1-C1'	5.00	124.30	118.80
1	L5	4864	U	N3-C2-O2	-5.00	118.70	122.20
1	L5	4314	C	N3-C2-O2	-5.00	118.40	121.90

There are no chirality outliers.

All (39) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
82	CB	55	ARG	Peptide
82	CB	807	GLN	Peptide
84	CD	166	GLY	Peptide
4	LA	110	GLY	Peptide
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	2	SER	Peptide
5	LB	258	HIS	Peptide
8	LE	129	GLY	Peptide
8	LE	176	THR	Peptide
11	LH	106	GLN	Peptide
11	LH	173	ARG	Peptide
12	LI	14	ASN	Peptide
13	LJ	94	LEU	Peptide
14	LL	154	VAL	Peptide
15	LM	87	ALA	Peptide
15	LM	88	ALA	Peptide
16	LN	124	ASP	Peptide
17	LO	110	PRO	Peptide
21	LS	5	GLY	Peptide

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Mol	Chain	Res	Type	Group
22	LT	136	ARG	Peptide
33	Le	91	CYS	Peptide
34	Lf	103	VAL	Peptide
34	Lf	106	TYR	Peptide
36	Lh	86	LYS	Peptide
38	Lj	39	TYR	Peptide
45	Lr	20	ARG	Peptide
49	SB	221	PRO	Peptide
50	SD	164	VAL	Peptide
52	SF	126	THR	Peptide
53	SH	15	LYS	Peptide
58	SQ	17	LYS	Peptide
58	SQ	18	THR	Peptide
58	SQ	43	GLU	Peptide
63	SV	78	ILE	Peptide
64	SX	125	VAL	Peptide
64	SX	126	ALA	Peptide
64	SX	86	PRO	Peptide
66	Sc	64	GLU	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	246/257 (96%)	221 (90%)	24 (10%)	1 (0%)	34	66
5	LB	400/403 (99%)	374 (94%)	24 (6%)	2 (0%)	29	61
6	LC	366/427 (86%)	335 (92%)	31 (8%)	0	100	100
7	LD	291/297 (98%)	273 (94%)	18 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	LE	232/288 (81%)	208 (90%)	24 (10%)	0	100	100
9	LF	223/248 (90%)	213 (96%)	10 (4%)	0	100	100
10	LG	239/266 (90%)	221 (92%)	18 (8%)	0	100	100
11	LH	188/192 (98%)	169 (90%)	19 (10%)	0	100	100
12	LI	198/214 (92%)	181 (91%)	17 (9%)	0	100	100
13	LJ	174/178 (98%)	154 (88%)	20 (12%)	0	100	100
14	LL	208/211 (99%)	192 (92%)	16 (8%)	0	100	100
15	LM	137/215 (64%)	127 (93%)	9 (7%)	1 (1%)	22	54
16	LN	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	15	45
17	LO	199/203 (98%)	190 (96%)	9 (4%)	0	100	100
18	LP	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
19	LQ	185/188 (98%)	174 (94%)	11 (6%)	0	100	100
20	LR	185/196 (94%)	179 (97%)	6 (3%)	0	100	100
21	LS	173/176 (98%)	159 (92%)	14 (8%)	0	100	100
22	LT	157/160 (98%)	146 (93%)	10 (6%)	1 (1%)	25	58
23	LU	99/128 (77%)	85 (86%)	13 (13%)	1 (1%)	15	45
24	LV	129/140 (92%)	121 (94%)	8 (6%)	0	100	100
25	LW	122/157 (78%)	117 (96%)	5 (4%)	0	100	100
26	LX	118/156 (76%)	112 (95%)	6 (5%)	0	100	100
27	LY	132/145 (91%)	120 (91%)	12 (9%)	0	100	100
28	LZ	133/136 (98%)	125 (94%)	8 (6%)	0	100	100
29	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
30	Lb	105/159 (66%)	99 (94%)	6 (6%)	0	100	100
31	Lc	96/115 (84%)	89 (93%)	7 (7%)	0	100	100
32	Ld	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
33	Le	126/135 (93%)	118 (94%)	7 (6%)	1 (1%)	19	51
34	Lf	107/110 (97%)	96 (90%)	9 (8%)	2 (2%)	8	28
35	Lg	112/117 (96%)	110 (98%)	2 (2%)	0	100	100
36	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
38	Lj	84/97 (87%)	77 (92%)	6 (7%)	1 (1%)	13	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	Lk	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
40	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
41	Lm	50/128 (39%)	50 (100%)	0	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	94 (91%)	9 (9%)	0	100	100
44	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
45	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
46	Lz	215/217 (99%)	171 (80%)	43 (20%)	1 (0%)	29	61
48	SA	219/295 (74%)	197 (90%)	21 (10%)	1 (0%)	29	61
49	SB	212/264 (80%)	197 (93%)	15 (7%)	0	100	100
50	SD	225/243 (93%)	201 (89%)	24 (11%)	0	100	100
51	SE	260/263 (99%)	243 (94%)	17 (6%)	0	100	100
52	SF	187/204 (92%)	166 (89%)	21 (11%)	0	100	100
53	SH	182/194 (94%)	162 (89%)	20 (11%)	0	100	100
54	SI	204/208 (98%)	195 (96%)	9 (4%)	0	100	100
55	SK	96/165 (58%)	87 (91%)	9 (9%)	0	100	100
56	SL	151/158 (96%)	138 (91%)	13 (9%)	0	100	100
57	SP	125/145 (86%)	111 (89%)	14 (11%)	0	100	100
58	SQ	142/146 (97%)	123 (87%)	19 (13%)	0	100	100
59	SR	133/135 (98%)	120 (90%)	13 (10%)	0	100	100
60	SS	143/152 (94%)	128 (90%)	15 (10%)	0	100	100
61	ST	141/145 (97%)	132 (94%)	8 (6%)	1 (1%)	22	54
62	SU	102/119 (86%)	92 (90%)	10 (10%)	0	100	100
63	SV	81/83 (98%)	74 (91%)	6 (7%)	1 (1%)	13	40
64	SX	139/143 (97%)	125 (90%)	12 (9%)	2 (1%)	11	36
65	Sa	100/115 (87%)	91 (91%)	8 (8%)	1 (1%)	15	45
66	Sc	62/69 (90%)	54 (87%)	8 (13%)	0	100	100
67	Sd	53/56 (95%)	47 (89%)	6 (11%)	0	100	100
68	Sg	311/317 (98%)	272 (88%)	39 (12%)	0	100	100
69	SC	220/293 (75%)	205 (93%)	15 (7%)	0	100	100
70	SG	235/249 (94%)	218 (93%)	17 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
71	SJ	183/194 (94%)	170 (93%)	13 (7%)	0	100	100
72	SM	120/132 (91%)	109 (91%)	11 (9%)	0	100	100
73	SN	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
74	SO	138/151 (91%)	123 (89%)	15 (11%)	0	100	100
75	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
76	SY	129/133 (97%)	117 (91%)	12 (9%)	0	100	100
77	SZ	73/125 (58%)	60 (82%)	12 (16%)	1 (1%)	11	36
78	Sb	81/84 (96%)	73 (90%)	8 (10%)	0	100	100
79	Se	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
80	Sf	65/156 (42%)	55 (85%)	10 (15%)	0	100	100
81	CA	350/394 (89%)	337 (96%)	13 (4%)	0	100	100
82	CB	842/858 (98%)	787 (94%)	52 (6%)	3 (0%)	34	66
84	CD	30/408 (7%)	19 (63%)	11 (37%)	0	100	100
All	All	12768/14565 (88%)	11751 (92%)	994 (8%)	23 (0%)	50	78

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
64	SX	127	ASN
33	Le	73	GLY
61	ST	41	LYS
77	SZ	45	ASN
82	CB	56	PHE
5	LB	302	ASN
15	LM	88	ALA
34	Lf	80	ASN
46	Lz	18	LEU
48	SA	12	GLU
65	Sa	47	ALA
4	LA	55	GLY
5	LB	4	ARG
22	LT	137	GLU
64	SX	126	ALA
34	Lf	107	PRO
38	Lj	40	PRO
82	CB	325	SER

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Mol	Chain	Res	Type
23	LU	59	GLY
16	LN	83	LYS
63	SV	79	VAL
82	CB	810	PRO

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%)	187 (98%)	3 (2%)	62	86
5	LB	348/349 (100%)	345 (99%)	3 (1%)	78	93
6	LC	306/348 (88%)	305 (100%)	1 (0%)	92	98
7	LD	246/250 (98%)	245 (100%)	1 (0%)	91	97
8	LE	209/252 (83%)	208 (100%)	1 (0%)	88	96
9	LF	194/215 (90%)	193 (100%)	1 (0%)	88	96
10	LG	203/223 (91%)	199 (98%)	4 (2%)	55	82
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	172/181 (95%)	171 (99%)	1 (1%)	86	96
13	LJ	148/149 (99%)	144 (97%)	4 (3%)	44	77
14	LL	176/177 (99%)	174 (99%)	2 (1%)	73	92
15	LM	118/161 (73%)	117 (99%)	1 (1%)	81	94
16	LN	171/172 (99%)	170 (99%)	1 (1%)	86	96
17	LO	173/174 (99%)	171 (99%)	2 (1%)	71	91
18	LP	134/163 (82%)	133 (99%)	1 (1%)	84	95
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	86	96
20	LR	166/175 (95%)	165 (99%)	1 (1%)	86	96
21	LS	156/157 (99%)	154 (99%)	2 (1%)	69	90
22	LT	139/140 (99%)	137 (99%)	2 (1%)	67	89
23	LU	91/115 (79%)	90 (99%)	1 (1%)	73	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	LV	101/107 (94%)	100 (99%)	1 (1%)	76	92
25	LW	103/126 (82%)	101 (98%)	2 (2%)	57	84
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	122 (98%)	2 (2%)	62	86
28	LZ	117/118 (99%)	115 (98%)	2 (2%)	60	86
29	La	120/121 (99%)	119 (99%)	1 (1%)	81	94
30	Lb	88/126 (70%)	88 (100%)	0	100	100
31	Lc	83/97 (86%)	80 (96%)	3 (4%)	35	69
32	Ld	98/110 (89%)	97 (99%)	1 (1%)	76	92
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%)	96 (98%)	2 (2%)	55	82
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%)	72 (99%)	1 (1%)	67	89
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	46 (98%)	1 (2%)	53	81
41	Lm	48/116 (41%)	47 (98%)	1 (2%)	53	81
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	93 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	108 (99%)	1 (1%)	78	93
46	Lz	195/196 (100%)	191 (98%)	4 (2%)	53	81
48	SA	183/243 (75%)	182 (100%)	1 (0%)	88	96
49	SB	195/231 (84%)	190 (97%)	5 (3%)	46	77
50	SD	190/202 (94%)	187 (98%)	3 (2%)	62	86
51	SE	224/225 (100%)	224 (100%)	0	100	100
52	SF	159/170 (94%)	158 (99%)	1 (1%)	86	96
53	SH	166/174 (95%)	163 (98%)	3 (2%)	59	85
54	SI	178/180 (99%)	177 (99%)	1 (1%)	86	96
55	SK	89/136 (65%)	87 (98%)	2 (2%)	52	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	SL	137/142 (96%)	133 (97%)	4 (3%)	42	76
57	SP	113/130 (87%)	113 (100%)	0	100	100
58	SQ	119/121 (98%)	119 (100%)	0	100	100
59	SR	122/122 (100%)	120 (98%)	2 (2%)	62	86
60	SS	126/132 (96%)	125 (99%)	1 (1%)	81	94
61	ST	113/115 (98%)	112 (99%)	1 (1%)	78	93
62	SU	94/107 (88%)	93 (99%)	1 (1%)	73	92
63	SV	67/67 (100%)	65 (97%)	2 (3%)	41	75
64	SX	113/115 (98%)	111 (98%)	2 (2%)	59	85
65	Sa	89/98 (91%)	89 (100%)	0	100	100
66	Sc	57/62 (92%)	57 (100%)	0	100	100
67	Sd	48/49 (98%)	47 (98%)	1 (2%)	53	81
68	Sg	272/275 (99%)	271 (100%)	1 (0%)	91	97
69	SC	188/225 (84%)	187 (100%)	1 (0%)	88	96
70	SG	207/218 (95%)	203 (98%)	4 (2%)	57	84
71	SJ	161/168 (96%)	160 (99%)	1 (1%)	86	96
72	SM	102/108 (94%)	98 (96%)	4 (4%)	32	66
73	SN	130/131 (99%)	130 (100%)	0	100	100
74	SO	110/119 (92%)	108 (98%)	2 (2%)	59	85
75	SW	112/113 (99%)	112 (100%)	0	100	100
76	SY	113/115 (98%)	112 (99%)	1 (1%)	78	93
77	SZ	66/103 (64%)	66 (100%)	0	100	100
78	Sb	75/76 (99%)	75 (100%)	0	100	100
79	Se	47/48 (98%)	46 (98%)	1 (2%)	53	81
80	Sf	60/140 (43%)	58 (97%)	2 (3%)	38	72
81	CA	303/336 (90%)	303 (100%)	0	100	100
82	CB	723/730 (99%)	719 (99%)	4 (1%)	86	96
84	CD	19/328 (6%)	18 (95%)	1 (5%)	22	54
All	All	11106/12391 (90%)	10999 (99%)	107 (1%)	77	92

All (107) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	15	VAL
4	LA	102	LEU
4	LA	207	VAL
5	LB	17	LEU
5	LB	258	HIS
5	LB	297	LYS
6	LC	188	ARG
7	LD	85	LYS
8	LE	56	ARG
9	LF	29	LYS
10	LG	26	LYS
10	LG	111	LYS
10	LG	175	ARG
10	LG	259	LYS
12	LI	78	LYS
13	LJ	43	LEU
13	LJ	95	ARG
13	LJ	171	ASP
13	LJ	178	LYS
14	LL	145	LYS
14	LL	210	LYS
15	LM	25	VAL
16	LN	114	ARG
17	LO	117	ARG
17	LO	187	LYS
18	LP	57	CYS
19	LQ	83	VAL
20	LR	165	LYS
21	LS	24	THR
21	LS	85	ASP
22	LT	36	LYS
22	LT	85	LEU
23	LU	113	ARG
24	LV	48	ARG
25	LW	25	ASP
25	LW	116	LYS
27	LY	78	TYR
27	LY	84	ARG
28	LZ	21	ARG
28	LZ	30	ASP
29	La	92	LYS
31	Lc	23	LYS
31	Lc	103	ASP

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Mol	Chain	Res	Type
31	Lc	106	ARG
32	Ld	67	ARG
35	Lg	54	ARG
35	Lg	63	VAL
38	Lj	22	CYS
40	Ll	46	ARG
41	Lm	127	VAL
45	Lr	103	ARG
46	Lz	7	ARG
46	Lz	122	ARG
46	Lz	161	LYS
46	Lz	215	ARG
48	SA	52	LYS
49	SB	56	LYS
49	SB	76	ASN
49	SB	199	LYS
49	SB	205	TYR
49	SB	222	LYS
50	SD	76	ARG
50	SD	167	TYR
50	SD	178	ARG
52	SF	155	CYS
53	SH	27	LEU
53	SH	32	MET
53	SH	57	ARG
54	SI	140	LYS
55	SK	6	LYS
55	SK	98	ARG
56	SL	19	ASN
56	SL	22	ARG
56	SL	69	ARG
56	SL	90	ARG
59	SR	45	LYS
59	SR	72	LYS
60	SS	142	ARG
61	ST	41	LYS
62	SU	116	ILE
63	SV	10	ASP
63	SV	56	CYS
64	SX	105	PHE
64	SX	112	VAL
67	Sd	48	LYS

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Mol	Chain	Res	Type
68	Sg	212	LYS
69	SC	257	LYS
70	SG	31	ARG
70	SG	98	ARG
70	SG	200	LYS
70	SG	211	LYS
71	SJ	66	LYS
72	SM	63	LYS
72	SM	84	LYS
72	SM	96	ARG
72	SM	121	LYS
74	SO	149	ARG
74	SO	150	ARG
76	SY	132	LYS
79	Se	26	LYS
80	Sf	104	LYS
80	Sf	109	ASP
82	CB	20	ARG
82	CB	203	ILE
82	CB	456	ARG
82	CB	785	LYS
84	CD	163	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (132) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	132	ASN
5	LB	204	GLN
5	LB	213	GLN
5	LB	315	ASN
6	LC	50	GLN
6	LC	317	ASN
7	LD	111	ASN
7	LD	191	ASN
7	LD	250	ASN
7	LD	282	GLN
8	LE	190	HIS
9	LF	39	GLN
10	LG	141	ASN
10	LG	225	ASN
11	LH	7	ASN
11	LH	106	GLN

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Mol	Chain	Res	Type
12	LI	203	HIS
13	LJ	104	ASN
13	LJ	112	HIS
14	LL	205	GLN
15	LM	34	ASN
15	LM	125	ASN
16	LN	196	ASN
17	LO	184	ASN
18	LP	34	GLN
18	LP	64	ASN
18	LP	80	GLN
18	LP	97	ASN
19	LQ	44	ASN
19	LQ	125	GLN
20	LR	40	GLN
20	LR	86	ASN
20	LR	130	ASN
20	LR	143	HIS
21	LS	77	ASN
21	LS	122	HIS
25	LW	50	ASN
25	LW	95	ASN
29	La	34	ASN
29	La	85	GLN
30	Lb	60	ASN
31	Lc	15	ASN
33	Le	23	HIS
33	Le	43	ASN
34	Lf	56	ASN
34	Lf	80	ASN
37	Li	26	HIS
38	Lj	57	ASN
38	Lj	66	HIS
43	Lo	45	GLN
43	Lo	102	GLN
44	Lp	56	HIS
45	Lr	100	ASN
46	Lz	72	GLN
46	Lz	73	HIS
46	Lz	96	ASN
48	SA	131	HIS
49	SB	43	ASN

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Mol	Chain	Res	Type
49	SB	124	HIS
49	SB	149	GLN
50	SD	101	GLN
50	SD	145	GLN
51	SE	138	HIS
51	SE	157	ASN
51	SE	209	HIS
51	SE	232	ASN
52	SF	79	HIS
52	SF	82	ASN
52	SF	118	ASN
52	SF	148	ASN
52	SF	203	ASN
53	SH	114	GLN
53	SH	165	ASN
54	SI	35	ASN
54	SI	64	ASN
54	SI	84	ASN
55	SK	32	HIS
55	SK	39	ASN
55	SK	42	ASN
55	SK	44	HIS
57	SP	24	GLN
57	SP	41	GLN
59	SR	31	ASN
59	SR	62	GLN
59	SR	83	ASN
60	SS	19	ASN
60	SS	72	GLN
60	SS	105	ASN
62	SU	18	HIS
62	SU	100	GLN
63	SV	35	ASN
64	SX	97	ASN
67	Sd	5	GLN
68	Sg	76	GLN
68	Sg	159	ASN
68	Sg	162	ASN
68	Sg	181	ASN
69	SC	134	ASN
69	SC	178	HIS
70	SG	81	HIS

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Mol	Chain	Res	Type
70	SG	110	ASN
71	SJ	75	ASN
71	SJ	125	HIS
71	SJ	177	ASN
71	SJ	182	GLN
72	SM	28	HIS
73	SN	49	GLN
74	SO	32	HIS
75	SW	16	ASN
75	SW	70	ASN
76	SY	112	ASN
76	SY	124	ASN
77	SZ	64	ASN
77	SZ	89	GLN
80	Sf	111	ASN
81	CA	7	GLN
81	CA	10	GLN
81	CA	162	GLN
81	CA	171	ASN
81	CA	178	ASN
81	CA	203	GLN
81	CA	242	GLN
82	CB	3	ASN
82	CB	8	GLN
82	CB	30	HIS
82	CB	84	ASN
82	CB	108	HIS
82	CB	184	ASN
82	CB	186	ASN
82	CB	202	ASN
82	CB	270	ASN
82	CB	705	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3705/5070 (73%)	969 (26%)	19 (0%)
2	L7	119/121 (98%)	15 (12%)	0
3	L8	155/157 (98%)	33 (21%)	1 (0%)
47	S2	1717/1869 (91%)	469 (27%)	8 (0%)
83	CC	74/75 (98%)	29 (39%)	3 (4%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	5770/7292 (79%)	1515 (26%)	31 (0%)

All (1515) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	15	A
1	L5	17	A
1	L5	25	A
1	L5	26	C
1	L5	30	C
1	L5	39	A
1	L5	48	G
1	L5	56	A
1	L5	59	A
1	L5	64	A
1	L5	65	A
1	L5	69	A
1	L5	72	C
1	L5	73	A
1	L5	74	G
1	L5	84	A
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	119	G
1	L5	120	A
1	L5	122	U
1	L5	132	G
1	L5	133	C
1	L5	134	G
1	L5	135	G
1	L5	136	C
1	L5	137	G
1	L5	145	G
1	L5	152	U
1	L5	159	C
1	L5	164	G
1	L5	165	A

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Mol	Chain	Res	Type
1	L5	166	C
1	L5	172	C
1	L5	181	C
1	L5	182	G
1	L5	183	C
1	L5	184	U
1	L5	185	C
1	L5	187	U
1	L5	188	G
1	L5	189	G
1	L5	200	U
1	L5	207	G
1	L5	209	U
1	L5	216	C
1	L5	218	A
1	L5	219	G
1	L5	220	C
1	L5	232	G
1	L5	233	U
1	L5	234	G
1	L5	255	C
1	L5	256	G
1	L5	258	G
1	L5	260	C
1	L5	261	G
1	L5	263	G
1	L5	264	C
1	L5	265	C
1	L5	266	C
1	L5	267	G
1	L5	269	G
1	L5	276	C
1	L5	280	G
1	L5	292	G
1	L5	297	U
1	L5	306	A
1	L5	315	G
1	L5	316	U
1	L5	340	C
1	L5	349	A
1	L5	350	C
1	L5	354	U

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Mol	Chain	Res	Type
1	L5	355	A
1	L5	373	G
1	L5	387	G
1	L5	388	A
1	L5	396	A
1	L5	406	C
1	L5	407	A
1	L5	408	A
1	L5	409	G
1	L5	410	A
1	L5	411	G
1	L5	412	G
1	L5	431	G
1	L5	432	U
1	L5	438	G
1	L5	440	U
1	L5	449	C
1	L5	450	G
1	L5	452	A
1	L5	453	G
1	L5	454	U
1	L5	456	C
1	L5	457	G
1	L5	465	G
1	L5	467	U
1	L5	468	U
1	L5	472	C
1	L5	479	G
1	L5	484	U
1	L5	485	C
1	L5	486	C
1	L5	489	C
1	L5	493	G
1	L5	494	U
1	L5	497	G
1	L5	498	C
1	L5	499	G
1	L5	500	G
1	L5	501	C
1	L5	502	C
1	L5	503	C
1	L5	504	G

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Mol	Chain	Res	Type
1	L5	505	G
1	L5	506	C
1	L5	509	A
1	L5	510	U
1	L5	513	U
1	L5	514	U
1	L5	516	C
1	L5	517	C
1	L5	518	G
1	L5	643	C
1	L5	645	G
1	L5	646	G
1	L5	655	C
1	L5	657	C
1	L5	658	C
1	L5	659	G
1	L5	665	C
1	L5	666	G
1	L5	667	A
1	L5	668	C
1	L5	669	C
1	L5	672	C
1	L5	673	C
1	L5	674	G
1	L5	685	C
1	L5	686	A
1	L5	687	U
1	L5	688	U
1	L5	696	C
1	L5	700	G
1	L5	703	G
1	L5	704	C
1	L5	731	G
1	L5	738	C
1	L5	739	G
1	L5	740	G
1	L5	742	G
1	L5	753	C
1	L5	754	U
1	L5	757	G
1	L5	758	G
1	L5	759	G

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Mol	Chain	Res	Type
1	L5	760	G
1	L5	904	C
1	L5	906	C
1	L5	907	C
1	L5	913	U
1	L5	914	U
1	L5	915	A
1	L5	917	A
1	L5	918	G
1	L5	923	C
1	L5	924	C
1	L5	926	G
1	L5	932	A
1	L5	933	G
1	L5	935	A
1	L5	936	C
1	L5	937	U
1	L5	941	C
1	L5	943	A
1	L5	945	U
1	L5	946	C
1	L5	956	A
1	L5	959	G
1	L5	960	A
1	L5	961	G
1	L5	962	C
1	L5	963	G
1	L5	965	G
1	L5	966	A
1	L5	967	C
1	L5	970	G
1	L5	971	U
1	L5	982	U
1	L5	985	C
1	L5	988	C
1	L5	989	U
1	L5	990	C
1	L5	992	C
1	L5	993	G
1	L5	995	C
1	L5	996	G
1	L5	1048	G

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Mol	Chain	Res	Type
1	L5	1049	C
1	L5	1050	C
1	L5	1051	G
1	L5	1066	G
1	L5	1070	G
1	L5	1074	G
1	L5	1075	G
1	L5	1082	C
1	L5	1083	U
1	L5	1095	A
1	L5	1168	G
1	L5	1169	G
1	L5	1170	G
1	L5	1171	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	1202	C
1	L5	1203	G
1	L5	1204	C
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	1218	G
1	L5	1219	G
1	L5	1222	A
1	L5	1235	G
1	L5	1241	C
1	L5	1242	G
1	L5	1243	C
1	L5	1246	G
1	L5	1247	U
1	L5	1253	G

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Mol	Chain	Res	Type
1	L5	1254	A
1	L5	1255	A
1	L5	1257	A
1	L5	1258	G
1	L5	1260	G
1	L5	1262	G
1	L5	1266	G
1	L5	1267	C
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	1277	G
1	L5	1280	C
1	L5	1284	G
1	L5	1287	G
1	L5	1294	A
1	L5	1295	C
1	L5	1296	G
1	L5	1301	C
1	L5	1324	A
1	L5	1326	A
1	L5	1337	A
1	L5	1354	A
1	L5	1358	G
1	L5	1359	G
1	L5	1360	G
1	L5	1365	C
1	L5	1367	C
1	L5	1368	A
1	L5	1377	G
1	L5	1378	C
1	L5	1379	C
1	L5	1381	U
1	L5	1387	A
1	L5	1393	G
1	L5	1394	G
1	L5	1397	A
1	L5	1403	G
1	L5	1404	G

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Mol	Chain	Res	Type
1	L5	1405	C
1	L5	1407	C
1	L5	1409	C
1	L5	1410	U
1	L5	1411	C
1	L5	1412	G
1	L5	1414	C
1	L5	1415	G
1	L5	1417	C
1	L5	1420	A
1	L5	1433	A
1	L5	1437	C
1	L5	1439	C
1	L5	1440	U
1	L5	1442	C
1	L5	1443	A
1	L5	1446	C
1	L5	1447	C
1	L5	1482	G
1	L5	1483	C
1	L5	1493	G
1	L5	1497	A
1	L5	1498	G
1	L5	1502	G
1	L5	1515	A
1	L5	1517	G
1	L5	1518	A
1	L5	1519	C
1	L5	1534	A
1	L5	1547	A
1	L5	1566	C
1	L5	1578	U
1	L5	1586	G
1	L5	1591	U
1	L5	1596	U
1	L5	1612	G
1	L5	1613	A
1	L5	1624	G
1	L5	1625	G
1	L5	1631	A
1	L5	1633	G
1	L5	1634	A

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Mol	Chain	Res	Type
1	L5	1638	A
1	L5	1641	G
1	L5	1642	A
1	L5	1654	G
1	L5	1660	U
1	L5	1661	C
1	L5	1670	G
1	L5	1676	C
1	L5	1677	U
1	L5	1678	C
1	L5	1681	G
1	L5	1691	G
1	L5	1694	C
1	L5	1697	G
1	L5	1699	A
1	L5	1700	G
1	L5	1703	C
1	L5	1704	C
1	L5	1705	G
1	L5	1707	C
1	L5	1709	C
1	L5	1715	C
1	L5	1717	C
1	L5	1718	C
1	L5	1719	A
1	L5	1731	C
1	L5	1734	G
1	L5	1740	C
1	L5	1741	G
1	L5	1742	A
1	L5	1750	G
1	L5	1753	G
1	L5	1755	C
1	L5	1757	U
1	L5	1758	G
1	L5	1760	G
1	L5	1761	G
1	L5	1762	C
1	L5	1763	C
1	L5	1765	A
1	L5	1766	A
1	L5	1767	A

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Mol	Chain	Res	Type
1	L5	1768	C
1	L5	1770	A
1	L5	1772	C
1	L5	1773	U
1	L5	1775	A
1	L5	1776	A
1	L5	1787	A
1	L5	1792	U
1	L5	1797	G
1	L5	1804	A
1	L5	1806	G
1	L5	1810	G
1	L5	1815	G
1	L5	1820	C
1	L5	1821	G
1	L5	1822	U
1	L5	1836	G
1	L5	1837	A
1	L5	1842	G
1	L5	1843	A
1	L5	1855	G
1	L5	1869	G
1	L5	1878	G
1	L5	1882	U
1	L5	1892	A
1	L5	1897	A
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	1931	C
1	L5	1932	A
1	L5	1935	C
1	L5	1936	C
1	L5	1940	G
1	L5	1945	G
1	L5	1947	U
1	L5	1948	G
1	L5	1949	U
1	L5	1951	G

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Mol	Chain	Res	Type
1	L5	1959	U
1	L5	1960	A
1	L5	1961	G
1	L5	1962	A
1	L5	1966	C
1	L5	1967	A
1	L5	1968	G
1	L5	1970	A
1	L5	1971	C
1	L5	1972	G
1	L5	1974	U
1	L5	1975	G
1	L5	1976	G
1	L5	1977	C
1	L5	1979	A
1	L5	1980	U
1	L5	1981	G
1	L5	1982	G
1	L5	1983	A
1	L5	1985	G
1	L5	1986	U
1	L5	1987	C
1	L5	1988	G
1	L5	1989	G
1	L5	1990	A
1	L5	1991	A
1	L5	1992	U
1	L5	1993	C
1	L5	1994	C
1	L5	1995	G
1	L5	1996	C
1	L5	1997	U
1	L5	1998	A
1	L5	1999	A
1	L5	2000	G
1	L5	2001	G
1	L5	2002	A
1	L5	2003	G
1	L5	2004	U
1	L5	2005	G
1	L5	2006	U
1	L5	2007	G

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Mol	Chain	Res	Type
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	2014	C
1	L5	2015	U
1	L5	2018	C
1	L5	2020	U
1	L5	2021	G
1	L5	2024	G
1	L5	2025	A
1	L5	2026	A
1	L5	2034	G
1	L5	2044	U
1	L5	2046	G
1	L5	2048	U
1	L5	2054	U
1	L5	2055	G
1	L5	2056	G
1	L5	2069	A
1	L5	2084	C
1	L5	2085	G
1	L5	2089	G
1	L5	2091	C
1	L5	2092	G
1	L5	2093	A
1	L5	2095	A
1	L5	2096	G
1	L5	2097	U
1	L5	2098	G
1	L5	2100	A
1	L5	2101	C
1	L5	2102	G
1	L5	2107	C
1	L5	2108	G
1	L5	2111	G
1	L5	2112	G
1	L5	2250	C
1	L5	2252	G
1	L5	2253	A

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Mol	Chain	Res	Type
1	L5	2256	C
1	L5	2258	C
1	L5	2259	G
1	L5	2260	C
1	L5	2263	A
1	L5	2277	C
1	L5	2289	C
1	L5	2300	A
1	L5	2301	G
1	L5	2306	G
1	L5	2313	A
1	L5	2316	G
1	L5	2332	A
1	L5	2333	G
1	L5	2348	G
1	L5	2351	C
1	L5	2360	A
1	L5	2364	G
1	L5	2369	U
1	L5	2395	A
1	L5	2396	A
1	L5	2397	G
1	L5	2412	A
1	L5	2417	A
1	L5	2418	A
1	L5	2421	G
1	L5	2425	U
1	L5	2437	C
1	L5	2441	C
1	L5	2450	G
1	L5	2453	A
1	L5	2464	C
1	L5	2465	C
1	L5	2467	U
1	L5	2474	G
1	L5	2475	G
1	L5	2478	C
1	L5	2479	G
1	L5	2483	G
1	L5	2484	A
1	L5	2485	U
1	L5	2487	G

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Mol	Chain	Res	Type
1	L5	2488	C
1	L5	2489	C
1	L5	2490	U
1	L5	2494	U
1	L5	2503	G
1	L5	2504	C
1	L5	2505	C
1	L5	2506	G
1	L5	2513	A
1	L5	2518	G
1	L5	2519	U
1	L5	2537	A
1	L5	2544	G
1	L5	2546	G
1	L5	2547	G
1	L5	2554	U
1	L5	2559	G
1	L5	2560	C
1	L5	2561	C
1	L5	2565	A
1	L5	2567	G
1	L5	2573	A
1	L5	2583	C
1	L5	2586	G
1	L5	2587	A
1	L5	2589	C
1	L5	2601	A
1	L5	2606	G
1	L5	2618	G
1	L5	2638	G
1	L5	2639	U
1	L5	2652	G
1	L5	2653	C
1	L5	2661	U
1	L5	2662	G
1	L5	2664	G
1	L5	2669	C
1	L5	2675	G
1	L5	2676	A
1	L5	2686	G
1	L5	2687	U
1	L5	2695	A

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Mol	Chain	Res	Type
1	L5	2696	A
1	L5	2707	U
1	L5	2708	U
1	L5	2709	C
1	L5	2711	G
1	L5	2713	C
1	L5	2721	G
1	L5	2724	G
1	L5	2725	A
1	L5	2726	G
1	L5	2738	C
1	L5	2739	C
1	L5	2742	G
1	L5	2743	A
1	L5	2746	A
1	L5	2756	G
1	L5	2761	U
1	L5	2763	U
1	L5	2764	A
1	L5	2769	U
1	L5	2770	C
1	L5	2787	A
1	L5	2788	U
1	L5	2790	U
1	L5	2806	A
1	L5	2815	A
1	L5	2825	A
1	L5	2826	U
1	L5	2827	G
1	L5	2835	A
1	L5	2838	G
1	L5	2848	G
1	L5	2855	G
1	L5	2867	C
1	L5	2877	G
1	L5	2892	C
1	L5	2895	A
1	L5	2897	G
1	L5	2900	U
1	L5	2902	G
1	L5	2903	G
1	L5	2904	U

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Mol	Chain	Res	Type
1	L5	2905	C
1	L5	2906	G
1	L5	2908	U
1	L5	2909	C
1	L5	3585	G
1	L5	3588	C
1	L5	3590	G
1	L5	3591	C
1	L5	3594	C
1	L5	3595	U
1	L5	3596	A
1	L5	3597	G
1	L5	3604	A
1	L5	3605	C
1	L5	3606	U
1	L5	3615	G
1	L5	3616	U
1	L5	3618	C
1	L5	3626	G
1	L5	3630	A
1	L5	3635	A
1	L5	3644	U
1	L5	3646	A
1	L5	3662	A
1	L5	3664	G
1	L5	3670	C
1	L5	3672	G
1	L5	3673	C
1	L5	3674	G
1	L5	3711	A
1	L5	3713	U
1	L5	3714	G
1	L5	3727	A
1	L5	3729	U
1	L5	3735	G
1	L5	3736	A
1	L5	3748	A
1	L5	3750	G
1	L5	3753	G
1	L5	3757	G
1	L5	3758	U
1	L5	3759	A

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Mol	Chain	Res	Type
1	L5	3760	A
1	L5	3761	C
1	L5	3769	C
1	L5	3771	C
1	L5	3775	A
1	L5	3776	G
1	L5	3777	G
1	L5	3786	U
1	L5	3802	U
1	L5	3811	G
1	L5	3812	C
1	L5	3814	U
1	L5	3817	A
1	L5	3818	U
1	L5	3819	G
1	L5	3823	G
1	L5	3838	U
1	L5	3839	G
1	L5	3840	U
1	L5	3841	C
1	L5	3851	U
1	L5	3867	A
1	L5	3876	A
1	L5	3877	A
1	L5	3878	C
1	L5	3879	G
1	L5	3881	G
1	L5	3885	G
1	L5	3887	C
1	L5	3890	A
1	L5	3892	U
1	L5	3897	G
1	L5	3901	A
1	L5	3906	A
1	L5	3907	G
1	L5	3908	A
1	L5	3915	U
1	L5	3916	G
1	L5	3938	G
1	L5	3939	G
1	L5	3942	A
1	L5	3944	G

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Mol	Chain	Res	Type
1	L5	3947	A
1	L5	3948	C
1	L5	3949	A
1	L5	3950	U
1	L5	3951	G
1	L5	3953	G
1	L5	3955	G
1	L5	3956	G
1	L5	3957	U
1	L5	3958	G
1	L5	3959	U
1	L5	3960	A
1	L5	3962	A
1	L5	3963	A
1	L5	3964	U
1	L5	3965	A
1	L5	3966	A
1	L5	3967	G
1	L5	3969	G
1	L5	3970	G
1	L5	3971	G
1	L5	3972	A
1	L5	3973	G
1	L5	3974	G
1	L5	3975	C
1	L5	3977	C
1	L5	4034	G
1	L5	4035	G
1	L5	4036	G
1	L5	4038	C
1	L5	4039	G
1	L5	4041	C
1	L5	4042	G
1	L5	4043	G
1	L5	4044	U
1	L5	4045	G
1	L5	4046	A
1	L5	4048	A
1	L5	4049	U
1	L5	4051	C
1	L5	4052	C
1	L5	4053	A

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Mol	Chain	Res	Type
1	L5	4054	C
1	L5	4055	U
1	L5	4056	A
1	L5	4057	C
1	L5	4058	U
1	L5	4059	C
1	L5	4062	A
1	L5	4063	U
1	L5	4064	C
1	L5	4065	G
1	L5	4069	U
1	L5	4076	G
1	L5	4084	G
1	L5	4086	G
1	L5	4097	G
1	L5	4099	G
1	L5	4101	C
1	L5	4102	C
1	L5	4104	G
1	L5	4107	G
1	L5	4108	G
1	L5	4110	C
1	L5	4111	U
1	L5	4113	U
1	L5	4114	C
1	L5	4115	G
1	L5	4116	C
1	L5	4117	U
1	L5	4119	C
1	L5	4121	G
1	L5	4127	A
1	L5	4133	C
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	4162	C
1	L5	4163	U
1	L5	4168	G
1	L5	4170	A

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Mol	Chain	Res	Type
1	L5	4183	G
1	L5	4191	G
1	L5	4196	G
1	L5	4197	G
1	L5	4203	A
1	L5	4222	G
1	L5	4228	G
1	L5	4229	U
1	L5	4232	U
1	L5	4233	A
1	L5	4249	G
1	L5	4251	A
1	L5	4254	G
1	L5	4255	A
1	L5	4256	A
1	L5	4257	A
1	L5	4265	U
1	L5	4268	A
1	L5	4273	A
1	L5	4281	A
1	L5	4291	G
1	L5	4304	A
1	L5	4305	G
1	L5	4306	U
1	L5	4314	C
1	L5	4319	C
1	L5	4329	G
1	L5	4330	G
1	L5	4332	C
1	L5	4339	A
1	L5	4349	C
1	L5	4371	G
1	L5	4373	G
1	L5	4374	U
1	L5	4376	A
1	L5	4377	G
1	L5	4378	A
1	L5	4379	A
1	L5	4380	A
1	L5	4387	C
1	L5	4391	G
1	L5	4394	A

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Mol	Chain	Res	Type
1	L5	4405	G
1	L5	4422	A
1	L5	4426	C
1	L5	4448	G
1	L5	4449	A
1	L5	4452	U
1	L5	4453	C
1	L5	4463	U
1	L5	4464	A
1	L5	4466	C
1	L5	4475	G
1	L5	4488	A
1	L5	4500	U
1	L5	4512	U
1	L5	4513	A
1	L5	4518	A
1	L5	4519	C
1	L5	4524	G
1	L5	4531	U
1	L5	4545	G
1	L5	4548	A
1	L5	4549	G
1	L5	4556	U
1	L5	4560	C
1	L5	4567	G
1	L5	4569	U
1	L5	4573	G
1	L5	4575	G
1	L5	4584	A
1	L5	4589	A
1	L5	4590	A
1	L5	4600	G
1	L5	4617	G
1	L5	4626	A
1	L5	4635	A
1	L5	4636	U
1	L5	4637	G
1	L5	4647	G
1	L5	4652	G
1	L5	4656	A
1	L5	4658	G
1	L5	4659	G

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Mol	Chain	Res	Type
1	L5	4670	C
1	L5	4672	A
1	L5	4679	G
1	L5	4684	A
1	L5	4687	A
1	L5	4694	G
1	L5	4695	C
1	L5	4707	A
1	L5	4708	A
1	L5	4709	U
1	L5	4719	G
1	L5	4720	C
1	L5	4733	C
1	L5	4734	A
1	L5	4735	G
1	L5	4741	C
1	L5	4742	G
1	L5	4745	G
1	L5	4747	C
1	L5	4750	G
1	L5	4754	G
1	L5	4757	C
1	L5	4759	C
1	L5	4761	G
1	L5	4765	G
1	L5	4771	C
1	L5	4772	C
1	L5	4775	C
1	L5	4776	G
1	L5	4859	C
1	L5	4860	G
1	L5	4863	G
1	L5	4870	G
1	L5	4871	C
1	L5	4875	G
1	L5	4877	G
1	L5	4881	U
1	L5	4882	U
1	L5	4883	C
1	L5	4887	C
1	L5	4889	G
1	L5	4891	G

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Mol	Chain	Res	Type
1	L5	4895	C
1	L5	4896	G
1	L5	4900	C
1	L5	4901	G
1	L5	4910	G
1	L5	4911	A
1	L5	4912	G
1	L5	4914	C
1	L5	4922	C
1	L5	4923	C
1	L5	4925	U
1	L5	4927	G
1	L5	4928	C
1	L5	4931	G
1	L5	4934	A
1	L5	4940	C
1	L5	4941	G
1	L5	4943	A
1	L5	4947	U
1	L5	4951	G
1	L5	4960	G
1	L5	4961	G
1	L5	4963	G
1	L5	4966	A
1	L5	4973	U
1	L5	4976	U
1	L5	4985	U
1	L5	4988	U
1	L5	4989	U
1	L5	4990	C
1	L5	4991	U
1	L5	5006	U
1	L5	5009	G
1	L5	5013	C
1	L5	5014	A
1	L5	5017	G
1	L5	5024	C
1	L5	5025	C
1	L5	5028	G
1	L5	5029	C
1	L5	5031	G
1	L5	5034	A

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Mol	Chain	Res	Type
1	L5	5040	U
1	L5	5041	G
1	L5	5047	C
1	L5	5050	C
1	L5	5054	C
1	L5	5055	G
1	L5	5061	A
1	L5	5069	U
2	L7	4	U
2	L7	5	A
2	L7	7	G
2	L7	22	A
2	L7	24	C
2	L7	33	U
2	L7	38	U
2	L7	42	A
2	L7	53	U
2	L7	54	A
2	L7	63	C
2	L7	64	G
2	L7	66	G
2	L7	100	A
2	L7	110	G
3	L8	2	G
3	L8	25	G
3	L8	34	U
3	L8	35	C
3	L8	38	U
3	L8	39	G
3	L8	48	A
3	L8	52	A
3	L8	59	A
3	L8	60	G
3	L8	62	A
3	L8	63	U
3	L8	68	G
3	L8	82	A
3	L8	83	C
3	L8	84	A
3	L8	85	U
3	L8	86	U
3	L8	87	G

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Mol	Chain	Res	Type
3	L8	94	G
3	L8	103	A
3	L8	105	C
3	L8	110	U
3	L8	111	U
3	L8	114	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	150	C
3	L8	151	G
47	S2	14	C
47	S2	17	C
47	S2	20	G
47	S2	25	A
47	S2	33	G
47	S2	41	G
47	S2	42	A
47	S2	46	A
47	S2	49	C
47	S2	56	G
47	S2	59	U
47	S2	62	G
47	S2	64	A
47	S2	67	C
47	S2	68	A
47	S2	72	C
47	S2	73	C
47	S2	74	G
47	S2	76	U
47	S2	92	A
47	S2	103	A
47	S2	113	G
47	S2	115	U
47	S2	116	U
47	S2	126	G
47	S2	129	C
47	S2	130	G
47	S2	139	C

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Mol	Chain	Res	Type
47	S2	143	U
47	S2	147	A
47	S2	149	A
47	S2	154	U
47	S2	158	A
47	S2	159	A
47	S2	160	U
47	S2	161	U
47	S2	162	C
47	S2	163	U
47	S2	175	A
47	S2	179	C
47	S2	184	G
47	S2	188	C
47	S2	190	G
47	S2	196	C
47	S2	197	U
47	S2	198	U
47	S2	199	C
47	S2	200	G
47	S2	203	G
47	S2	204	G
47	S2	206	G
47	S2	207	G
47	S2	208	G
47	S2	213	G
47	S2	214	U
47	S2	291	G
47	S2	292	A
47	S2	293	C
47	S2	295	C
47	S2	302	A
47	S2	306	C
47	S2	308	G
47	S2	309	G
47	S2	310	C
47	S2	311	C
47	S2	312	G
47	S2	313	A
47	S2	316	G
47	S2	318	A
47	S2	319	C

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Mol	Chain	Res	Type
47	S2	320	G
47	S2	322	C
47	S2	323	C
47	S2	324	C
47	S2	325	C
47	S2	326	C
47	S2	327	G
47	S2	328	U
47	S2	329	G
47	S2	331	C
47	S2	332	G
47	S2	339	A
47	S2	340	C
47	S2	360	A
47	S2	362	C
47	S2	364	A
47	S2	365	C
47	S2	367	U
47	S2	368	U
47	S2	370	G
47	S2	374	G
47	S2	380	G
47	S2	383	G
47	S2	385	G
47	S2	386	C
47	S2	399	C
47	S2	407	G
47	S2	408	A
47	S2	409	C
47	S2	417	C
47	S2	418	A
47	S2	421	G
47	S2	426	A
47	S2	436	G
47	S2	438	G
47	S2	448	A
47	S2	449	A
47	S2	450	C
47	S2	452	G
47	S2	464	A
47	S2	465	A
47	S2	466	G

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Mol	Chain	Res	Type
47	S2	467	G
47	S2	471	G
47	S2	472	C
47	S2	473	A
47	S2	474	G
47	S2	476	A
47	S2	482	G
47	S2	483	C
47	S2	487	U
47	S2	488	U
47	S2	492	C
47	S2	502	C
47	S2	517	C
47	S2	525	A
47	S2	530	U
47	S2	531	A
47	S2	532	C
47	S2	533	A
47	S2	534	G
47	S2	536	A
47	S2	537	C
47	S2	538	U
47	S2	540	U
47	S2	542	U
47	S2	546	G
47	S2	547	G
47	S2	548	C
47	S2	551	U
47	S2	552	G
47	S2	554	A
47	S2	555	A
47	S2	556	U
47	S2	557	U
47	S2	558	G
47	S2	559	G
47	S2	563	G
47	S2	564	A
47	S2	576	A
47	S2	581	U
47	S2	583	A
47	S2	587	A
47	S2	588	G

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Mol	Chain	Res	Type
47	S2	589	G
47	S2	591	U
47	S2	597	G
47	S2	600	G
47	S2	604	A
47	S2	607	U
47	S2	608	C
47	S2	614	C
47	S2	617	G
47	S2	622	C
47	S2	623	G
47	S2	627	U
47	S2	630	U
47	S2	631	U
47	S2	643	A
47	S2	644	G
47	S2	659	G
47	S2	660	C
47	S2	663	C
47	S2	664	A
47	S2	668	A
47	S2	671	A
47	S2	672	A
47	S2	673	G
47	S2	684	G
47	S2	687	C
47	S2	688	U
47	S2	689	U
47	S2	690	G
47	S2	692	G
47	S2	693	A
47	S2	696	G
47	S2	697	G
47	S2	698	G
47	S2	732	U
47	S2	734	C
47	S2	736	C
47	S2	738	C
47	S2	739	C
47	S2	749	U
47	S2	751	G
47	S2	752	G

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Mol	Chain	Res	Type
47	S2	753	C
47	S2	788	G
47	S2	791	C
47	S2	792	C
47	S2	794	A
47	S2	798	G
47	S2	810	A
47	S2	811	A
47	S2	821	G
47	S2	822	U
47	S2	823	U
47	S2	827	A
47	S2	830	A
47	S2	834	C
47	S2	835	C
47	S2	836	G
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	847	A
47	S2	869	A
47	S2	870	A
47	S2	872	A
47	S2	874	G
47	S2	877	C
47	S2	880	G
47	S2	882	U
47	S2	883	U
47	S2	886	A
47	S2	887	U
47	S2	888	U
47	S2	889	U
47	S2	891	G
47	S2	892	U
47	S2	896	U
47	S2	897	U
47	S2	898	U
47	S2	899	U
47	S2	900	C

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Mol	Chain	Res	Type
47	S2	901	G
47	S2	903	A
47	S2	909	G
47	S2	910	G
47	S2	913	A
47	S2	914	U
47	S2	919	A
47	S2	920	A
47	S2	930	C
47	S2	933	G
47	S2	934	G
47	S2	943	U
47	S2	950	C
47	S2	958	G
47	S2	963	A
47	S2	969	U
47	S2	970	G
47	S2	971	G
47	S2	972	A
47	S2	990	A
47	S2	992	A
47	S2	999	G
47	S2	1017	U
47	S2	1018	U
47	S2	1023	A
47	S2	1027	A
47	S2	1028	A
47	S2	1033	G
47	S2	1036	A
47	S2	1045	U
47	S2	1061	U
47	S2	1062	A
47	S2	1067	C
47	S2	1080	A
47	S2	1083	A
47	S2	1085	C
47	S2	1088	U
47	S2	1089	G
47	S2	1109	C
47	S2	1110	G
47	S2	1114	U
47	S2	1115	U

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Mol	Chain	Res	Type
47	S2	1116	C
47	S2	1118	C
47	S2	1119	A
47	S2	1121	G
47	S2	1126	G
47	S2	1133	A
47	S2	1138	C
47	S2	1139	C
47	S2	1143	A
47	S2	1150	A
47	S2	1153	C
47	S2	1154	U
47	S2	1161	U
47	S2	1195	A
47	S2	1207	G
47	S2	1208	A
47	S2	1215	C
47	S2	1216	C
47	S2	1217	A
47	S2	1221	G
47	S2	1224	G
47	S2	1227	G
47	S2	1241	A
47	S2	1242	U
47	S2	1243	U
47	S2	1251	A
47	S2	1253	A
47	S2	1256	G
47	S2	1257	G
47	S2	1259	A
47	S2	1265	A
47	S2	1274	G
47	S2	1275	G
47	S2	1283	C
47	S2	1284	A
47	S2	1285	G
47	S2	1286	G
47	S2	1293	A
47	S2	1294	G
47	S2	1295	A
47	S2	1298	G
47	S2	1301	A

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Mol	Chain	Res	Type
47	S2	1302	G
47	S2	1303	C
47	S2	1306	U
47	S2	1308	U
47	S2	1311	C
47	S2	1312	G
47	S2	1318	G
47	S2	1332	A
47	S2	1333	U
47	S2	1342	U
47	S2	1371	U
47	S2	1372	U
47	S2	1378	A
47	S2	1382	A
47	S2	1396	A
47	S2	1401	A
47	S2	1402	A
47	S2	1406	G
47	S2	1408	U
47	S2	1410	C
47	S2	1412	C
47	S2	1415	C
47	S2	1419	C
47	S2	1420	G
47	S2	1421	A
47	S2	1422	G
47	S2	1423	C
47	S2	1424	G
47	S2	1433	C
47	S2	1434	C
47	S2	1435	C
47	S2	1436	C
47	S2	1438	A
47	S2	1446	A
47	S2	1447	G
47	S2	1449	G
47	S2	1454	A
47	S2	1456	G
47	S2	1462	U
47	S2	1463	U
47	S2	1464	C
47	S2	1473	G

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Mol	Chain	Res	Type
47	S2	1487	A
47	S2	1488	C
47	S2	1489	A
47	S2	1490	G
47	S2	1495	G
47	S2	1497	G
47	S2	1498	A
47	S2	1505	U
47	S2	1507	G
47	S2	1508	A
47	S2	1509	U
47	S2	1519	U
47	S2	1520	G
47	S2	1521	C
47	S2	1533	A
47	S2	1537	A
47	S2	1546	G
47	S2	1552	G
47	S2	1553	C
47	S2	1555	U
47	S2	1556	A
47	S2	1558	C
47	S2	1560	U
47	S2	1570	G
47	S2	1573	G
47	S2	1574	C
47	S2	1575	G
47	S2	1580	A
47	S2	1584	G
47	S2	1586	U
47	S2	1587	G
47	S2	1588	A
47	S2	1594	A
47	S2	1598	G
47	S2	1600	G
47	S2	1601	A
47	S2	1606	G
47	S2	1621	U
47	S2	1623	A
47	S2	1632	G
47	S2	1634	A
47	S2	1637	A

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Mol	Chain	Res	Type
47	S2	1638	G
47	S2	1639	G
47	S2	1640	A
47	S2	1648	G
47	S2	1654	G
47	S2	1663	A
47	S2	1665	G
47	S2	1671	G
47	S2	1680	G
47	S2	1686	G
47	S2	1698	C
47	S2	1699	A
47	S2	1700	C
47	S2	1701	C
47	S2	1702	G
47	S2	1715	A
47	S2	1719	A
47	S2	1721	U
47	S2	1722	G
47	S2	1742	C
47	S2	1743	G
47	S2	1744	G
47	S2	1745	A
47	S2	1752	C
47	S2	1753	C
47	S2	1754	G
47	S2	1757	G
47	S2	1758	G
47	S2	1759	G
47	S2	1760	G
47	S2	1761	U
47	S2	1771	G
47	S2	1772	C
47	S2	1773	C
47	S2	1774	C
47	S2	1775	U
47	S2	1777	G
47	S2	1782	G
47	S2	1783	C
47	S2	1784	G
47	S2	1786	U
47	S2	1802	C

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Mol	Chain	Res	Type
47	S2	1805	G
47	S2	1806	A
47	S2	1821	U
47	S2	1822	A
47	S2	1823	A
47	S2	1824	A
47	S2	1825	A
47	S2	1826	G
47	S2	1829	G
47	S2	1830	U
47	S2	1831	A
47	S2	1835	A
47	S2	1838	U
47	S2	1839	U
47	S2	1849	G
47	S2	1852	C
47	S2	1861	G
47	S2	1862	G
47	S2	1863	A
47	S2	1864	U
47	S2	1865	C
83	CC	9	A
83	CC	16	C
83	CC	17	G
83	CC	18	G
83	CC	19	C
83	CC	20	U
83	CC	22	U
83	CC	28	C
83	CC	31	G
83	CC	32	C
83	CC	33	U
83	CC	34	U
83	CC	35	U
83	CC	36	C
83	CC	37	A
83	CC	38	C
83	CC	39	C
83	CC	42	G
83	CC	45	G
83	CC	46	A
83	CC	47	C

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Mol	Chain	Res	Type
83	CC	48	C
83	CC	51	G
83	CC	57	A
83	CC	59	U
83	CC	60	C
83	CC	72	G
83	CC	73	C
83	CC	75	A

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	183	C
1	L5	278	G
1	L5	406	C
1	L5	493	G
1	L5	504	G
1	L5	914	U
1	L5	1082	C
1	L5	1633	G
1	L5	2019	C
1	L5	2033	A
1	L5	2416	G
1	L5	2675	G
1	L5	2760	G
1	L5	2786	C
1	L5	3614	G
1	L5	3673	C
1	L5	4045	G
1	L5	4378	A
1	L5	4913	G
3	L8	83	C
47	S2	112	U
47	S2	291	G
47	S2	417	C
47	S2	420	G
47	S2	563	G
47	S2	668	A
47	S2	688	U
47	S2	1434	C
83	CC	35	U
83	CC	37	A

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Mol	Chain	Res	Type
83	CC	74	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 264 ligands modelled in this entry, 264 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

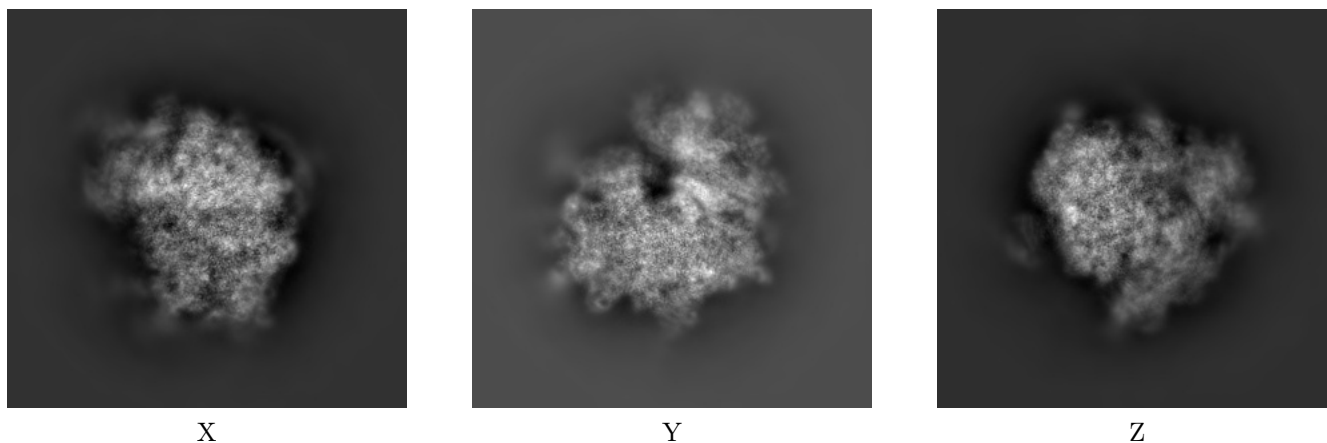
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11100. 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](#)

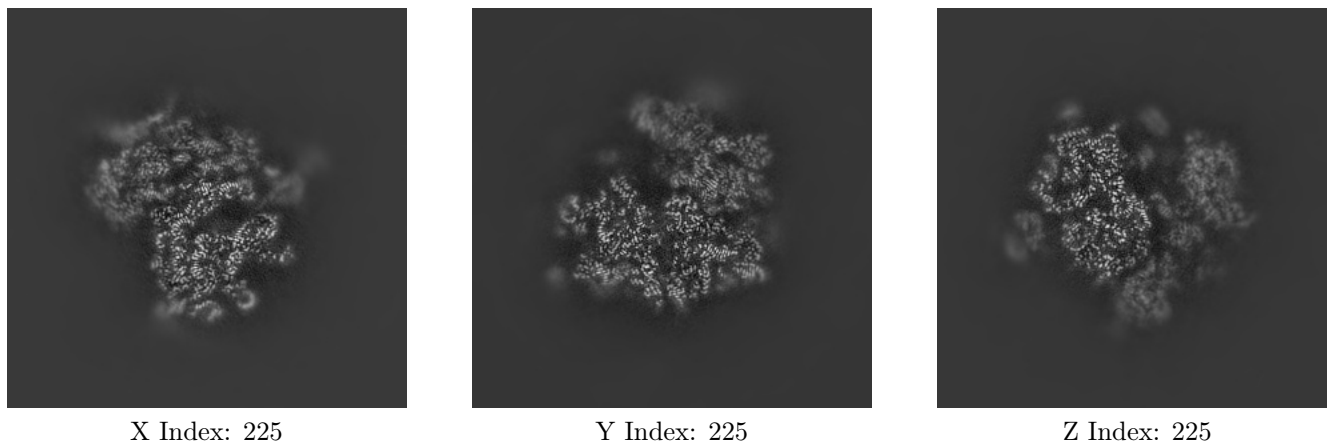
6.1.1 Primary map



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

6.2 Central slices [i](#)

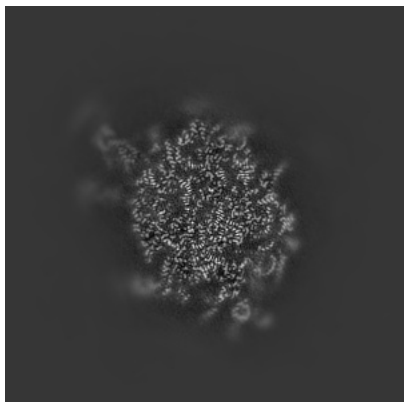
6.2.1 Primary map



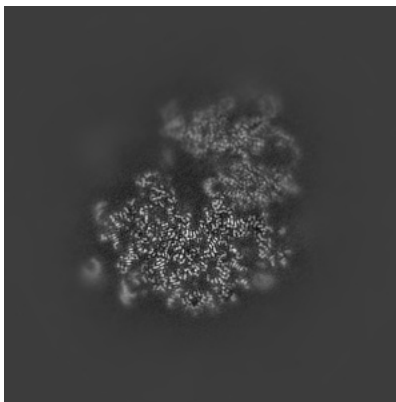
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

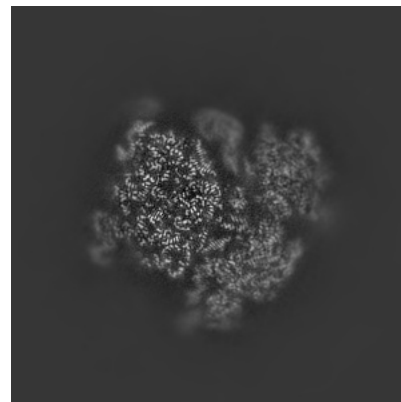
6.3.1 Primary map



X Index: 195



Y Index: 239

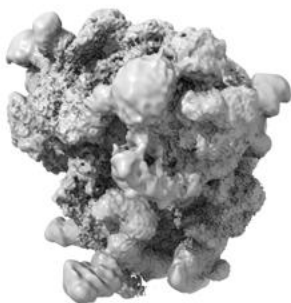


Z Index: 245

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

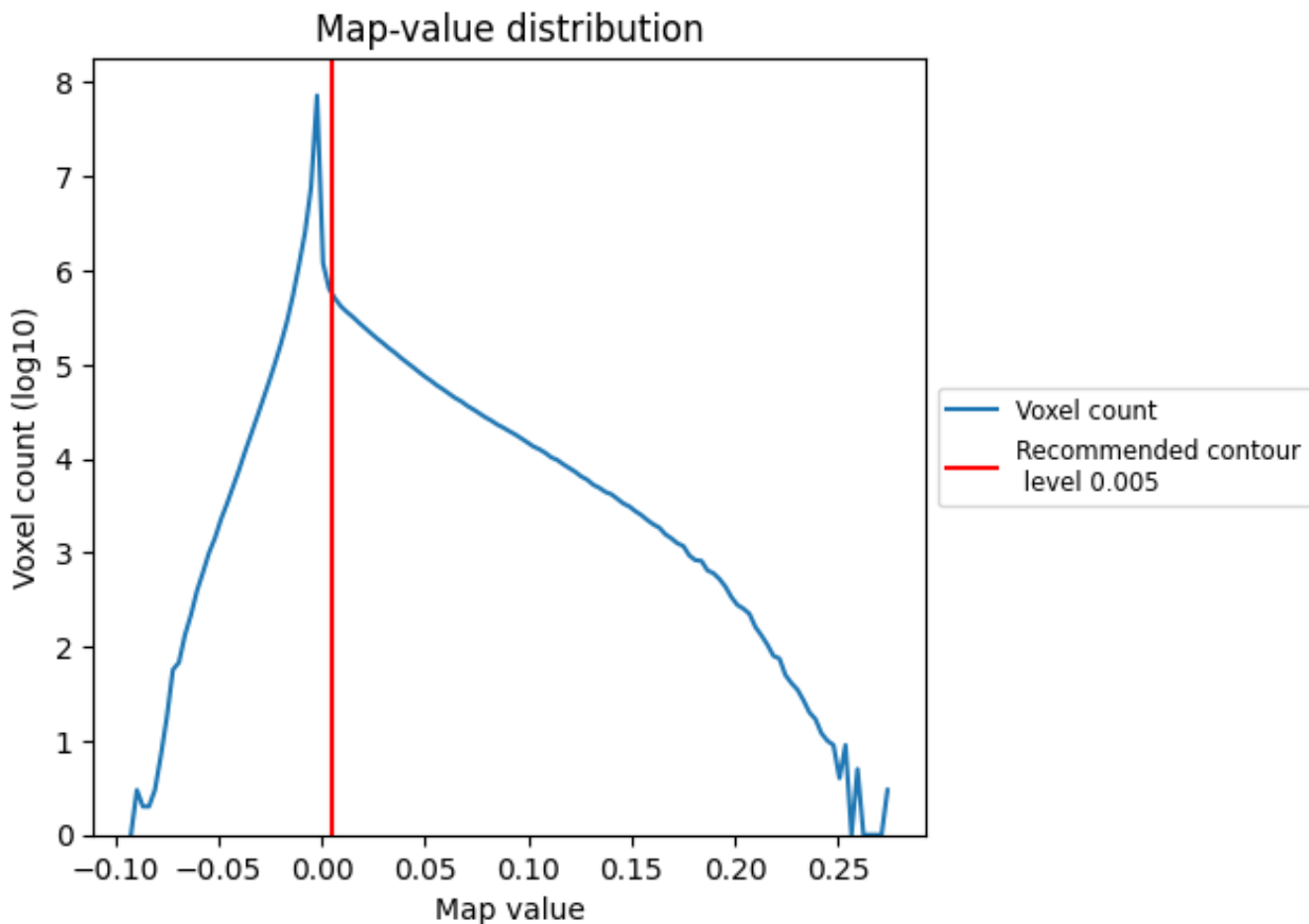
6.5 Mask visualisation

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

7 Map analysis [i](#)

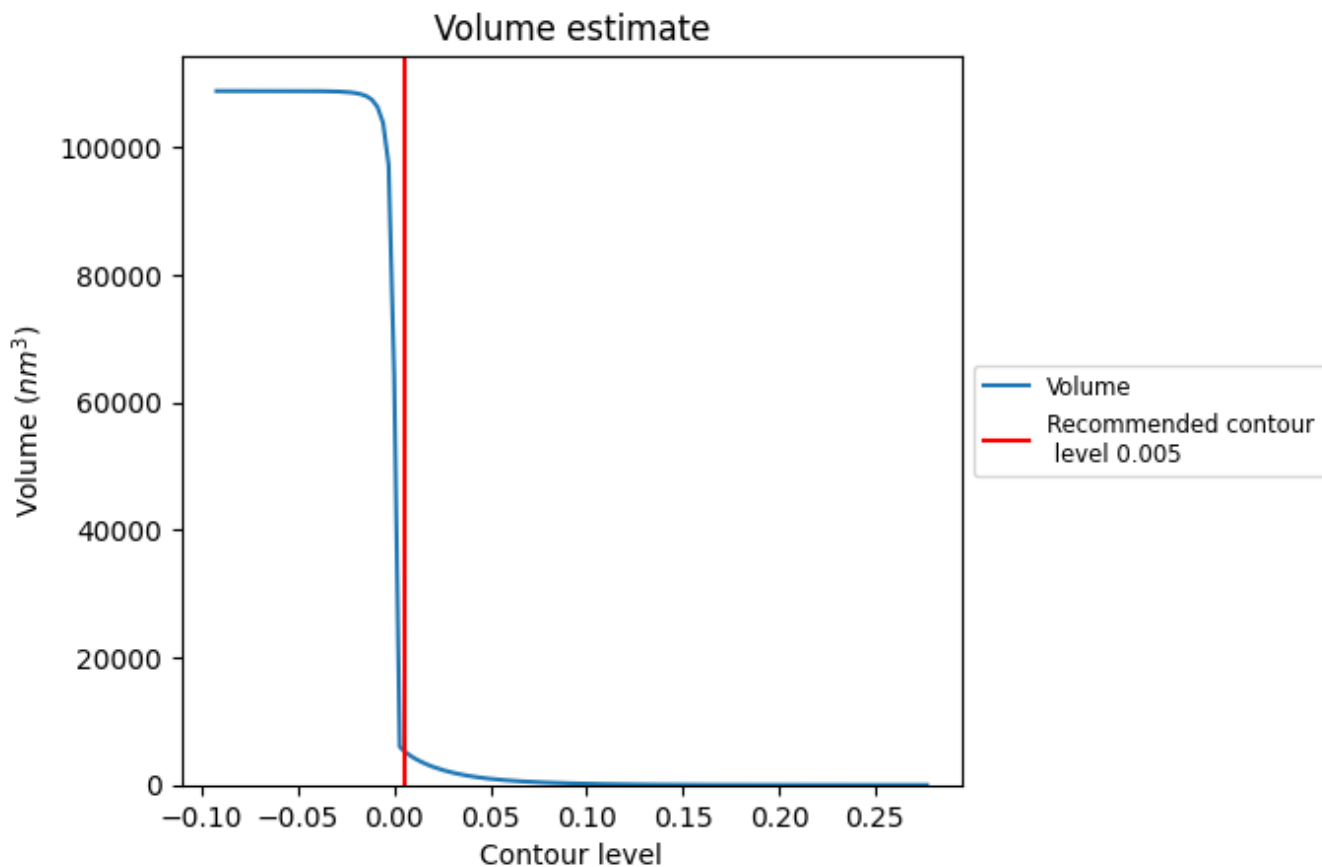
This section contains the results of statistical analysis of the map.

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.

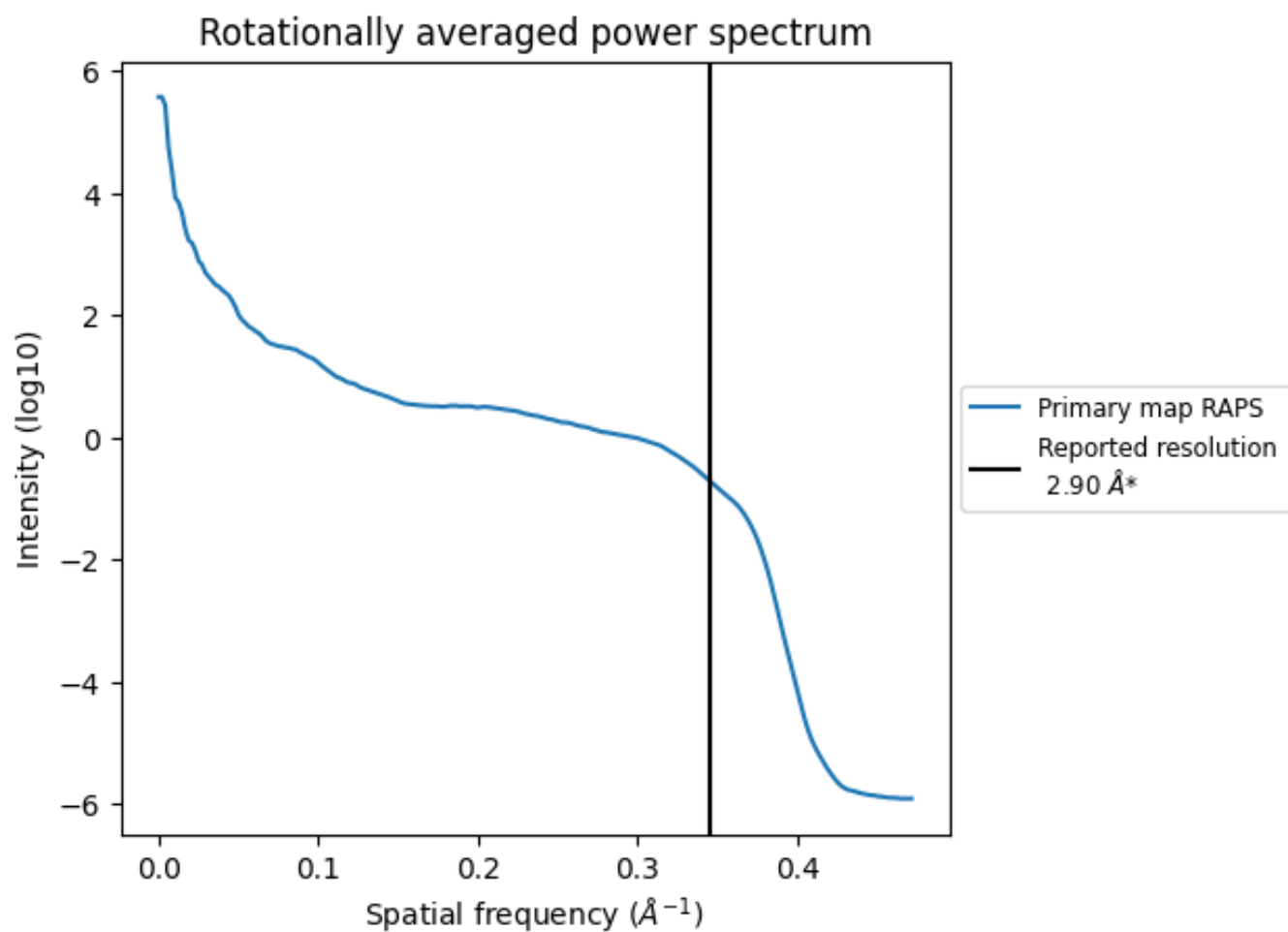
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 5376 nm^3 ; this corresponds to an approximate mass of 4856 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](#)

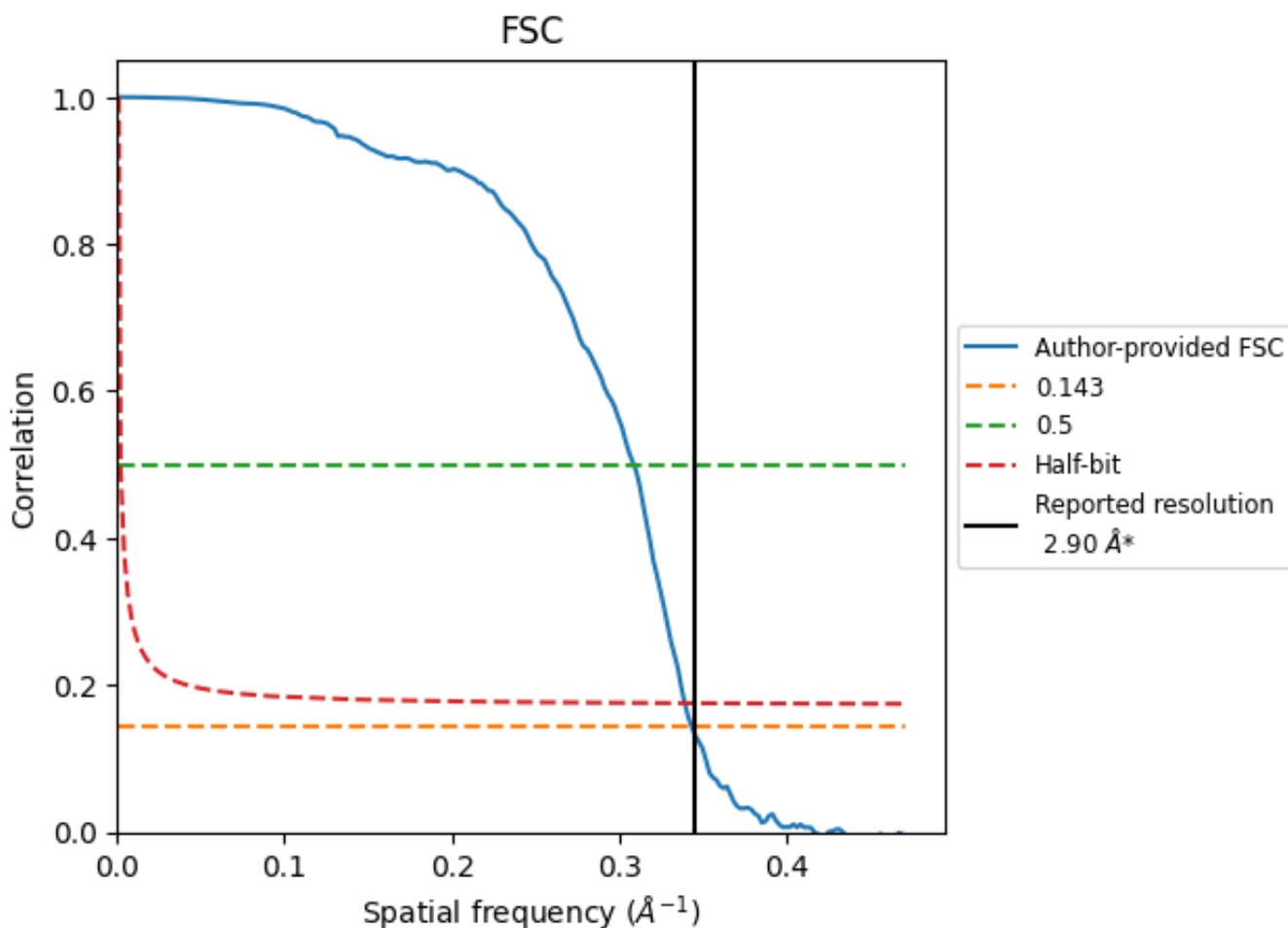


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8 Fourier-Shell correlation [\(i\)](#)

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

8.1 FSC [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

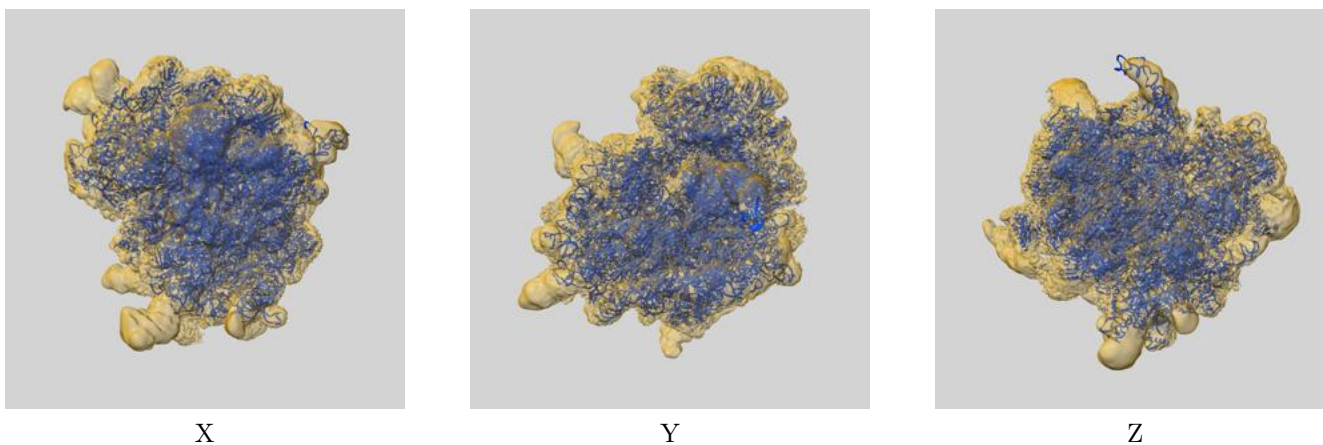
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.91	3.24	2.95
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

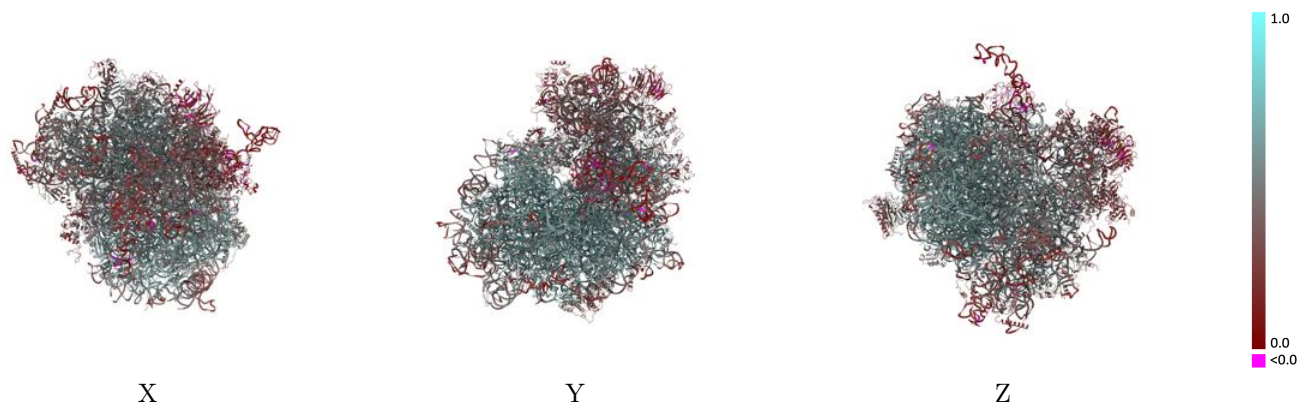
This section contains information regarding the fit between EMDB map EMD-11100 and PDB model 6Z6N. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



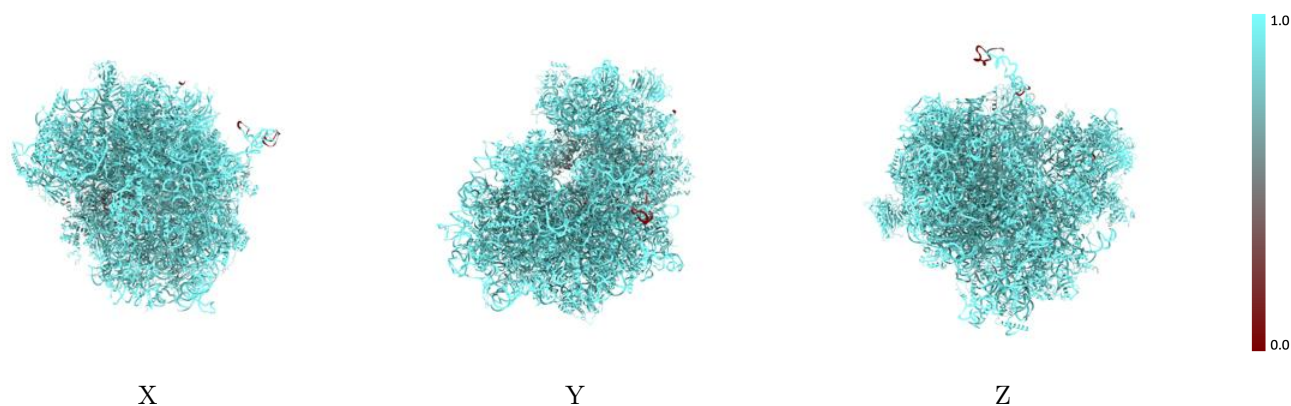
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



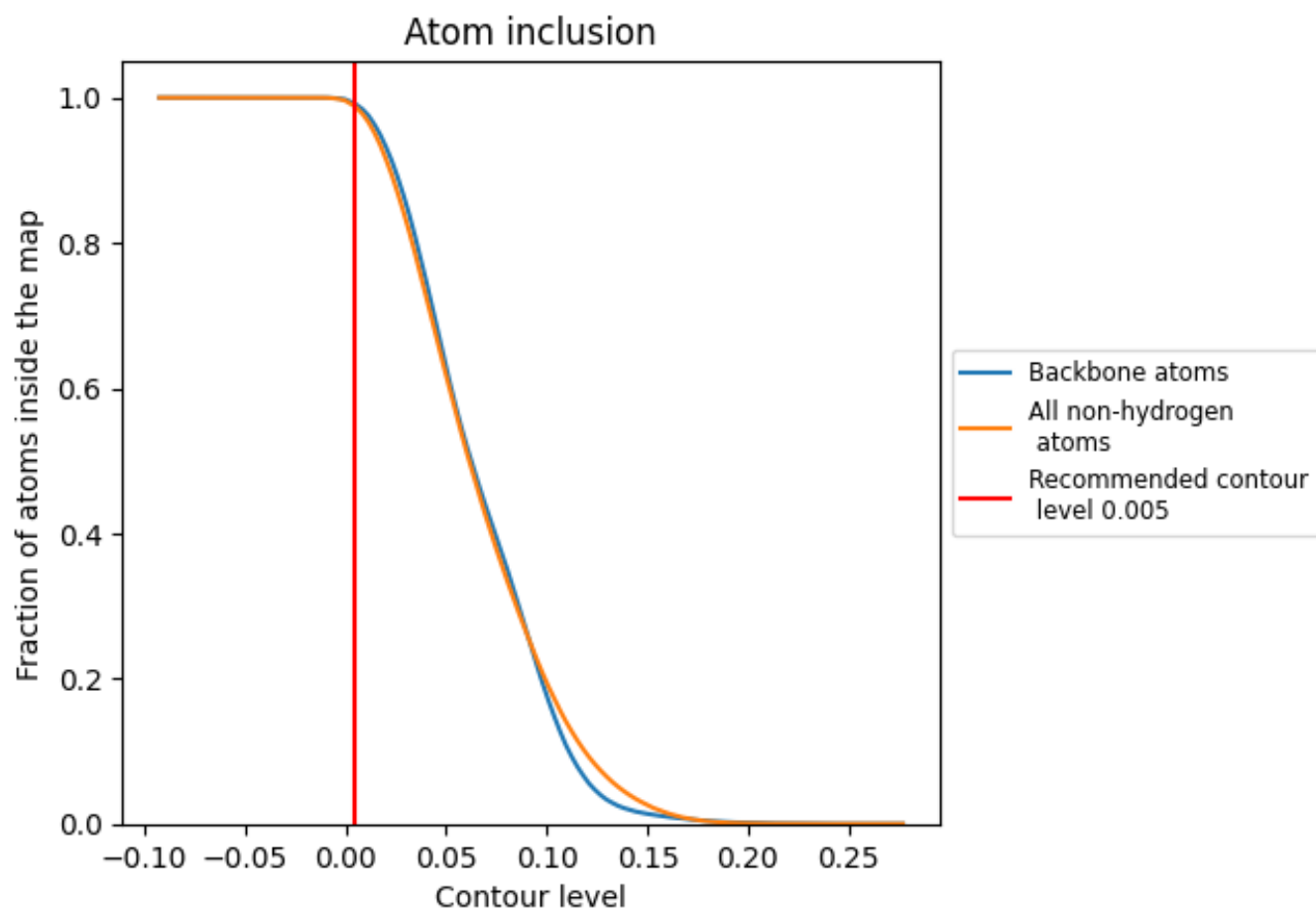
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9875	0.4910
CA	0.9930	0.3530
CB	0.7872	0.3720
CC	0.9880	0.2560
CD	0.8692	0.2290
L5	0.9978	0.5420
L7	1.0000	0.5960
L8	0.9985	0.5750
LA	0.9918	0.6150
LB	0.9956	0.5850
LC	0.9965	0.5800
LD	0.9991	0.5320
LE	0.9962	0.5020
LF	0.9934	0.5850
LG	0.9915	0.5020
LH	0.9966	0.5530
LI	0.9912	0.5740
LJ	0.9920	0.4600
LL	0.9927	0.5450
LM	0.9973	0.5460
LN	0.9969	0.6200
LO	0.9956	0.5950
LP	0.9983	0.6000
LQ	0.9931	0.6060
LR	0.9833	0.5280
LS	0.9964	0.6020
LT	0.9929	0.5750
LU	0.9988	0.4670
LV	0.9896	0.5980
LW	0.9878	0.4130
LX	0.9958	0.5670
LY	0.9972	0.5590
LZ	1.0000	0.5470
La	0.9973	0.6090
Lb	0.9787	0.5060



















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Chain	Atom inclusion	Q-score
Lc	 0.9839	 0.5440
Ld	 0.9988	 0.5660
Le	 0.9921	 0.6120
Lf	 0.9976	 0.6140
Lg	 0.9966	 0.5780
Lh	 0.9929	 0.5440
Li	 0.9962	 0.5470
Lj	 0.9970	 0.6200
Lk	 0.9928	 0.5090
Ll	 0.9882	 0.6050
Lm	 0.9856	 0.5780
Ln	 0.9856	 0.5750
Lo	 0.9845	 0.5810
Lp	 0.9855	 0.5940
Lr	 0.9990	 0.5800
Lz	 0.8996	 0.1130
S2	 0.9986	 0.4420
SA	 0.9835	 0.4150
SB	 0.9941	 0.4580
SC	 0.9911	 0.4750
SD	 0.9843	 0.3170
SE	 0.9926	 0.4640
SF	 0.9794	 0.3610
SG	 0.9952	 0.3550
SH	 0.9857	 0.3570
SI	 0.9736	 0.4610
SJ	 0.9850	 0.4280
SK	 0.9975	 0.2590
SL	 0.9142	 0.5030
SM	 0.9181	 0.1690
SN	 0.9872	 0.5020
SO	 0.9422	 0.4720
SP	 0.9822	 0.2620
SQ	 0.9982	 0.3290
SR	 0.9868	 0.3540
SS	 0.9922	 0.3120
ST	 0.9917	 0.3090
SU	 0.9975	 0.2920
SV	 0.9984	 0.4250
SW	 0.9901	 0.5000
SX	 0.9832	 0.4770
SY	 0.9990	 0.3810

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Chain	Atom inclusion	Q-score
SZ	 0.9846	 0.2400
Sa	 0.9835	 0.5000
Sb	 0.9906	 0.4460
Sc	 0.9712	 0.3510
Sd	 0.9842	 0.3890
Se	 0.9820	 0.3920
Sf	 0.9963	 0.1540
Sg	 0.9833	 0.2050