



Full wwPDB EM Validation Report ⓘ

May 20, 2023 – 09:19 am BST

PDB ID : 7Z3N
EMDB ID : EMD-14479
Title : Cryo-EM structure of the ribosome-associated RAC complex on the 80S ribosome - RAC-1 conformation
Authors : Kisonaite, M.; Wild, K.; Sinning, I.
Deposited on : 2022-03-02
Resolution : 3.20 Å(reported)
Based on initial model : 7OLC

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.dev50
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.32.2

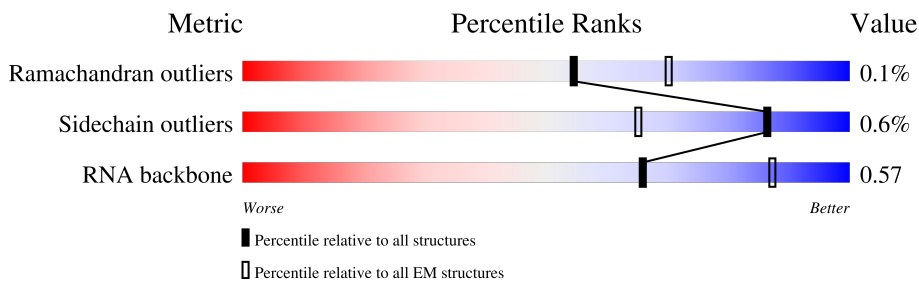
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	1	3337	
2	2	1796	
3	3	120	
4	4	156	
5	A	316	
6	B	302	
7	C	446	
8	D	578	

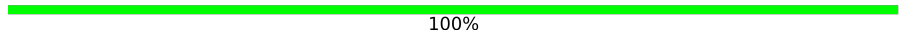
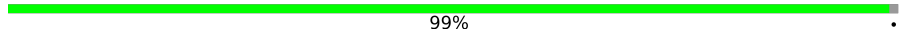
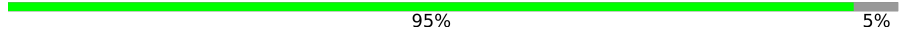

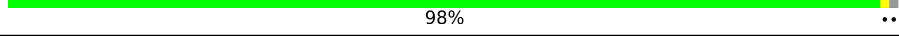
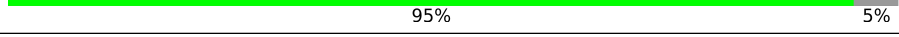
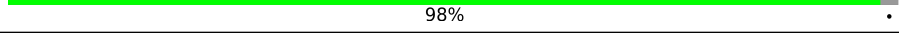
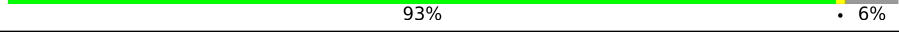
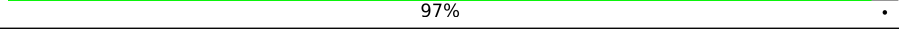
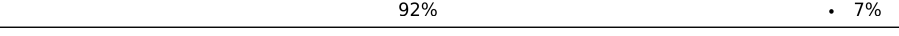
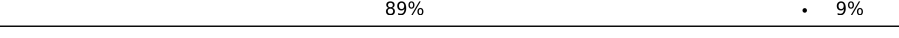
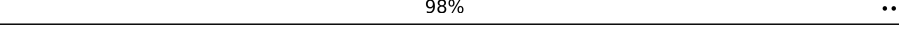
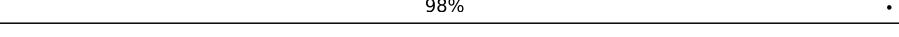
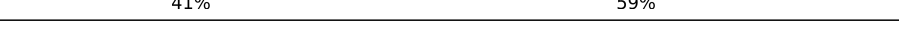


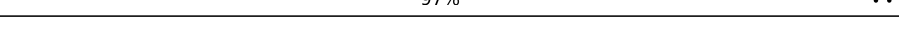
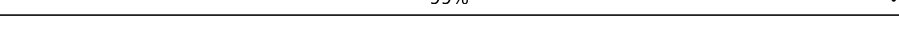
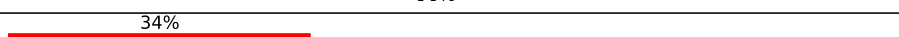






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Mol	Chain	Length	Quality of chain
9	LA	254	98%
10	LB	392	99%
11	LC	365	99%
12	LD	304	98%
13	LE	200	97%
14	LF	249	99%
15	LG	262	89% 10%
16	LH	192	98%
17	LI	219	99%
18	LJ	173	95%
19	LK	165	93% 6%
20	LL	213	98%
21	LM	142	99%
22	LN	203	99%
23	LO	204	100%
24	LP	187	99%
25	LQ	213	85% 14%
26	LR	192	96%
27	LS	174	99%
28	LT	160	99%
29	LU	127	80% 20%
30	LV	139	97%
31	LW	161	83% 17%
32	LX	156	77% 22%
33	LY	138	97%

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Mol	Chain	Length	Quality of chain
34	LZ	135	 100%
35	La	149	 99%
36	Lb	65	 95% 5%
37	Lc	108	 90% 10%
38	Ld	120	 98%
39	Le	131	 95% 5%
40	Lf	109	 98%
41	Lg	119	 93% 6%
42	Lh	126	 97%
43	Li	110	 92% 7%
44	Lj	95	 89% 9%
45	Lk	81	 98%
46	Ll	51	 98%
47	Lm	128	 41% 59%
48	Ln	25	 76% 20%
48	Lr	25	 20% 76% 20%
49	Lo	106	 97%
50	Lp	92	 99%
51	Lq	147	 96%
52	Ls	312	 34% 60% 39%
53	NC	27	 85% 100%
54	SA	285	 72% 27%
55	SB	255	 6% 91% 9%
56	SC	263	 82% 18%
57	SD	254	 20% 83% 16%

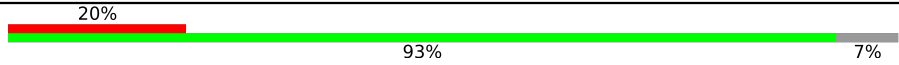


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Mol	Chain	Length	Quality of chain
58	SE	264	11% 98% ..
59	SF	212	26% 92% • 6%
60	SG	239	5% 96% ..
61	SH	203	7% 96% •
62	SI	202	8% 99%
63	SJ	190	9% 93% • 6%
64	SK	159	14% 56% 44%
65	SL	161	12% 93% 7%
66	SM	144	72% 81% • 18%
67	SN	151	• 99% ..
68	SO	150	• 89% • 10%
69	SP	153	20% 73% • 25%
70	SQ	143	15% 97% •
71	SR	143	6% 88% • 10%
72	SS	156	18% 87% • 12%
73	ST	153	25% 91% • 7%
74	SU	116	21% 88% • 11%
75	SV	98	• 88% 12%
76	SW	130	• 98% ..
77	SX	145	• 97% ..
78	SY	136	12% 94% • •
79	SZ	99	9% 69% • 30%
80	Sa	119	• 86% • 13%
81	Sb	82	5% 99% •
82	Sc	68	10% 90% 10%

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Mol	Chain	Length	Quality of chain
83	Sd	56	
84	Se	62	
85	Sf	154	

2 Entry composition [i](#)

There are 88 unique types of molecules in this entry. The entry contains 213543 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	3191	68242	30465	12334	22252	3191	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	1772	37781	16882	6728	12399	1772	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	3	119	2535	1132	453	831	119	0	0

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	4	156	3319	1484	589	1090	156	0	0

- Molecule 5 is a protein called Putative guanine nucleotide-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A	312	2438	1534	424	468	12	0	0

- Molecule 6 is a protein called HABP4_PA1-RBP1 domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	B	31	243	144	49	50	0	0

- Molecule 7 is a protein called Putative ribosome associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	C	444	3548	2211	661	672	4	0	0

- Molecule 8 is a protein called Putative heat shock protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	D	519	3942	2470	689	780	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	LA	252	1925	1203	385	334	3	0	0

- Molecule 10 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LB	387	3088	1964	576	535	13	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LC	363	2758	1741	527	481	9	0	0

- Molecule 12 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LD	300	2440	1545	431	461	3	0	0

- Molecule 13 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LE	194	1518	974	274	267	3	0	0

- Molecule 14 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	247	Total	C	N	O	S	0	0
			2017	1294	376	344	3		

- Molecule 15 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	235	Total	C	N	O	S	0	0
			1900	1218	351	326	5		

- Molecule 16 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	191	Total	C	N	O	S	0	0
			1505	955	269	275	6		

- Molecule 17 is a protein called 60S ribosomal protein L10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	217	Total	C	N	O	S	0	0
			1760	1109	343	299	9		

- Molecule 18 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	167	Total	C	N	O	S	0	0
			1367	854	268	239	6		

- Molecule 19 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	LK	155	Total	C	N	O	0	0
			762	452	155	155		

- Molecule 20 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	209	Total	C	N	O	S	0	0
			1666	1037	340	287	2		

- Molecule 21 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	LM	141	1125	714	216	194	1	0	0

- Molecule 22 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	LN	202	1703	1062	360	277	4	0	0

- Molecule 23 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	LO	203	1613	1036	305	267	5	0	0

- Molecule 24 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	LP	186	1472	912	295	262	3	0	0

- Molecule 25 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	LQ	183	1481	935	306	238	2	0	0

- Molecule 26 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	LR	184	1506	928	324	249	5	0	0

- Molecule 27 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	LS	173	1425	917	266	238	4	0	0

- Molecule 28 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LT	158	Total	C	N	O	S	0	0
			1266	803	246	215	2		

- Molecule 29 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LU	102	Total	C	N	O	S	0	0
			827	538	143	145	1		

- Molecule 30 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LV	135	Total	C	N	O	S	0	0
			994	633	185	169	7		

- Molecule 31 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LW	133	Total	C	N	O	S	0	0
			1075	667	221	185	2		

- Molecule 32 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	LX	121	Total	C	N	O	0	0
			965	620	175	170		

- Molecule 33 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LY	134	Total	C	N	O	S	0	0
			1065	664	215	184	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LZ	135	Total	C	N	O	S	0	0
			1111	713	207	187	4		

- Molecule 35 is a protein called 60S ribosomal protein L28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	La	148	1180	745	239	194	2	0	0

- Molecule 36 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Lb	62	508	310	112	86		0	0

- Molecule 37 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	Lc	97	722	458	125	134	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Ld	119	965	607	188	168	2	0	0

- Molecule 39 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Le	124	1001	629	205	161	6	0	0

- Molecule 40 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	Lf	107	853	540	170	142	1	0	0

- Molecule 41 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	Lg	112	891	554	181	152	4	0	0

- Molecule 42 is a protein called Dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	Lh	122	1003	637	198	168	0	0

- Molecule 43 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	Li	102	836	515	184	136	1	0	0

- Molecule 44 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	Lj	86	684	418	152	109	5	0	0

- Molecule 45 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	Lk	80	658	415	126	115	2	0	0

- Molecule 46 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
46	Ll	50	435	275	97	63	0	0

- Molecule 47 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	Lm	52	418	261	86	65	6	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lm	1	MET	SER	conflict	UNP G0S8G4
Lm	2	GLN	ARG	conflict	UNP G0S8G4

- Molecule 48 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ln	24	Total	C	N	O	S	0	0
			224	136	61	26	1		
48	Lr	24	Total	C	N	O	S	0	0
			224	136	61	26	1		

- Molecule 49 is a protein called 60S ribosomal protein L44-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lo	104	Total	C	N	O	S	0	0
			822	520	161	136	5		

- Molecule 50 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lp	91	Total	C	N	O	S	0	0
			697	430	138	123	6		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
51	Lq	141	Total	C	N	O	0	0
			1083	678	215	190		

- Molecule 52 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ls	189	Total	C	N	O	S	0	0
			1449	927	250	265	7		

- Molecule 53 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	NC	27	Total	C	N	O	0	0
			135	81	27	27		

- Molecule 54 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SA	208	Total	C	N	O	S	0	0
			1641	1051	289	295	6		

- Molecule 55 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SB	232	Total	C	N	O	S	0	0
			1871	1190	351	325	5		

- Molecule 56 is a protein called 40S ribosomal protein S2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SC	216	Total	C	N	O	S	0	0
			1672	1074	294	301	3		

- Molecule 57 is a protein called 40S ribosomal protein S3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SD	214	Total	C	N	O	S	0	0
			1688	1068	307	305	8		

- Molecule 58 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SE	261	Total	C	N	O	S	0	0
			2072	1314	389	362	7		

- Molecule 59 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SF	199	Total	C	N	O	S	0	0
			1557	971	294	285	7		

- Molecule 60 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SG	232	Total	C	N	O	S	0	0
			1875	1171	376	323	5		

- Molecule 61 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	SH	195	Total	C	N	O	0	0
			1562	983	300	279		

- Molecule 62 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	SI	201	1621	1009	330	281	1	0	0

- Molecule 63 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	SJ	179	1466	933	290	241	2	0	0

- Molecule 64 is a protein called 40S ribosomal protein s10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	SK	89	742	487	124	129	2	0	0

- Molecule 65 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	SL	150	1222	780	236	201	5	0	0

- Molecule 66 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	SM	118	923	577	167	171	8	0	0

- Molecule 67 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	SN	150	1182	756	220	205	1	0	0

- Molecule 68 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	SO	135	1002	614	199	184	5	0	0

- Molecule 69 is a protein called 40S ribosomal protein s15-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SP	115	Total	C	N	O	S	0	0
			917	583	172	159	3		

- Molecule 70 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SQ	138	Total	C	N	O	S	0	0
			1081	693	202	184	2		

- Molecule 71 is a protein called 40S ribosomal protein S17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SR	128	Total	C	N	O	S	0	0
			1045	657	190	195	3		

- Molecule 72 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SS	137	Total	C	N	O	S	0	0
			1118	699	222	196	1		

- Molecule 73 is a protein called 40S ribosomal protein S19-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	ST	142	Total	C	N	O	S	0	0
			1117	694	221	201	1		

- Molecule 74 is a protein called 40S ribosomal protein S20-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SU	103	Total	C	N	O	S	0	0
			819	517	150	148	4		

- Molecule 75 is a protein called 40S ribosomal protein S21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SV	86	Total	C	N	O	S	0	0
			664	408	124	128	4		

- Molecule 76 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	SW	129	1037	659	195	178	5	0	0

- Molecule 77 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	SX	142	1099	694	215	188	2	0	0

- Molecule 78 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	SY	132	1061	668	209	182	2	0	0

- Molecule 79 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	SZ	69	546	345	101	98	2	0	0

- Molecule 80 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	Sa	104	839	518	177	137	7	0	0

- Molecule 81 is a protein called Ribosomal protein s27-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
81	Sb	81	611	386	111	107	7	0	0

- Molecule 82 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
82	Sc	61	484	298	97	88	1	0	0

- Molecule 83 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
83	Sd	52	419	261	84	70	4	0	0

- Molecule 84 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
84	Se	40	322	202	67	53	0	0

- Molecule 85 is a protein called 40S ribosomal protein S27a-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
85	Sf	73	604	382	115	101	6	0	0

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

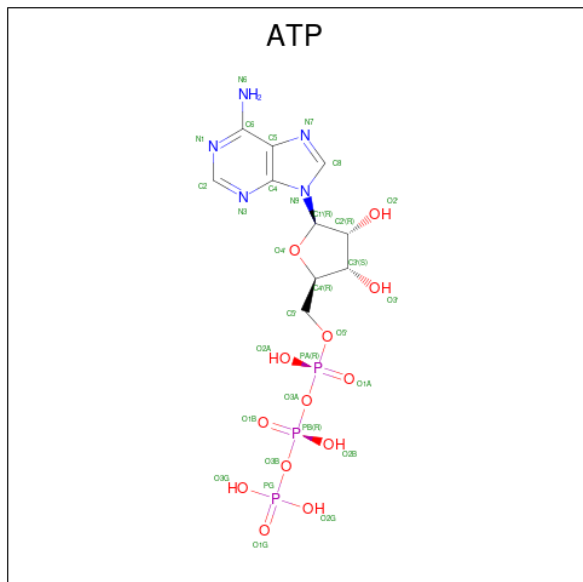
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
86	1	360	360	360	0
86	2	66	66	66	0
86	3	6	6	6	0
86	4	10	10	10	0
86	D	1	1	1	0
86	LB	1	1	1	0
86	LC	1	1	1	0
86	LI	1	1	1	0
86	LJ	1	1	1	0
86	LN	1	1	1	0
86	LP	1	1	1	0
86	LV	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
86	LW	1	Total	Mg	0
			1	1	
86	Lb	1	Total	Mg	0
			1	1	
86	SN	1	Total	Mg	0
			1	1	
86	SO	1	Total	Mg	0
			1	1	
86	SQ	1	Total	Mg	0
			1	1	

- Molecule 87 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
87	D	1	Total	C	N	O	P	0
			31	10	5	13	3	

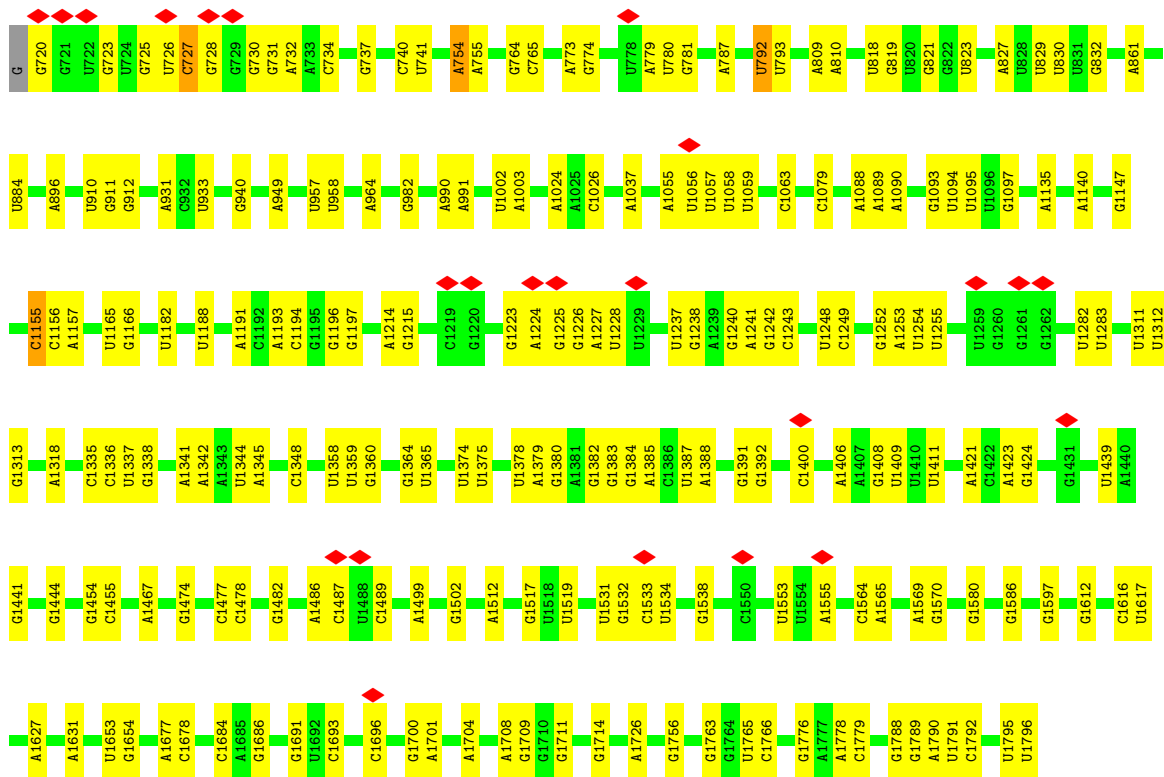
- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
88	Lg	1	Total	Zn	0
			1	1	
88	Lj	1	Total	Zn	0
			1	1	
88	Lm	1	Total	Zn	0
			1	1	

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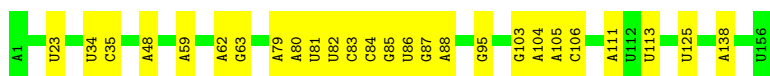
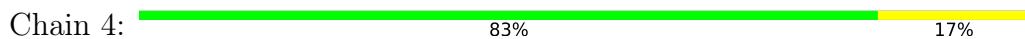
Mol	Chain	Residues	Atoms		AltConf
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0
88	Sa	1	Total 1	Zn 1	0
88	Sb	1	Total 1	Zn 1	0
88	Sd	1	Total 1	Zn 1	0



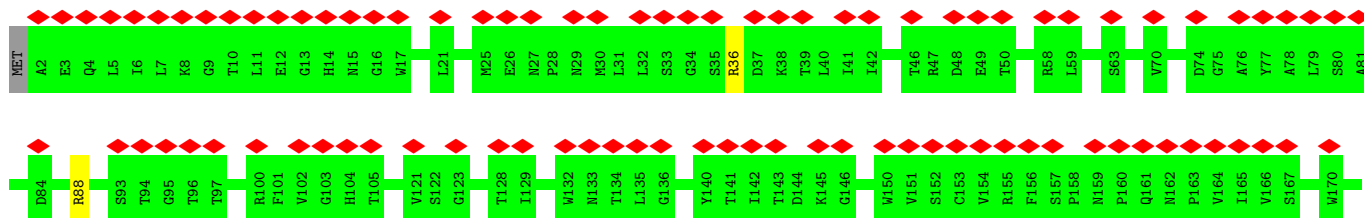
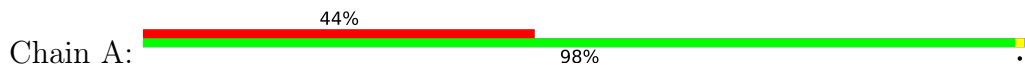
• Molecule 3: 5S rRNA

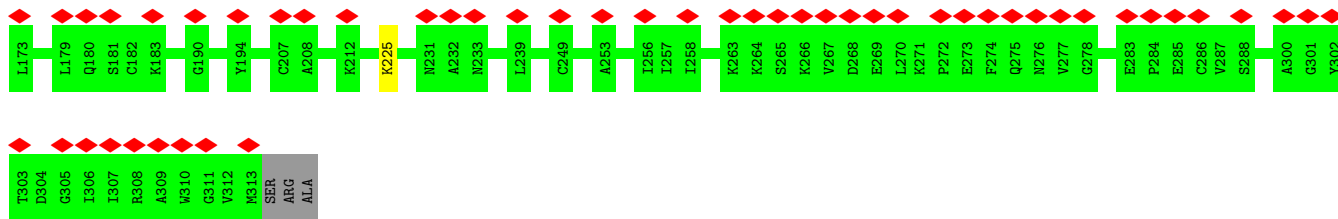


• Molecule 4: 5.8S rRNA

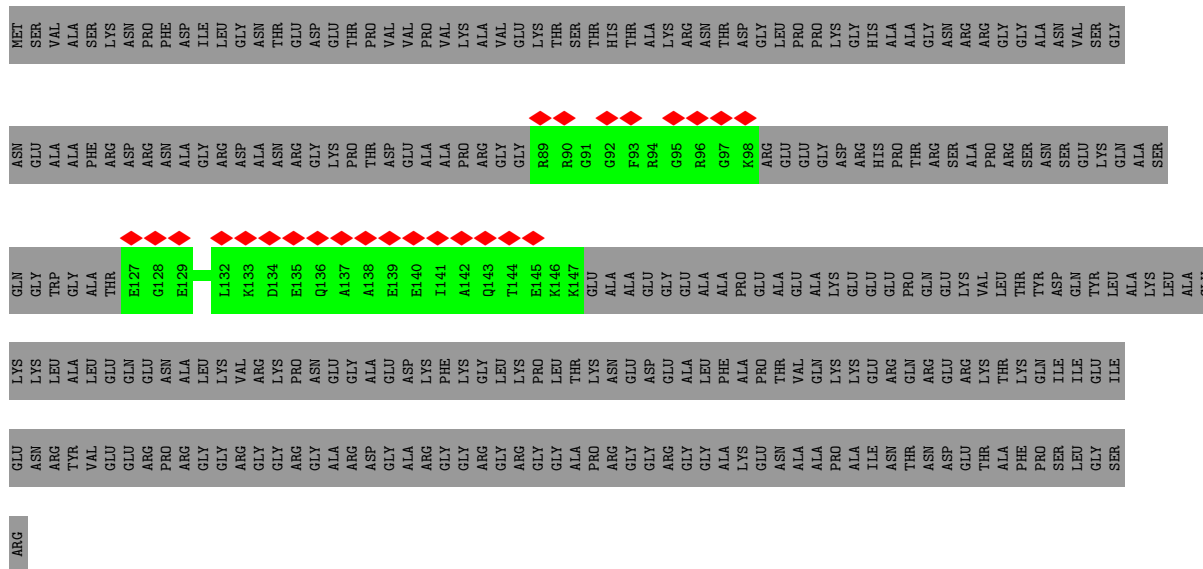


• Molecule 5: Putative guanine nucleotide-binding protein

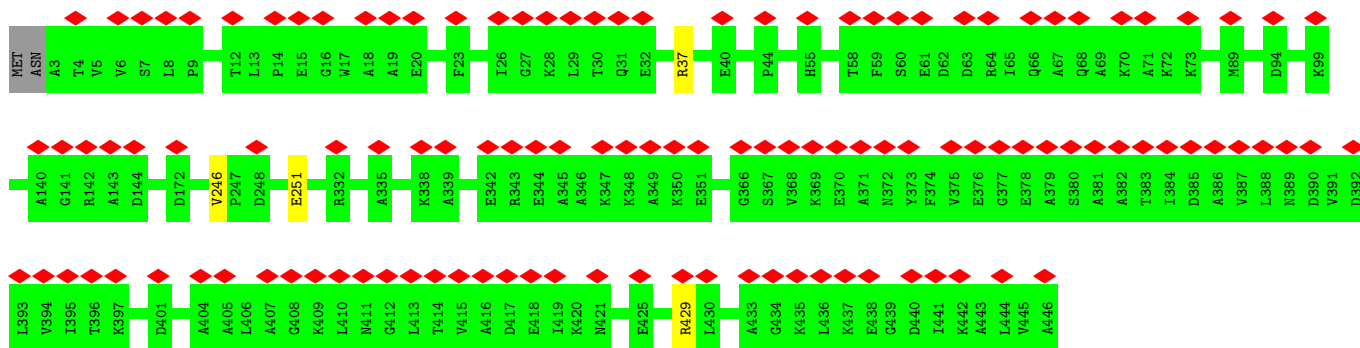




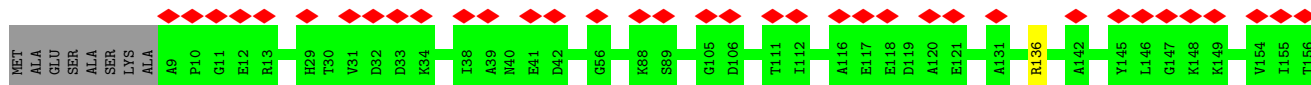
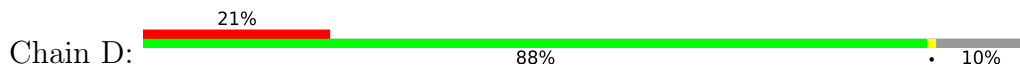
• Molecule 6: HABP4_PAI-RBP1 domain-containing protein



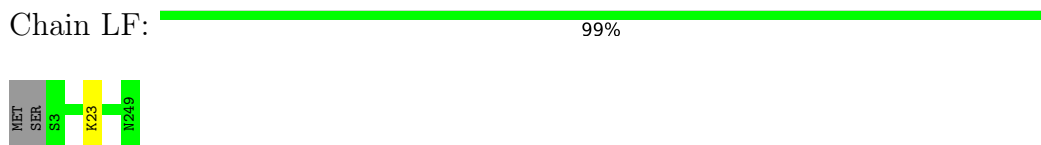
• Molecule 7: Putative ribosome associated protein



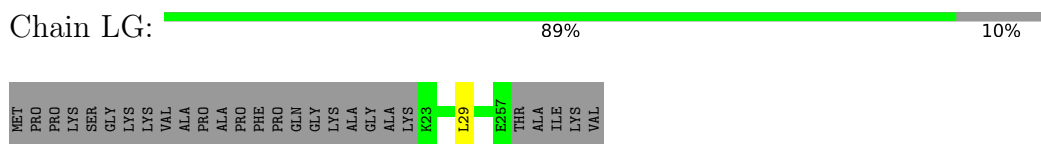
• Molecule 8: Putative heat shock protein



- Molecule 14: 60S ribosomal protein l7-like protein



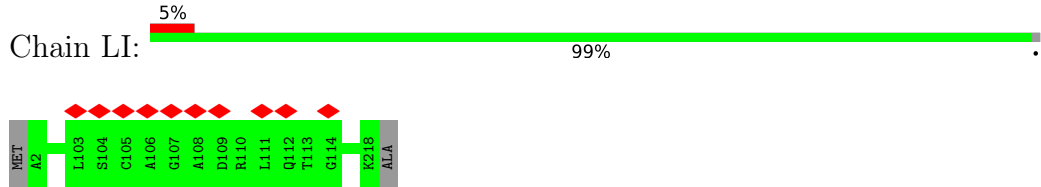
- Molecule 15: 60S ribosomal protein L8



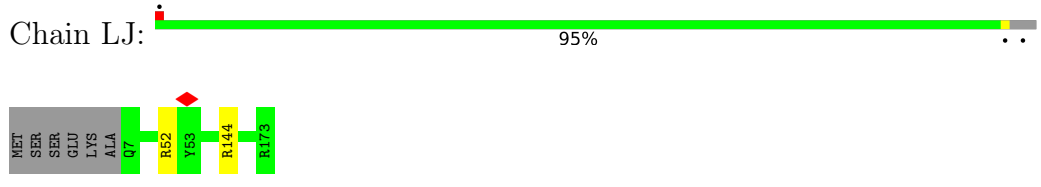
- Molecule 16: uL6



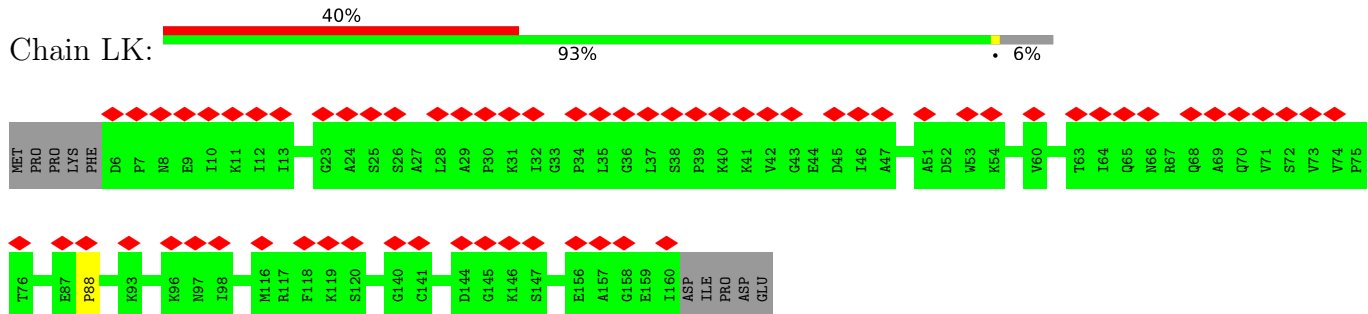
- Molecule 17: 60S ribosomal protein L10-like protein



- Molecule 18: Putative ribosomal protein



- Molecule 19: 60S ribosomal protein L12-like protein

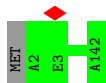


- Molecule 20: 60S ribosomal protein L13





- Molecule 21: 60S ribosomal protein L14-like protein



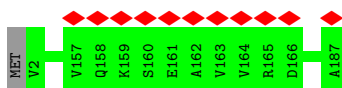
- Molecule 22: Ribosomal protein L15



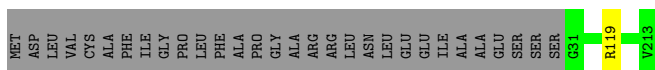
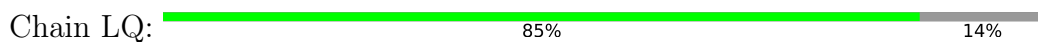
- Molecule 23: 60S ribosomal protein L16-like protein



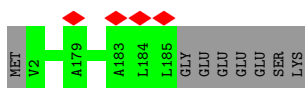
- Molecule 24: 60S ribosomal protein l17-like protein



- Molecule 25: Ribosomal protein L18-like protein



- Molecule 26: Ribosomal protein L19



- Molecule 27: 60S ribosomal protein L20

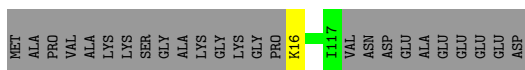
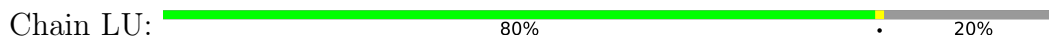




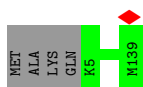
- Molecule 28: 60S ribosomal protein l21-like protein



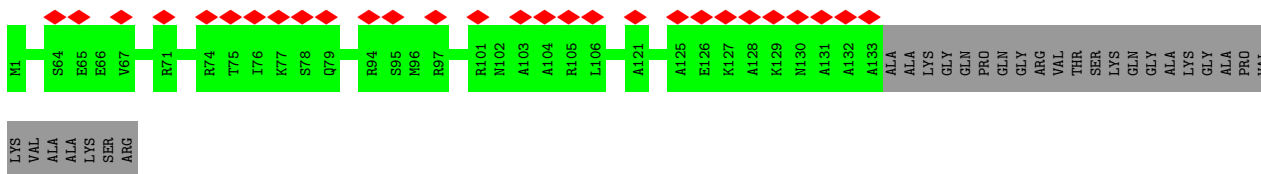
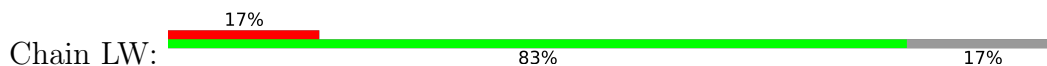
- Molecule 29: 60S ribosomal protein L22-like protein



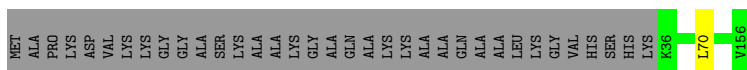
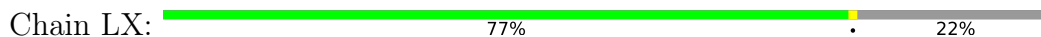
- Molecule 30: 60S ribosomal protein l23-like protein



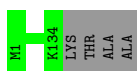
- Molecule 31: eL24



- Molecule 32: 60S ribosomal protein L25-like protein



- Molecule 33: 60S ribosomal protein L26-like protein



- Molecule 34: 60S ribosomal protein L27

Chain LZ:  100%

There are no outlier residues recorded for this chain.

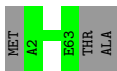
- Molecule 35: 60S ribosomal protein L28-like protein

Chain La:  99%



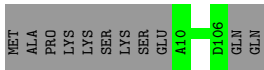
- Molecule 36: 60S ribosomal protein L29

Chain Lb:  95% 5%



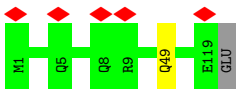
- Molecule 37: 60S ribosomal protein l30-like protein

Chain Lc:  90% 10%



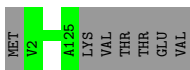
- Molecule 38: Putative 60S ribosomal protein

Chain Ld:  98% ..



- Molecule 39: 60S ribosomal protein L32-like protein

Chain Le:  95% 5%



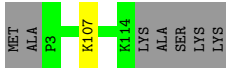
- Molecule 40: 60S ribosomal protein l33-like protein

Chain Lf:  98%



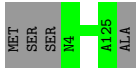
- Molecule 41: Ribosomal protein l34-like protein

Chain Lg:  93% 6%



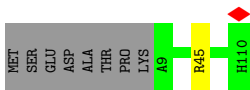
- Molecule 42: Dolichyl-diphosphooligosaccharide--protein glycotransferase

Chain Lh: 97%



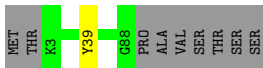
- Molecule 43: 60S ribosomal protein L36

Chain Li: 92% 7%



- Molecule 44: Ribosomal protein L37

Chain Lj: 89% 9%



- Molecule 45: eL38

Chain Lk: 98%



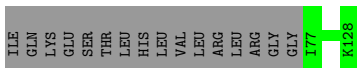
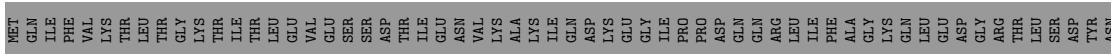
- Molecule 46: Ribosomal protein eL39

Chain Ll: 98%

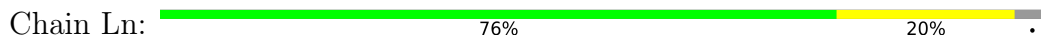


- Molecule 47: Putative ribosomal protein

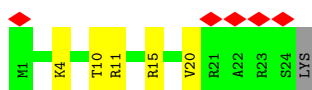
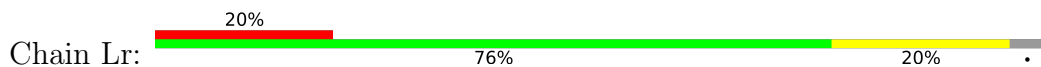
Chain Lm: 41% 59%



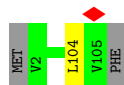
- Molecule 48: 60S ribosomal protein L41-A



• Molecule 48: 60S ribosomal protein L41-A



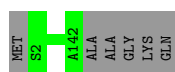
• Molecule 49: 60S ribosomal protein L44-like protein



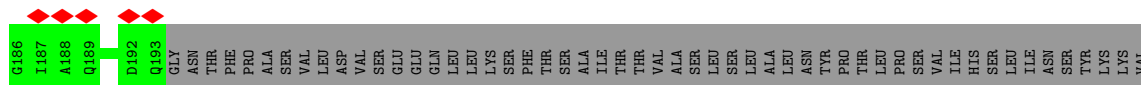
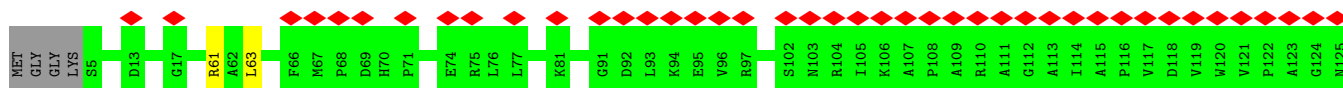
• Molecule 50: 60S ribosomal protein L43-like protein



• Molecule 51: Putative 60S ribosomal protein

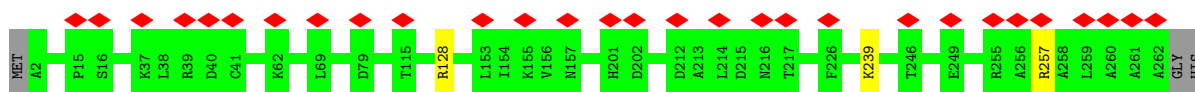


• Molecule 52: 60S acidic ribosomal protein P0



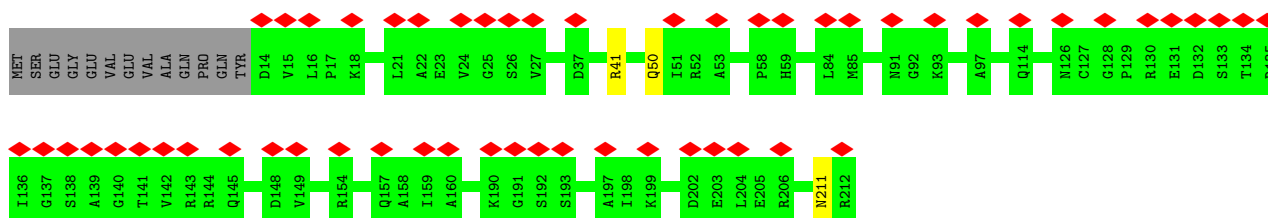
- Molecule 58: 40S ribosomal protein S4

Chain SE: 11% 98%



- Molecule 59: 40S ribosomal protein s5-like protein

Chain SF: 26% 92% 6%



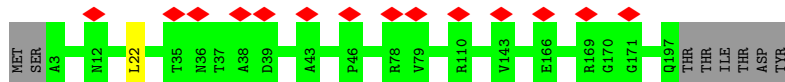
- Molecule 60: 40S ribosomal protein S6

Chain SG: 5% 96%



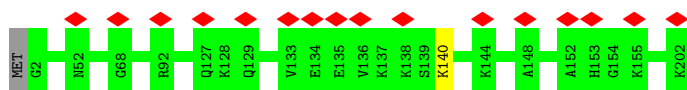
- Molecule 61: 40S ribosomal protein S7

Chain SH: 7% 96%



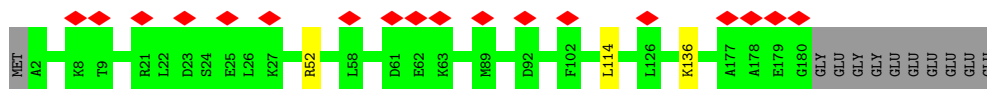
- Molecule 62: 40S ribosomal protein S8

Chain SI: 8% 99%

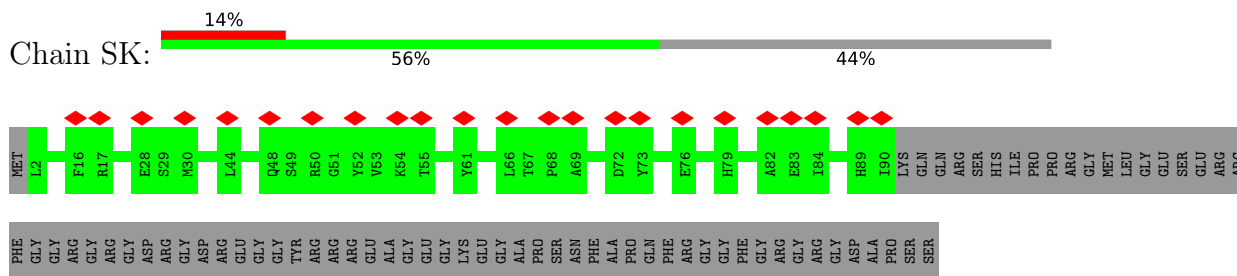


- Molecule 63: 40S ribosomal protein s9-like protein

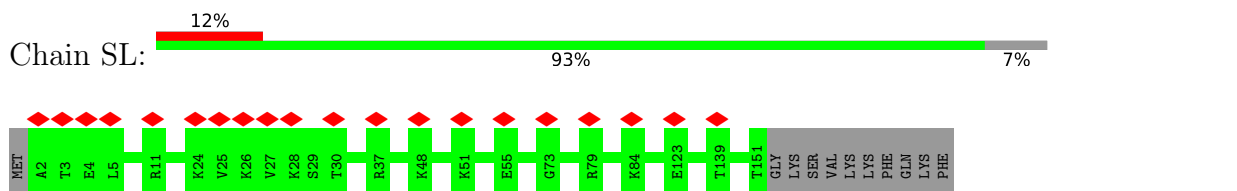
Chain SJ: 9% 93% 6%



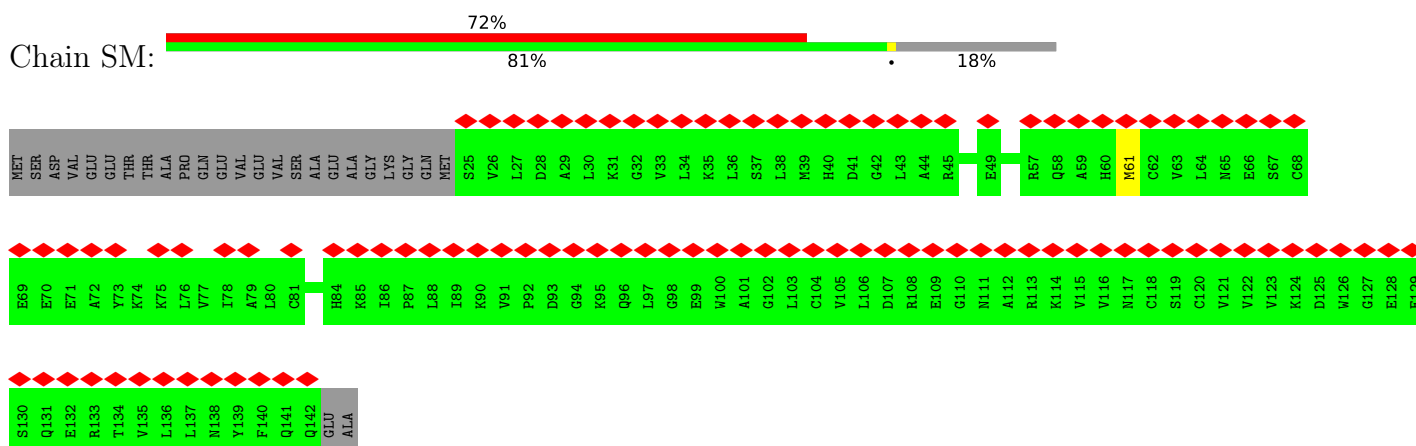
- Molecule 64: 40S ribosomal protein s10-like protein



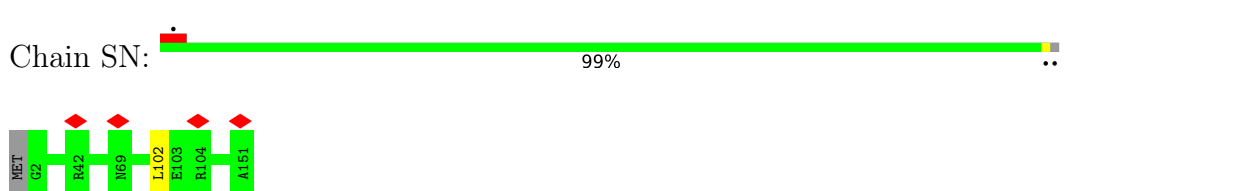
• Molecule 65: 40S ribosomal protein S11-like protein



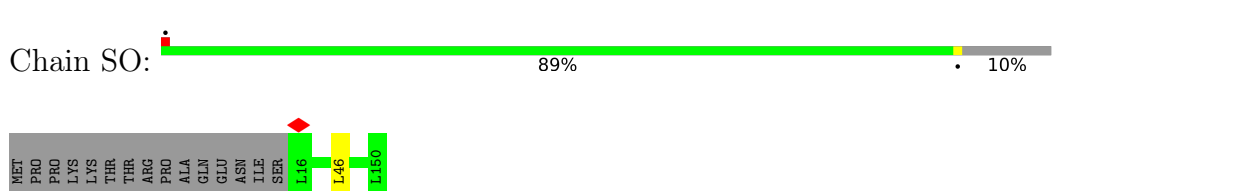
• Molecule 66: 40S ribosomal protein S12



• Molecule 67: 40S ribosomal protein S13-like protein

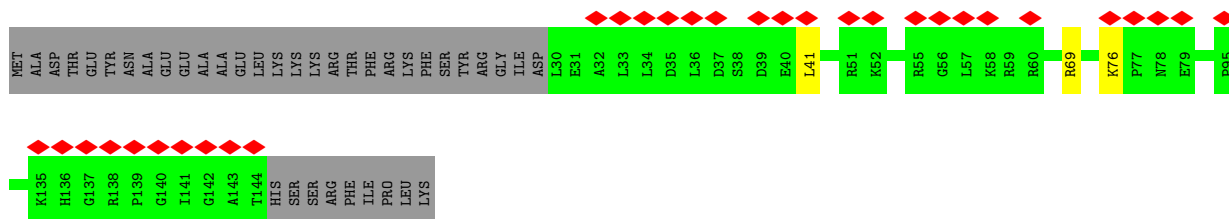


• Molecule 68: 40S ribosomal protein S14-like protein

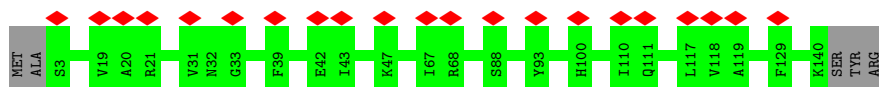


• Molecule 69: 40S ribosomal protein s15-like protein

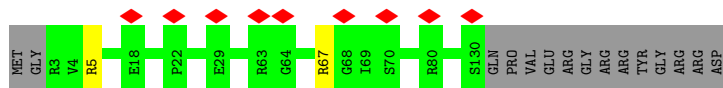
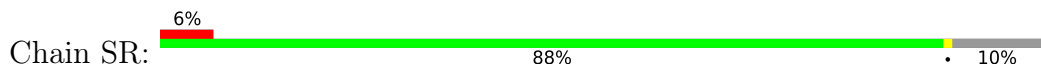




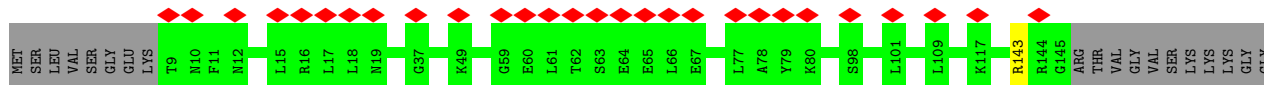
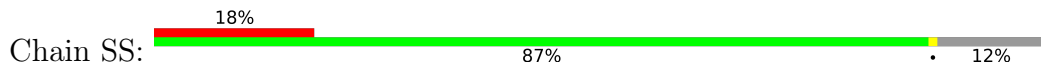
- Molecule 70: 40S ribosomal protein S16-like protein



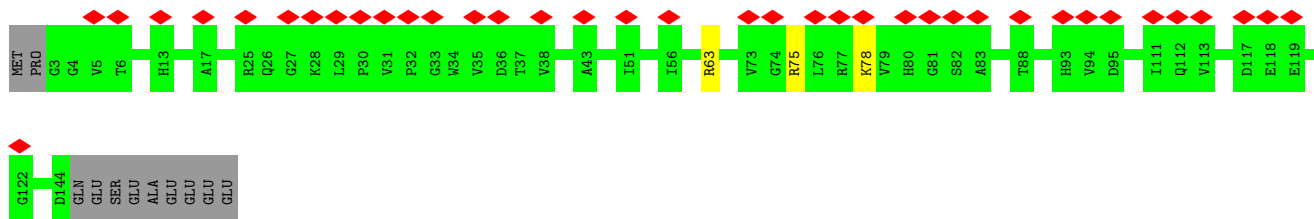
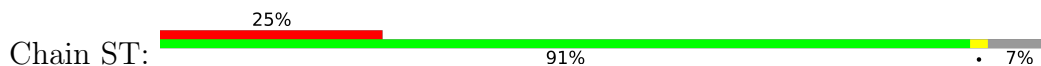
- Molecule 71: 40S ribosomal protein S17-like protein



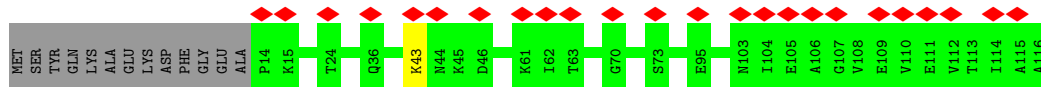
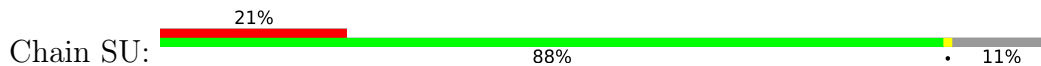
- Molecule 72: Putative ribosomal protein



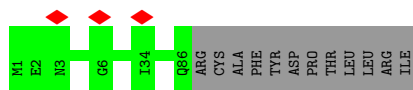
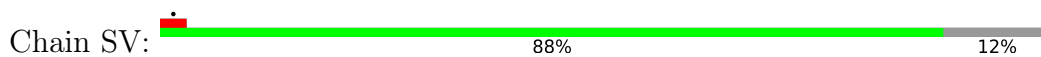
- Molecule 73: 40S ribosomal protein S19-like protein



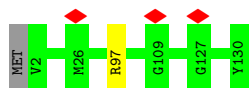
- Molecule 74: 40S ribosomal protein S20-like protein



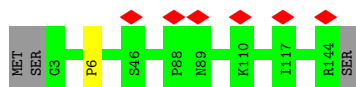
- Molecule 75: 40S ribosomal protein S21-like protein



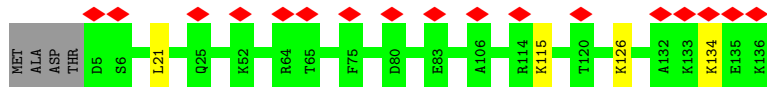
- Molecule 76: 40S ribosomal protein S22-like protein



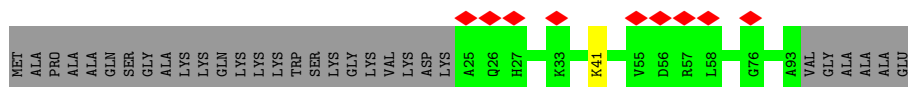
- Molecule 77: 40S ribosomal protein s23-like protein



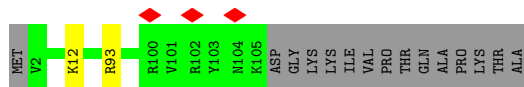
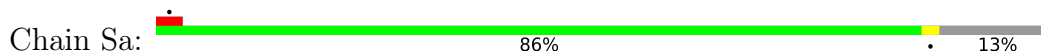
- Molecule 78: 40S ribosomal protein S24



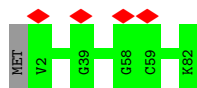
- Molecule 79: 40S ribosomal protein S25



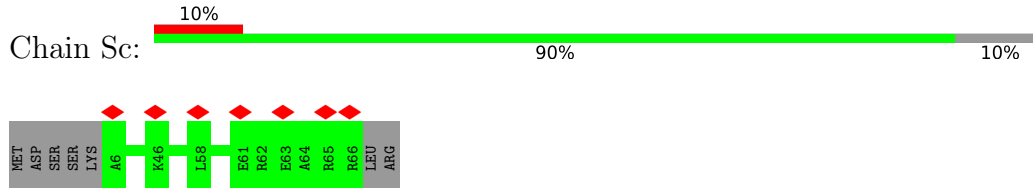
- Molecule 80: 40S ribosomal protein S26



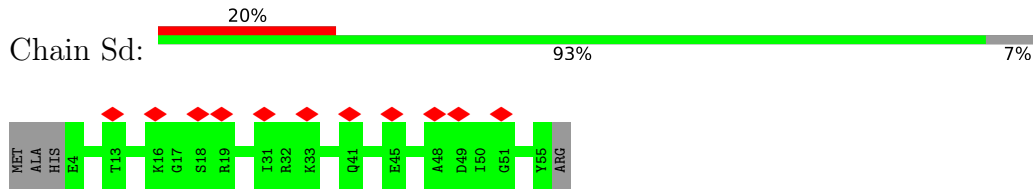
- Molecule 81: Ribosomal protein s27-like protein



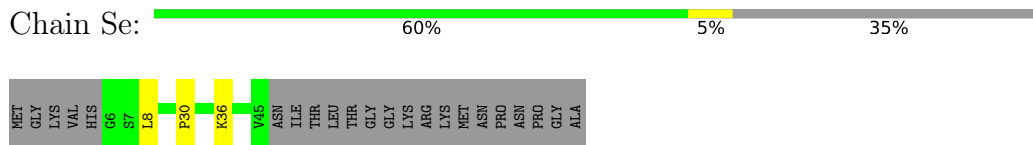
- Molecule 82: 40S ribosomal protein S28-like protein



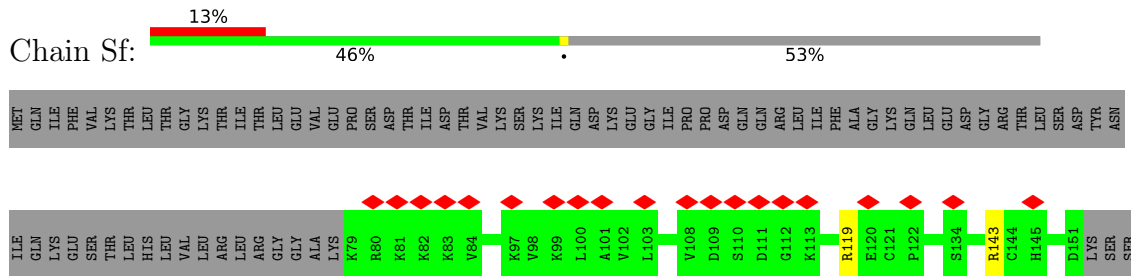
- Molecule 83: Ribosomal protein uS14



- Molecule 84: 40S ribosomal protein S30



- Molecule 85: 40S ribosomal protein S27a-like protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	305951	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 ($e^-/\text{\AA}^2$)	39.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	25.266	Depositor
Minimum map value	-11.982	Depositor
Average map value	-0.007	Depositor
Map value standard deviation	0.913	Depositor
Recommended contour level	1.8	Depositor
Map size (Å)	534.60004, 534.60004, 534.60004	wwPDB
Map dimensions	486, 486, 486	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.19	0/76339	0.78	16/119028 (0.0%)
2	2	0.20	0/42256	0.80	16/65852 (0.0%)
3	3	0.18	0/2833	0.77	0/4413
4	4	0.17	0/3710	0.77	0/5778
5	A	0.27	0/2495	0.61	0/3390
6	B	0.25	0/242	0.59	0/314
7	C	0.27	0/3606	0.59	0/4836
8	D	0.27	0/4002	0.58	1/5437 (0.0%)
9	LA	0.25	0/1964	0.60	0/2641
10	LB	0.24	0/3156	0.56	0/4238
11	LC	0.26	0/2815	0.55	0/3795
12	LD	0.27	0/2487	0.57	1/3341 (0.0%)
13	LE	0.28	0/1547	0.57	0/2081
14	LF	0.27	0/2055	0.57	0/2758
15	LG	0.26	0/1929	0.57	1/2579 (0.0%)
16	LH	0.26	0/1525	0.58	1/2050 (0.0%)
17	LI	0.26	0/1797	0.61	0/2413
18	LJ	0.28	0/1389	0.72	0/1856
19	LK	0.26	0/761	0.55	0/1056
20	LL	0.26	0/1695	0.62	0/2276
21	LM	0.26	0/1144	0.59	0/1539
22	LN	0.25	0/1740	0.64	0/2332
23	LO	0.27	0/1638	0.58	0/2197
24	LP	0.26	0/1495	0.64	0/2014
25	LQ	0.25	0/1507	0.60	0/2017
26	LR	0.27	0/1525	0.63	0/2028
27	LS	0.26	0/1460	0.57	0/1965
28	LT	0.26	0/1292	0.60	0/1738
29	LU	0.30	0/840	0.62	0/1123
30	LV	0.26	0/1012	0.59	0/1361
31	LW	0.27	0/1088	0.64	0/1443
32	LX	0.26	0/981	0.62	1/1324 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LY	0.27	0/1079	0.61	0/1443
34	LZ	0.26	0/1134	0.62	0/1519
35	La	0.25	0/1212	0.59	0/1627
36	Lb	0.27	0/518	0.64	0/684
37	Lc	0.28	0/731	0.57	0/983
38	Ld	0.28	0/979	0.61	0/1308
39	Le	0.25	0/1019	0.58	0/1358
40	Lf	0.27	0/874	0.60	0/1176
41	Lg	0.25	0/904	0.65	0/1210
42	Lh	0.28	0/1014	0.63	0/1349
43	Li	0.29	0/844	0.70	0/1115
44	Lj	0.26	0/697	0.68	0/922
45	Lk	0.27	0/666	0.63	1/884 (0.1%)
46	Ll	0.24	0/445	0.59	0/593
47	Lm	0.27	0/424	0.68	0/561
48	Ln	0.42	0/225	1.00	0/289
48	Lr	0.42	0/225	1.00	0/289
49	Lo	0.25	0/835	0.56	1/1105 (0.1%)
50	Lp	0.25	0/705	0.63	0/940
51	Lq	0.26	0/1101	0.61	0/1482
52	Ls	0.26	0/1477	0.59	1/1995 (0.1%)
54	SA	0.29	0/1683	0.65	1/2299 (0.0%)
55	SB	0.27	0/1900	0.66	0/2551
56	SC	0.28	0/1703	0.67	0/2303
57	SD	0.27	0/1712	0.69	0/2299
58	SE	0.27	0/2112	0.65	0/2842
59	SF	0.29	0/1578	0.66	0/2130
60	SG	0.28	0/1906	0.64	0/2547
61	SH	0.27	0/1587	0.66	1/2140 (0.0%)
62	SI	0.27	0/1654	0.64	0/2213
63	SJ	0.28	0/1489	0.73	2/1993 (0.1%)
64	SK	0.27	0/764	0.63	0/1038
65	SL	0.26	0/1249	0.62	0/1678
66	SM	0.27	0/934	0.66	1/1255 (0.1%)
67	SN	0.28	0/1205	0.64	1/1627 (0.1%)
68	SO	0.28	0/1014	0.71	1/1361 (0.1%)
69	SP	0.27	0/932	0.68	1/1248 (0.1%)
70	SQ	0.27	0/1098	0.64	0/1472
71	SR	0.31	0/1060	0.72	0/1424
72	SS	0.26	0/1133	0.65	0/1520
73	ST	0.29	0/1137	0.70	1/1533 (0.1%)
74	SU	0.26	0/828	0.66	0/1112
75	SV	0.26	0/671	0.62	0/900

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SW	0.30	0/1055	0.68	0/1416
77	SX	0.50	1/1116 (0.1%)	0.88	3/1489 (0.2%)
78	SY	0.26	0/1075	0.68	1/1431 (0.1%)
79	SZ	0.24	0/550	0.66	0/736
80	Sa	0.26	0/852	0.63	0/1136
81	Sb	0.27	0/623	0.63	0/843
82	Sc	0.26	0/487	0.69	0/653
83	Sd	0.27	0/427	0.65	0/570
84	Se	0.63	1/325 (0.3%)	1.09	4/427 (0.9%)
85	Sf	0.24	0/614	0.57	0/813
All	All	0.23	2/227906 (0.0%)	0.73	57/333044 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
77	SX	6	PRO	CG-CD	-12.92	1.08	1.50
84	Se	30	PRO	CG-CD	-9.09	1.20	1.50

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	SX	6	PRO	N-CD-CG	-15.07	80.59	103.20
84	Se	30	PRO	CA-N-CD	-10.39	96.95	111.50
84	Se	30	PRO	N-CD-CG	-10.19	87.91	103.20
1	1	1205	G	O4'-C1'-N9	8.96	115.37	108.20
77	SX	6	PRO	CA-CB-CG	-8.44	87.97	104.00
8	D	450	VAL	CG1-CB-CG2	-8.04	98.04	110.90
2	2	224	C	N1-C2-O2	7.97	123.68	118.90
2	2	1400	C	N3-C2-O2	-7.68	116.52	121.90
2	2	754	A	O4'-C1'-N9	7.09	113.87	108.20
2	2	225	C	N3-C2-O2	-6.58	117.30	121.90
77	SX	6	PRO	CA-N-CD	-6.54	102.35	111.50
73	ST	63	ARG	CB-CG-CD	6.48	128.45	111.60
78	SY	21	LEU	CA-CB-CG	6.21	129.57	115.30
63	SJ	52	ARG	CA-CB-CG	6.17	126.97	113.40
54	SA	21	LEU	CA-CB-CG	6.09	129.31	115.30
1	1	2200	C	N3-C2-O2	-6.02	117.69	121.90
1	1	2667	C	N3-C2-O2	-5.99	117.71	121.90
2	2	224	C	N3-C2-O2	-5.95	117.74	121.90
32	LX	70	LEU	CA-CB-CG	5.94	128.95	115.30
2	2	1392	G	N3-C4-N9	-5.92	122.45	126.00
1	1	1587	U	P-O3'-C3'	5.91	126.79	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
63	SJ	114	LEU	CA-CB-CG	5.88	128.83	115.30
1	1	2075	U	OP2-P-O3'	5.85	118.08	105.20
2	2	233	G	N1-C2-N2	-5.81	110.97	116.20
84	Se	30	PRO	CA-CB-CG	-5.79	93.00	104.00
84	Se	8	LEU	CA-CB-CG	5.77	128.57	115.30
12	LD	113	LEU	CA-CB-CG	5.74	128.50	115.30
1	1	2200	C	N1-C2-O2	5.72	122.33	118.90
1	1	41	A	O4'-C1'-N9	5.57	112.65	108.20
2	2	1454	G	C4-N9-C1'	5.55	133.72	126.50
1	1	1266	C	N1-C2-O2	5.55	122.23	118.90
1	1	1622	A	O4'-C1'-N9	-5.54	103.77	108.20
1	1	1158	C	N1-C2-O2	5.52	122.21	118.90
2	2	1063	C	N3-C2-O2	-5.49	118.06	121.90
2	2	1155	C	O4'-C1'-N1	-5.47	103.82	108.20
61	SH	22	LEU	CA-CB-CG	5.39	127.70	115.30
1	1	1159	C	C6-N1-C1'	5.37	127.25	120.80
2	2	792	U	P-O3'-C3'	5.36	126.13	119.70
69	SP	41	LEU	CA-CB-CG	5.32	127.53	115.30
15	LG	29	LEU	CA-CB-CG	5.29	127.47	115.30
1	1	1478	U	C2-N1-C1'	5.25	123.99	117.70
2	2	1391	G	N3-C4-N9	5.22	129.13	126.00
1	1	1600	U	N1-C2-N3	5.17	118.00	114.90
68	SO	46	LEU	CA-CB-CG	5.17	127.18	115.30
67	SN	102	LEU	CA-CB-CG	5.15	127.15	115.30
45	Lk	13	GLU	CA-CB-CG	5.13	124.69	113.40
49	Lo	104	LEU	CA-CB-CG	5.12	127.08	115.30
66	SM	61	MET	CA-CB-CG	5.12	122.00	113.30
2	2	233	G	N3-C2-N2	5.12	123.48	119.90
16	LH	130	MET	CB-CG-SD	5.12	127.75	112.40
2	2	1392	G	C5-C6-O6	5.11	131.67	128.60
52	Ls	63	LEU	CA-CB-CG	5.10	127.02	115.30
1	1	1159	C	C2-N1-C1'	-5.07	113.22	118.80
2	2	727	C	O5'-P-OP1	-5.06	101.15	105.70
1	1	2075	U	P-O3'-C3'	5.05	125.76	119.70
2	2	1454	G	N3-C4-N9	5.04	129.03	126.00
1	1	3324	C	C2-N1-C1'	5.01	124.31	118.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	A	310/316 (98%)	287 (93%)	23 (7%)	0	100	100
6	B	27/302 (9%)	19 (70%)	8 (30%)	0	100	100
7	C	442/446 (99%)	423 (96%)	18 (4%)	1 (0%)	47	79
8	D	511/578 (88%)	496 (97%)	11 (2%)	4 (1%)	19	58
9	LA	250/254 (98%)	239 (96%)	11 (4%)	0	100	100
10	LB	385/392 (98%)	365 (95%)	20 (5%)	0	100	100
11	LC	361/365 (99%)	346 (96%)	15 (4%)	0	100	100
12	LD	298/304 (98%)	290 (97%)	8 (3%)	0	100	100
13	LE	192/200 (96%)	178 (93%)	14 (7%)	0	100	100
14	LF	245/249 (98%)	237 (97%)	8 (3%)	0	100	100
15	LG	233/262 (89%)	229 (98%)	4 (2%)	0	100	100
16	LH	189/192 (98%)	184 (97%)	5 (3%)	0	100	100
17	LI	215/219 (98%)	202 (94%)	13 (6%)	0	100	100
18	LJ	165/173 (95%)	160 (97%)	5 (3%)	0	100	100
19	LK	153/165 (93%)	135 (88%)	17 (11%)	1 (1%)	22	61
20	LL	207/213 (97%)	201 (97%)	6 (3%)	0	100	100
21	LM	139/142 (98%)	134 (96%)	5 (4%)	0	100	100
22	LN	200/203 (98%)	192 (96%)	8 (4%)	0	100	100
23	LO	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
24	LP	184/187 (98%)	177 (96%)	7 (4%)	0	100	100
25	LQ	181/213 (85%)	174 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	LR	182/192 (95%)	176 (97%)	6 (3%)	0	100	100
27	LS	171/174 (98%)	166 (97%)	5 (3%)	0	100	100
28	LT	156/160 (98%)	154 (99%)	2 (1%)	0	100	100
29	LU	100/127 (79%)	99 (99%)	1 (1%)	0	100	100
30	LV	133/139 (96%)	130 (98%)	3 (2%)	0	100	100
31	LW	131/161 (81%)	129 (98%)	2 (2%)	0	100	100
32	LX	119/156 (76%)	112 (94%)	7 (6%)	0	100	100
33	LY	132/138 (96%)	130 (98%)	2 (2%)	0	100	100
34	LZ	133/135 (98%)	132 (99%)	1 (1%)	0	100	100
35	La	146/149 (98%)	137 (94%)	9 (6%)	0	100	100
36	Lb	60/65 (92%)	59 (98%)	1 (2%)	0	100	100
37	Lc	95/108 (88%)	95 (100%)	0	0	100	100
38	Ld	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
39	Le	122/131 (93%)	119 (98%)	3 (2%)	0	100	100
40	Lf	105/109 (96%)	100 (95%)	5 (5%)	0	100	100
41	Lg	110/119 (92%)	105 (96%)	5 (4%)	0	100	100
42	Lh	120/126 (95%)	116 (97%)	4 (3%)	0	100	100
43	Li	100/110 (91%)	95 (95%)	5 (5%)	0	100	100
44	Lj	84/95 (88%)	78 (93%)	5 (6%)	1 (1%)	13	49
45	Lk	78/81 (96%)	77 (99%)	1 (1%)	0	100	100
46	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
47	Lm	50/128 (39%)	50 (100%)	0	0	100	100
48	Ln	22/25 (88%)	22 (100%)	0	0	100	100
48	Lr	22/25 (88%)	22 (100%)	0	0	100	100
49	Lo	102/106 (96%)	99 (97%)	3 (3%)	0	100	100
50	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
51	Lq	139/147 (95%)	135 (97%)	4 (3%)	0	100	100
52	Ls	187/312 (60%)	182 (97%)	5 (3%)	0	100	100
54	SA	206/285 (72%)	195 (95%)	11 (5%)	0	100	100
55	SB	230/255 (90%)	214 (93%)	16 (7%)	0	100	100
56	SC	214/263 (81%)	206 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	SD	210/254 (83%)	199 (95%)	11 (5%)	0	100	100
58	SE	259/264 (98%)	245 (95%)	14 (5%)	0	100	100
59	SF	197/212 (93%)	187 (95%)	10 (5%)	0	100	100
60	SG	230/239 (96%)	223 (97%)	7 (3%)	0	100	100
61	SH	193/203 (95%)	187 (97%)	6 (3%)	0	100	100
62	SI	199/202 (98%)	196 (98%)	3 (2%)	0	100	100
63	SJ	177/190 (93%)	172 (97%)	5 (3%)	0	100	100
64	SK	87/159 (55%)	84 (97%)	3 (3%)	0	100	100
65	SL	148/161 (92%)	145 (98%)	3 (2%)	0	100	100
66	SM	116/144 (81%)	105 (90%)	11 (10%)	0	100	100
67	SN	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
68	SO	133/150 (89%)	124 (93%)	9 (7%)	0	100	100
69	SP	113/153 (74%)	109 (96%)	4 (4%)	0	100	100
70	SQ	136/143 (95%)	128 (94%)	8 (6%)	0	100	100
71	SR	126/143 (88%)	121 (96%)	5 (4%)	0	100	100
72	SS	135/156 (86%)	125 (93%)	10 (7%)	0	100	100
73	ST	140/153 (92%)	135 (96%)	5 (4%)	0	100	100
74	SU	101/116 (87%)	95 (94%)	6 (6%)	0	100	100
75	SV	84/98 (86%)	82 (98%)	2 (2%)	0	100	100
76	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
77	SX	140/145 (97%)	130 (93%)	10 (7%)	0	100	100
78	SY	130/136 (96%)	128 (98%)	2 (2%)	0	100	100
79	SZ	67/99 (68%)	67 (100%)	0	0	100	100
80	Sa	102/119 (86%)	99 (97%)	3 (3%)	0	100	100
81	Sb	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
82	Sc	59/68 (87%)	57 (97%)	2 (3%)	0	100	100
83	Sd	50/56 (89%)	47 (94%)	3 (6%)	0	100	100
84	Se	38/62 (61%)	38 (100%)	0	0	100	100
85	Sf	71/154 (46%)	64 (90%)	7 (10%)	0	100	100
All	All	12586/14205 (89%)	12071 (96%)	508 (4%)	7 (0%)	54	83

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	C	251	GLU
8	D	450	VAL
8	D	556	ASP
19	LK	88	PRO
44	Lj	39	TYR
8	D	421	PRO
8	D	555	THR

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
5	A	271/274 (99%)	268 (99%)	3 (1%)	73 88
6	B	22/224 (10%)	22 (100%)	0	100 100
7	C	358/367 (98%)	355 (99%)	3 (1%)	81 93
8	D	427/474 (90%)	422 (99%)	5 (1%)	71 88
9	LA	196/198 (99%)	194 (99%)	2 (1%)	76 90
10	LB	327/331 (99%)	327 (100%)	0	100 100
11	LC	284/285 (100%)	283 (100%)	1 (0%)	91 95
12	LD	250/253 (99%)	250 (100%)	0	100 100
13	LE	162/166 (98%)	162 (100%)	0	100 100
14	LF	213/215 (99%)	212 (100%)	1 (0%)	88 95
15	LG	203/222 (91%)	203 (100%)	0	100 100
16	LH	168/169 (99%)	167 (99%)	1 (1%)	86 94
17	LI	182/183 (100%)	182 (100%)	0	100 100
18	LJ	145/150 (97%)	143 (99%)	2 (1%)	67 86
20	LL	172/176 (98%)	172 (100%)	0	100 100
21	LM	116/117 (99%)	116 (100%)	0	100 100
22	LN	179/180 (99%)	177 (99%)	2 (1%)	73 88
23	LO	161/162 (99%)	161 (100%)	0	100 100
24	LP	151/152 (99%)	151 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	LQ	155/178 (87%)	154 (99%)	1 (1%)	86	94
26	LR	153/160 (96%)	153 (100%)	0	100	100
27	LS	153/154 (99%)	153 (100%)	0	100	100
28	LT	134/135 (99%)	134 (100%)	0	100	100
29	LU	90/108 (83%)	89 (99%)	1 (1%)	73	88
30	LV	99/102 (97%)	99 (100%)	0	100	100
31	LW	107/125 (86%)	107 (100%)	0	100	100
32	LX	108/129 (84%)	108 (100%)	0	100	100
33	LY	117/119 (98%)	117 (100%)	0	100	100
34	LZ	121/121 (100%)	121 (100%)	0	100	100
35	La	121/122 (99%)	121 (100%)	0	100	100
36	Lb	53/55 (96%)	53 (100%)	0	100	100
37	Lc	78/88 (89%)	78 (100%)	0	100	100
38	Ld	104/105 (99%)	103 (99%)	1 (1%)	76	90
39	Le	107/114 (94%)	107 (100%)	0	100	100
40	Lf	88/90 (98%)	88 (100%)	0	100	100
41	Lg	97/102 (95%)	96 (99%)	1 (1%)	76	90
42	Lh	109/112 (97%)	109 (100%)	0	100	100
43	Li	86/93 (92%)	85 (99%)	1 (1%)	71	88
44	Lj	70/78 (90%)	70 (100%)	0	100	100
45	Lk	76/77 (99%)	76 (100%)	0	100	100
46	Ll	45/46 (98%)	45 (100%)	0	100	100
47	Lm	47/115 (41%)	47 (100%)	0	100	100
48	Ln	22/23 (96%)	17 (77%)	5 (23%)	1	4
48	Lr	22/23 (96%)	17 (77%)	5 (23%)	1	4
49	Lo	88/90 (98%)	88 (100%)	0	100	100
50	Lp	73/74 (99%)	73 (100%)	0	100	100
51	Lq	109/112 (97%)	109 (100%)	0	100	100
52	Ls	155/255 (61%)	154 (99%)	1 (1%)	86	94
54	SA	178/225 (79%)	177 (99%)	1 (1%)	86	94
55	SB	203/223 (91%)	203 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	SC	181/206 (88%)	181 (100%)	0	100	100
57	SD	182/206 (88%)	180 (99%)	2 (1%)	73	88
58	SE	219/221 (99%)	216 (99%)	3 (1%)	67	86
59	SF	167/178 (94%)	164 (98%)	3 (2%)	59	82
60	SG	198/204 (97%)	196 (99%)	2 (1%)	76	90
61	SH	169/177 (96%)	169 (100%)	0	100	100
62	SI	163/164 (99%)	162 (99%)	1 (1%)	86	94
63	SJ	154/162 (95%)	153 (99%)	1 (1%)	86	94
64	SK	77/126 (61%)	77 (100%)	0	100	100
65	SL	133/143 (93%)	133 (100%)	0	100	100
66	SM	101/121 (84%)	101 (100%)	0	100	100
67	SN	129/130 (99%)	129 (100%)	0	100	100
68	SO	102/117 (87%)	102 (100%)	0	100	100
69	SP	99/132 (75%)	97 (98%)	2 (2%)	55	80
70	SQ	111/115 (96%)	111 (100%)	0	100	100
71	SR	119/131 (91%)	117 (98%)	2 (2%)	60	83
72	SS	120/135 (89%)	119 (99%)	1 (1%)	81	93
73	ST	114/124 (92%)	112 (98%)	2 (2%)	59	82
74	SU	93/103 (90%)	92 (99%)	1 (1%)	73	88
75	SV	69/80 (86%)	69 (100%)	0	100	100
76	SW	112/113 (99%)	111 (99%)	1 (1%)	78	91
77	SX	113/116 (97%)	113 (100%)	0	100	100
78	SY	112/115 (97%)	109 (97%)	3 (3%)	44	75
79	SZ	60/80 (75%)	59 (98%)	1 (2%)	60	83
80	Sa	91/103 (88%)	89 (98%)	2 (2%)	52	79
81	Sb	70/71 (99%)	70 (100%)	0	100	100
82	Sc	54/61 (88%)	54 (100%)	0	100	100
83	Sd	43/46 (94%)	43 (100%)	0	100	100
84	Se	34/51 (67%)	33 (97%)	1 (3%)	42	74
85	Sf	66/139 (48%)	64 (97%)	2 (3%)	41	73
All	All	10610/11721 (90%)	10543 (99%)	67 (1%)	86	94

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	A	36	ARG
5	A	88	ARG
5	A	225	LYS
7	C	37	ARG
7	C	246	VAL
7	C	429	ARG
8	D	136	ARG
8	D	265	LYS
8	D	285	LYS
8	D	359	ARG
8	D	365	ARG
9	LA	139	HIS
9	LA	194	ASN
11	LC	94	MET
14	LF	23	LYS
16	LH	143	LYS
18	LJ	52	ARG
18	LJ	144	ARG
22	LN	26	ARG
22	LN	38	ARG
25	LQ	119	ARG
29	LU	16	LYS
38	Ld	49	GLN
41	Lg	107	LYS
43	Li	45	ARG
48	Ln	4	LYS
48	Ln	10	THR
48	Ln	11	ARG
48	Ln	15	ARG
48	Ln	20	VAL
48	Lr	4	LYS
48	Lr	10	THR
48	Lr	11	ARG
48	Lr	15	ARG
48	Lr	20	VAL
52	Ls	61	ARG
54	SA	168	LYS
57	SD	43	ARG
57	SD	144	LYS
58	SE	128	ARG
58	SE	239	LYS
58	SE	257	ARG

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Mol	Chain	Res	Type
59	SF	41	ARG
59	SF	50	GLN
59	SF	211	ASN
60	SG	98	ARG
60	SG	192	HIS
62	SI	140	LYS
63	SJ	136	LYS
69	SP	69	ARG
69	SP	76	LYS
71	SR	5	ARG
71	SR	67	ARG
72	SS	143	ARG
73	ST	75	ARG
73	ST	78	LYS
74	SU	43	LYS
76	SW	97	ARG
78	SY	115	LYS
78	SY	126	LYS
78	SY	134	LYS
79	SZ	41	LYS
80	Sa	12	LYS
80	Sa	93	ARG
84	Se	36	LYS
85	Sf	119	ARG
85	Sf	143	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
5	A	244	ASN
7	C	153	GLN
7	C	265	ASN
8	D	85	GLN
8	D	328	ASN
8	D	363	ASN
9	LA	100	ASN
10	LB	174	GLN
10	LB	346	HIS
24	LP	175	GLN
27	LS	5	GLN
32	LX	81	ASN
32	LX	107	GLN

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Mol	Chain	Res	Type
42	Lh	37	GLN
54	SA	86	GLN
57	SD	29	GLN
59	SF	118	GLN
59	SF	173	ASN
60	SG	65	GLN
60	SG	189	HIS
60	SG	213	GLN
61	SH	17	GLN
61	SH	18	ASN
62	SI	119	GLN
62	SI	146	GLN
63	SJ	108	GLN
63	SJ	121	HIS
64	SK	45	GLN
64	SK	48	GLN
67	SN	32	GLN
71	SR	31	ASN
71	SR	48	ASN
72	SS	26	GLN
73	ST	127	GLN
76	SW	42	GLN
77	SX	22	GLN
81	Sb	61	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3188/3337 (95%)	524 (16%)	51 (1%)
2	2	1770/1796 (98%)	374 (21%)	48 (2%)
3	3	118/120 (98%)	9 (7%)	1 (0%)
4	4	155/156 (99%)	26 (16%)	3 (1%)
All	All	5231/5409 (96%)	933 (17%)	103 (1%)

All (933) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	27	A
1	1	41	A
1	1	44	A
1	1	50	A

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Mol	Chain	Res	Type
1	1	60	G
1	1	61	A
1	1	66	A
1	1	67	A
1	1	93	G
1	1	97	G
1	1	111	G
1	1	114	C
1	1	117	A
1	1	118	U
1	1	119	U
1	1	123	A
1	1	132	U
1	1	133	C
1	1	134	G
1	1	135	G
1	1	144	G
1	1	152	G
1	1	153	A
1	1	165	G
1	1	170	A
1	1	179	C
1	1	181	G
1	1	184	U
1	1	185	U
1	1	204	C
1	1	207	A
1	1	212	G
1	1	213	A
1	1	214	G
1	1	215	A
1	1	225	A
1	1	234	C
1	1	251	U
1	1	262	G
1	1	276	G
1	1	277	A
1	1	279	U
1	1	288	A
1	1	308	C
1	1	316	A
1	1	332	C

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Mol	Chain	Res	Type
1	1	343	C
1	1	363	U
1	1	369	G
1	1	385	G
1	1	391	U
1	1	392	A
1	1	394	C
1	1	395	A
1	1	396	C
1	1	414	G
1	1	415	A
1	1	422	U
1	1	432	C
1	1	433	U
1	1	434	U
1	1	445	G
1	1	446	A
1	1	447	U
1	1	448	C
1	1	456	G
1	1	458	U
1	1	460	U
1	1	461	C
1	1	469	C
1	1	471	C
1	1	472	U
1	1	475	G
1	1	476	C
1	1	481	C
1	1	485	G
1	1	489	A
1	1	511	U
1	1	512	A
1	1	527	G
1	1	538	G
1	1	539	G
1	1	547	A
1	1	549	A
1	1	559	G
1	1	560	U
1	1	570	G
1	1	580	A

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Mol	Chain	Res	Type
1	1	583	A
1	1	591	C
1	1	592	U
1	1	593	G
1	1	597	G
1	1	599	A
1	1	608	U
1	1	609	A
1	1	610	A
1	1	624	C
1	1	637	A
1	1	648	A
1	1	665	A
1	1	669	U
1	1	679	A
1	1	697	A
1	1	700	G
1	1	703	A
1	1	704	A
1	1	715	A
1	1	722	G
1	1	746	U
1	1	748	U
1	1	749	U
1	1	758	U
1	1	759	U
1	1	763	G
1	1	767	G
1	1	783	A
1	1	788	A
1	1	799	A
1	1	812	A
1	1	843	C
1	1	856	U
1	1	861	U
1	1	862	G
1	1	878	A
1	1	889	G
1	1	890	G
1	1	896	A
1	1	898	G
1	1	899	A

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Mol	Chain	Res	Type
1	1	919	G
1	1	926	A
1	1	941	C
1	1	942	U
1	1	943	C
1	1	959	A
1	1	960	C
1	1	961	C
1	1	962	U
1	1	984	A
1	1	992	G
1	1	998	C
1	1	999	G
1	1	1003	G
1	1	1006	A
1	1	1007	U
1	1	1008	U
1	1	1009	U
1	1	1010	U
1	1	1011	U
1	1	1012	A
1	1	1013	G
1	1	1015	C
1	1	1017	U
1	1	1030	A
1	1	1032	C
1	1	1047	A
1	1	1048	A
1	1	1055	G
1	1	1064	C
1	1	1065	U
1	1	1068	A
1	1	1077	U
1	1	1078	U
1	1	1079	C
1	1	1080	G
1	1	1081	A
1	1	1086	A
1	1	1087	U
1	1	1088	C
1	1	1100	G
1	1	1114	G

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Mol	Chain	Res	Type
1	1	1131	G
1	1	1134	U
1	1	1136	A
1	1	1142	A
1	1	1161	G
1	1	1163	G
1	1	1164	U
1	1	1165	G
1	1	1175	C
1	1	1184	C
1	1	1189	G
1	1	1195	A
1	1	1204	U
1	1	1205	G
1	1	1215	C
1	1	1218	U
1	1	1219	G
1	1	1220	G
1	1	1221	C
1	1	1222	C
1	1	1224	U
1	1	1225	G
1	1	1226	G
1	1	1227	A
1	1	1228	A
1	1	1229	G
1	1	1231	C
1	1	1233	G
1	1	1245	G
1	1	1246	A
1	1	1247	C
1	1	1248	U
1	1	1264	U
1	1	1268	G
1	1	1272	G
1	1	1278	G
1	1	1290	G
1	1	1291	A
1	1	1292	U
1	1	1296	G
1	1	1313	A
1	1	1314	U

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Mol	Chain	Res	Type
1	1	1331	A
1	1	1332	G
1	1	1333	A
1	1	1335	A
1	1	1336	C
1	1	1337	G
1	1	1339	U
1	1	1369	A
1	1	1382	A
1	1	1383	G
1	1	1402	A
1	1	1404	G
1	1	1417	G
1	1	1420	C
1	1	1433	G
1	1	1458	G
1	1	1464	A
1	1	1465	A
1	1	1466	G
1	1	1485	G
1	1	1491	C
1	1	1495	U
1	1	1506	U
1	1	1516	U
1	1	1537	U
1	1	1538	U
1	1	1539	C
1	1	1540	A
1	1	1543	G
1	1	1545	G
1	1	1552	G
1	1	1554	G
1	1	1555	C
1	1	1560	U
1	1	1561	G
1	1	1562	U
1	1	1563	G
1	1	1567	A
1	1	1585	A
1	1	1587	U
1	1	1588	C
1	1	1609	U

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Mol	Chain	Res	Type
1	1	1611	C
1	1	1619	C
1	1	1622	A
1	1	1623	A
1	1	1624	C
1	1	1625	U
1	1	1637	C
1	1	1685	U
1	1	1696	A
1	1	1697	C
1	1	1704	U
1	1	1727	G
1	1	1730	A
1	1	1731	G
1	1	1740	A
1	1	1741	C
1	1	1742	U
1	1	1745	U
1	1	1746	G
1	1	1748	C
1	1	1750	G
1	1	1760	G
1	1	1774	U
1	1	1775	U
1	1	1777	A
1	1	1794	A
1	1	1796	A
1	1	1797	A
1	1	1798	U
1	1	1799	U
1	1	1800	C
1	1	1801	U
1	1	1819	A
1	1	1820	U
1	1	1821	A
1	1	1822	A
1	1	1826	C
1	1	1829	C
1	1	1830	A
1	1	1858	G
1	1	1859	A
1	1	1860	U

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Mol	Chain	Res	Type
1	1	1866	A
1	1	1886	G
1	1	1888	A
1	1	1906	C
1	1	1933	G
1	1	1934	G
1	1	1935	C
1	1	1936	A
1	1	1937	C
1	1	1938	G
1	1	1939	U
1	1	1941	G
1	1	2045	G
1	1	2046	C
1	1	2047	G
1	1	2048	U
1	1	2054	U
1	1	2055	A
1	1	2063	A
1	1	2065	U
1	1	2076	A
1	1	2084	G
1	1	2085	G
1	1	2094	A
1	1	2107	A
1	1	2121	A
1	1	2123	G
1	1	2132	G
1	1	2133	U
1	1	2134	G
1	1	2139	U
1	1	2151	A
1	1	2168	U
1	1	2170	A
1	1	2171	A
1	1	2172	U
1	1	2173	G
1	1	2186	A
1	1	2192	A
1	1	2207	A
1	1	2212	G
1	1	2216	G

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Mol	Chain	Res	Type
1	1	2219	A
1	1	2221	U
1	1	2228	C
1	1	2233	A
1	1	2235	G
1	1	2236	G
1	1	2242	A
1	1	2244	A
1	1	2248	C
1	1	2251	G
1	1	2270	G
1	1	2273	U
1	1	2276	A
1	1	2278	G
1	1	2281	U
1	1	2297	U
1	1	2299	U
1	1	2335	A
1	1	2336	A
1	1	2337	C
1	1	2338	G
1	1	2339	G
1	1	2356	G
1	1	2360	A
1	1	2364	A
1	1	2365	A
1	1	2366	G
1	1	2367	A
1	1	2374	U
1	1	2382	A
1	1	2409	U
1	1	2410	A
1	1	2459	U
1	1	2460	C
1	1	2463	A
1	1	2464	U
1	1	2465	U
1	1	2474	A
1	1	2477	U
1	1	2478	A
1	1	2487	A
1	1	2488	G

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Mol	Chain	Res	Type
1	1	2489	C
1	1	2492	G
1	1	2498	A
1	1	2501	U
1	1	2502	G
1	1	2503	C
1	1	2504	G
1	1	2505	U
1	1	2506	C
1	1	2508	A
1	1	2510	C
1	1	2513	C
1	1	2521	A
1	1	2529	U
1	1	2530	C
1	1	2531	G
1	1	2532	C
1	1	2533	G
1	1	2543	G
1	1	2544	G
1	1	2552	A
1	1	2553	C
1	1	2565	G
1	1	2566	G
1	1	2573	G
1	1	2578	OMG
1	1	2585	A
1	1	2611	U
1	1	2615	A
1	1	2622	G
1	1	2633	A
1	1	2636	G
1	1	2648	A
1	1	2650	A
1	1	2653	A
1	1	2655	A
1	1	2663	A
1	1	2673	G
1	1	2687	G
1	1	2688	U
1	1	2711	U
1	1	2712	G

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Mol	Chain	Res	Type
1	1	2714	C
1	1	2721	A
1	1	2731	C
1	1	2732	C
1	1	2736	G
1	1	2737	A
1	1	2755	G
1	1	2758	A
1	1	2759	G
1	1	2760	A
1	1	2763	A
1	1	2769	C
1	1	2776	A
1	1	2777	U
1	1	2778	A
1	1	2788	U
1	1	2798	G
1	1	2803	C
1	1	2804	A
1	1	2828	U
1	1	2830	G
1	1	2831	A
1	1	2846	A
1	1	2858	C
1	1	2863	U
1	1	2882	U
1	1	2894	U
1	1	2895	A
1	1	2900	A
1	1	2906	G
1	1	2930	A
1	1	2942	C
1	1	2970	A
1	1	3007	A
1	1	3008	U
1	1	3014	U
1	1	3017	G
1	1	3036	G
1	1	3044	A
1	1	3050	C
1	1	3051	C
1	1	3059	G

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Mol	Chain	Res	Type
1	1	3074	G
1	1	3080	A
1	1	3088	A
1	1	3089	U
1	1	3100	A
1	1	3101	C
1	1	3111	C
1	1	3112	U
1	1	3113	A
1	1	3119	A
1	1	3122	U
1	1	3127	G
1	1	3128	A
1	1	3130	G
1	1	3131	U
1	1	3132	A
1	1	3135	A
1	1	3141	G
1	1	3146	C
1	1	3147	G
1	1	3162	C
1	1	3163	A
1	1	3164	G
1	1	3170	U
1	1	3188	G
1	1	3189	U
1	1	3200	A
1	1	3201	A
1	1	3211	U
1	1	3214	A
1	1	3217	U
1	1	3218	U
1	1	3219	A
1	1	3223	A
1	1	3225	G
1	1	3227	G
1	1	3229	G
1	1	3230	G
1	1	3231	G
1	1	3235	A
1	1	3245	C
1	1	3248	A

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Mol	Chain	Res	Type
1	1	3257	A
1	1	3258	U
1	1	3259	G
1	1	3260	U
1	1	3282	U
1	1	3286	G
1	1	3292	U
1	1	3299	U
1	1	3309	U
1	1	3310	G
1	1	3319	C
1	1	3324	C
1	1	3325	U
1	1	3331	U
1	1	3332	A
1	1	3333	G
2	2	17	C
2	2	25	C
2	2	26	A
2	2	27	U
2	2	34	G
2	2	42	G
2	2	47	A
2	2	57	G
2	2	68	A
2	2	69	G
2	2	73	U
2	2	74	U
2	2	75	A
2	2	76	U
2	2	77	A
2	2	82	G
2	2	83	A
2	2	103	A
2	2	113	C
2	2	115	U
2	2	126	G
2	2	127	U
2	2	128	A
2	2	129	C
2	2	130	C
2	2	131	U

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Mol	Chain	Res	Type
2	2	132	U
2	2	133	A
2	2	134	C
2	2	135	U
2	2	136	A
2	2	137	C
2	2	138	A
2	2	155	U
2	2	156	U
2	2	173	C
2	2	175	G
2	2	177	A
2	2	185	A
2	2	186	C
2	2	187	U
2	2	188	U
2	2	189	C
2	2	190	G
2	2	192	A
2	2	210	A
2	2	212	U
2	2	213	A
2	2	214	A
2	2	215	A
2	2	216	A
2	2	218	C
2	2	219	C
2	2	222	U
2	2	223	G
2	2	224	C
2	2	228	U
2	2	229	C
2	2	230	G
2	2	231	G
2	2	232	G
2	2	233	G
2	2	234	C
2	2	235	U
2	2	236	U
2	2	237	U
2	2	247	C
2	2	258	C

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Mol	Chain	Res	Type
2	2	262	A
2	2	269	C
2	2	270	G
2	2	272	C
2	2	273	C
2	2	274	U
2	2	275	U
2	2	276	G
2	2	277	C
2	2	278	G
2	2	284	G
2	2	287	G
2	2	296	A
2	2	311	C
2	2	313	A
2	2	317	U
2	2	319	G
2	2	321	C
2	2	326	G
2	2	334	G
2	2	335	C
2	2	338	G
2	2	349	A
2	2	353	G
2	2	356	A
2	2	357	A
2	2	358	C
2	2	367	A
2	2	377	C
2	2	396	A
2	2	397	A
2	2	399	C
2	2	401	G
2	2	414	A
2	2	415	G
2	2	421	C
2	2	422	A
2	2	423	G
2	2	431	G
2	2	436	U
2	2	441	C
2	2	445	C

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Mol	Chain	Res	Type
2	2	451	A
2	2	452	C
2	2	465	A
2	2	472	A
2	2	474	A
2	2	490	U
2	2	491	U
2	2	492	C
2	2	493	G
2	2	505	U
2	2	510	U
2	2	511	G
2	2	512	A
2	2	535	A
2	2	536	G
2	2	537	G
2	2	538	A
2	2	539	A
2	2	540	C
2	2	541	A
2	2	552	A
2	2	553	A
2	2	554	G
2	2	555	U
2	2	556	C
2	2	562	C
2	2	567	A
2	2	571	G
2	2	576	A
2	2	577	A
2	2	579	U
2	2	591	A
2	2	592	G
2	2	608	U
2	2	611	A
2	2	612	G
2	2	616	A
2	2	617	A
2	2	619	A
2	2	620	A
2	2	621	G
2	2	636	U

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Mol	Chain	Res	Type
2	2	641	C
2	2	646	C
2	2	647	C
2	2	652	G
2	2	674	G
2	2	677	U
2	2	678	G
2	2	679	G
2	2	680	G
2	2	681	C
2	2	686	C
2	2	688	U
2	2	689	U
2	2	690	U
2	2	692	C
2	2	693	U
2	2	703	C
2	2	705	G
2	2	710	C
2	2	723	G
2	2	725	G
2	2	726	U
2	2	727	C
2	2	728	G
2	2	730	G
2	2	731	G
2	2	732	A
2	2	734	C
2	2	737	G
2	2	740	C
2	2	741	U
2	2	754	A
2	2	755	A
2	2	764	G
2	2	765	C
2	2	773	A
2	2	774	G
2	2	779	A
2	2	780	U
2	2	781	G
2	2	787	A
2	2	792	U

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Mol	Chain	Res	Type
2	2	793	U
2	2	809	A
2	2	810	A
2	2	818	U
2	2	819	G
2	2	821	G
2	2	823	U
2	2	827	A
2	2	829	U
2	2	830	U
2	2	832	G
2	2	861	A
2	2	884	U
2	2	896	A
2	2	910	U
2	2	911	G
2	2	912	G
2	2	931	A
2	2	933	U
2	2	940	G
2	2	949	A
2	2	957	U
2	2	958	U
2	2	964	A
2	2	982	G
2	2	990	A
2	2	991	A
2	2	1002	U
2	2	1003	A
2	2	1024	A
2	2	1026	C
2	2	1037	A
2	2	1055	A
2	2	1056	U
2	2	1057	U
2	2	1058	U
2	2	1059	U
2	2	1079	C
2	2	1088	A
2	2	1089	A
2	2	1090	A
2	2	1093	G

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Mol	Chain	Res	Type
2	2	1094	U
2	2	1095	U
2	2	1097	G
2	2	1135	A
2	2	1140	A
2	2	1147	G
2	2	1155	C
2	2	1156	C
2	2	1157	A
2	2	1166	G
2	2	1182	U
2	2	1188	U
2	2	1191	A
2	2	1193	A
2	2	1194	C
2	2	1196	G
2	2	1197	G
2	2	1214	A
2	2	1215	G
2	2	1223	G
2	2	1224	A
2	2	1225	G
2	2	1226	G
2	2	1227	A
2	2	1228	U
2	2	1237	U
2	2	1238	G
2	2	1240	G
2	2	1241	A
2	2	1242	G
2	2	1243	C
2	2	1248	U
2	2	1249	C
2	2	1252	G
2	2	1253	A
2	2	1254	U
2	2	1255	U
2	2	1282	U
2	2	1283	U
2	2	1311	U
2	2	1312	U
2	2	1313	G

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Mol	Chain	Res	Type
2	2	1318	A
2	2	1335	C
2	2	1336	C
2	2	1337	U
2	2	1338	G
2	2	1341	A
2	2	1342	A
2	2	1344	U
2	2	1345	A
2	2	1348	C
2	2	1358	U
2	2	1359	U
2	2	1360	G
2	2	1364	G
2	2	1365	U
2	2	1374	U
2	2	1375	U
2	2	1378	U
2	2	1379	A
2	2	1380	G
2	2	1382	G
2	2	1383	G
2	2	1384	G
2	2	1385	A
2	2	1387	U
2	2	1388	A
2	2	1406	A
2	2	1408	G
2	2	1409	U
2	2	1411	U
2	2	1421	A
2	2	1423	A
2	2	1424	G
2	2	1439	U
2	2	1441	G
2	2	1444	G
2	2	1455	C
2	2	1467	A
2	2	1474	G
2	2	1478	C
2	2	1482	G
2	2	1486	A

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Mol	Chain	Res	Type
2	2	1487	C
2	2	1489	C
2	2	1499	A
2	2	1502	G
2	2	1512	A
2	2	1517	G
2	2	1519	U
2	2	1532	G
2	2	1533	C
2	2	1534	U
2	2	1538	G
2	2	1553	U
2	2	1555	A
2	2	1564	C
2	2	1565	A
2	2	1570	G
2	2	1580	G
2	2	1586	G
2	2	1597	G
2	2	1612	G
2	2	1617	U
2	2	1627	A
2	2	1631	A
2	2	1653	U
2	2	1654	G
2	2	1677	A
2	2	1678	C
2	2	1684	C
2	2	1686	G
2	2	1691	G
2	2	1693	C
2	2	1696	C
2	2	1700	G
2	2	1701	A
2	2	1704	A
2	2	1708	A
2	2	1709	G
2	2	1711	G
2	2	1714	G
2	2	1726	A
2	2	1756	G
2	2	1763	G

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Mol	Chain	Res	Type
2	2	1765	U
2	2	1766	C
2	2	1776	G
2	2	1778	A
2	2	1779	C
2	2	1788	G
2	2	1789	G
2	2	1790	A
2	2	1791	U
2	2	1792	C
2	2	1795	U
2	2	1796	U
3	3	7	G
3	3	54	U
3	3	55	A
3	3	65	G
3	3	73	U
3	3	90	G
3	3	92	C
3	3	101	A
3	3	111	G
4	4	23	U
4	4	34	U
4	4	35	C
4	4	48	A
4	4	59	A
4	4	62	A
4	4	63	G
4	4	79	A
4	4	80	A
4	4	81	U
4	4	82	U
4	4	83	C
4	4	84	C
4	4	85	G
4	4	86	U
4	4	87	G
4	4	88	A
4	4	95	G
4	4	103	G
4	4	104	A
4	4	105	A

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Mol	Chain	Res	Type
4	4	106	C
4	4	111	A
4	4	113	U
4	4	125	U
4	4	138	A

All (103) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	133	C
1	1	250	C
1	1	275	G
1	1	431	A
1	1	459	C
1	1	469	C
1	1	484	A
1	1	609	A
1	1	703	A
1	1	898	G
1	1	960	C
1	1	1009	U
1	1	1016	U
1	1	1047	A
1	1	1219	G
1	1	1224	U
1	1	1226	G
1	1	1246	A
1	1	1267	C
1	1	1277	A
1	1	1290	G
1	1	1338	A
1	1	1587	U
1	1	1741	C
1	1	1774	U
1	1	1796	A
1	1	2064	C
1	1	2075	U
1	1	2167	C
1	1	2172	U
1	1	2220	C
1	1	2227	U
1	1	2232	U

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Mol	Chain	Res	Type
1	1	2502	G
1	1	2503	C
1	1	2532	C
1	1	2552	A
1	1	2621	G
1	1	2731	C
1	1	3074	G
1	1	3079	U
1	1	3121	G
1	1	3163	A
1	1	3210	U
1	1	3224	C
1	1	3230	G
1	1	3258	U
1	1	3281	G
1	1	3298	U
1	1	3323	C
1	1	3332	A
2	2	75	A
2	2	102	A
2	2	125	A
2	2	131	U
2	2	184	G
2	2	187	U
2	2	211	U
2	2	222	U
2	2	228	U
2	2	231	G
2	2	233	G
2	2	269	C
2	2	273	C
2	2	274	U
2	2	275	U
2	2	352	G
2	2	414	A
2	2	509	A
2	2	539	A
2	2	552	A
2	2	555	U
2	2	604	G
2	2	678	G
2	2	720	G

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Mol	Chain	Res	Type
2	2	725	G
2	2	740	C
2	2	754	A
2	2	792	U
2	2	827	A
2	2	1094	U
2	2	1165	U
2	2	1193	A
2	2	1197	G
2	2	1224	A
2	2	1241	A
2	2	1252	G
2	2	1282	U
2	2	1337	U
2	2	1341	A
2	2	1374	U
2	2	1378	U
2	2	1387	U
2	2	1477	C
2	2	1531	U
2	2	1564	C
2	2	1569	A
2	2	1616	C
2	2	1653	U
3	3	72	G
4	4	86	U
4	4	103	G
4	4	104	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	1	2578	1	18,26,27	1.10	2 (11%)	19,38,41	0.84	1 (5%)
23	SAC	LO	2	23	7,8,9	1.01	0	8,9,11	0.85	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	1	2578	1	-	2/5/27/28	0/3/3/3
23	SAC	LO	2	23	-	2/7/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2578	OMG	C8-N7	-2.70	1.30	1.35
1	1	2578	OMG	C5-C6	-2.26	1.42	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2578	OMG	O6-C6-C5	2.31	128.88	124.37

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	LO	2	SAC	N-CA-CB-OG
23	LO	2	SAC	C-CA-CB-OG
1	1	2578	OMG	O4'-C4'-C5'-O5'
1	1	2578	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 464 ligands modelled in this entry, 463 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	ATP	D	601	86	26,33,33	0.60	0	31,52,52	0.74	2 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	ATP	D	601	86	-	6/18/38/38	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	D	601	ATP	C5'-O5'-PA-O3A	2.28	123.82	120.35
87	D	601	ATP	PB-O3B-PG	2.06	139.89	132.83

There are no chirality outliers.

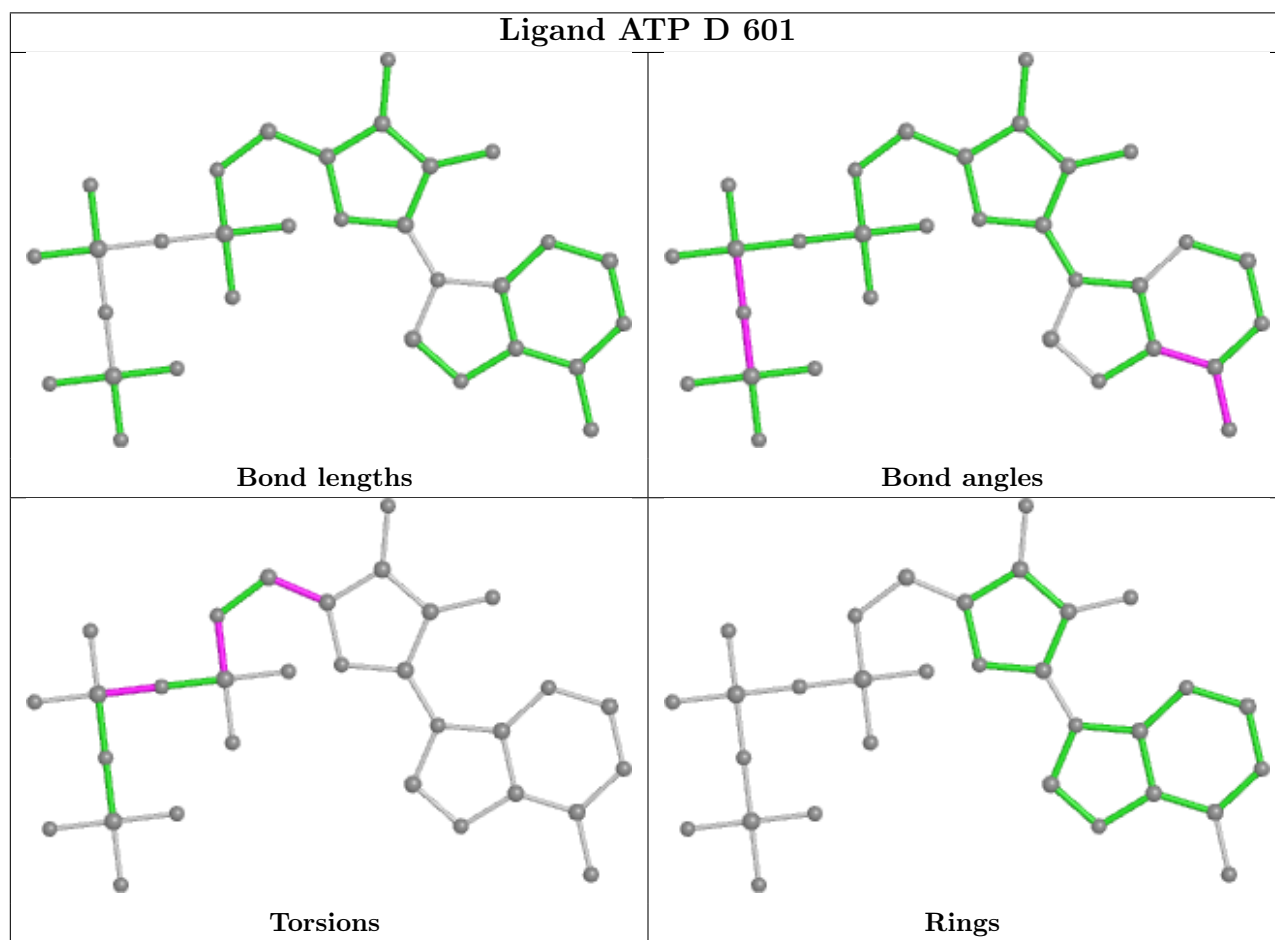
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
87	D	601	ATP	C5'-O5'-PA-O3A
87	D	601	ATP	C3'-C4'-C5'-O5'
87	D	601	ATP	O4'-C4'-C5'-O5'
87	D	601	ATP	PA-O3A-PB-O2B
87	D	601	ATP	C5'-O5'-PA-O1A
87	D	601	ATP	C5'-O5'-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

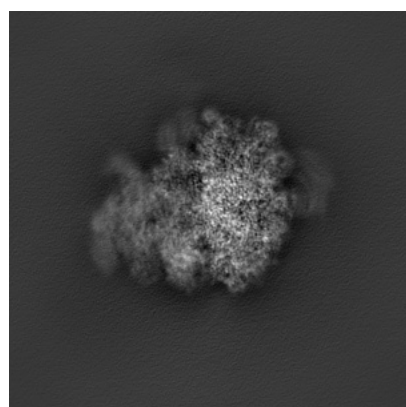
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14479. These allow visual inspection of the internal detail of the map and identification of artifacts.

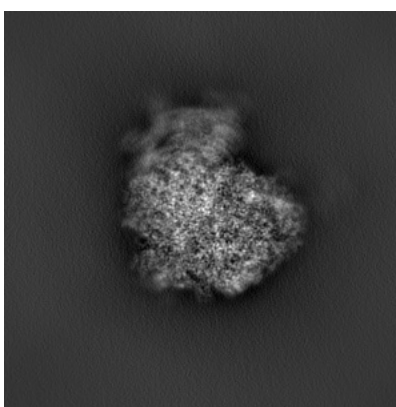
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

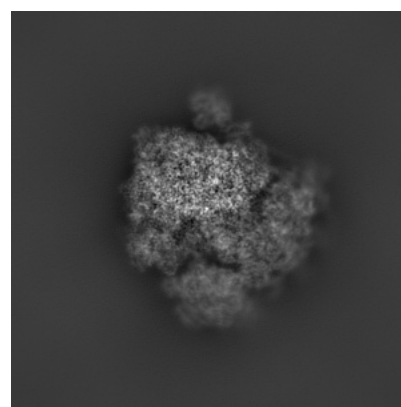
6.1.1 Primary map



X



Y

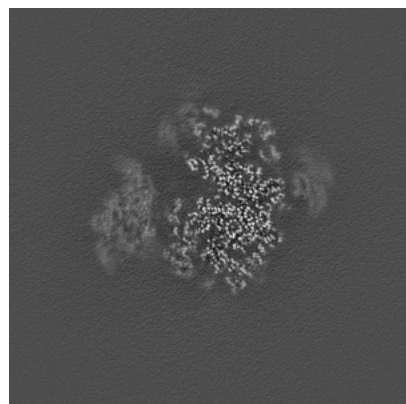


Z

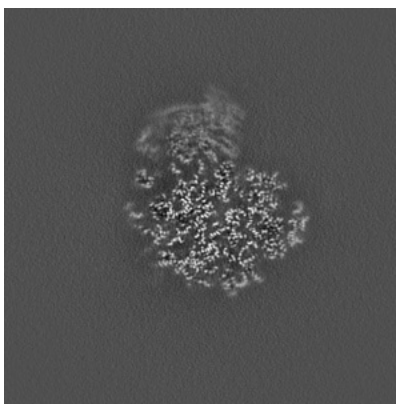
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

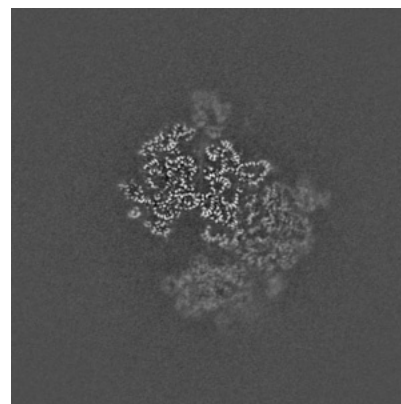
6.2.1 Primary map



X Index: 243



Y Index: 243

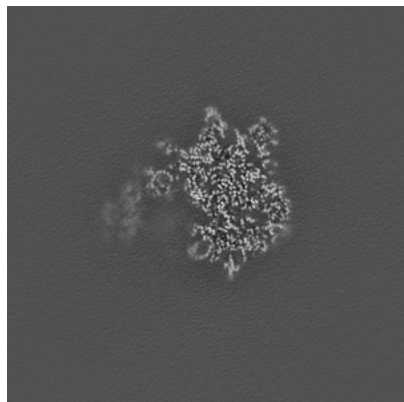


Z Index: 243

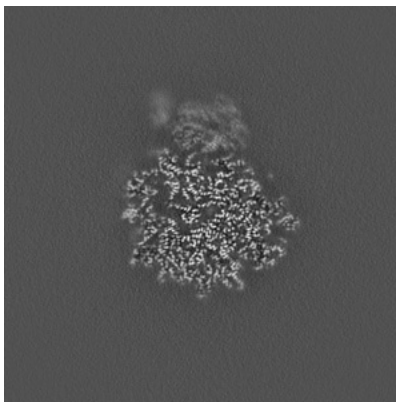
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

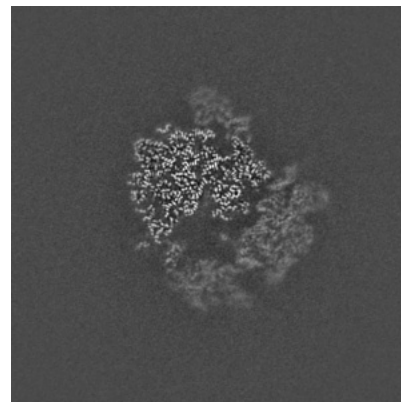
6.3.1 Primary map



X Index: 201



Y Index: 267

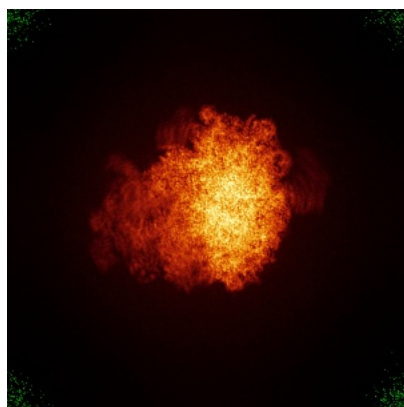


Z Index: 258

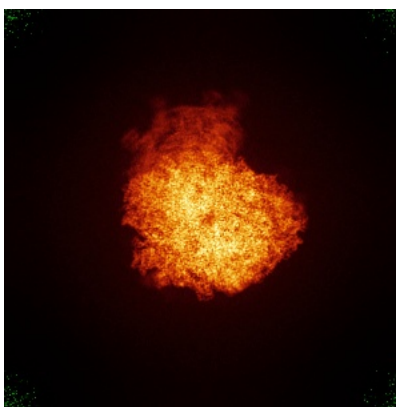
The images above show the largest variance slices of the map in three orthogonal directions.

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

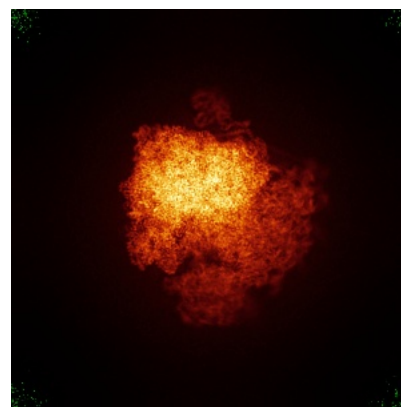
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

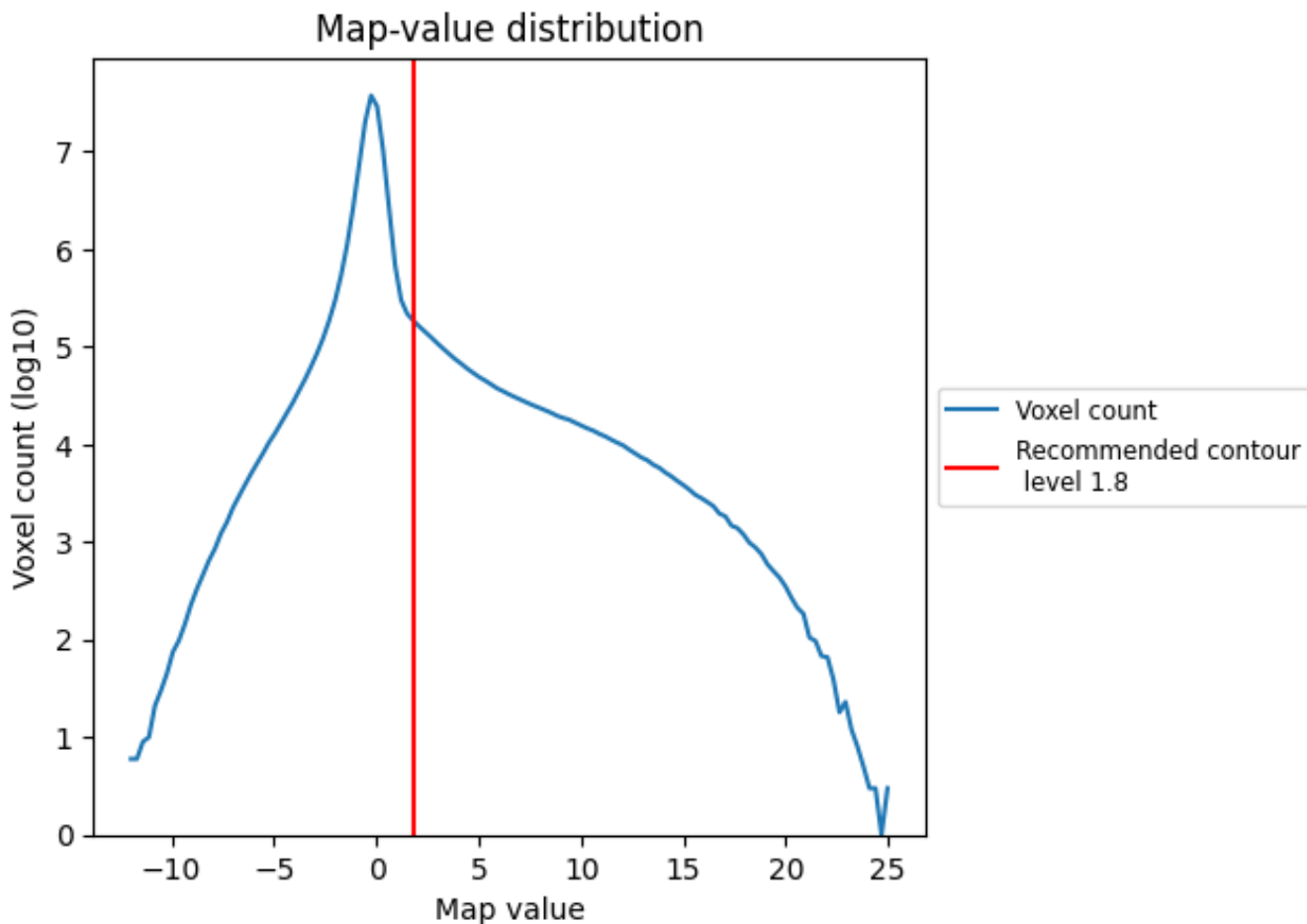
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

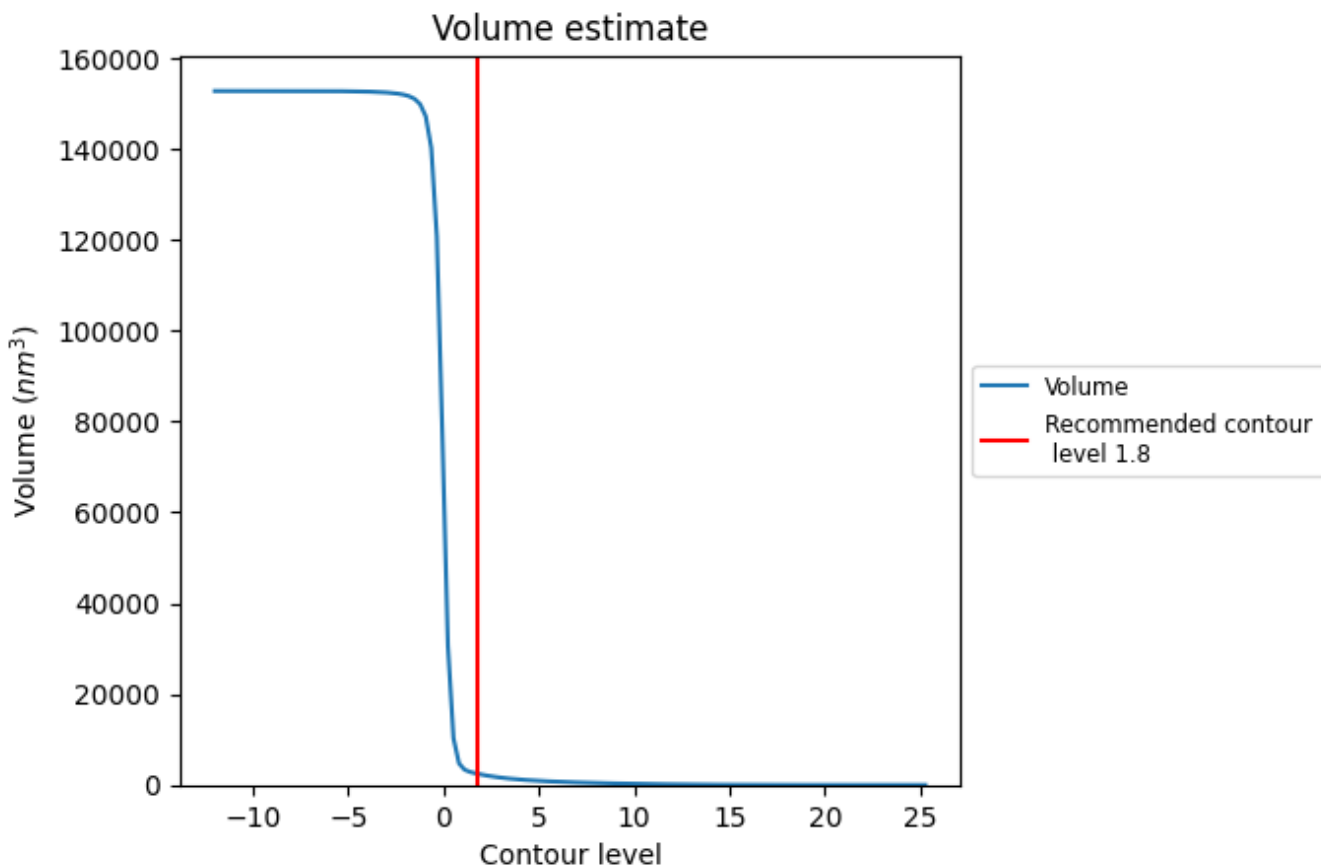
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

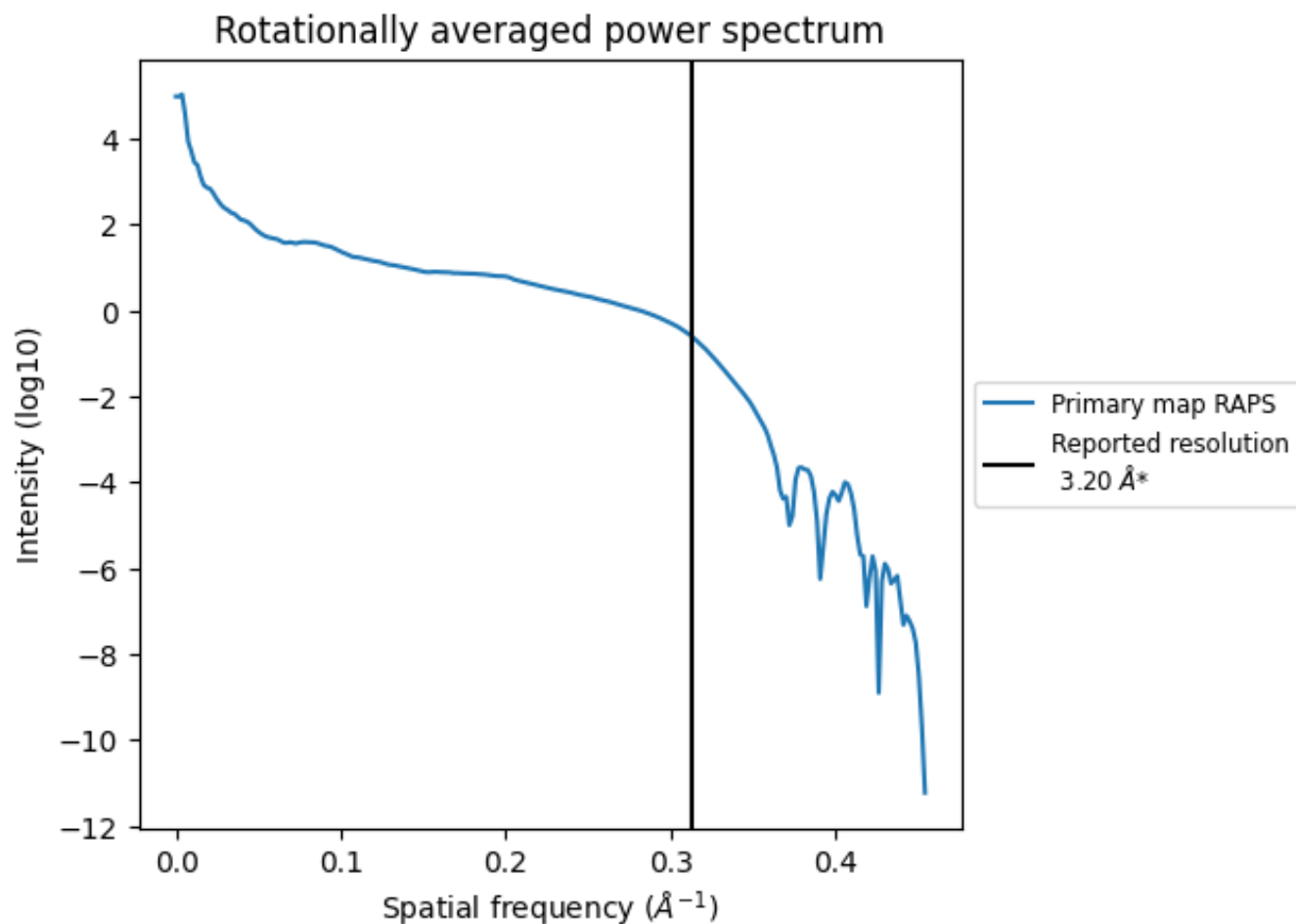
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2455 nm³; this corresponds to an approximate mass of 2218 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 [\(i\)](#)

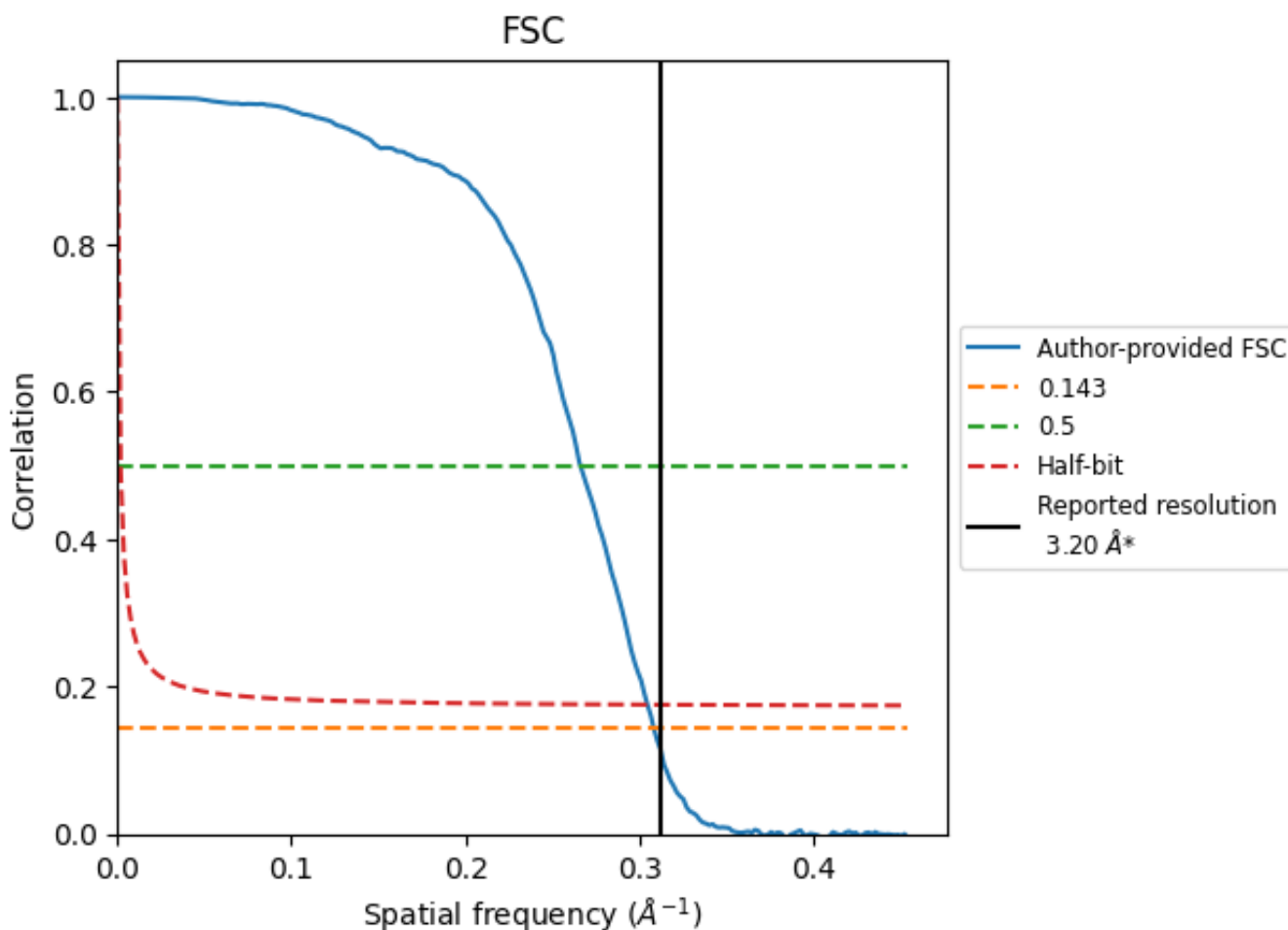


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

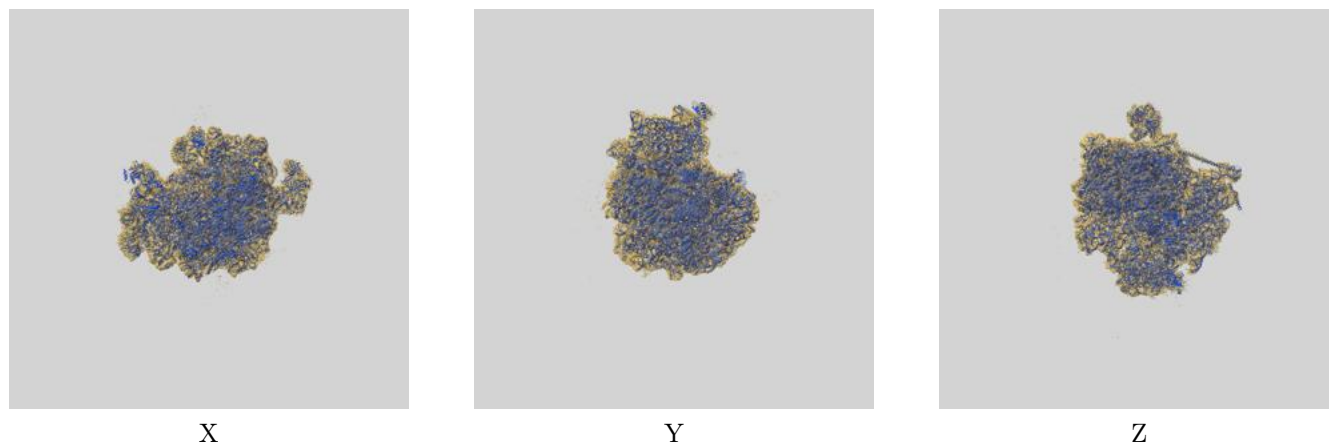
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.24	3.76	3.28
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

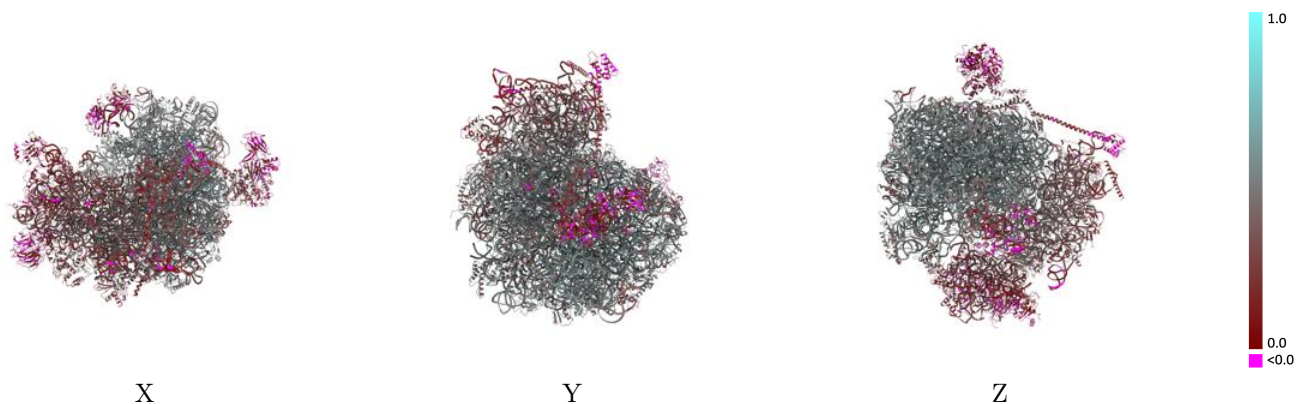
This section contains information regarding the fit between EMDB map EMD-14479 and PDB model 7Z3N. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



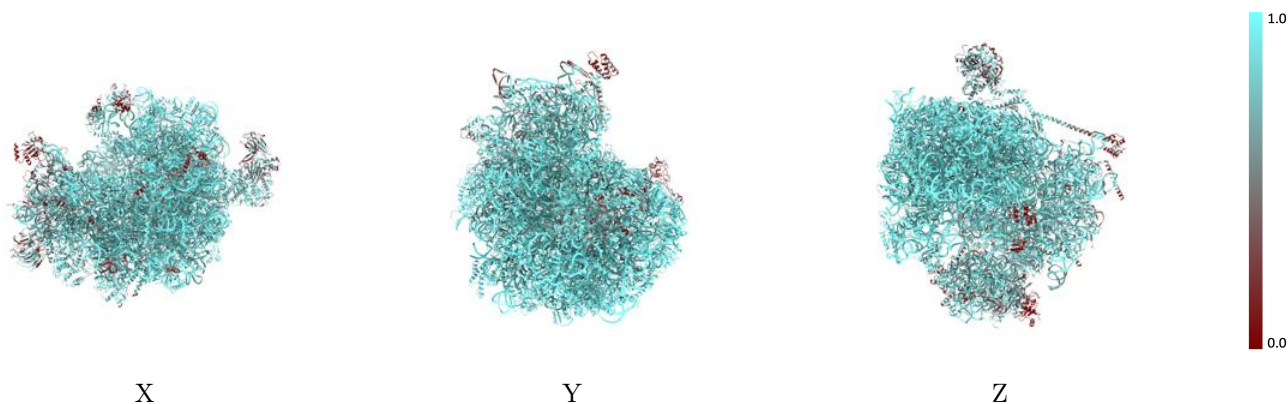
The images above show the 3D surface view of the map at the recommended contour level 1.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



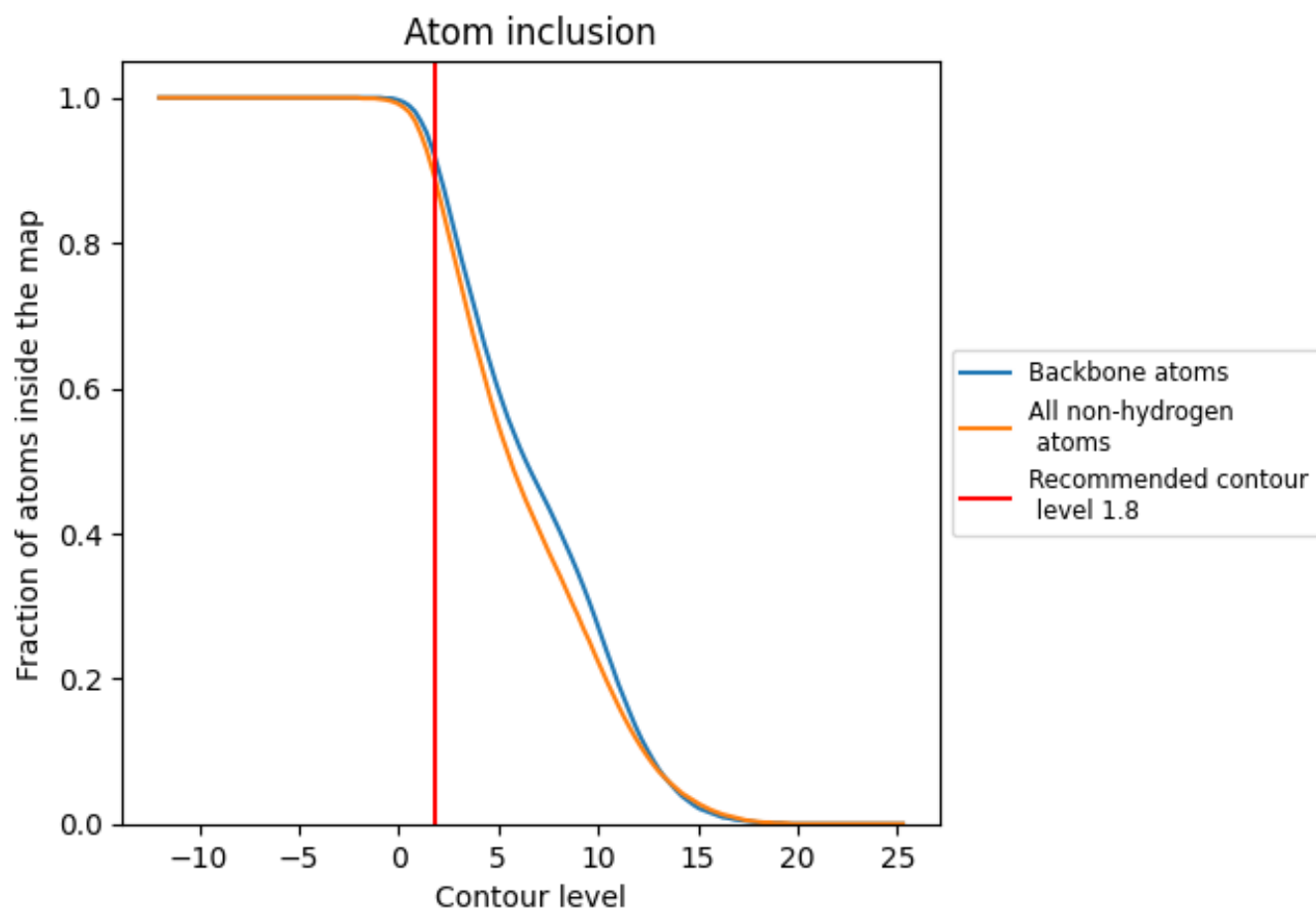
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.8).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 89% 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 (1.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.4120
1	 0.9880	 0.4980
2	 0.8990	 0.3370
3	 0.9980	 0.5030
4	 0.9910	 0.5000
A	 0.4790	 0.0780
B	 0.2210	 0.2020
C	 0.6150	 0.1840
D	 0.6300	 0.1330
LA	 0.9210	 0.5190
LB	 0.9500	 0.5120
LC	 0.9510	 0.5120
LD	 0.9420	 0.4510
LE	 0.9410	 0.4580
LF	 0.9420	 0.5010
LG	 0.9370	 0.4780
LH	 0.9400	 0.4780
LI	 0.9170	 0.4930
LJ	 0.9280	 0.4250
LK	 0.5540	 0.0760
LL	 0.9560	 0.4950
LM	 0.9410	 0.4810
LN	 0.9520	 0.5280
LO	 0.9520	 0.5010
LP	 0.8870	 0.4810
LQ	 0.9520	 0.5230
LR	 0.8990	 0.4550
LS	 0.9580	 0.5150
LT	 0.9530	 0.5120
LU	 0.9300	 0.4270
LV	 0.9370	 0.5110
LW	 0.7230	 0.3370
LX	 0.9310	 0.4820
LY	 0.9590	 0.5010
LZ	 0.9470	 0.4850























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Chain	Atom inclusion	Q-score
La	 0.9600	 0.5320
Lb	 0.9250	 0.4680
Lc	 0.9270	 0.4700
Ld	 0.8700	 0.4710
Le	 0.9490	 0.5300
Lf	 0.9540	 0.5330
Lg	 0.9350	 0.5080
Lh	 0.9310	 0.4610
Li	 0.9160	 0.4590
Lj	 0.9540	 0.5340
Lk	 0.8970	 0.4310
Ll	 0.9300	 0.4980
Lm	 0.9560	 0.5050
Ln	 0.7980	 0.4250
Lo	 0.9390	 0.5050
Lp	 0.9030	 0.4970
Lq	 0.9500	 0.5070
Lr	 0.6110	 0.2540
Ls	 0.4020	 0.1260
NC	 0.1630	 0.3150
SA	 0.8330	 0.3400
SB	 0.8310	 0.3800
SC	 0.8080	 0.3360
SD	 0.6140	 0.2280
SE	 0.7390	 0.3350
SF	 0.6190	 0.2630
SG	 0.8100	 0.3030
SH	 0.7880	 0.3120
SI	 0.7820	 0.3660
SJ	 0.7260	 0.3100
SK	 0.6310	 0.1850
SL	 0.7050	 0.3840
SM	 0.1260	 0.1360
SN	 0.8100	 0.3910
SO	 0.8760	 0.4160
SP	 0.6340	 0.1810
SQ	 0.6910	 0.2270
SR	 0.7400	 0.2330
SS	 0.6790	 0.1810
ST	 0.6450	 0.2010
SU	 0.6450	 0.2100
SV	 0.8390	 0.3370

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Chain	Atom inclusion	Q-score
SW	 0.8200	 0.3750
SX	 0.7890	 0.3600
SY	 0.7750	 0.2890
SZ	 0.7070	 0.1960
Sa	 0.8710	 0.4350
Sb	 0.8140	 0.3790
Sc	 0.7630	 0.3220
Sd	 0.6670	 0.2440
Se	 0.8520	 0.3280
Sf	 0.6220	 0.1060