



## wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Sep 12, 2019 – 04:40 PM EDT

PDB ID : 6P5K  
EMDB ID: : EMD-20257  
Title : Structure of a mammalian 80S ribosome in complex with the Israeli Acute Paralysis Virus IRES (Class 3)  
Authors : Acosta-Reyes, F.J.; Neupane, R.; Frank, J.; Fernandez, I.S.  
Deposited on : 2019-05-30  
Resolution : 3.10 Å(reported)

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report  
for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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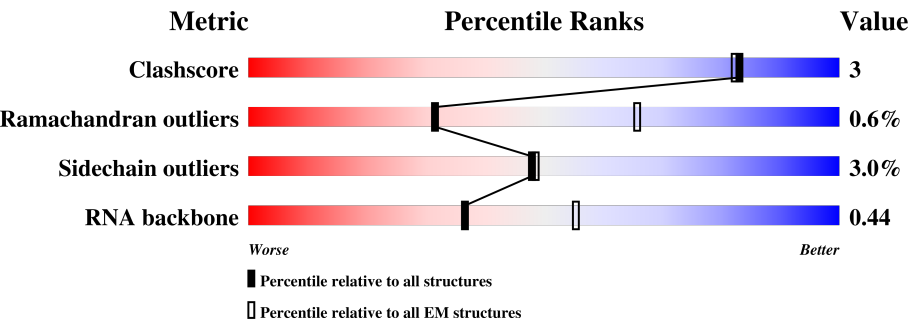
MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.10 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.























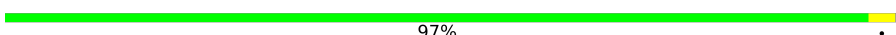




Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	5	3594	68% 29% .
2	7	119	85% 14% .
3	8	156	69% 27% ..
4	AA	257	71% 23% . .
5	AB	403	85% 12% .
6	AC	392	79% 11% . 8%
7	AD	297	92% 6% .
8	AE	291	66% 7% . 26%

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Mol	Chain	Length	Quality of chain
9	AF	249	
10	AG	242	
11	AH	192	
12	AI	214	
13	AJ	178	
14	AL	211	
15	AM	198	
16	AN	204	
17	AO	203	
18	AP	184	
19	AQ	188	
20	AR	196	
21	AS	176	
22	AT	160	
23	AU	128	
24	AV	140	
25	AW	157	
26	AX	156	
27	AY	145	
28	AZ	136	
29	Aa	148	
30	Ab	226	
31	Ac	115	
32	Ad	125	
33	Ae	135	



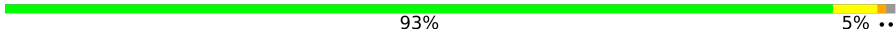













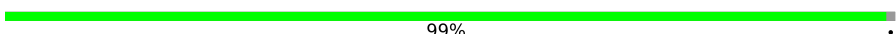

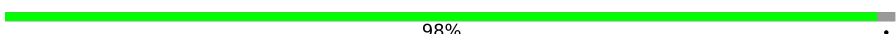


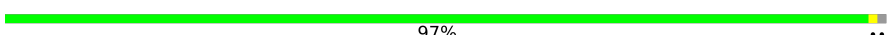
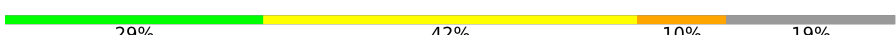
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Mol	Chain	Length	Quality of chain
34	Af	110	91% 7% ..
35	Ag	126	90% 10%
36	Ah	123	97% ..
37	Ai	105	94% . .
38	Aj	97	86% . 11%
39	Ak	70	90% 9% .
40	Al	51	98% .
41	Am	52	96% .
42	An	25	96% .
43	Ao	106	95% . .
44	Ap	92	97% ..
45	Ar	137	89% . 9%
46	AK	217	80% 16% . .
47	2	1869	62% 25% . 9%
48	B	295	67% 6% 26%
49	C	264	69% 11% . 19%
50	D	255	75% 11% 13%
51	E	281	74% 6% . 19%
52	F	263	85% 14% .
53	G	204	85% 5% . 9%
54	H	249	86% 9% 5%
55	I	194	88% 7% 5%
56	J	207	89% 11%
57	K	194	81% 13% . 5%
58	L	149	61% . 36%

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Mol	Chain	Length	Quality of chain
59	M	158	
60	N	132	
61	O	151	
62	P	151	
63	Q	145	
64	R	172	
65	S	135	
66	T	152	
67	U	145	
68	V	119	
69	W	83	
70	X	130	
71	Y	143	
72	Z	134	
73	a	125	
74	b	115	
75	c	84	
76	d	69	
77	e	56	
78	f	133	
79	g	156	
80	h	317	
81	1	253	

## 2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 215976 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3594	Total	C	N	O	P	0	0
			77074	34325	14116	25039	3594		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 4 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AA	248	Total	C	N	O	S	0	0
			1895	1186	389	314	6		

- Molecule 5 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AB	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 6 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AC	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 7 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AD	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 8 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AE	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 9 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AF	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 10 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AG	225	Total	C	N	O	S	0	0
			1819	1161	351	303	4		

- Molecule 11 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AH	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 12 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AI	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 13 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AJ	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 14 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AL	201	Total	C	N	O	S	0	0
			1627	1020	341	262	4		

- Molecule 15 is a protein called L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AM	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 16 is a protein called eL15.

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

- Molecule 17 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	199	Total	C	N	O	S	0	0
			1631	1052	319	255	5		

- Molecule 18 is a protein called uL22.

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

- Molecule 19 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AQ	187	Total	C	N	O	S	0	0
			1526	964	306	252	4		

- Molecule 20 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AR	180	Total	C	N	O	S	0	0
			1503	931	324	238	10		

- Molecule 21 is a protein called eL20.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	AS	176	Total	C	N	O	S	0	0
			1457	928	283	235	11		

- Molecule 22 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AU	99	Total	C	N	O	S	0	0
			818	520	146	150	2		

- Molecule 24 is a protein called uL14.

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

- Molecule 25 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AW	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called eL23.

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

- Molecule 27 is a protein called uL24.

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

- Molecule 28 is a protein called eL27.

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

- Molecule 29 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Aa	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 30 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ab	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 31 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ac	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 32 is a protein called eL31.

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

- Molecule 33 is a protein called eL32.

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

- Molecule 34 is a protein called eL33.

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

- Molecule 35 is a protein called eL34.

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

- Molecule 36 is a protein called eL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ah	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 37 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ai	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 38 is a protein called eL37.

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

- Molecule 39 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ak	69	Total	C	N	O	S	0	0
			569	366	101	99	3		

- Molecule 40 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Al	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 41 is a protein called eL40.

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

- Molecule 42 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	An	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 43 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ao	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 44 is a protein called eL43.

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

- Molecule 45 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ar	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 46 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AK	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 48 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B	217	Total	C	N	O	S	0	0
			1706	1085	295	317	9		

- Molecule 49 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	C	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 50 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	D	221	Total	C	N	O	S	0	0
			1712	1107	296	299	10		

- Molecule 51 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	E	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 52 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	F	262	Total	C	N	O	S	0	0
			2073	1323	384	357	9		

- Molecule 53 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	G	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 54 is a protein called eS6.

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

- Molecule 55 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	I	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 56 is a protein called eS8.

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

- Molecule 57 is a protein called uS4.

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

- Molecule 58 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	L	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 59 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	M	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 60 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	N	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 61 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	O	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 62 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	P	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 63 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Q	119	Total	C	N	O	S	0	0
			990	630	186	167	7		

- Molecule 64 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	R	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 65 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	S	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 66 is a protein called uS13.

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

- Molecule 67 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	U	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 68 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	V	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 69 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	W	83	Total	C	N	O	S	0	0
			630	387	118	120	5		

- Molecule 70 is a protein called uS8.

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

- Molecule 71 is a protein called uS12.

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

- Molecule 72 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Z	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 73 is a protein called eS25.

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

- Molecule 74 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	b	98	Total	C	N	O	S	0	0
			778	485	158	129	6		

- Molecule 75 is a protein called eS27.

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

- Molecule 76 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	d	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 77 is a protein called eS29.



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

- Molecule 78 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	f	56	Total	C	N	O	S	0	0
			447	276	98	72	1		

- Molecule 79 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	g	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 80 is a protein called RACK1.

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

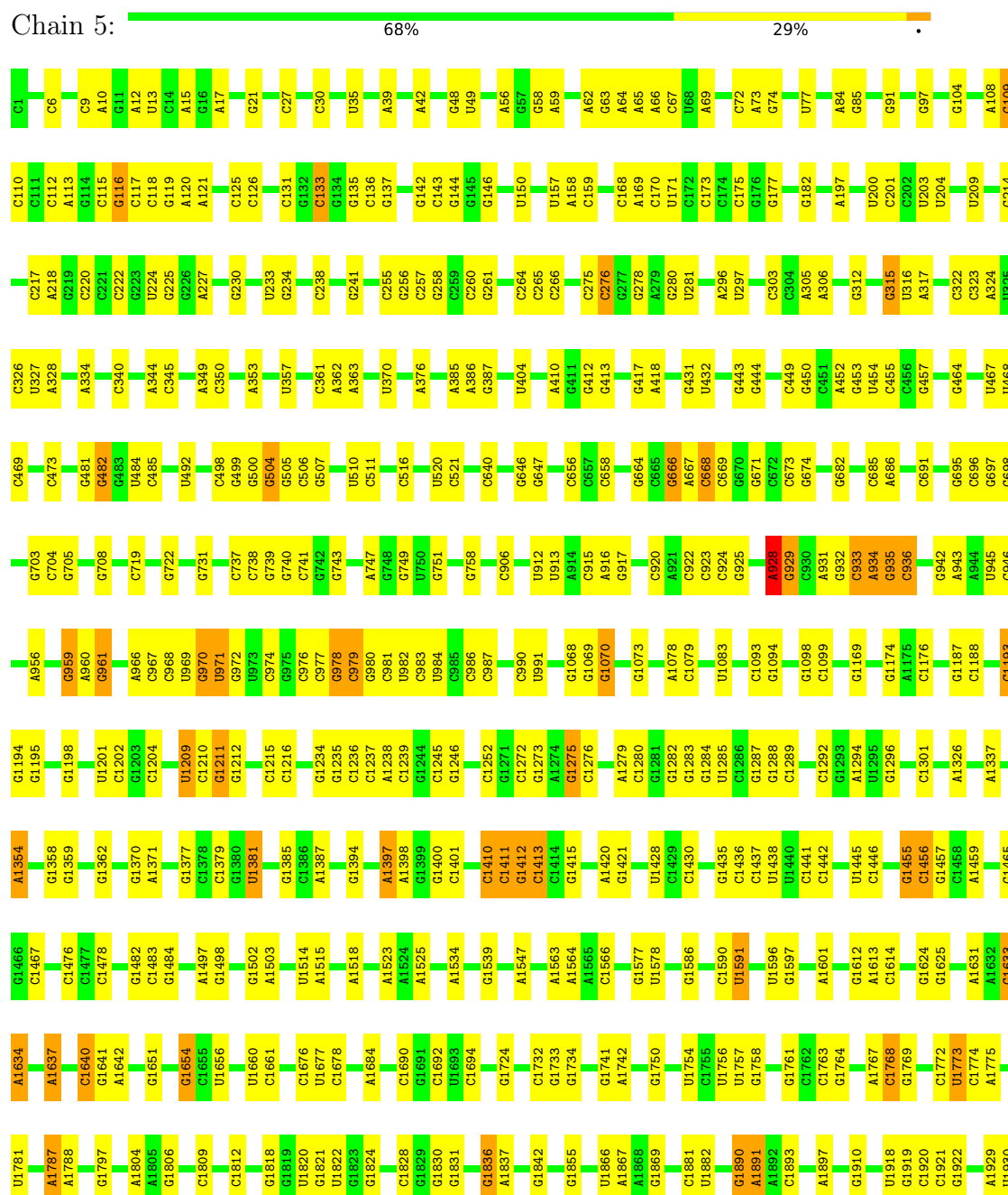
- Molecule 81 is a RNA chain called IAPV-IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	1	205	Total	C	N	O	P	0	0
			4366	1951	775	1435	205		

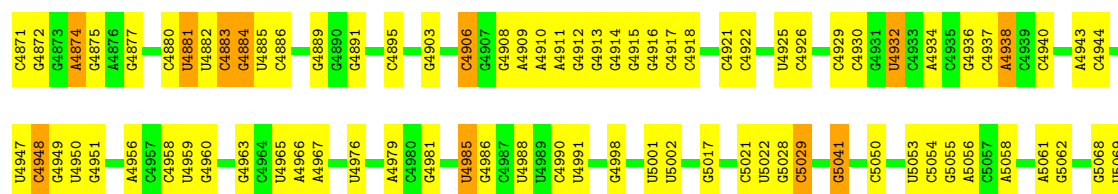
### 3 Residue-property plots

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

#### • Molecule 1: 28S rRNA

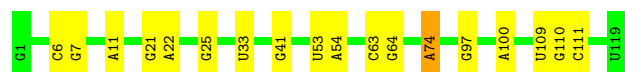


A4656	C4519	G4377	A4257	C4133	G3970	U3713	G2898	C2770	U2661	G2547	A2268	A2025	C1931
A4657	C4522	C4387	C4258	C4134	A3971	U3853	C2899	G2771	C2662	C2548	G2275	U2027	A1932
A4658	G4529	C4391	U4260	G4135	G3973	G3857	U2900	C2772	C2669	G2549	G2275	U2027	C1935
A4664	G4523	G4391	U4265	G4136	G3974	C3870	C3598	C2779	C2670	G2552	G2280	C2031	G1940
A4667	G4527	A4394	G4266	C4148	C4037	U3729	G3603	C2780	C2673	G2553	G2289	U2032	G1948
C4670	A4528	U4395	A4268	G4150	A4046	G3735	A3604	C2783	A2674	U2554	G2289	A2033	G1948
U4677	U4530	C4398	A4271	G4154	A4047	G3878	G3605	A2787	G2675	G2556	G2297	G2045	G1952
U4687	U4531	C4401	G4272	C4155	A4048	G3879	U3606	U2788	G2686	G2557	U2298	G2046	G1952
A4693	A4535	G4402	A4273	G4156	A4048	C3887	A3611	A2789	U2687	G2562	A2300	U2048	U1957
C4693	A4546	U4403	A4280	C4162	A4050	U4049	G3611	U2790	G2693	C2563	G2301	G2052	A1958
U4699	C4547	G4404	A4281	U4163	A4053	G3888	G3615	C2794	C2694	G2564	G2306	G2052	A1959
A4700	A4548	G4405	A4281	U4163	A4054	G3889	U3616	G2795	A2695	G2565	G2306	G2055	A1960
U4709	G4549	G4405	G4291	G4168	U4055	C3892	G3618	G2796	A2696	G2566	A2313	G2056	A1962
U4709	U4419	C4402	U4296	G4169	A4056	U3893	G3619	A2798	U2701	G2569	G2314	C2062	G1968
U4719	U4420	G4402	U4297	A4170	C4057	G3993	G3755	A2799	U2701	C2572	G2316	C2062	G1969
C4720	A4421	A4422	G4297	C4171	U4058	C3896	A3760	A2806	G2706	U2575	G2331	G2065	G1972
C4720	U4423	U4423	U4300	A4172	C4059	C3897	C3761	G2811	U2707	G2575	A2332	G2066	G1973
U4728	A4424	A4424	U4301	G4180	U4060	G3898	U3762	C2709	U2708	G2578	G2333	A2069	G1974
C4738	G4425	G4425	C4303	U4181	G4061	A3901	C3765	C2814	C2710	C2583	C2337	U2070	G1975
C4739	U4433	U4433	C4303	G4182	C4064	A3904	G3765	A2815	U2485	C2492	C2351	G2084	G1976
U4750	G4433	G4433	C4304	G4183	C4065	C3904	A3774	G2827	G2714	G2486	G2357	G2085	C1977
C4751	U4440	U4440	U4304	G4184	C4066	A3905	A3774	U2828	G2715	G2487	G2345	G2088	A1983
C4751	G4451	U4451	C4305	G4185	A4072	A3906	A3774	U2829	C2716	C2488	G2346	A2088	A1984
U4752	U4452	U4452	U4306	G4185	C4073	C3907	G3777	G2830	C2716	C2489	G2347	G2089	G1985
U4753	C4453	C4453	U4312	G4191	U4074	A3908	U3778	A2835	G2721	U2490	G2348	U2090	U1986
C4754	U4454	U4454	C4313	G4197	G4076	U3915	G3780	A2835	G2721	C2594	C2351	C2091	C1987
C4755	U4455	U4455	C4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
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C4757	U4457	U4457	C4313	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
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C4759	G4459	U4459	C4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4760	U4460	U4460	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4761	U4461	U4461	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4762	U4462	U4462	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4763	U4463	U4463	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
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C4766	U4466	U4466	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4767	U4467	U4467	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4768	U4468	U4468	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
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C4770	U4470	U4470	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4771	U4471	U4471	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4772	U4472	U4472	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4773	U4473	U4473	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
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C4775	U4475	U4475	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4776	U4476	U4476	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4777	U4477	U4477	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4863	U4478	U4478	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4864	U4479	U4479	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4865	U4480	U4480	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4866	U4481	U4481	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4867	U4482	U4482	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4868	U4483	U4483	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
C4869	U4484	U4484	U4314	G4197	G4076	C3916	G3780	A2835	G2721	C2594	C2351	C2092	C1987
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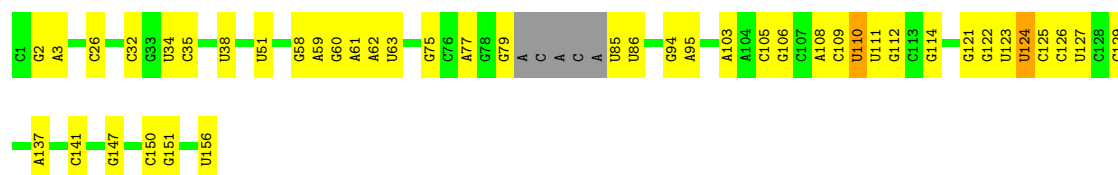
• Molecule 2: 5S rRNA

Chain 7: 85% 14%



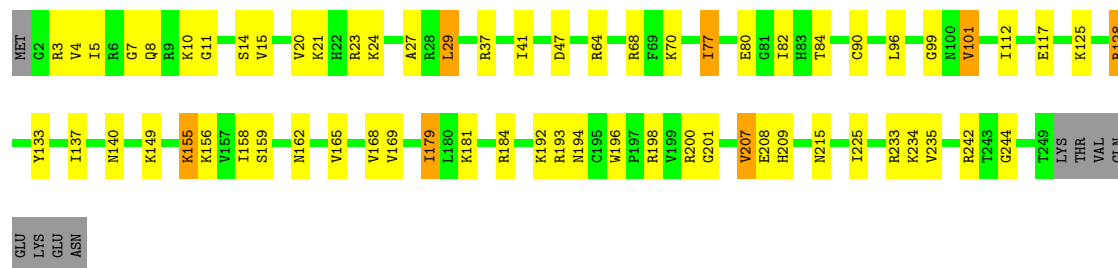
• Molecule 3: 5.8S rRNA

Chain 8: 69% 27%



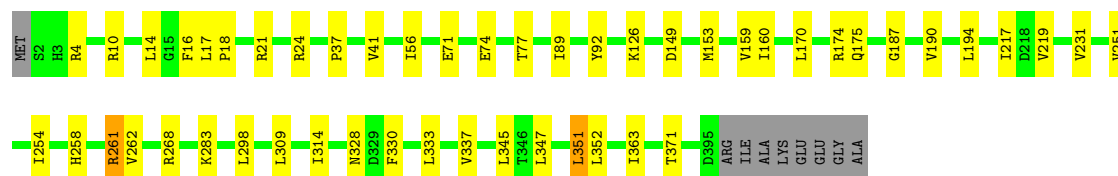
• Molecule 4: uL2

Chain AA: 71% 23%



• Molecule 5: uL3

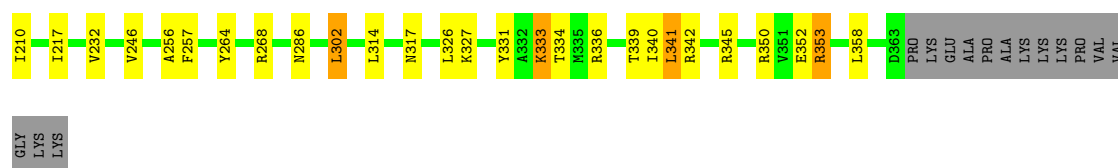
Chain AB: 85% 12%



• Molecule 6: uL4

Chain AC: 79% 11% 8%

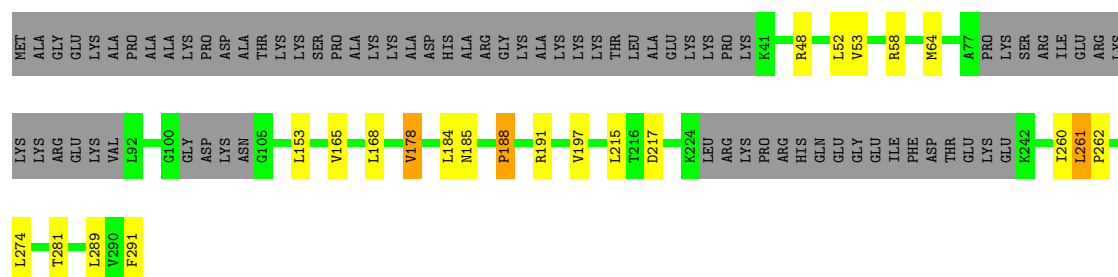




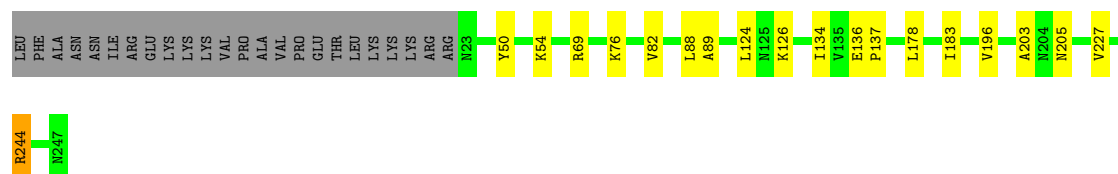
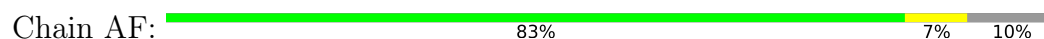
- Molecule 7: uL18



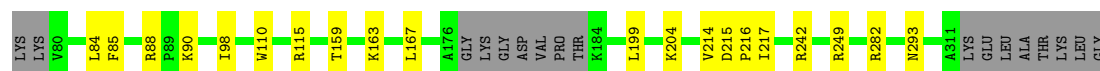
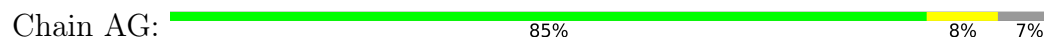
- Molecule 8: eL6



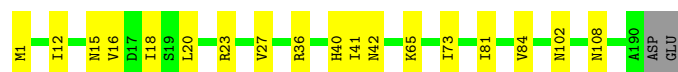
- Molecule 9: uL30




- Molecule 10: eL8



- Molecule 11: uL6



- Molecule 12: uL16

Chain AI:  88% 8% .



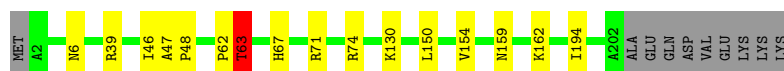
- Molecule 13: uL11

Chain AJ:  90% 6% .



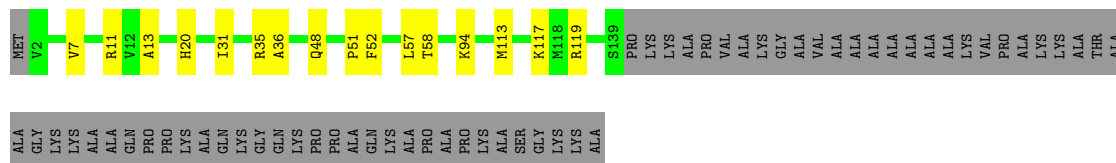
- Molecule 14: eL13

Chain AL:  88% 7% 5%



- Molecule 15: L14e

Chain AM:  62% 8% 30%



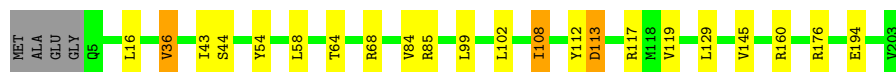
- Molecule 16: eL15

Chain AN:  86% 12% .




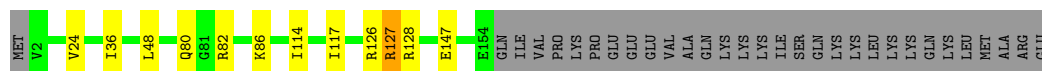
- Molecule 17: uL13

Chain AO:  87% 9% ..




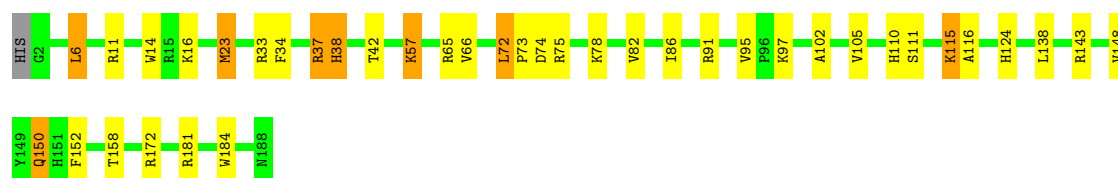
- Molecule 18: uL22

Chain AP:  77% 6% 17%




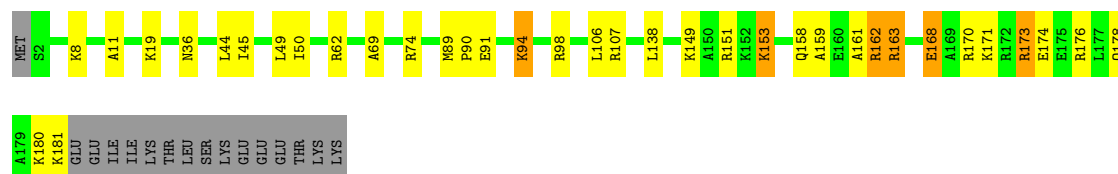
- Molecule 19: eL18

Chain AQ:  79% 16% . .




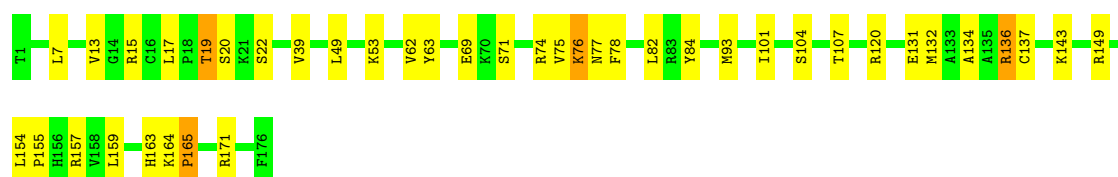
- Molecule 20: eL19

Chain AR:  73% 15% . 8%




- Molecule 21: eL20

Chain AS:  77% 21% .



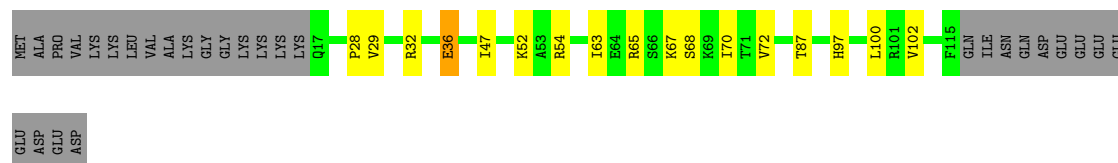
- Molecule 22: eL21

Chain AT:  89% 9% ..




- Molecule 23: eL22

Chain AU:  64% 13% . 23%



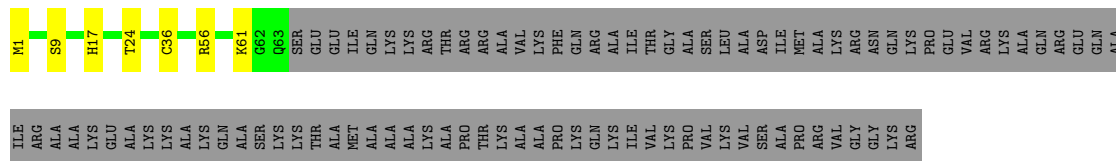
- Molecule 24: uL14

Chain AV:  77% 14% . 8%



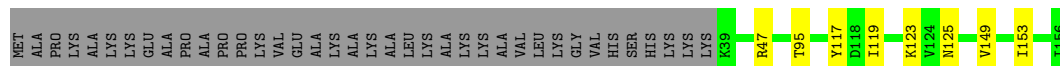
- Molecule 25: eL24

Chain AW:  36% 60%




- Molecule 26: eL23

Chain AX:  71% 5% 24%



- Molecule 27: uL24

Chain AY:  81% 11% 8%



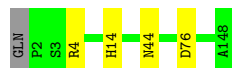
- Molecule 28: eL27

Chain AZ:  90% 10%



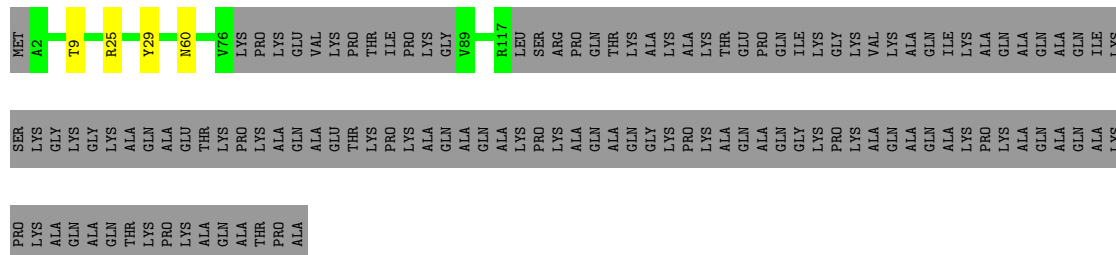
- Molecule 29: uL15

Chain Aa:  97%




- Molecule 30: eL29

Chain Ab:  44% 54%




- Molecule 31: eL30

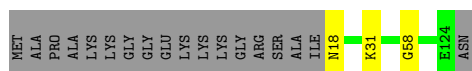


Chain Ac:  83% 15%



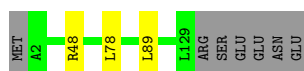
• Molecule 32: eL31

Chain Ad:  83% 14%



• Molecule 33: eL32

Chain Ae:  93% 5%



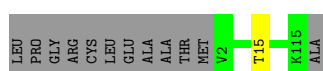
• Molecule 34: eL33

Chain Af:  91% 7% ..



• Molecule 35: eL34

Chain Ag:  90% 10%



• Molecule 36: eL35

Chain Ah:  97% ..




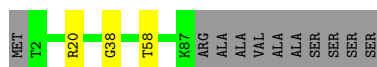
• Molecule 37: eL36

Chain Ai:  94% ..



• Molecule 38: eL37

Chain Aj:  86% 11%



- Molecule 39: eL38

Chain Ak: 90% 9% .



- Molecule 40: eL39

Chain Al: 98% .



- Molecule 41: eL40

Chain Am: 96% .



- Molecule 42: eL41

Chain An: 96% .



- Molecule 43: eL42

Chain Ao: 95% . .



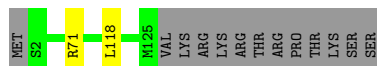
- Molecule 44: eL43

Chain Ap: 97% . .



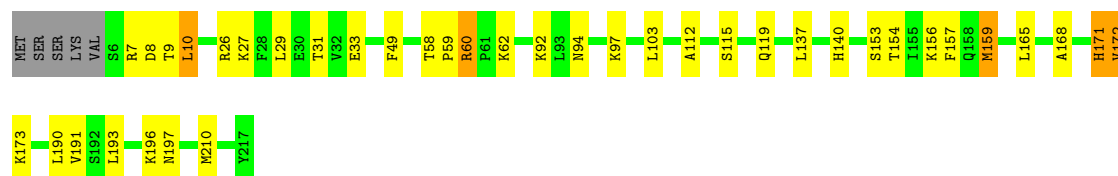
- Molecule 45: eL28

Chain Ar: 89% . 9%



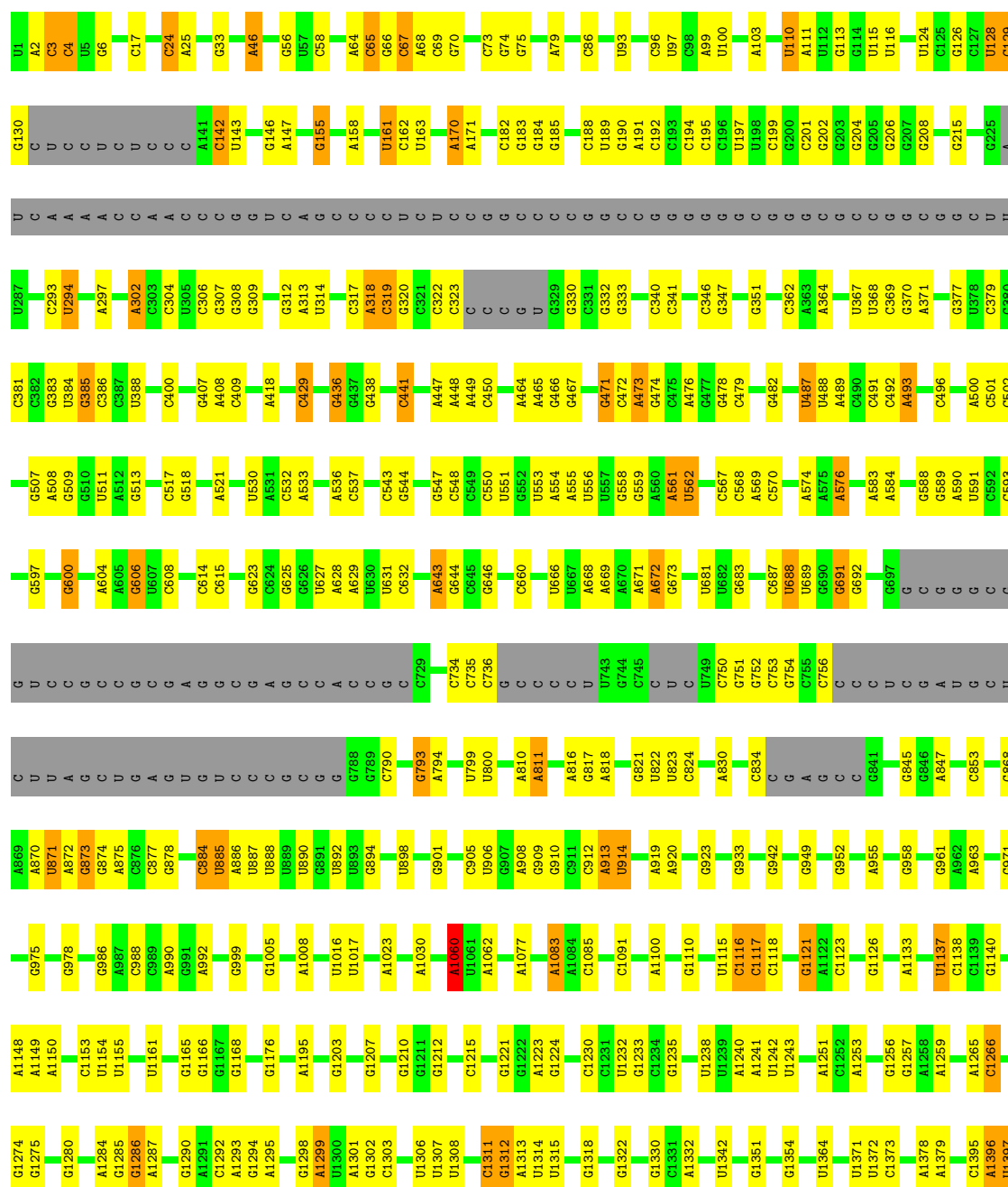
- Molecule 46: uL1

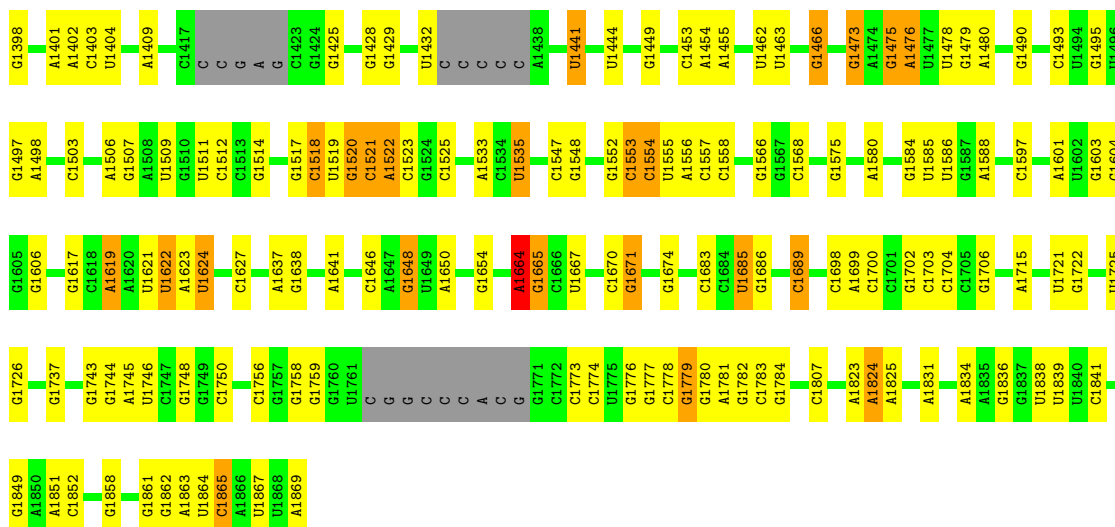
Chain AK:



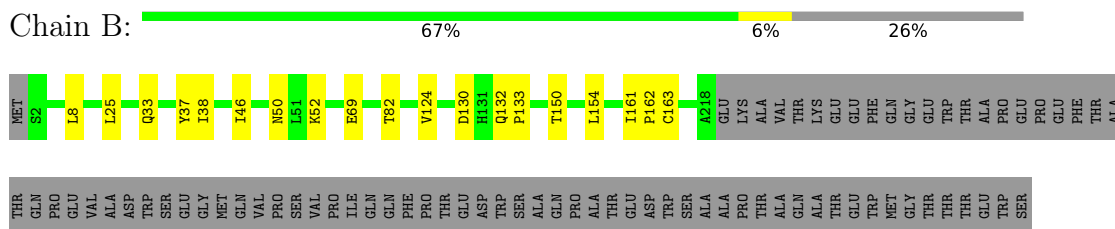
- Molecule 47: 18S rRNA

Chain 2:

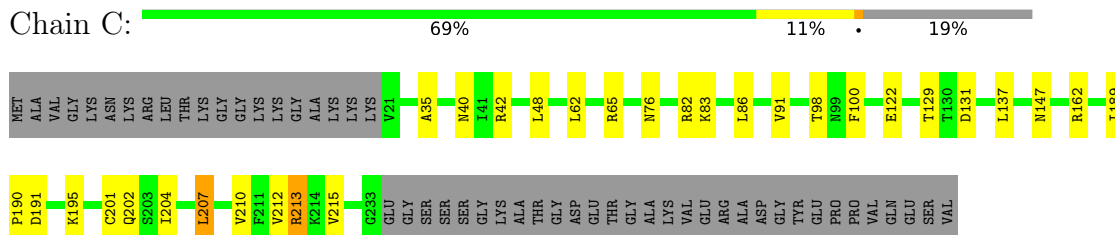




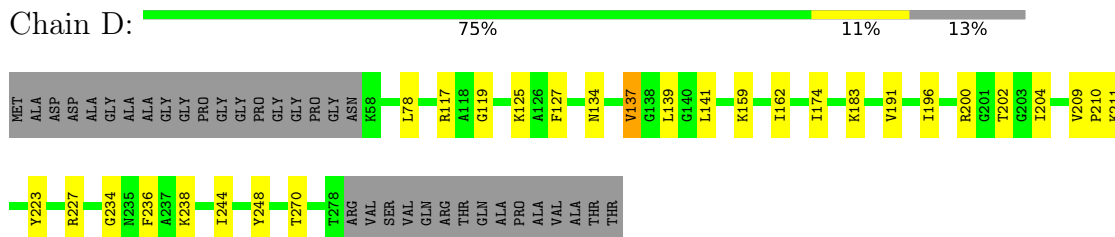
- Molecule 48: uS2



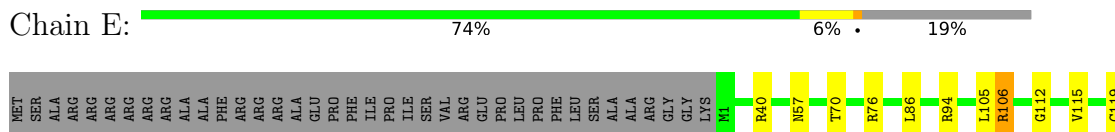
- Molecule 49: eS1



- Molecule 50: uS5



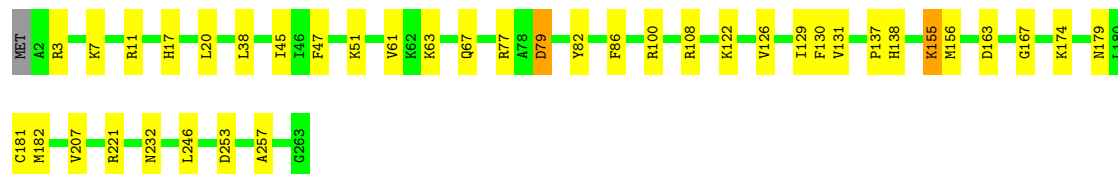
- Molecule 51: uS3





• Molecule 52: eS4

Chain F: 85% 14%



• Molecule 53: uS7

Chain G: 85% 5% 9%



• Molecule 54: eS6

Chain H: 86% 9% 5%



• Molecule 55: eS7

Chain I: 88% 7% 5%



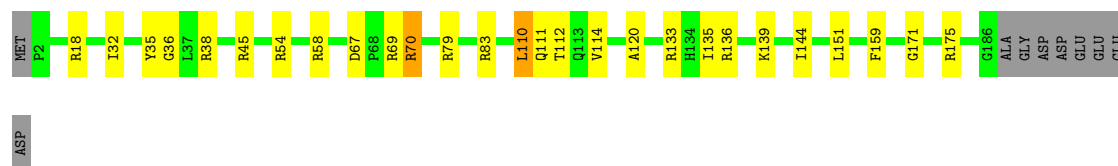
• Molecule 56: eS8

Chain J: 89% 11%



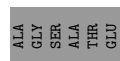
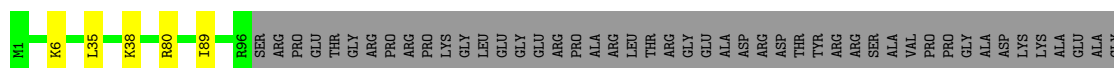
• Molecule 57: uS4

Chain K: 81% 13% 5%




• Molecule 58: eS10

Chain L:  61% 36%




- Molecule 59: uS17

Chain M:  83% 8% 9%



- Molecule 60: eS12

Chain N:  78% 11% 11%




- Molecule 61: uS15

Chain O:  93% 5% ..



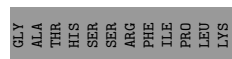
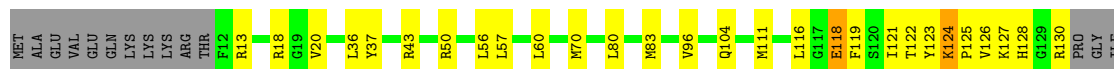
- Molecule 62: uS11

Chain P:  83% 7% 10%



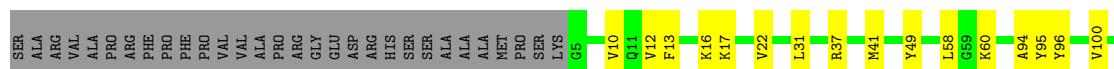
- Molecule 63: uS19

Chain Q:  63% 18% 18%



- Molecule 64: uS9

Chain R:  72% 11% 17%





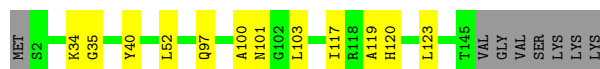
- Molecule 65: eS17

Chain S: 91% 7% .



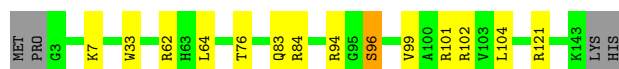
- Molecule 66: uS13

Chain T: 87% 8% 5%



- Molecule 67: eS19

Chain U: 88% 9% ..



- Molecule 68: uS10

Chain V: 74% 8% 16%



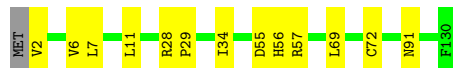
- Molecule 69: eS21

Chain W: 86% 13% .



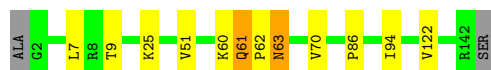
- Molecule 70: uS8

Chain X: 89% 10% .




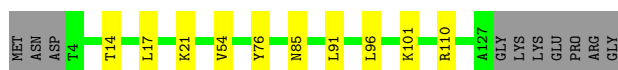
- Molecule 71: uS12

Chain Y: 90% 7% ..



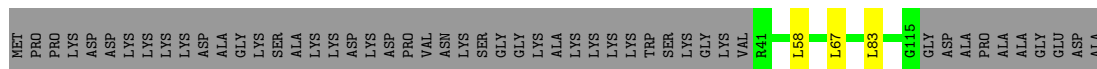
- Molecule 72: eS24

Chain Z:  85% 7% 7%




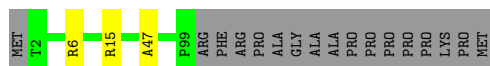
- Molecule 73: eS25

Chain a:  58% 40%



- Molecule 74: eS26

Chain b:  83% 15%




- Molecule 75: eS27

Chain c:  99%



- Molecule 76: eS28

Chain d:  88% 10%



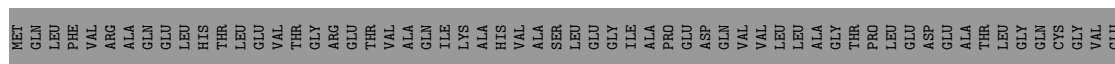
- Molecule 77: eS29

Chain e:  98%



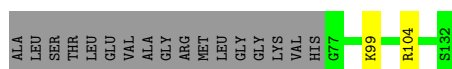
- Molecule 78: eS30

Chain f:  41% 58%



- Molecule 79: eS31

Chain g:  42% 56%





MET  
GLN  
ILE  
PHE  
VAL  
LYS  
THR  
LEU  
THR  
GLY  
LYS  
THR  
ILE  
THR  
LEU  
GLY  
VAL  
GLU  
PRO  
SER  
ASP  
THR  
ILE  
GLU  
ASN  
VAL  
LYS  
ALA  
LYS  
ILE  
GLN  
ASP  
LYS  
GLU  
ASP  
GLY  
ILE  
PRO  
PRO  
ASP  
GLN  
GLN  
ARG  
LEU  
ILE  
PHE  
ALA  
GLY  
LYS  
GLN  
LEU  
LEU  
ASP  
GLY  
ARG  
THR  
SER  
ASP  
TYR  
ASN

ILE  
GLN  
LYS  
GLU  
SER  
THR  
LEU  
HIS  
LEU  
VAL  
LEU  
ARG  
LEU  
ARG  
GLY  
GLU  
ALA  
LYS  
LYS  
ARG  
LYS  
THR  
K83  
K96  
R138  
F150  
ASN  
LYS  
PRO  
GLU  
ASP  
LYS

• Molecule 80: RACK1

Chain h: 97% ..

MET  
T2  
K38  
S63  
N159  
N178  
I314  
GLY  
THR  
ARG

• Molecule 81: IAPV-IRES

Chain 1: 29% 42% 10% 19%

G  
A  
G  
C  
G  
G  
U  
U  
U  
C  
U  
G  
G  
A  
A  
U  
U  
C  
A  
U  
A  
U  
U  
G  
G  
A  
A  
G  
U  
U  
A  
A  
G  
G  
C6416  
A6420  
U6424  
A6425  
U6426  
G6427  
G6428  
U6429  
U6430  
A6431  
G6432  
G6433  
G6434  
A6435

U6436  
C6437  
A6443  
G6444  
G6445  
U6450  
U6451  
A6455  
U6456  
A6457  
A6458  
A6459  
C6460  
U6461  
C6462  
U6463  
U6466  
G6467  
A6470  
G6471  
G6472  
C6473  
U6474  
U6475  
G6479  
U6480  
G6481  
A6482  
U6483  
G6484  
U6485  
U6486  
C6487  
G6488  
A6489  
G6490  
A6491  
G6492  
G6493  
C6494  
U6501  
A6502  
U6506  
G6507  
G6512  
C6513  
G6514  
U6515  
G6516  
G6517  
G6518

U6519  
G6520  
G6521  
C6522  
A6523  
G6524  
C6525  
C6526  
G6527  
C6528  
A6529  
C6530  
C6531  
A6532  
A6533  
A6534  
U6535  
C6536  
C6537  
U6538  
C6539  
U6540  
A6541  
U6542  
U6543  
G6544  
G6545  
A6548  
G6549  
G6550  
A6551  
C6552  
C6553  
A6554  
C6555  
C6556  
U6557  
G6558  
U6559  
A6560  
C6561  
U6562  
G6563  
G6564  
G6565  
A6566  
A6567  
C6575  
A6576  
G6577  
U6578  
C6579  
G6580  
U6583  
G6584  
G6585  
U6586

A6587  
A6588  
C6589  
A6590  
C6591  
A6592  
U6593  
G6594  
C6595  
G6596  
G6597  
C6598  
G6599  
U6600  
U6601  
C6602  
G6603  
G6604  
A6605  
A6606  
A6607  
U6608  
A6609  
C6610  
C6611  
A6612  
U6613  
C6616  
U6617  
G6618  
C6619  
C6620  
G  
A  
U  
G

## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	68697	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	42.09	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	5	0.21	0/86215	0.69	11/134459 (0.0%)
10	AG	0.67	0/1850	0.81	0/2491
11	AH	0.69	0/1535	0.82	0/2063
12	AI	0.66	0/1702	0.79	0/2272
13	AJ	0.68	0/1385	0.81	0/1852
14	AL	0.66	0/1658	0.83	0/2219
15	AM	0.67	0/1158	0.80	0/1547
16	AN	0.65	0/1746	0.82	0/2338
17	AO	0.66	0/1663	0.80	0/2223
18	AP	0.66	0/1268	0.79	0/1700
19	AQ	0.65	0/1557	0.81	0/2086
2	7	0.19	0/2836	0.66	0/4421
20	AR	0.66	0/1519	0.79	0/2006
21	AS	0.65	0/1498	0.80	0/2012
22	AT	0.65	0/1326	0.80	0/1770
23	AU	0.68	0/832	0.79	0/1116
24	AV	0.69	0/983	0.82	0/1319
25	AW	0.66	0/541	0.77	0/720
26	AX	0.65	0/984	0.76	0/1323
27	AY	0.67	0/1132	0.81	0/1504
28	AZ	0.66	0/1130	0.82	0/1507
29	Aa	0.66	0/1191	0.80	0/1590
3	8	0.21	0/3581	0.69	0/5577
30	Ab	0.67	0/861	0.83	0/1138
31	Ac	0.69	0/771	0.79	0/1034
32	Ad	0.66	0/903	0.82	0/1216
33	Ae	0.66	0/1071	0.80	0/1429
34	Af	0.65	0/895	0.82	0/1198
35	Ag	0.68	0/916	0.85	0/1220
36	Ah	0.67	0/1021	0.81	0/1348
37	Ai	0.68	0/841	0.82	0/1112
38	Aj	0.66	0/720	0.85	0/952
39	Ak	0.66	0/575	0.79	0/759
4	AA	0.66	0/1933	0.83	0/2592

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
40	Al	0.64	0/459	0.81	0/608
41	Am	0.66	0/435	0.83	0/575
42	An	0.63	0/240	0.88	0/305
43	Ao	0.66	0/864	0.81	0/1140
44	Ap	0.69	0/718	0.81	0/953
45	Ar	0.68	0/1010	0.83	0/1354
46	AK	0.69	0/1733	0.81	0/2324
47	2	0.21	0/40509	0.69	7/63128 (0.0%)
48	B	0.67	0/1744	0.78	0/2371
49	C	0.68	0/1756	0.80	0/2350
5	AB	0.66	0/3240	0.80	0/4339
50	D	0.68	0/1748	0.79	0/2362
51	E	0.69	0/1796	0.80	0/2417
52	F	0.67	0/2115	0.79	0/2843
53	G	0.69	0/1492	0.79	0/2005
54	H	0.68	0/1946	0.84	0/2590
55	I	0.69	0/1510	0.77	0/2022
56	J	0.67	0/1715	0.80	0/2287
57	K	0.68	0/1550	0.82	0/2069
58	L	0.66	0/834	0.77	0/1125
59	M	0.67	0/1195	0.81	0/1597
6	AC	0.66	0/2937	0.80	0/3946
60	N	0.71	0/918	0.79	0/1233
61	O	0.68	0/1226	0.79	0/1649
62	P	0.69	0/1029	0.84	0/1380
63	Q	0.67	0/1009	0.81	0/1346
64	R	0.69	0/1146	0.83	0/1534
65	S	0.69	0/1082	0.78	0/1452
66	T	0.68	0/1208	0.82	0/1618
67	U	0.69	0/1115	0.82	0/1493
68	V	0.69	0/805	0.80	0/1081
69	W	0.71	0/638	0.82	0/855
7	AD	0.66	0/2437	0.78	0/3264
70	X	0.68	0/1051	0.80	0/1406
71	Y	0.68	0/1116	0.83	0/1490
72	Z	0.68	0/1028	0.81	0/1366
73	a	0.69	0/604	0.79	0/810
74	b	0.68	0/791	0.81	0/1062
75	c	0.68	0/665	0.78	0/891
76	d	0.70	0/490	0.81	0/656
77	e	0.68	0/470	0.76	0/623
78	f	0.69	0/451	0.83	0/592
79	g	0.68	0/567	0.83	0/753

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
8	AE	0.67	0/1762	0.81	0/2362
80	h	0.69	0/2493	0.80	0/3394
81	1	0.24	0/4881	0.73	1/7604 (0.0%)
9	AF	0.66	0/1911	0.79	0/2549
All	All	0.46	0/232236	0.73	19/341286 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
14	AL	0	1
18	AP	0	1
34	Af	0	2
46	AK	0	3
5	AB	0	3
51	E	0	1
65	S	0	1
7	AD	0	1
71	Y	0	1
8	AE	0	1
All	All	0	15

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	928	A	C2'-C3'-O3'	6.33	123.82	113.70
1	5	1455	G	C2'-C3'-O3'	5.93	123.19	113.70
1	5	4884	G	C2'-C3'-O3'	5.90	123.14	113.70
1	5	4180	G	C2'-C3'-O3'	5.77	122.92	113.70
47	2	1137	U	C2'-C3'-O3'	5.46	122.44	113.70

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	AB	16	PHE	Peptide
5	AB	258	HIS	Peptide
5	AB	351	LEU	Peptide

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Mol	Chain	Res	Type	Group
7	AD	36	LEU	Peptide
8	AE	188	PRO	Peptide

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	77074	0	38936	200	0
2	7	2538	0	1286	3	0
3	8	3208	0	1629	7	0
4	AA	1895	0	1984	51	0
5	AB	3172	0	3310	22	0
6	AC	2883	0	3053	32	0
7	AD	2391	0	2424	10	0
8	AE	1729	0	1887	16	0
9	AF	1875	0	1995	12	0
10	AG	1819	0	1956	9	0
11	AH	1516	0	1597	6	0
12	AI	1664	0	1712	9	0
13	AJ	1362	0	1399	4	0
14	AL	1627	0	1743	6	0
15	AM	1137	0	1211	9	0
16	AN	1701	0	1749	15	0
17	AO	1631	0	1780	14	0
18	AP	1242	0	1274	6	0
19	AQ	1526	0	1623	29	0
20	AR	1503	0	1657	23	0
21	AS	1457	0	1490	23	0
22	AT	1298	0	1366	10	0
23	AU	818	0	838	15	0
24	AV	969	0	1031	9	0
25	AW	528	0	541	5	0
26	AX	967	0	1040	4	0
27	AY	1115	0	1205	8	0
28	AZ	1107	0	1182	7	0
29	Aa	1162	0	1209	0	0
30	Ab	848	0	920	0	0
31	Ac	761	0	794	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	Ad	888	0	930	0	0
33	Ae	1053	0	1147	0	0
34	Af	876	0	912	0	0
35	Ag	906	0	1002	0	0
36	Ah	1013	0	1147	0	0
37	Ai	830	0	916	0	0
38	Aj	705	0	741	0	0
39	Ak	569	0	634	0	0
40	Al	447	0	480	0	0
41	Am	429	0	469	0	0
42	An	239	0	289	0	0
43	Ao	851	0	924	0	0
44	Ap	708	0	760	0	0
45	Ar	994	0	1051	0	0
46	AK	1705	0	1810	16	0
47	2	36229	0	18300	121	0
48	B	1706	0	1697	10	0
49	C	1729	0	1803	18	0
50	D	1712	0	1808	17	0
51	E	1768	0	1866	9	0
52	F	2073	0	2173	24	0
53	G	1471	0	1522	7	0
54	H	1923	0	2089	16	0
55	I	1488	0	1582	7	0
56	J	1686	0	1772	14	0
57	K	1525	0	1640	16	0
58	L	810	0	836	2	0
59	M	1175	0	1249	7	0
60	N	908	0	939	6	0
61	O	1202	0	1289	5	0
62	P	1016	0	1039	7	0
63	Q	990	0	1038	23	0
64	R	1128	0	1195	12	0
65	S	1068	0	1121	6	0
66	T	1190	0	1249	9	0
67	U	1097	0	1130	8	0
68	V	795	0	862	6	0
69	W	630	0	631	6	0
70	X	1034	0	1080	7	0
71	Y	1098	0	1167	7	0
72	Z	1011	0	1083	4	0
73	a	598	0	656	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
74	b	778	0	828	0	0
75	c	651	0	672	0	0
76	d	488	0	514	0	0
77	e	459	0	452	0	0
78	f	447	0	495	0	0
79	g	555	0	567	0	0
80	h	2436	0	2393	0	0
81	1	4366	0	2204	33	0
All	All	215976	0	159974	798	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 798 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:D:119:GLY:HA2	81:1:6620:C:H42	1.45	0.82
6:AC:340:ILE:HD13	8:AE:53:VAL:CG2	2.12	0.79
46:AK:7:ARG:HA	46:AK:191:VAL:HG11	1.63	0.79
4:AA:155:LYS:N	4:AA:155:LYS:HE3	1.98	0.78
6:AC:340:ILE:HD13	8:AE:53:VAL:HG21	1.66	0.77

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	AA	246/257 (96%)	223 (91%)	20 (8%)	3 (1%)	14 48
5	AB	392/403 (97%)	357 (91%)	33 (8%)	2 (0%)	31 68
6	AC	360/392 (92%)	334 (93%)	22 (6%)	4 (1%)	16 50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	AD	291/297 (98%)	275 (94%)	15 (5%)	1 (0%)	43	77
8	AE	208/291 (72%)	188 (90%)	20 (10%)	0	100	100
9	AF	223/249 (90%)	209 (94%)	13 (6%)	1 (0%)	36	72
10	AG	221/242 (91%)	206 (93%)	14 (6%)	1 (0%)	31	68
11	AH	188/192 (98%)	175 (93%)	12 (6%)	1 (0%)	31	68
12	AI	201/214 (94%)	181 (90%)	20 (10%)	0	100	100
13	AJ	168/178 (94%)	158 (94%)	8 (5%)	2 (1%)	14	48
14	AL	199/211 (94%)	190 (96%)	7 (4%)	2 (1%)	17	53
15	AM	136/198 (69%)	128 (94%)	7 (5%)	1 (1%)	24	61
16	AN	201/204 (98%)	183 (91%)	16 (8%)	2 (1%)	17	53
17	AO	197/203 (97%)	188 (95%)	9 (5%)	0	100	100
18	AP	151/184 (82%)	146 (97%)	5 (3%)	0	100	100
19	AQ	185/188 (98%)	172 (93%)	13 (7%)	0	100	100
20	AR	178/196 (91%)	170 (96%)	8 (4%)	0	100	100
21	AS	174/176 (99%)	158 (91%)	14 (8%)	2 (1%)	16	50
22	AT	157/160 (98%)	144 (92%)	11 (7%)	2 (1%)	13	46
23	AU	97/128 (76%)	87 (90%)	10 (10%)	0	100	100
24	AV	127/140 (91%)	115 (91%)	11 (9%)	1 (1%)	21	59
25	AW	61/157 (39%)	59 (97%)	2 (3%)	0	100	100
26	AX	116/156 (74%)	106 (91%)	10 (9%)	0	100	100
27	AY	132/145 (91%)	123 (93%)	9 (7%)	0	100	100
28	AZ	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
29	Aa	145/148 (98%)	129 (89%)	15 (10%)	1 (1%)	24	61
30	Ab	100/226 (44%)	92 (92%)	6 (6%)	2 (2%)	8	35
31	Ac	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
32	Ad	105/125 (84%)	98 (93%)	6 (6%)	1 (1%)	17	53
33	Ae	126/135 (93%)	119 (94%)	7 (6%)	0	100	100
34	Af	107/110 (97%)	99 (92%)	6 (6%)	2 (2%)	9	36
35	Ag	112/126 (89%)	109 (97%)	3 (3%)	0	100	100
36	Ah	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
37	Ai	100/105 (95%)	93 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	Aj	84/97 (87%)	77 (92%)	6 (7%)	1 (1%)	14	48
39	Ak	67/70 (96%)	61 (91%)	3 (4%)	3 (4%)	3	17
40	Al	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
41	Am	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
42	An	23/25 (92%)	23 (100%)	0	0	100	100
43	Ao	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
44	Ap	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
45	Ar	122/137 (89%)	113 (93%)	9 (7%)	0	100	100
46	AK	210/217 (97%)	168 (80%)	36 (17%)	6 (3%)	5	27
48	B	215/295 (73%)	198 (92%)	17 (8%)	0	100	100
49	C	211/264 (80%)	193 (92%)	16 (8%)	2 (1%)	19	56
50	D	219/255 (86%)	204 (93%)	14 (6%)	1 (0%)	31	68
51	E	226/281 (80%)	203 (90%)	21 (9%)	2 (1%)	19	56
52	F	260/263 (99%)	233 (90%)	26 (10%)	1 (0%)	36	72
53	G	181/204 (89%)	164 (91%)	13 (7%)	4 (2%)	7	33
54	H	235/249 (94%)	213 (91%)	21 (9%)	1 (0%)	36	72
55	I	181/194 (93%)	166 (92%)	14 (8%)	1 (1%)	27	64
56	J	204/207 (99%)	185 (91%)	16 (8%)	3 (2%)	11	43
57	K	183/194 (94%)	167 (91%)	15 (8%)	1 (0%)	31	68
58	L	94/149 (63%)	84 (89%)	10 (11%)	0	100	100
59	M	139/158 (88%)	125 (90%)	13 (9%)	1 (1%)	24	61
60	N	115/132 (87%)	96 (84%)	19 (16%)	0	100	100
61	O	147/151 (97%)	134 (91%)	11 (8%)	2 (1%)	12	44
62	P	134/151 (89%)	123 (92%)	11 (8%)	0	100	100
63	Q	117/145 (81%)	98 (84%)	16 (14%)	3 (3%)	6	29
64	R	140/172 (81%)	126 (90%)	14 (10%)	0	100	100
65	S	130/135 (96%)	119 (92%)	11 (8%)	0	100	100
66	T	142/152 (93%)	127 (89%)	14 (10%)	1 (1%)	24	61
67	U	139/145 (96%)	126 (91%)	12 (9%)	1 (1%)	24	61
68	V	98/119 (82%)	89 (91%)	9 (9%)	0	100	100
69	W	81/83 (98%)	76 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	X	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	21	59
71	Y	139/143 (97%)	126 (91%)	10 (7%)	3 (2%)	7	33
72	Z	122/134 (91%)	110 (90%)	12 (10%)	0	100	100
73	a	73/125 (58%)	65 (89%)	8 (11%)	0	100	100
74	b	96/115 (84%)	82 (85%)	13 (14%)	1 (1%)	17	53
75	c	81/84 (96%)	74 (91%)	7 (9%)	0	100	100
76	d	60/69 (87%)	57 (95%)	2 (3%)	1 (2%)	10	40
77	e	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
78	f	54/133 (41%)	49 (91%)	5 (9%)	0	100	100
79	g	66/156 (42%)	54 (82%)	11 (17%)	1 (2%)	11	43
80	h	311/317 (98%)	262 (84%)	49 (16%)	0	100	100
All	All	11321/12917 (88%)	10354 (92%)	895 (8%)	72 (1%)	31	64

5 of 72 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	AT	80	VAL
46	AK	140	HIS
6	AC	126	SER
9	AF	196	VAL
14	AL	6	ASN

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AA	189/199 (95%)	169 (89%)	20 (11%)	7	28
5	AB	342/348 (98%)	330 (96%)	12 (4%)	39	73
6	AC	302/323 (94%)	284 (94%)	18 (6%)	21	54
7	AD	247/250 (99%)	244 (99%)	3 (1%)	74	89
8	AE	190/251 (76%)	183 (96%)	7 (4%)	37	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	AF	196/218 (90%)	191 (97%)	5 (3%)	49	78
10	AG	194/208 (93%)	189 (97%)	5 (3%)	49	78
11	AH	169/171 (99%)	162 (96%)	7 (4%)	33	68
12	AI	175/181 (97%)	172 (98%)	3 (2%)	63	85
13	AJ	143/149 (96%)	142 (99%)	1 (1%)	85	94
14	AL	167/176 (95%)	161 (96%)	6 (4%)	38	72
15	AM	117/151 (78%)	116 (99%)	1 (1%)	81	92
16	AN	171/172 (99%)	166 (97%)	5 (3%)	45	76
17	AO	171/173 (99%)	166 (97%)	5 (3%)	45	76
18	AP	134/163 (82%)	130 (97%)	4 (3%)	44	75
19	AQ	166/167 (99%)	148 (89%)	18 (11%)	7	28
20	AR	159/175 (91%)	146 (92%)	13 (8%)	12	42
21	AS	155/155 (100%)	142 (92%)	13 (8%)	12	41
22	AT	139/140 (99%)	135 (97%)	4 (3%)	45	76
23	AU	91/116 (78%)	88 (97%)	3 (3%)	41	74
24	AV	100/107 (94%)	95 (95%)	5 (5%)	27	61
25	AW	55/126 (44%)	55 (100%)	0	100	100
26	AX	106/134 (79%)	105 (99%)	1 (1%)	81	92
27	AY	124/135 (92%)	119 (96%)	5 (4%)	34	69
28	AZ	117/118 (99%)	115 (98%)	2 (2%)	63	85
29	Aa	119/120 (99%)	116 (98%)	3 (2%)	50	80
30	Ab	84/172 (49%)	82 (98%)	2 (2%)	52	80
31	Ac	84/98 (86%)	82 (98%)	2 (2%)	52	80
32	Ad	98/110 (89%)	96 (98%)	2 (2%)	58	83
33	Ae	114/121 (94%)	111 (97%)	3 (3%)	49	78
34	Af	88/89 (99%)	82 (93%)	6 (7%)	17	50
35	Ag	98/106 (92%)	97 (99%)	1 (1%)	78	91
36	Ah	109/110 (99%)	106 (97%)	3 (3%)	47	77
37	Ai	86/89 (97%)	83 (96%)	3 (4%)	39	73
38	Aj	73/80 (91%)	71 (97%)	2 (3%)	48	78
39	Ak	64/65 (98%)	61 (95%)	3 (5%)	29	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	Al	47/48 (98%)	47 (100%)	0	100	100
41	Am	48/48 (100%)	46 (96%)	2 (4%)	32	67
42	An	24/24 (100%)	23 (96%)	1 (4%)	32	67
43	Ao	92/94 (98%)	89 (97%)	3 (3%)	41	74
44	Ap	74/75 (99%)	72 (97%)	2 (3%)	48	78
45	Ar	108/121 (89%)	106 (98%)	2 (2%)	60	84
46	AK	190/196 (97%)	179 (94%)	11 (6%)	22	56
48	B	180/245 (74%)	178 (99%)	2 (1%)	76	90
49	C	194/231 (84%)	189 (97%)	5 (3%)	49	78
50	D	186/205 (91%)	181 (97%)	5 (3%)	48	78
51	E	190/232 (82%)	184 (97%)	6 (3%)	42	74
52	F	223/225 (99%)	216 (97%)	7 (3%)	43	75
53	G	158/170 (93%)	157 (99%)	1 (1%)	87	94
54	H	207/218 (95%)	206 (100%)	1 (0%)	90	95
55	I	165/174 (95%)	163 (99%)	2 (1%)	74	89
56	J	178/179 (99%)	177 (99%)	1 (1%)	87	94
57	K	161/168 (96%)	156 (97%)	5 (3%)	43	75
58	L	87/125 (70%)	86 (99%)	1 (1%)	76	90
59	M	130/142 (92%)	127 (98%)	3 (2%)	53	80
60	N	99/108 (92%)	97 (98%)	2 (2%)	58	83
61	O	130/131 (99%)	129 (99%)	1 (1%)	83	93
62	P	106/119 (89%)	105 (99%)	1 (1%)	81	92
63	Q	108/130 (83%)	100 (93%)	8 (7%)	15	47
64	R	117/140 (84%)	114 (97%)	3 (3%)	49	78
65	S	119/121 (98%)	119 (100%)	0	100	100
66	T	125/132 (95%)	123 (98%)	2 (2%)	65	87
67	U	111/116 (96%)	109 (98%)	2 (2%)	62	85
68	V	92/107 (86%)	89 (97%)	3 (3%)	41	74
69	W	68/68 (100%)	63 (93%)	5 (7%)	15	47
70	X	112/113 (99%)	111 (99%)	1 (1%)	81	92
71	Y	113/114 (99%)	112 (99%)	1 (1%)	81	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	Z	107/115 (93%)	104 (97%)	3 (3%)	47	77
73	a	66/103 (64%)	63 (96%)	3 (4%)	30	65
74	b	86/99 (87%)	84 (98%)	2 (2%)	53	80
75	c	75/76 (99%)	75 (100%)	0	100	100
76	d	55/62 (89%)	55 (100%)	0	100	100
77	e	48/49 (98%)	48 (100%)	0	100	100
78	f	46/106 (43%)	44 (96%)	2 (4%)	32	66
79	g	61/140 (44%)	60 (98%)	1 (2%)	65	87
80	h	272/275 (99%)	268 (98%)	4 (2%)	67	87
All	All	9894/11010 (90%)	9594 (97%)	300 (3%)	48	75

5 of 300 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	AS	19	THR
29	Aa	44	ASN
68	V	50	VAL
21	AS	77	ASN
23	AU	97	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
26	AX	125	ASN
46	AK	94	ASN
70	X	64	ASN
29	Aa	85	GLN
38	Aj	13	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3569/3594 (99%)	960 (26%)	74 (2%)
2	7	118/119 (99%)	15 (12%)	1 (0%)
3	8	149/156 (95%)	36 (24%)	4 (2%)
47	2	1685/1869 (90%)	456 (27%)	31 (1%)
81	1	204/253 (80%)	110 (53%)	9 (4%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	5725/5991 (95%)	1577 (27%)	119 (2%)

5 of 1577 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	6	C
1	5	9	C
1	5	10	A
1	5	12	A
1	5	13	U

5 of 119 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	3765	G
1	5	4635	A
47	2	1744	G
1	5	3888	G
1	5	4155	C

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	25

The worst 5 of 25 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	40.49
1	5	1252:C	O3'	1271:G	P	36.06
1	5	1219:G	O3'	1233:G	P	21.64
1	5	1405:C	O3'	1409:G	P	19.72
1	5	1696:C	O3'	1720:C	P	19.06