



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

Dec 3, 2019 – 06:48 PM EST

PDB ID : 5MC6  
EMDB ID: : EMD-3461  
Title : Cryo-EM structure of a native ribosome-Ski2-Ski3-Ski8 complex from *S. cerevisiae*  
Authors : Schmidt, C.; Kowalinski, E.; Shanmuganathan, V.; Defenouillere, Q.; Braunger, K.; Heuer, A.; Pech, M.; Namane, A.; Berninghausen, O.; Fromont-Racine, M.; Jacquier, A.; Conti, E.; Becker, T.; Beckmann, R.  
Deposited on : 2016-11-09  
Resolution : 3.80 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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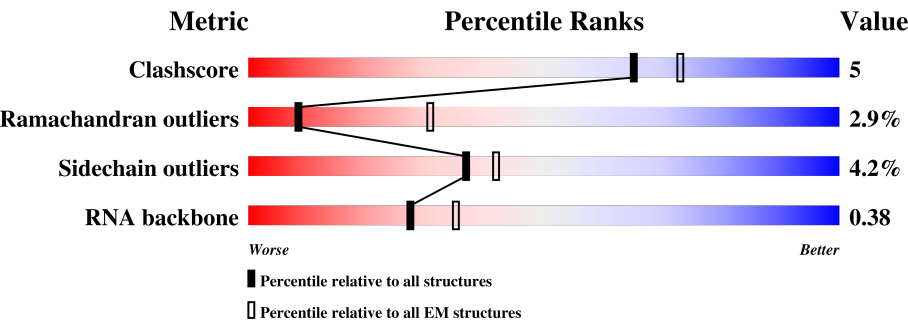
MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : 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 3.80 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.























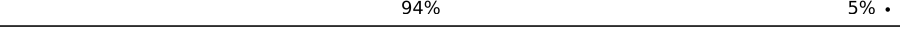
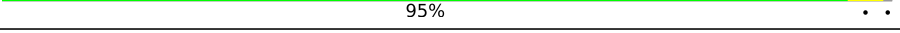
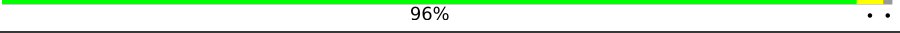


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

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	2	1800	<div><div>50%</div><div>41%</div><div>7%</div><div>.</div></div>
2	A	240	<div><div>78%</div><div>14%</div><div>7%</div><div>.</div></div>
3	B	225	<div><div>74%</div><div>16%</div><div>8%</div><div>.</div></div>
4	C	105	<div><div>69%</div><div>22%</div><div>9%</div><div>.</div></div>
5	D	143	<div><div>67%</div><div>17%</div><div>15%</div><div>.</div></div>
6	E	142	<div><div>75%</div><div>12%</div><div>13%</div><div>.</div></div>
7	F	143	<div><div>81%</div><div>14%</div><div>..</div></div>
8	G	136	<div><div>54%</div><div>11%</div><div>33%</div><div>.</div></div>


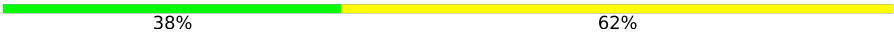



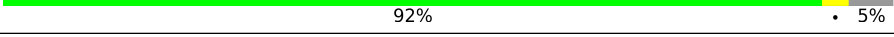
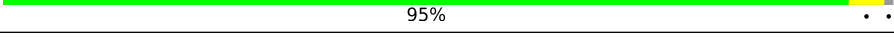
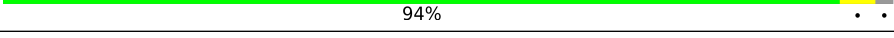
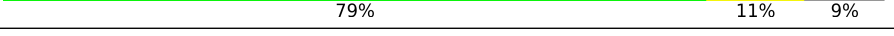

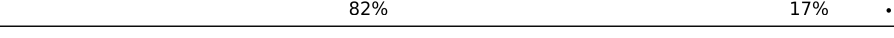
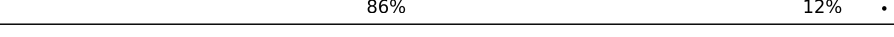

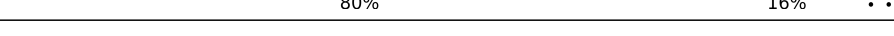


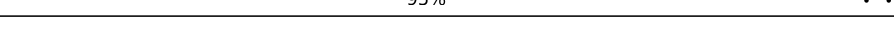

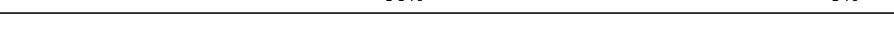






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Mol	Chain	Length	Quality of chain
9	H	146	 77% 18% . .
10	I	144	 78% 19% ..
11	J	121	 74% 13% . 12%
12	K	108	 50% 13% . 35%
13	L	67	 85% 9% 6%
14	M	56	 86% 7% . 5%
15	N	152	 29% 5% 66%
16	O	319	 89% 10%
17	P	252	 75% 6% . 18%
18	Q	255	 71% 13% . 16%
19	R	254	 76% 10% 13%
20	S	261	 89% 11%
21	T	236	 83% 12% .
22	U	190	 83% 13% ..
23	V	200	 65% 23% 5% . 6%
24	W	197	 82% 8% . 10%
25	X	156	 88% 11% ..
26	Y	151	 87% 11% ..
27	Z	137	 80% 12% . 7%
28	a	87	 94% 5% .
29	b	130	 95% . .
30	c	145	 96% . .
31	d	135	 87% 9% ..
32	e	119	 68% 13% 18%
33	f	82	 93% 6% .




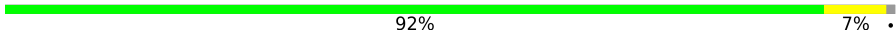
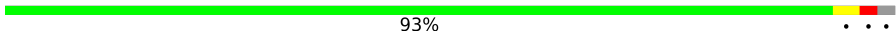



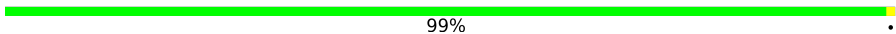
















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Mol	Chain	Length	Quality of chain
34	g	63	 92% 5%
35	l	34	 38% 62%
36	m	76	 55% 43%
37	n	77	 60% 40%
38	h	1287	 83% 13%
39	i	1432	 92% 5%
40	j	397	 95%
40	k	397	 94%
41	AA	256	 79% 11% 9%
42	AB	137	 86% 13%
43	AC	100	 82% 17%
44	AD	191	 86% 12%
45	AE	155	 56% 6% 37%
46	AF	88	 80% 16%
47	AG	174	 83% 13%
48	AH	142	 75% 11% 15%
49	AI	78	 95%
50	AJ	199	 86% 10%
51	AK	127	 90% 9%
52	AL	51	 86% 12%
53	AM	138	 87% 12%
54	AN	136	 82% 17%
55	AO	128	 36% 59%
56	AP	106	 89% 9%
57	AQ	204	 85% 13%





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Mol	Chain	Length	Quality of chain
58	AR	149	 81% 13% ..
59	AS	25	 44% 52% .
60	AT	92	 84% 14% ..
61	AU	199	 92% 7% .
62	AV	59	 93% . . .
63	AW	254	 80% 19% .
64	AX	184	 85% 13% ..
65	AY	105	 82% 10% . 8%
66	AZ	210	 99% .
67	BA	387	 84% 15% .
68	BB	186	 84% 16% .
69	BC	113	 76% 19% . .
70	BD	221	 85% 13% .
71	BE	362	 84% 15% .
72	BF	189	 86% 13% ..
73	BG	130	 87% 11% .
74	BH	172	 91% 9% .
75	BI	297	 87% 11% .
76	BJ	160	 87% 13% .
77	BK	107	 83% 15% ..
78	BL	121	 78% 5% 17%
79	BM	176	 75% 12% . 11%
80	BN	121	 83% 9% 7%
81	BO	244	 80% 10% 9%
82	BP	120	 89% 9% ..

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Mol	Chain	Length	Quality of chain
83	BQ	3396	 51% 36% 6% 7%
84	BR	121	 54% 40% 6%
85	BS	158	 53% 41% 7%
86	BT	157	 50% 41% 5% ..

## 2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 229285 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1767	Total	C	N	O	P	0	0
			37645	16830	6656	12392	1767		

- Molecule 2 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 3 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 4 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	96	Total	C	N	O	S	0	0
			813	527	133	151	2		

- Molecule 5 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	121	Total	C	N	O	S	0	0
			877	552	153	170	2		

- Molecule 6 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 7 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	F	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 8 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	91	Total	C	N	O	S	0	0
			746	467	144	133	2		

- Molecule 9 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 10 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 11 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 12 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	K	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 13 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 14 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 15 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 16 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	318	Total	C	N	O	S	0	0
			2436	1541	418	469	8		

- Molecule 17 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 18 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 19 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	220	Total	C	N	O	S	0	0
			1671	1072	297	300	2		

- Molecule 20 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 21 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 22 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	184	Total	C	N	O	S	0	0
			1481	951	265	265			

- Molecule 23 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 24 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	178	Total	C	N	O	S	0	0
			1434	905	276	252	1		

- Molecule 25 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 26 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 27 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 28 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 29 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 30 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 31 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	132	Total	C	N	O		0	0
			1060	669	206	185			

- Molecule 32 is a protein called 40S ribosomal protein S26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 34 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	60	Total	C	N	O	S	0	0
			473	297	98	77	1		

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	34	Total	C	N	O	P	0	0
			692	311	84	263	34		

- Molecule 36 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	76	Total	C	N	O	P	0	0
			1611	721	281	534	75		

- Molecule 37 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	77	Total	C	N	O	P	0	0
			1644	731	290	546	77		

- Molecule 38 is a protein called Antiviral helicase SKI2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	1121	Total	C	N	O	S	0	0
			8814	5643	1504	1625	42		

- Molecule 39 is a protein called Superciller protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	1365	Total	C	N	O	S	0	0
			9827	6302	1663	1825	37		

- Molecule 40 is a protein called Antiviral protein SKI8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	392	Total	C	N	O	S	0	0
			2933	1861	500	558	14		
40	k	388	Total	C	N	O	S	0	0
			2919	1851	502	552	14		

- Molecule 41 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AA	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 42 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AB	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AC	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 44 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AD	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 45 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AE	98	Total	C	N	O	S	0	0
			699	443	137	118	1		

- Molecule 46 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AF	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 47 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AG	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 48 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AH	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 49 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	AI	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 50 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	AJ	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 51 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	AK	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 52 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AL	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 53 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 54 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	AN	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 55 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AO	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 56 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AP	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 57 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AQ	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 58 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AR	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 59 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 60 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AT	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 61 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AU	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 62 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	AV	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 63 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 64 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AX	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 65 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AY	97	Total	C	N	O	S	0	0
			742	479	124	138	1		

- Molecule 66 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	210	Total	C	N	O		0	0
			1050	630	210	210			

- Molecule 67 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BA	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 68 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BB	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 69 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BC	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 70 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BD	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 71 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BE	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 72 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	BF	188	Total	C	N	O	S	0	0
			1521	935	326	260			

- Molecule 73 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BG	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 74 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BH	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 75 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BI	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 76 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	BJ	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 77 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	BK	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 78 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	BL	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 79 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BM	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 80 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	BN	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 81 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BO	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 82 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BP	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 83 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	BQ	3165	Total	C	N	O	P	0	0
			67695	30238	12201	22091	3165		

- Molecule 84 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	BR	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 85 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	BS	158	Total	C	N	O	P	0	0
			3352	1500	586	1108	158		

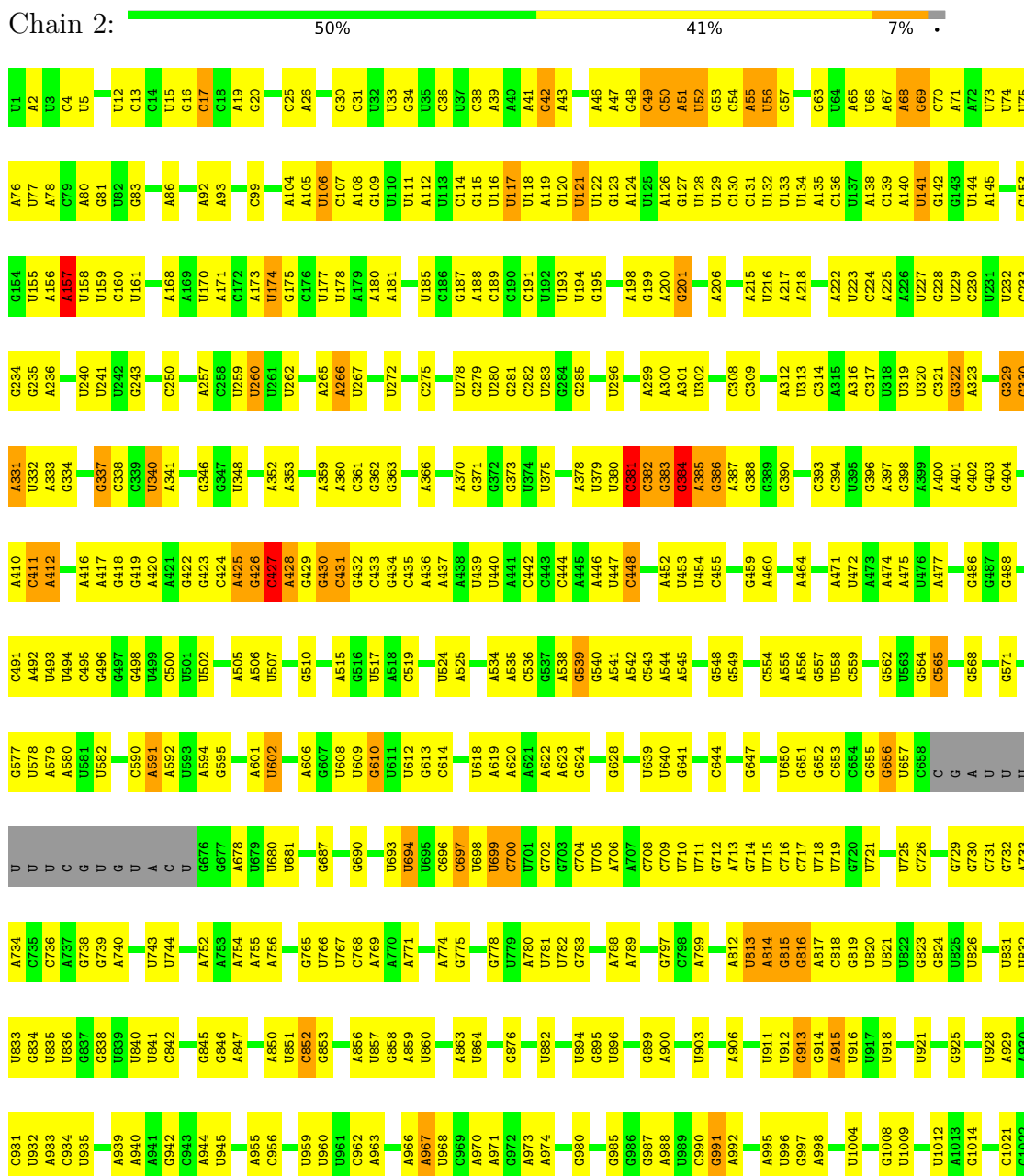
- Molecule 86 is a protein called Eukaryotic translation initiation factor 5A-1.

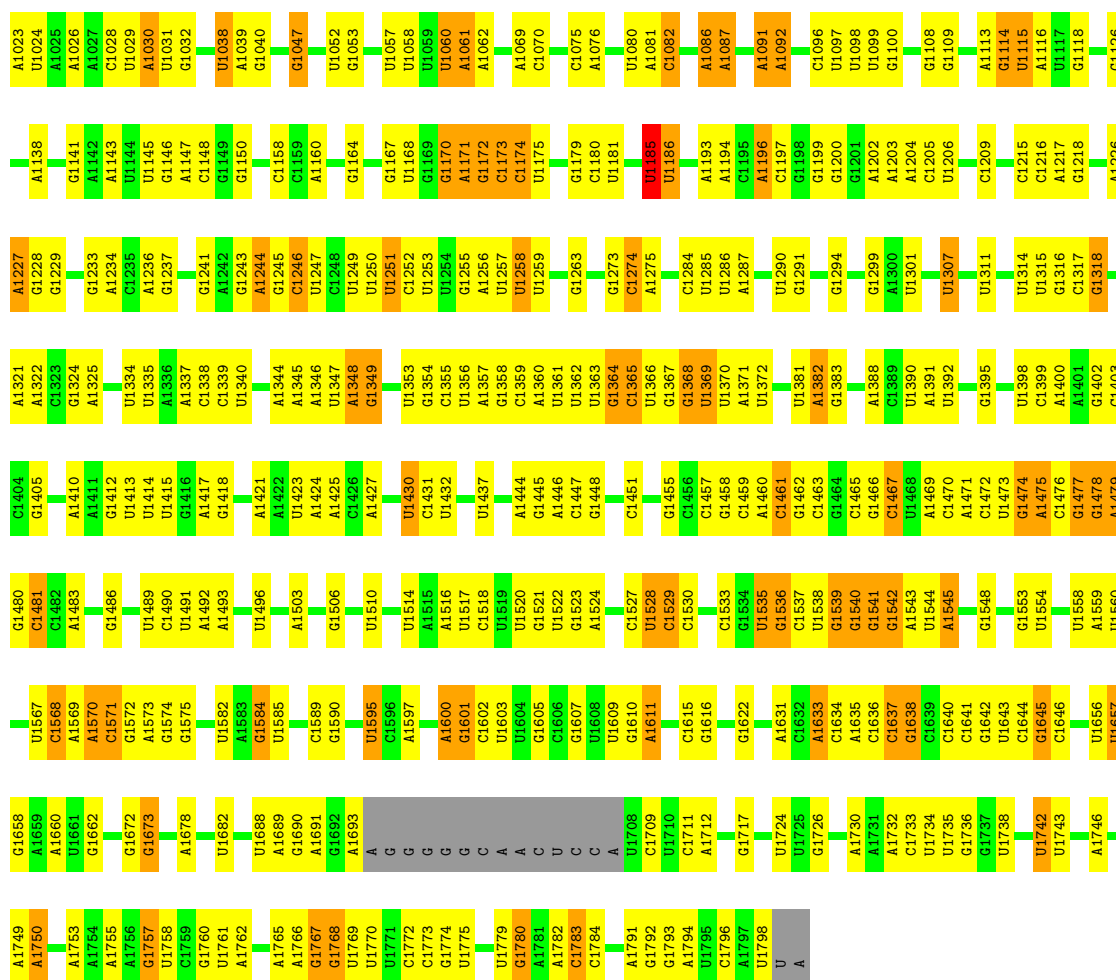
Mol	Chain	Residues	Atoms					AltConf	Trace
86	BT	154	Total	C	N	O	S	0	0
			1143	709	195	230	9		

### 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.

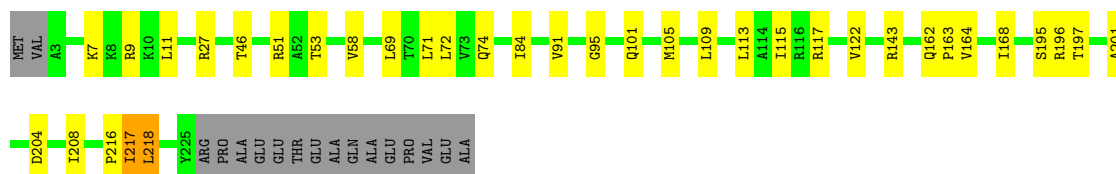
#### • Molecule 1: 18S ribosomal RNA





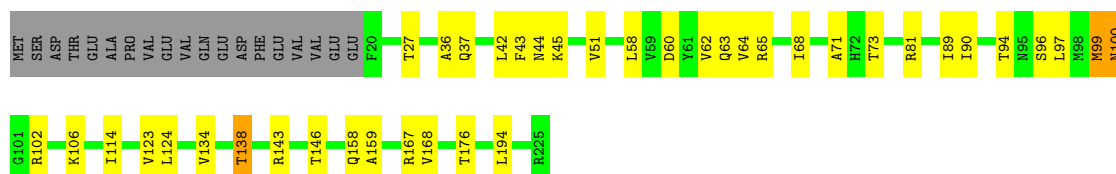
• Molecule 2: 40S ribosomal protein S3

Chain A: 78% 14% 7%



• Molecule 3: 40S ribosomal protein S5

Chain B: 74% 16% 8%



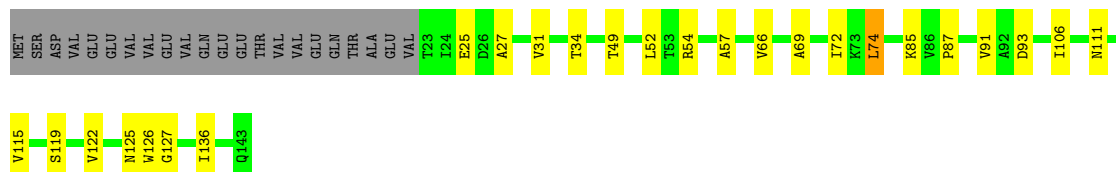
• Molecule 4: 40S ribosomal protein S10-A

Chain C:  69% 22% 9%



- Molecule 5: 40S ribosomal protein S12

Chain D:  67% 17% 15%




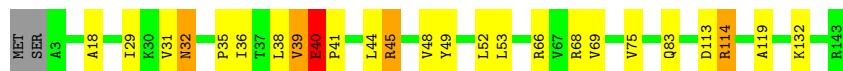
- Molecule 6: 40S ribosomal protein S15

Chain E:  75% 12% 13%



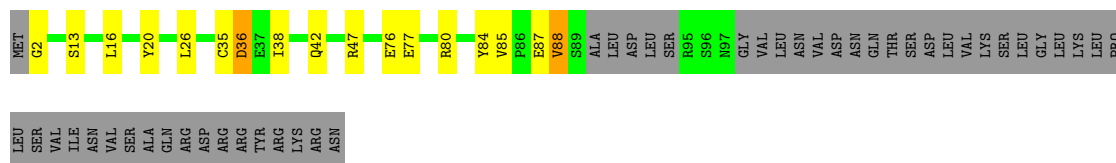
- Molecule 7: 40S ribosomal protein S16-A

Chain F:  81% 14% ..




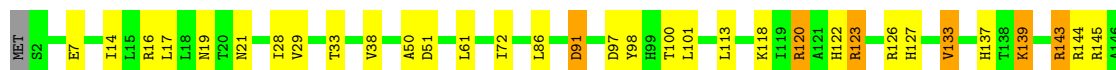
- Molecule 8: 40S ribosomal protein S17-B

Chain G:  54% 11% 33%



- Molecule 9: 40S ribosomal protein S18-A

Chain H:  77% 18% ..



- Molecule 10: 40S ribosomal protein S19-A

Chain I:  78% 19% ..



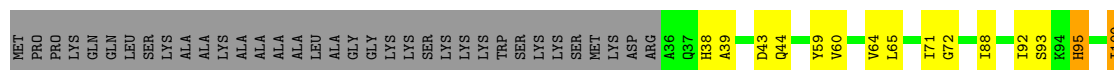
- Molecule 11: 40S ribosomal protein S20

Chain J: 74% 13% 12%



- Molecule 12: 40S ribosomal protein S25-A

Chain K: 50% 13% 35%



- Molecule 13: 40S ribosomal protein S28-B

Chain L: 85% 9% 6%



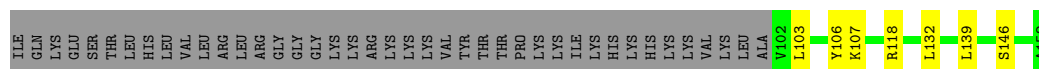
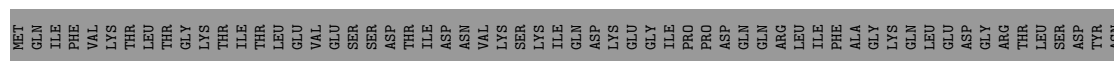
- Molecule 14: 40S ribosomal protein S29-A

Chain M: 86% 7% 5%



- Molecule 15: Ubiquitin-40S ribosomal protein S31

Chain N: 29% 5% 66%



- Molecule 16: Guanine nucleotide-binding protein subunit beta-like protein

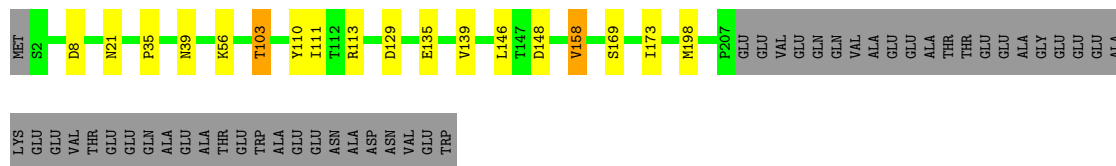
Chain O: 89% 10%





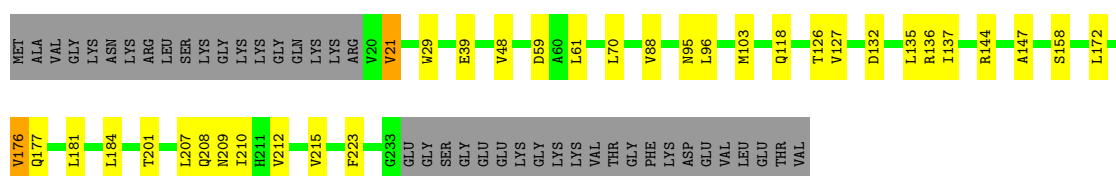
• Molecule 17: 40S ribosomal protein S0-A

Chain P: 75% 6% 18%



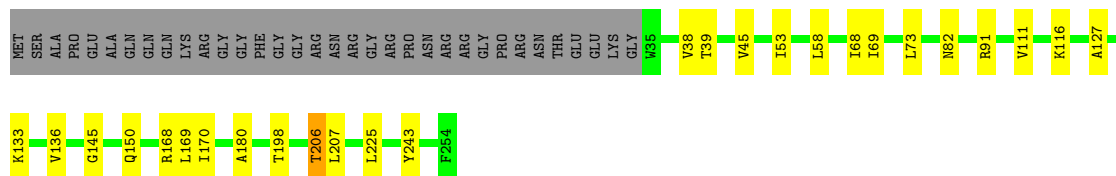
• Molecule 18: 40S ribosomal protein S1-A

Chain Q: 71% 13% 16%



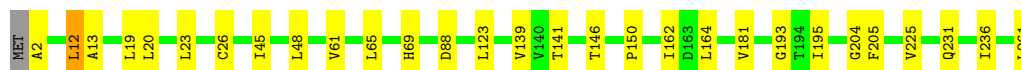
• Molecule 19: 40S ribosomal protein S2

Chain R: 76% 10% 13%



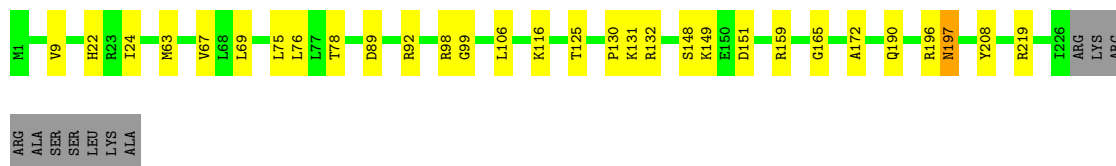
• Molecule 20: 40S ribosomal protein S4-A

Chain S: 89% 11%




• Molecule 21: 40S ribosomal protein S6-A

Chain T: 83% 12%



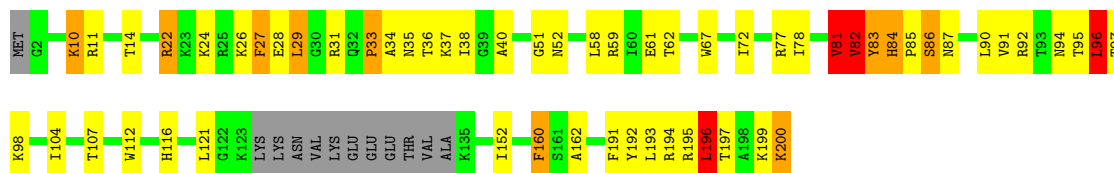
• Molecule 22: 40S ribosomal protein S7-A

Chain U:  83% 13% ..




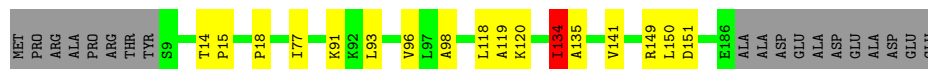
- Molecule 23: 40S ribosomal protein S8-A

Chain V:  65% 23% 5% • 6%




- Molecule 24: 40S ribosomal protein S9-A

Chain W:  82% 8% • 10%




- Molecule 25: 40S ribosomal protein S11-A

Chain X:  88% 11% ..




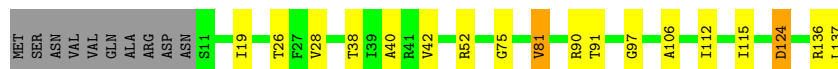
- Molecule 26: 40S ribosomal protein S13

Chain Y:  87% 11% ..



- Molecule 27: 40S ribosomal protein S14-A

Chain Z:  80% 12% • 7%



- Molecule 28: 40S ribosomal protein S21-A

Chain a:  94% 5% •



- Molecule 29: 40S ribosomal protein S22-A

Chain b:  95% ..



- Molecule 30: 40S ribosomal protein S23-A

Chain c:  96% ..



- Molecule 31: 40S ribosomal protein S24-A

Chain d:  87% 9% ..



- Molecule 32: 40S ribosomal protein S26-A

Chain e:  68% 13% 18%



- Molecule 33: 40S ribosomal protein S27-A

Chain f:  93% 6% .

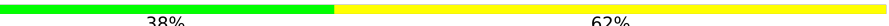


- Molecule 34: 40S ribosomal protein S30-A

Chain g:  92% . 5%



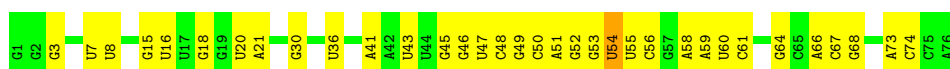
- Molecule 35: mRNA

Chain l:  38% 62%



- Molecule 36: A-site tRNA

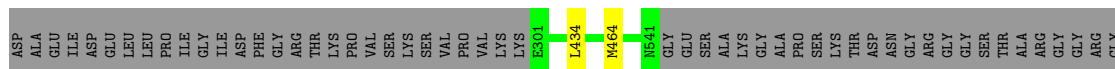
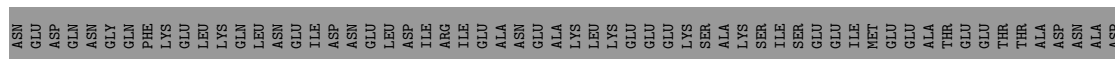
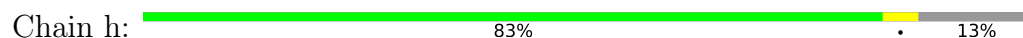
Chain m:  55% 43% .



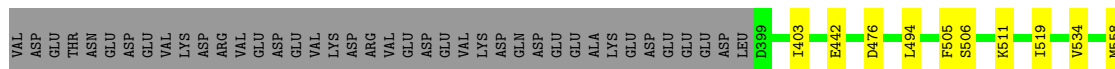
- Molecule 37: P-site tRNA



- Molecule 38: Antiviral helicase SKI2



- Molecule 39: Superkiller protein 3



- Molecule 40: Antiviral protein SKI8




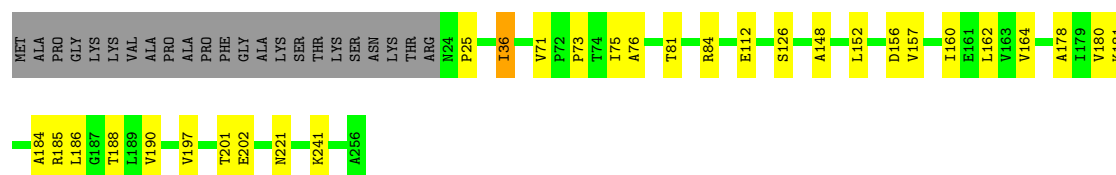
- Molecule 40: Antiviral protein SKI8

Chain k:  94% .

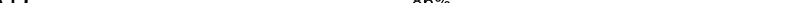


- Molecule 41: 60S ribosomal protein L8-A

Chain AA:  79% 11% 9%




- Molecule 42: 60S ribosomal protein L23-A

Chain AB:  86% 13%



- Molecule 43: 60S ribosomal protein L36-A

Chain AC: 



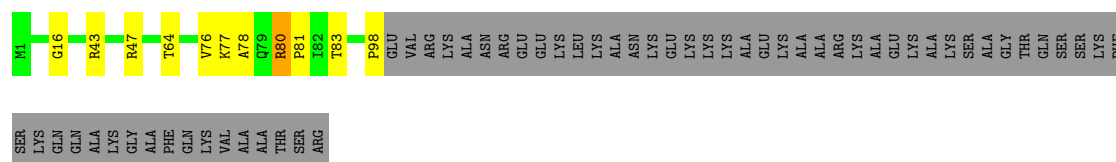
- Molecule 44: 60S ribosomal protein L9-A

Chain AD:  86% 12%




- Molecule 45: 60S ribosomal protein L24-A

Chain AE:  56% 6% 37%



- Molecule 46: 60S ribosomal protein L37-A

Chain AF: 



- Molecule 47: 60S ribosomal protein L11-A

Chain AG: 83% 13% ..



- Molecule 48: 60S ribosomal protein L25

Chain AH: 75% 11% 15%



- Molecule 49: 60S ribosomal protein L38

Chain AI: 95% ..



- Molecule 50: 60S ribosomal protein L13-A

Chain AJ: 86% 10% ..



- Molecule 51: 60S ribosomal protein L26-A

Chain AK: 90% 9% .



- Molecule 52: 60S ribosomal protein L39

Chain AL: 86% 12% .




- Molecule 53: 60S ribosomal protein L14-A

Chain AM: 87% 12% .



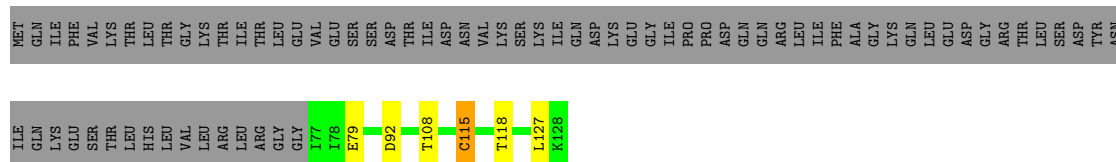
- Molecule 54: 60S ribosomal protein L27-A

Chain AN:  82% 17%



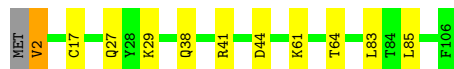
- Molecule 55: Ubiquitin-60S ribosomal protein L40

Chain AO:  36% 59%




- Molecule 56: 60S ribosomal protein L42-A

Chain AP:  89% 9%




- Molecule 57: 60S ribosomal protein L15-A

Chain AQ:  85% 13%



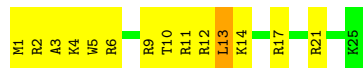
- Molecule 58: 60S ribosomal protein L28

Chain AR:  81% 13%




- Molecule 59: 60S ribosomal protein L41-A

Chain AS:  44% 52%



- Molecule 60: 60S ribosomal protein L43-A

Chain AT:  84% 14%



- Molecule 61: 60S ribosomal protein L16-A

Chain AU:  92% 7% .




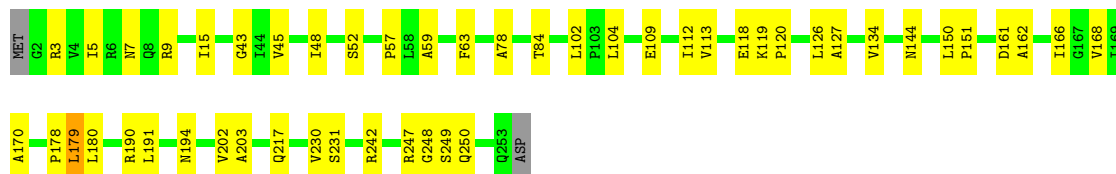
- Molecule 62: 60S ribosomal protein L29

Chain AV:  93% . . .




- Molecule 63: 60S ribosomal protein L2-A

Chain AW:  80% 19% .




- Molecule 64: 60S ribosomal protein L17-A

Chain AX:  85% 13% ..



- Molecule 65: 60S ribosomal protein L30

Chain AY:  82% 10% . 8%




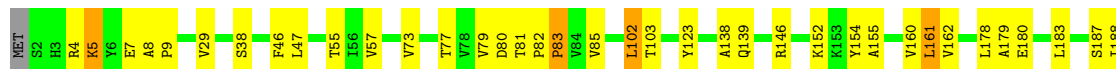
- Molecule 66: uL1

Chain AZ:  99% .



- Molecule 67: 60S ribosomal protein L3

Chain BA:  84% 15% .





- Molecule 68: 60S ribosomal protein L18-A

Chain BB: 84% 16%



- Molecule 69: 60S ribosomal protein L31-A

Chain BC: 76% 19%



- Molecule 70: 60S ribosomal protein L10

Chain BD: 85% 13%



- Molecule 71: 60S ribosomal protein L4-A

Chain BE: 84% 15%



- Molecule 72: 60S ribosomal protein L19-A

Chain BF: 86% 13%

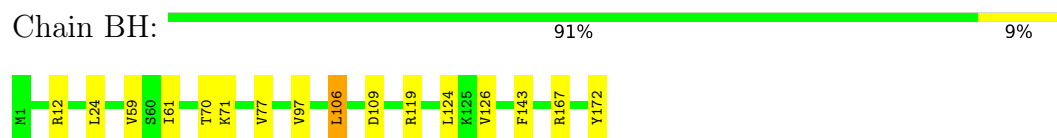


- Molecule 73: 60S ribosomal protein L32

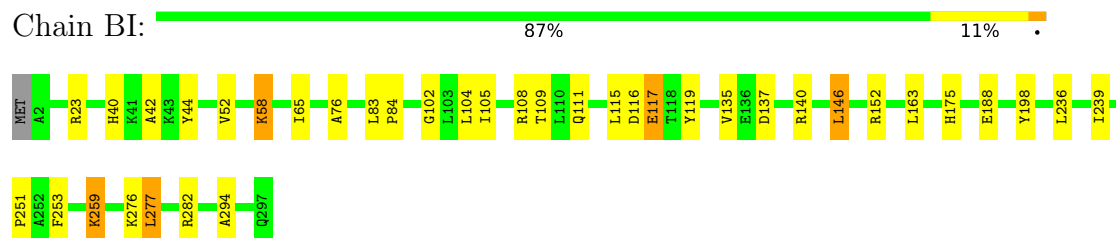
Chain BG: 87% 11%



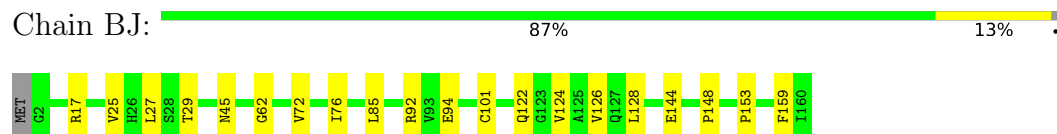
- Molecule 74: 60S ribosomal protein L20-A



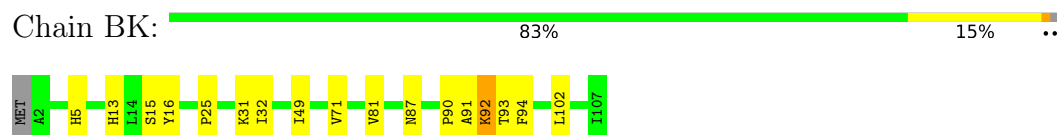
- Molecule 75: 60S ribosomal protein L5



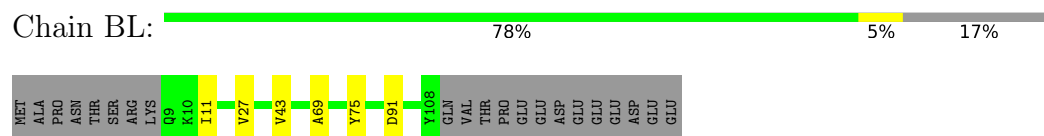
- Molecule 76: 60S ribosomal protein L21-A



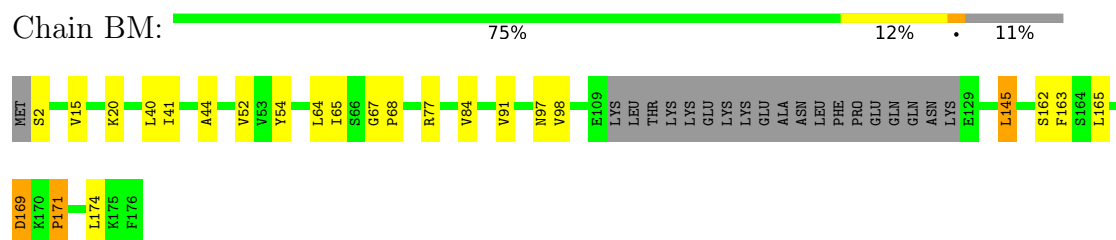
- Molecule 77: 60S ribosomal protein L33-A



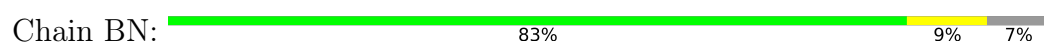
- Molecule 78: 60S ribosomal protein L22-A



- Molecule 79: 60S ribosomal protein L6-A



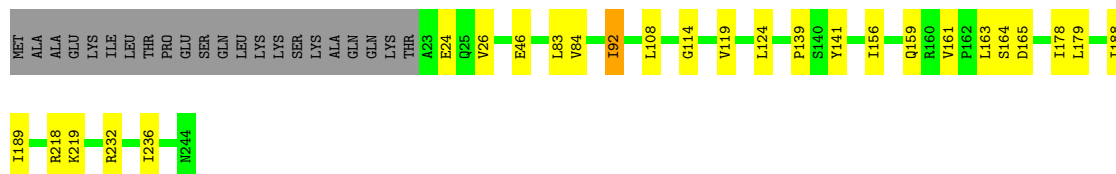
- Molecule 80: 60S ribosomal protein L34-A





- Molecule 81: 60S ribosomal protein L7-A

Chain BO: 80% 10% 9%



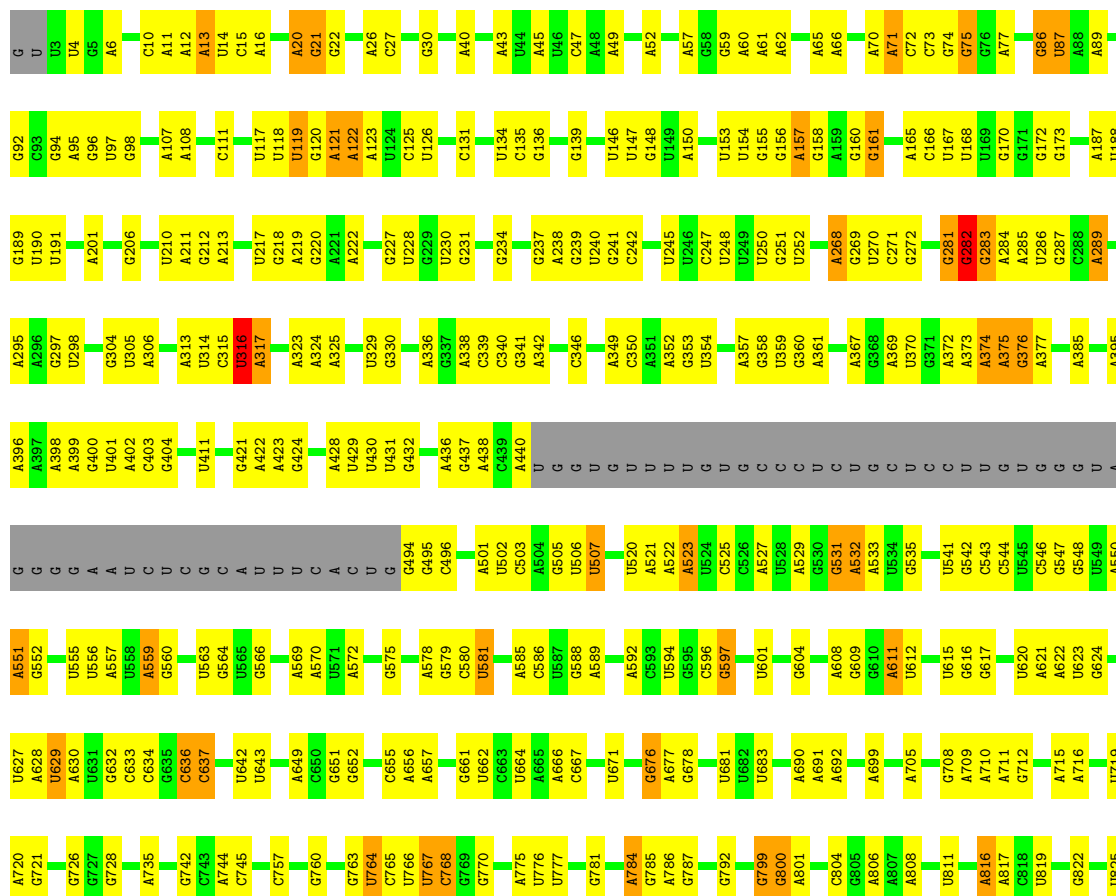
- Molecule 82: 60S ribosomal protein L35-A

Chain BP: 89% 9% ..



- Molecule 83: 25S ribosomal RNA

Chain BQ: 51% 36% 6% 7%

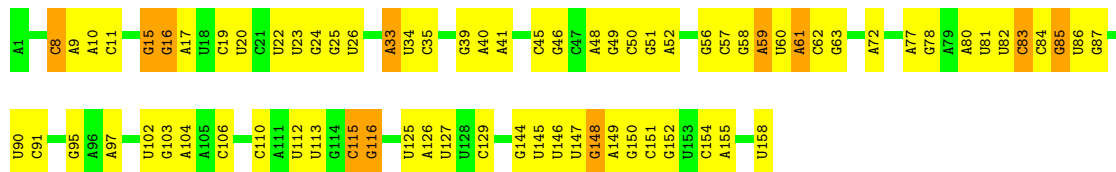


[illegible]



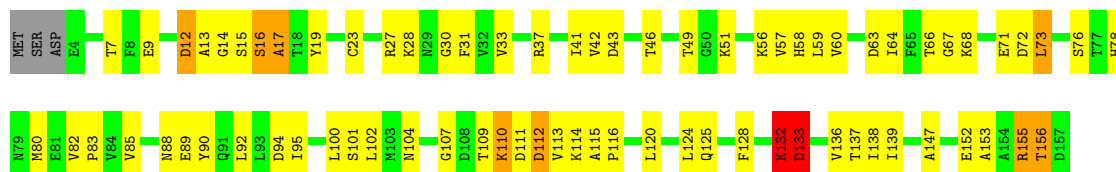
- Molecule 85: 5.8S ribosomal RNA

Chain BS:  53% 41% 7%



- Molecule 86: Eukaryotic translation initiation factor 5A-1

Chain BT:  50% 41% 5% ..



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	31503	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	2.8	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5CT

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	2	0.33	2/42103 (0.0%)	0.73	20/65603 (0.0%)
10	I	0.42	0/1130	0.68	0/1517
11	J	0.36	0/865	0.62	0/1169
12	K	0.40	0/571	0.65	0/768
13	L	0.37	0/499	0.69	0/670
14	M	0.38	0/452	0.63	0/600
15	N	0.39	0/404	0.61	0/542
16	O	0.35	0/2489	0.52	0/3389
17	P	0.39	0/1617	0.62	0/2215
18	Q	0.40	0/1735	0.62	0/2335
19	R	0.35	0/1702	0.57	0/2310
2	A	0.37	0/1759	0.62	0/2368
20	S	0.39	0/2109	0.61	0/2839
21	T	0.38	0/1823	0.62	0/2439
22	U	0.40	0/1506	0.57	0/2028
23	V	0.46	0/1514	0.78	1/2021 (0.0%)
24	W	0.40	0/1456	0.65	0/1949
25	X	0.42	2/1239 (0.2%)	0.56	0/1673
26	Y	0.39	0/1215	0.66	0/1638
27	Z	0.41	0/901	0.71	0/1217
28	a	0.38	0/693	0.64	0/935
29	b	0.35	0/1038	0.65	1/1395 (0.1%)
3	B	0.39	0/1629	0.67	0/2202
30	c	0.36	0/1139	0.61	0/1518
31	d	0.41	0/1074	0.70	2/1431 (0.1%)
32	e	0.61	0/782	0.80	0/1047
33	f	0.37	0/620	0.57	0/838
34	g	0.39	0/481	0.60	0/640
35	l	0.47	1/764 (0.1%)	0.79	0/1179
36	m	0.26	0/1799	0.72	1/2801 (0.0%)
37	n	0.36	1/1835 (0.1%)	0.71	0/2858
38	h	0.40	2/8985 (0.0%)	0.56	1/12155 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	i	0.38	0/10027	0.54	0/13707
4	C	0.39	0/833	0.59	0/1126
40	j	0.37	0/3001	0.52	0/4083
40	k	0.37	0/2988	0.54	0/4060
41	AA	0.42	0/1836	0.63	0/2481
42	AB	0.39	0/1018	0.66	0/1369
43	AC	0.43	0/778	0.73	0/1034
44	AD	0.41	0/1539	0.66	0/2073
45	AE	0.42	0/712	0.66	1/958 (0.1%)
46	AF	0.45	0/696	0.74	0/923
47	AG	0.43	0/1374	0.71	0/1842
48	AH	0.38	0/979	0.64	0/1321
49	AI	0.40	0/618	0.61	0/826
5	D	0.40	0/885	0.61	0/1202
50	AJ	0.45	0/1568	0.74	0/2106
51	AK	0.39	0/1004	0.67	0/1341
52	AL	0.44	0/443	0.74	0/588
53	AM	0.40	0/1068	0.70	0/1438
54	AN	0.41	0/1118	0.65	0/1497
55	AO	0.42	0/423	0.69	0/562
56	AP	0.41	0/860	0.66	0/1136
57	AQ	0.44	0/1757	0.77	1/2354 (0.0%)
58	AR	0.42	0/1204	0.73	1/1612 (0.1%)
59	AS	0.50	0/234	0.86	0/300
6	E	0.40	0/998	0.64	0/1341
60	AT	0.39	0/701	0.72	0/934
61	AU	0.41	0/1585	0.66	0/2128
62	AV	0.39	0/473	0.66	0/629
63	AW	0.39	0/1948	0.75	0/2617
64	AX	0.42	0/1443	0.73	0/1944
65	AY	0.41	0/750	0.63	0/1008
67	BA	0.41	0/3146	0.69	0/4228
68	BB	0.40	0/1465	0.73	0/1965
69	BC	0.39	0/890	0.67	0/1196
7	F	0.40	0/1125	0.69	1/1510 (0.1%)
70	BD	0.43	0/1807	0.71	0/2425
71	BE	0.41	0/2800	0.68	0/3790
72	BF	0.43	0/1538	0.71	0/2050
73	BG	0.39	0/1041	0.64	0/1394
74	BH	0.41	0/1481	0.67	0/1990
75	BI	0.42	0/2425	0.66	0/3271
76	BJ	0.40	0/1300	0.68	0/1743
77	BK	0.41	0/868	0.69	0/1168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
78	BL	0.44	0/812	0.60	0/1099
79	BM	0.40	0/1260	0.65	0/1694
8	G	0.49	2/754 (0.3%)	0.74	1/1005 (0.1%)
80	BN	0.41	0/890	0.71	0/1189
81	BO	0.42	0/1821	0.67	0/2451
82	BP	0.39	0/978	0.69	0/1301
83	BQ	0.34	4/75774 (0.0%)	0.75	37/118137 (0.0%)
84	BR	0.31	0/2883	0.73	1/4491 (0.0%)
85	BS	0.32	0/3745	0.73	1/5829 (0.0%)
86	BT	0.32	0/1142	0.61	0/1537
9	H	0.41	0/1211	0.75	0/1628
All	All	0.37	14/243945 (0.0%)	0.70	70/355920 (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
10	I	0	2
21	T	0	2
22	U	0	1
23	V	0	3
32	e	0	2
57	AQ	0	1
58	AR	0	2
63	AW	0	1
69	BC	0	1
70	BD	0	1
86	BT	0	1
9	H	0	1
All	All	0	18

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	52	U	O3'-P	23.25	1.89	1.61
83	BQ	683	U	N1-C2	10.32	1.47	1.38
37	n	1	G	OP3-P	-10.19	1.49	1.61
35	l	34	U	OP3-P	-10.13	1.49	1.61
83	BQ	683	U	C4-C5	8.78	1.51	1.43

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	52	U	P-O3'-C3'	-14.01	102.89	119.70
1	2	52	U	C5'-C4'-O4'	-13.02	93.47	109.10
83	BQ	2972	G	N9-C1'-C2'	-11.36	99.23	114.00
1	2	428	A	N9-C1'-C2'	-10.27	100.66	114.00
83	BQ	933	A	C2'-C3'-O3'	9.73	130.90	109.50

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	H	143	ARG	Peptide
10	I	88	VAL	Peptide
10	I	89	ARG	Peptide
21	T	196	ARG	Peptide
21	T	197	ASN	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	2	37645	0	18938	393	0
2	A	1734	0	1817	17	0
3	B	1609	0	1675	18	0
4	C	813	0	800	9	0
5	D	877	0	883	8	0
6	E	977	0	1002	8	0
7	F	1105	0	1166	14	0
8	G	746	0	781	9	0
9	H	1192	0	1220	49	0
10	I	1112	0	1124	9	0
11	J	855	0	917	8	0
12	K	563	0	603	11	0
13	L	497	0	535	2	0
14	M	442	0	428	2	0
15	N	397	0	399	2	0
16	O	2436	0	2386	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	P	1577	0	1567	3	0
18	Q	1709	0	1784	10	0
19	R	1671	0	1768	12	0
20	S	2068	0	2154	12	0
21	T	1799	0	1879	41	0
22	U	1481	0	1572	16	0
23	V	1489	0	1525	33	0
24	W	1434	0	1511	7	0
25	X	1213	0	1257	5	0
26	Y	1192	0	1255	8	0
27	Z	891	0	883	4	0
28	a	684	0	672	0	0
29	b	1021	0	1060	0	0
30	c	1121	0	1196	0	0
31	d	1060	0	1123	0	0
32	e	769	0	818	0	0
33	f	610	0	633	0	0
34	g	473	0	518	0	0
35	l	692	0	347	0	0
36	m	1611	0	817	0	0
37	n	1644	0	831	0	0
38	h	8814	0	8710	0	0
39	i	9827	0	8617	0	0
40	j	2933	0	2695	0	0
40	k	2919	0	2682	0	0
41	AA	1804	0	1877	14	0
42	AB	1003	0	1048	10	0
43	AC	771	0	849	5	0
44	AD	1518	0	1587	13	0
45	AE	699	0	638	37	0
46	AF	681	0	684	8	0
47	AG	1353	0	1381	30	0
48	AH	964	0	1025	4	0
49	AI	612	0	682	1	0
50	AJ	1543	0	1608	9	0
51	AK	993	0	1081	5	0
52	AL	436	0	475	1	0
53	AM	1053	0	1149	4	0
54	AN	1092	0	1155	9	0
55	AO	417	0	459	1	0
56	AP	847	0	918	24	0
57	AQ	1720	0	1779	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	AR	1173	0	1215	13	0
59	AS	233	0	282	57	0
60	AT	694	0	738	11	0
61	AU	1555	0	1659	3	0
62	AV	462	0	491	2	0
63	AW	1914	0	1980	53	0
64	AX	1420	0	1437	14	0
65	AY	742	0	797	4	0
66	AZ	1050	0	245	1	0
67	BA	3075	0	3142	33	0
68	BB	1441	0	1543	18	0
69	BC	876	0	912	8	0
70	BD	1770	0	1808	6	0
71	BE	2748	0	2859	19	0
72	BF	1521	0	1611	72	0
73	BG	1020	0	1090	5	0
74	BH	1445	0	1487	7	0
75	BI	2375	0	2325	15	0
76	BJ	1276	0	1323	5	0
77	BK	850	0	880	8	0
78	BL	796	0	812	2	0
79	BM	1239	0	1326	12	0
80	BN	880	0	945	5	0
81	BO	1784	0	1862	12	0
82	BP	969	0	1078	5	0
83	BQ	67695	0	34019	437	0
84	BR	2579	0	1304	16	0
85	BS	3352	0	1695	19	0
86	BT	1143	0	1102	96	0
All	All	229285	0	172910	1455	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 5.

The worst 5 of 1455 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)
83:BQ:2418:G:C2	86:BT:73:LEU:HD11	1.29	1.63
1:2:1645:G:C5'	83:BQ:2255:A:N6	1.76	1.47
1:2:815:G:N3	72:BF:162:ARG:CZ	1.82	1.42
56:AP:27:GLN:HE22	86:BT:14:GLY:N	1.03	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:987:G:C6	63:AW:249:SER:HA	1.58	1.38

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	
2	A	221/240 (92%)	194 (88%)	24 (11%)	3 (1%)	12	52
3	B	204/225 (91%)	172 (84%)	24 (12%)	8 (4%)	3	33
4	C	94/105 (90%)	72 (77%)	16 (17%)	6 (6%)	1	23
5	D	119/143 (83%)	92 (77%)	17 (14%)	10 (8%)	1	15
6	E	122/142 (86%)	101 (83%)	18 (15%)	3 (2%)	6	42
7	F	139/143 (97%)	119 (86%)	15 (11%)	5 (4%)	4	35
8	G	87/136 (64%)	73 (84%)	11 (13%)	3 (3%)	4	37
9	H	143/146 (98%)	123 (86%)	17 (12%)	3 (2%)	8	46
10	I	141/144 (98%)	112 (79%)	21 (15%)	8 (6%)	2	25
11	J	105/121 (87%)	94 (90%)	10 (10%)	1 (1%)	17	58
12	K	68/108 (63%)	54 (79%)	9 (13%)	5 (7%)	1	19
13	L	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
14	M	51/56 (91%)	41 (80%)	10 (20%)	0	100	100
15	N	49/152 (32%)	40 (82%)	6 (12%)	3 (6%)	1	24
16	O	316/319 (99%)	274 (87%)	37 (12%)	5 (2%)	11	50
17	P	204/252 (81%)	176 (86%)	20 (10%)	8 (4%)	3	33
18	Q	212/255 (83%)	170 (80%)	31 (15%)	11 (5%)	2	27
19	R	218/254 (86%)	184 (84%)	30 (14%)	4 (2%)	9	48
20	S	258/261 (99%)	213 (83%)	36 (14%)	9 (4%)	4	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	T	224/236 (95%)	188 (84%)	29 (13%)	7 (3%)	4	39
22	U	182/190 (96%)	142 (78%)	31 (17%)	9 (5%)	2	28
23	V	184/200 (92%)	128 (70%)	30 (16%)	26 (14%)	0	5
24	W	176/197 (89%)	149 (85%)	21 (12%)	6 (3%)	4	37
25	X	153/156 (98%)	129 (84%)	17 (11%)	7 (5%)	2	29
26	Y	148/151 (98%)	134 (90%)	11 (7%)	3 (2%)	8	47
27	Z	125/137 (91%)	103 (82%)	17 (14%)	5 (4%)	3	32
28	a	85/87 (98%)	67 (79%)	14 (16%)	4 (5%)	2	29
29	b	127/130 (98%)	116 (91%)	8 (6%)	3 (2%)	6	43
30	c	142/145 (98%)	120 (84%)	21 (15%)	1 (1%)	24	65
31	d	130/135 (96%)	109 (84%)	14 (11%)	7 (5%)	2	27
32	e	95/119 (80%)	70 (74%)	17 (18%)	8 (8%)	1	15
33	f	79/82 (96%)	61 (77%)	14 (18%)	4 (5%)	2	27
34	g	58/63 (92%)	48 (83%)	8 (14%)	2 (3%)	4	37
38	h	1107/1287 (86%)	965 (87%)	124 (11%)	18 (2%)	11	50
39	i	1355/1432 (95%)	1158 (86%)	172 (13%)	25 (2%)	9	48
40	j	388/397 (98%)	335 (86%)	46 (12%)	7 (2%)	9	48
40	k	382/397 (96%)	333 (87%)	40 (10%)	9 (2%)	6	43
41	AA	231/256 (90%)	194 (84%)	32 (14%)	5 (2%)	7	44
42	AB	134/137 (98%)	117 (87%)	14 (10%)	3 (2%)	7	44
43	AC	97/100 (97%)	80 (82%)	13 (13%)	4 (4%)	3	32
44	AD	189/191 (99%)	166 (88%)	19 (10%)	4 (2%)	8	46
45	AE	96/155 (62%)	73 (76%)	18 (19%)	5 (5%)	2	27
46	AF	85/88 (97%)	70 (82%)	14 (16%)	1 (1%)	14	56
47	AG	167/174 (96%)	143 (86%)	18 (11%)	6 (4%)	4	35
48	AH	119/142 (84%)	103 (87%)	14 (12%)	2 (2%)	10	49
49	AI	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	13	54
50	AJ	191/199 (96%)	158 (83%)	27 (14%)	6 (3%)	4	39
51	AK	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
52	AL	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	8	46
53	AM	134/138 (97%)	119 (89%)	12 (9%)	3 (2%)	7	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	AN	133/136 (98%)	118 (89%)	10 (8%)	5 (4%)	3	34
55	AO	50/128 (39%)	45 (90%)	3 (6%)	2 (4%)	3	32
56	AP	103/106 (97%)	86 (84%)	16 (16%)	1 (1%)	17	58
57	AQ	201/204 (98%)	175 (87%)	21 (10%)	5 (2%)	6	42
58	AR	146/149 (98%)	118 (81%)	21 (14%)	7 (5%)	2	28
59	AS	23/25 (92%)	23 (100%)	0	0	100	100
60	AT	89/92 (97%)	81 (91%)	7 (8%)	1 (1%)	16	57
61	AU	195/199 (98%)	177 (91%)	15 (8%)	3 (2%)	11	51
62	AV	56/59 (95%)	50 (89%)	5 (9%)	1 (2%)	9	48
63	AW	250/254 (98%)	218 (87%)	31 (12%)	1 (0%)	36	75
64	AX	181/184 (98%)	158 (87%)	19 (10%)	4 (2%)	7	44
65	AY	95/105 (90%)	86 (90%)	8 (8%)	1 (1%)	16	57
67	BA	384/387 (99%)	332 (86%)	41 (11%)	11 (3%)	5	40
68	BB	183/186 (98%)	163 (89%)	17 (9%)	3 (2%)	11	50
69	BC	107/113 (95%)	94 (88%)	11 (10%)	2 (2%)	9	48
70	BD	218/221 (99%)	185 (85%)	24 (11%)	9 (4%)	3	32
71	BE	359/362 (99%)	306 (85%)	38 (11%)	15 (4%)	3	31
72	BF	186/189 (98%)	167 (90%)	16 (9%)	3 (2%)	11	50
73	BG	125/130 (96%)	110 (88%)	13 (10%)	2 (2%)	11	50
74	BH	170/172 (99%)	151 (89%)	16 (9%)	3 (2%)	9	48
75	BI	294/297 (99%)	263 (90%)	22 (8%)	9 (3%)	4	39
76	BJ	157/160 (98%)	133 (85%)	18 (12%)	6 (4%)	3	34
77	BK	104/107 (97%)	93 (89%)	9 (9%)	2 (2%)	9	48
78	BL	98/121 (81%)	79 (81%)	16 (16%)	3 (3%)	4	39
79	BM	152/176 (86%)	137 (90%)	11 (7%)	4 (3%)	6	41
80	BN	110/121 (91%)	104 (94%)	3 (3%)	3 (3%)	5	41
81	BO	220/244 (90%)	199 (90%)	16 (7%)	5 (2%)	7	44
82	BP	117/120 (98%)	106 (91%)	10 (8%)	1 (1%)	19	60
86	BT	151/157 (96%)	127 (84%)	14 (9%)	10 (7%)	1	22
All	All	14299/15550 (92%)	12246 (86%)	1644 (12%)	409 (3%)	8	40

5 of 409 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	196	ARG
3	B	100	ASN
5	D	115	VAL
5	D	126	TRP
7	F	32	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	
2	A	182/195 (93%)	175 (96%)	7 (4%)	36	68
3	B	173/191 (91%)	162 (94%)	11 (6%)	19	55
4	C	88/98 (90%)	83 (94%)	5 (6%)	23	59
5	D	89/119 (75%)	85 (96%)	4 (4%)	30	65
6	E	101/118 (86%)	94 (93%)	7 (7%)	17	53
7	F	117/119 (98%)	113 (97%)	4 (3%)	40	71
8	G	80/124 (64%)	75 (94%)	5 (6%)	20	56
9	H	128/129 (99%)	117 (91%)	11 (9%)	11	45
10	I	115/116 (99%)	102 (89%)	13 (11%)	6	32
11	J	100/114 (88%)	94 (94%)	6 (6%)	21	58
12	K	61/89 (68%)	58 (95%)	3 (5%)	27	62
13	L	56/60 (93%)	54 (96%)	2 (4%)	38	70
14	M	47/49 (96%)	44 (94%)	3 (6%)	19	55
15	N	43/135 (32%)	42 (98%)	1 (2%)	53	78
16	O	259/262 (99%)	250 (96%)	9 (4%)	39	70
17	P	164/210 (78%)	157 (96%)	7 (4%)	32	65
18	Q	191/224 (85%)	182 (95%)	9 (5%)	29	64
19	R	180/205 (88%)	175 (97%)	5 (3%)	47	74
20	S	221/222 (100%)	217 (98%)	4 (2%)	62	83
21	T	188/201 (94%)	181 (96%)	7 (4%)	37	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	U	165/170 (97%)	160 (97%)	5 (3%)	44	73
23	V	150/161 (93%)	133 (89%)	17 (11%)	6	32
24	W	152/166 (92%)	150 (99%)	2 (1%)	71	87
25	X	129/137 (94%)	126 (98%)	3 (2%)	53	78
26	Y	127/128 (99%)	121 (95%)	6 (5%)	29	64
27	Z	81/105 (77%)	74 (91%)	7 (9%)	11	45
28	a	74/74 (100%)	72 (97%)	2 (3%)	48	75
29	b	110/111 (99%)	109 (99%)	1 (1%)	81	91
30	c	119/120 (99%)	115 (97%)	4 (3%)	40	71
31	d	111/113 (98%)	103 (93%)	8 (7%)	16	52
32	e	83/101 (82%)	77 (93%)	6 (7%)	16	52
33	f	70/71 (99%)	69 (99%)	1 (1%)	69	86
34	g	50/54 (93%)	50 (100%)	0	100	100
38	h	936/1139 (82%)	901 (96%)	35 (4%)	37	69
39	i	849/1279 (66%)	823 (97%)	26 (3%)	43	72
40	j	296/347 (85%)	288 (97%)	8 (3%)	48	75
40	k	295/347 (85%)	290 (98%)	5 (2%)	63	84
41	AA	187/208 (90%)	179 (96%)	8 (4%)	32	65
42	AB	104/105 (99%)	98 (94%)	6 (6%)	22	59
43	AC	81/82 (99%)	76 (94%)	5 (6%)	20	56
44	AD	171/171 (100%)	165 (96%)	6 (4%)	39	70
45	AE	57/129 (44%)	57 (100%)	0	100	100
46	AF	70/71 (99%)	65 (93%)	5 (7%)	16	52
47	AG	147/150 (98%)	140 (95%)	7 (5%)	28	63
48	AH	104/118 (88%)	98 (94%)	6 (6%)	22	59
49	AI	68/69 (99%)	67 (98%)	1 (2%)	67	85
50	AJ	154/159 (97%)	146 (95%)	8 (5%)	25	62
51	AK	109/110 (99%)	105 (96%)	4 (4%)	37	69
52	AL	45/46 (98%)	42 (93%)	3 (7%)	18	54
53	AM	107/109 (98%)	101 (94%)	6 (6%)	23	60
54	AN	115/116 (99%)	112 (97%)	3 (3%)	49	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	AO	47/116 (40%)	44 (94%)	3 (6%)	19	55
56	AP	90/91 (99%)	85 (94%)	5 (6%)	23	60
57	AQ	175/176 (99%)	168 (96%)	7 (4%)	34	66
58	AR	118/119 (99%)	111 (94%)	7 (6%)	21	58
59	AS	23/23 (100%)	21 (91%)	2 (9%)	11	44
60	AT	71/72 (99%)	69 (97%)	2 (3%)	47	74
61	AU	160/162 (99%)	155 (97%)	5 (3%)	43	72
62	AV	46/47 (98%)	45 (98%)	1 (2%)	55	79
63	AW	193/196 (98%)	187 (97%)	6 (3%)	43	72
64	AX	140/146 (96%)	133 (95%)	7 (5%)	27	62
65	AY	81/88 (92%)	78 (96%)	3 (4%)	37	69
67	BA	320/323 (99%)	304 (95%)	16 (5%)	27	62
68	BB	150/151 (99%)	144 (96%)	6 (4%)	34	66
69	BC	92/97 (95%)	84 (91%)	8 (9%)	11	44
70	BD	184/187 (98%)	169 (92%)	15 (8%)	12	47
71	BE	288/289 (100%)	277 (96%)	11 (4%)	36	68
72	BF	153/154 (99%)	148 (97%)	5 (3%)	41	72
73	BG	109/111 (98%)	106 (97%)	3 (3%)	47	74
74	BH	156/156 (100%)	150 (96%)	6 (4%)	36	68
75	BI	244/245 (100%)	235 (96%)	9 (4%)	37	69
76	BJ	136/137 (99%)	129 (95%)	7 (5%)	26	62
77	BK	90/91 (99%)	87 (97%)	3 (3%)	41	72
78	BL	87/107 (81%)	86 (99%)	1 (1%)	76	88
79	BM	134/153 (88%)	127 (95%)	7 (5%)	25	62
80	BN	95/103 (92%)	94 (99%)	1 (1%)	76	88
81	BO	186/205 (91%)	181 (97%)	5 (3%)	48	75
82	BP	104/105 (99%)	101 (97%)	3 (3%)	45	73
86	BT	118/132 (89%)	113 (96%)	5 (4%)	32	66
All	All	11689/13228 (88%)	11203 (96%)	486 (4%)	37	66

5 of 486 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	h	1244	TRP
42	AB	104	ASN
75	BI	140	ARG
39	i	247	TYR
40	j	18	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
39	i	982	GLN
50	AJ	37	ASN
79	BM	167	ASN
39	i	1066	GLN
40	k	176	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1764/1800 (98%)	729 (41%)	100 (5%)
35	l	33/34 (97%)	20 (60%)	0
36	m	75/76 (98%)	34 (45%)	0
37	n	76/77 (98%)	30 (39%)	0
83	BQ	3162/3396 (93%)	1066 (33%)	177 (5%)
84	BR	120/121 (99%)	35 (29%)	7 (5%)
85	BS	157/158 (99%)	50 (31%)	10 (6%)
All	All	5387/5662 (95%)	1964 (36%)	294 (5%)

5 of 1964 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	5	U
1	2	17	C
1	2	25	C

5 of 294 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
83	BQ	767	U
83	BQ	1355	A

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Mol	Chain	Res	Type
83	BQ	3317	U
83	BQ	816	A
83	BQ	993	G

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z  > 2$
86	5CT	BT	51	86	14,14,15	0.33	0	10,15,17	1.27	2 (20%)

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
86	5CT	BT	51	86	-	4/12/14/16	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	BT	51	5CT	C1-NZ-CE	-2.30	108.27	113.42
86	BT	51	5CT	C4-C3-C2	-2.03	109.19	113.47

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	BT	51	5CT	C2-C3-C4-N1

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Mol	Chain	Res	Type	Atoms
86	BT	51	5CT	CG-CD-CE-NZ
86	BT	51	5CT	C2-C1-NZ-CE
86	BT	51	5CT	CD-CE-NZ-C1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	BT	51	5CT	1	0

## 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	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	52:U	O3'	53:G	P	1.89