



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Nov 22, 2016 – 12:43 PM EST

PDB ID : 5LZW
EMDB ID: : EMD-4134
Title : Structure of the mammalian rescue complex with Pelota and Hbs1l assembled on a truncated mRNA.
Authors : Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.
Deposited on : 2016-10-02
Resolution : 3.53 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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
EM map analysis : **NOT EXECUTED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028320

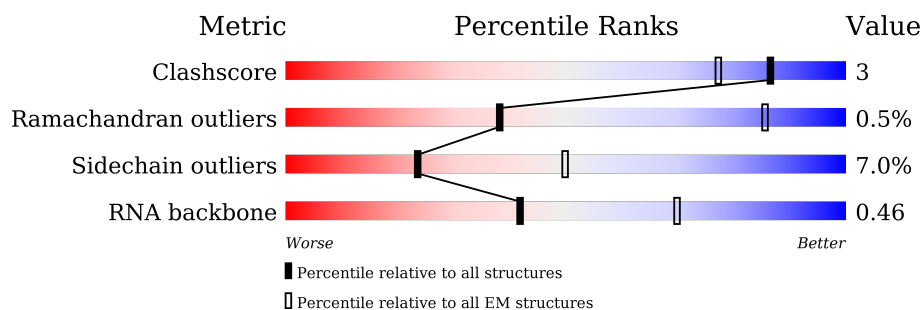
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.53 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.




















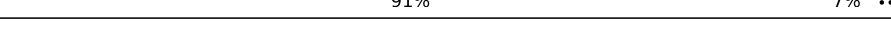
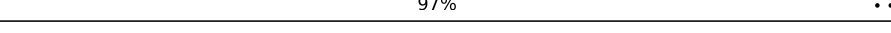




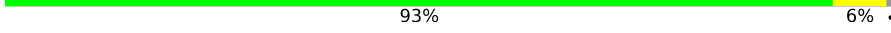
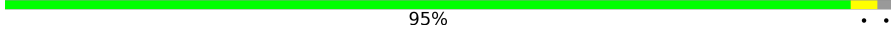
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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 ≥ 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	A	257	82% (green) 14% (yellow) .. (grey)
2	B	403	87% (green) 9% (yellow) .. (grey)
3	C	425	77% (green) 8% (yellow) . (orange) 15% (grey)
4	D	297	88% (green) 10% (yellow) . (orange)
5	E	291	65% (green) 8% (yellow) . (orange) 26% (grey)
6	F	247	80% (green) 10% (yellow) . (orange) 9% (grey)
7	G	319	67% (green) 6% (yellow) 27% (grey)
8	H	192	87% (green) 11% (yellow) .. (grey)



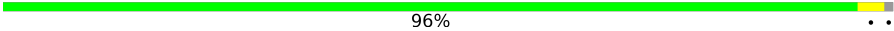
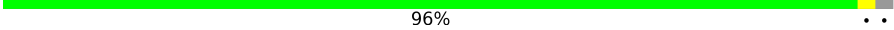



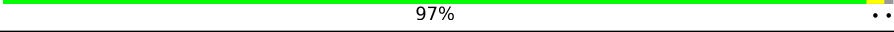



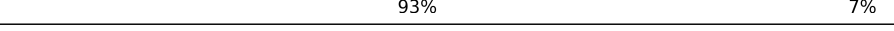







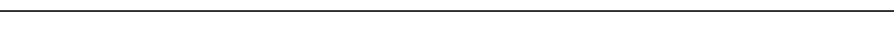

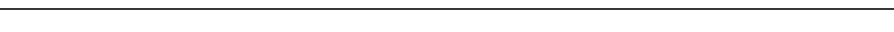
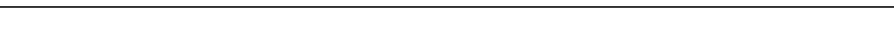


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Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	218	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	245	
28	c	115	
29	d	125	
30	e	135	
31	f	110	
32	g	116	
33	h	123	




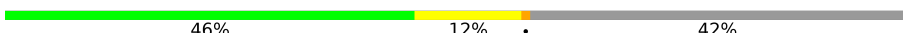





















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Mol	Chain	Length	Quality of chain
34	i	105	 94% . .
35	j	97	 85% . 11%
36	k	70	 96% . .
37	l	51	 96% . .
38	m	102	 48% . 49%
39	n	25	 92% 8%
40	o	106	 93% 5% .
41	p	92	 97% . .
42	r	137	 85% 5% 9%
43	s	318	 59% . 38%
44	t	165	 90% . 7%
45	1	15	 93% 7%
46	2	76	 79% 20% .
47	3	75	 64% 35% .
48	5	3543	 70% 27% .
49	7	120	 85% 15%
50	8	156	 70% 26% . .
51	9	1869	 60% 27% . 9%
52	AA	295	 62% 11% . 26%
53	BB	264	 70% 10% . 19%
54	CC	293	 62% 12% . 25%
55	DD	243	 80% 12% . 6%
56	EE	263	 86% 14%
57	FF	204	 81% 9% 9%
58	GG	249	 84% 11% 5%

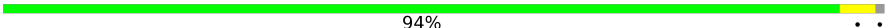



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Mol	Chain	Length	Quality of chain
59	HH	194	
60	II	208	
61	JJ	194	
62	KK	165	
63	LL	158	
64	MM	132	
65	NN	151	
66	OO	168	
67	PP	145	
68	QQ	146	
69	RR	135	
70	SS	152	
71	TT	145	
72	UU	119	
73	VV	83	
74	WW	130	
75	XX	143	
76	YY	130	
77	ZZ	125	
78	aa	115	
79	bb	84	
80	cc	69	
81	dd	56	
82	ee	133	
83	ff	156	

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Mol	Chain	Length	Quality of chain
84	gg	317	 94% . .
85	hh	8	 50% 50%
86	ii	403	 87% 5% 8%
87	jj	710	 56% . 40%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
90	GCP	9	1972	-	-	X	-

2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 222130 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 protein called uL2.

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

- Molecule 2 is a protein called uL3.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called uL4.

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

- Molecule 4 is a protein called uL18.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	LYS	initiating methionine	UNP G1SYJ6

- Molecule 5 is a protein called eL6.

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

- Molecule 6 is a protein called uL30.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

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

- Molecule 9 is a protein called uL16.

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

- Molecule 10 is a protein called uL5.

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

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 12 is a protein called eL14.

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

- Molecule 13 is a protein called eL15.

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

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

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

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 23 is a protein called uL23.

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

- Molecule 24 is a protein called uL24.

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

- Molecule 25 is a protein called eL27.

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

- Molecule 26 is a protein called uL15.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1	MET	GLN	conflict	UNP G1SNY0

- Molecule 27 is a protein called eL29.

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

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called eL32.

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

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called eL34.

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

- Molecule 33 is a protein called uL29.

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

- Molecule 34 is a protein called eL36.

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

- Molecule 35 is a protein called eL37.

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

- Molecule 36 is a protein called eL38.

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

- Molecule 37 is a protein called eL39.

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

- Molecule 38 is a protein called eL40.

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

- Molecule 39 is a protein called eL41.

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

- Molecule 40 is a protein called eL42.

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

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

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

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	1	15	Total	C	N	O	S	0	0
			125	82	20	22	1		

- Molecule 46 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 47 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	3	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 48 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 49 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 50 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 51 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	9	1698	Total	C	N	O	P	0	0
			36249	16180	6508	11864	1697		

- Molecule 52 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AA	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 53 is a protein called eS1.

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

- Molecule 54 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CC	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 55 is a protein called uS3.

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

- Molecule 56 is a protein called eS4.

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

- Molecule 57 is a protein called uS7.

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

- Molecule 58 is a protein called eS6.

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

- Molecule 59 is a protein called eS7.

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

- Molecule 60 is a protein called eS8.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 61 is a protein called uS4.

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

- Molecule 62 is a protein called eS10.

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

- Molecule 63 is a protein called uS17.

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

- Molecule 64 is a protein called eS12.

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

- Molecule 65 is a protein called uS15.

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

- Molecule 66 is a protein called uS11.

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

- Molecule 67 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	PP	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 68 is a protein called uS9.

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

- Molecule 69 is a protein called eS17.

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

- Molecule 70 is a protein called uS13.

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

- Molecule 71 is a protein called eS19.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 72 is a protein called uS10.

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

- Molecule 73 is a protein called eS21.

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

- Molecule 74 is a protein called uS8.

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

- Molecule 75 is a protein called uS12.

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

- Molecule 76 is a protein called eS24.

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

- Molecule 77 is a protein called eS25.

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

- Molecule 78 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 79 is a protein called eS27.

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

- Molecule 80 is a protein called eS28.

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

- Molecule 81 is a protein called uS14.

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

- Molecule 82 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	ee	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 83 is a protein called eS31.

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

- Molecule 84 is a protein called RACK1.

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

- Molecule 85 is a RNA chain called mRNA (truncated).

Mol	Chain	Residues	Atoms					AltConf	Trace
85	hh	8	Total	C	N	O	P	0	0
			169	76	29	56	8		

- Molecule 86 is a protein called Pelota.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	ii	372	Total	C	N	O	S	0	0
			2947	1844	528	559	16		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ii	221	MET	LEU	conflict	UNP Q9BRX2
ii	386	GLY	-	expression tag	UNP Q9BRX2
ii	387	SER	-	expression tag	UNP Q9BRX2
ii	388	GLU	-	expression tag	UNP Q9BRX2
ii	389	ASN	-	expression tag	UNP Q9BRX2
ii	390	LEU	-	expression tag	UNP Q9BRX2
ii	391	TYR	-	expression tag	UNP Q9BRX2
ii	392	PHE	-	expression tag	UNP Q9BRX2
ii	393	GLN	-	expression tag	UNP Q9BRX2
ii	394	GLY	-	expression tag	UNP Q9BRX2
ii	395	ALA	-	expression tag	UNP Q9BRX2
ii	396	HIS	-	expression tag	UNP Q9BRX2
ii	397	HIS	-	expression tag	UNP Q9BRX2
ii	398	HIS	-	expression tag	UNP Q9BRX2
ii	399	HIS	-	expression tag	UNP Q9BRX2
ii	400	HIS	-	expression tag	UNP Q9BRX2
ii	401	HIS	-	expression tag	UNP Q9BRX2
ii	402	SER	-	expression tag	UNP Q9BRX2
ii	403	THR	-	expression tag	UNP Q9BRX2

- Molecule 87 is a protein called Hbs1l.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	jj	425	Total	C	N	O	S	0	0
			3292	2100	565	609	18		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
jj	-25	MET	-	initiating methionine	UNP Q9Y450
jj	-24	ASP	-	expression tag	UNP Q9Y450
jj	-23	TYR	-	expression tag	UNP Q9Y450
jj	-22	LYS	-	expression tag	UNP Q9Y450
jj	-21	ASP	-	expression tag	UNP Q9Y450
jj	-20	HIS	-	expression tag	UNP Q9Y450
jj	-19	ASP	-	expression tag	UNP Q9Y450
jj	-18	GLY	-	expression tag	UNP Q9Y450
jj	-17	ASP	-	expression tag	UNP Q9Y450
jj	-16	TYR	-	expression tag	UNP Q9Y450
jj	-15	LYS	-	expression tag	UNP Q9Y450
jj	-14	ASP	-	expression tag	UNP Q9Y450
jj	-13	HIS	-	expression tag	UNP Q9Y450
jj	-12	ASP	-	expression tag	UNP Q9Y450
jj	-11	ILE	-	expression tag	UNP Q9Y450
jj	-10	ASP	-	expression tag	UNP Q9Y450
jj	-9	TYR	-	expression tag	UNP Q9Y450
jj	-8	LYS	-	expression tag	UNP Q9Y450
jj	-7	ASP	-	expression tag	UNP Q9Y450
jj	-6	ASP	-	expression tag	UNP Q9Y450
jj	-5	ASP	-	expression tag	UNP Q9Y450
jj	-4	ASP	-	expression tag	UNP Q9Y450
jj	-3	LYS	-	expression tag	UNP Q9Y450
jj	-2	ALA	-	expression tag	UNP Q9Y450
jj	-1	GLY	-	expression tag	UNP Q9Y450
jj	0	SER	-	expression tag	UNP Q9Y450

- Molecule 88 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
88	P	2	Total Mg 2 2	0
88	g	1	Total Mg 1 1	0
88	j	1	Total Mg 1 1	0
88	Q	1	Total Mg 1 1	0
88	e	1	Total Mg 1 1	0
88	B	1	Total Mg 1 1	0

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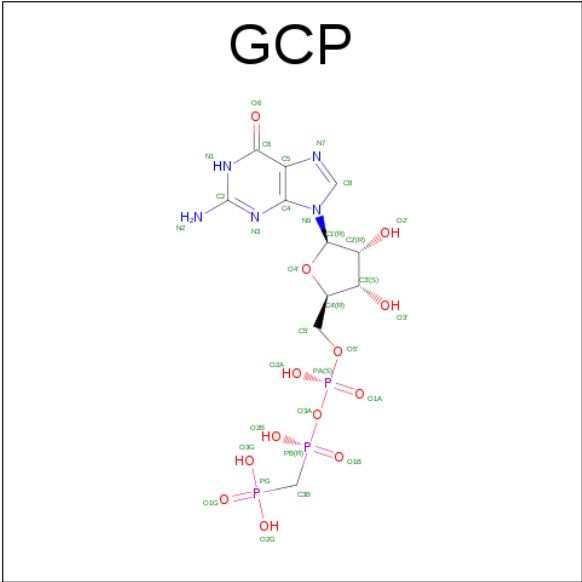
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
88	I	1	Total 1	Mg 1	0
88	jj	1	Total 1	Mg 1	0
88	V	1	Total 1	Mg 1	0
88	7	5	Total 5	Mg 5	0
88	a	1	Total 1	Mg 1	0
88	5	188	Total 188	Mg 188	0
88	8	6	Total 6	Mg 6	0
88	9	71	Total 71	Mg 71	0

- Molecule 89 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
89	p	1	Total 1	Zn 1	0
89	g	1	Total 1	Zn 1	0
89	j	1	Total 1	Zn 1	0
89	dd	1	Total 1	Zn 1	0
89	ff	1	Total 1	Zn 1	0
89	aa	1	Total 1	Zn 1	0
89	o	1	Total 1	Zn 1	0
89	m	1	Total 1	Zn 1	0

- Molecule 90 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

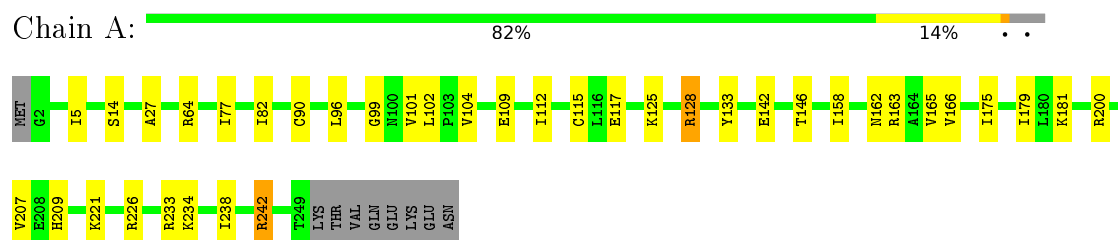


Mol	Chain	Residues	Atoms					AltConf
90	9	1	Total	C	N	O	P	0
			32	11	5	13	3	
90	jj	1	Total	C	N	O	P	0
			32	11	5	13	3	

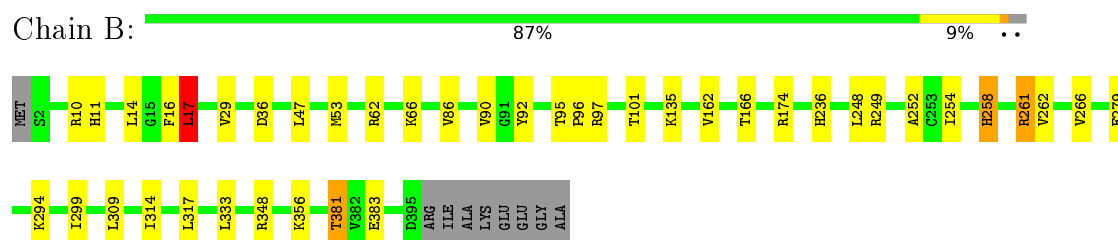
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

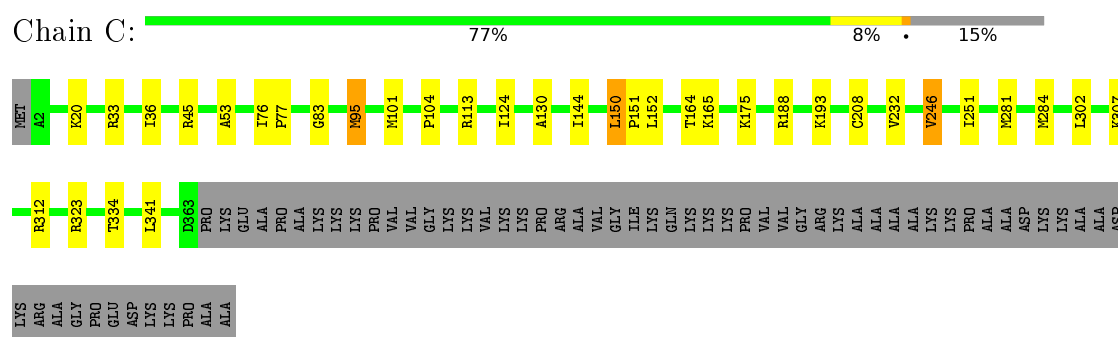
• Molecule 1: uL2



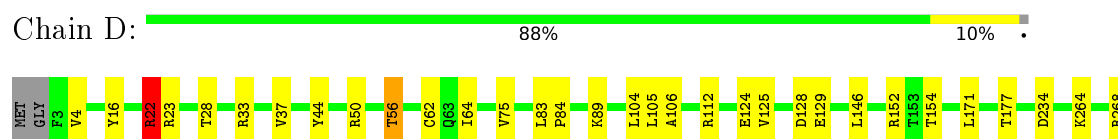
• Molecule 2: uL3



• Molecule 3: uL4



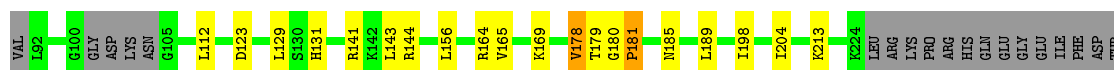
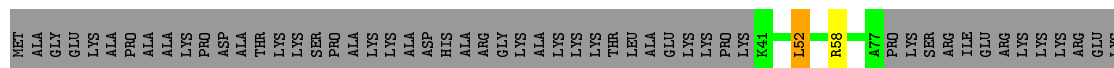
• Molecule 4: uL18





- Molecule 5: eL6

Chain E: 65% 8% 26%



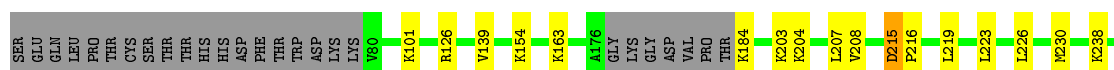
- Molecule 6: uL30

Chain F: 80% 10% 9%



- Molecule 7: eL8

Chain G: 67% 6% 27%



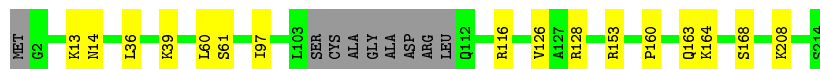
- Molecule 8: uL6

Chain H: 87% 11% 2%

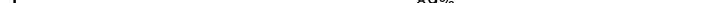


- Molecule 9: uL16

Chain I: 88% 7% 5%



- Molecule 10: uL5

Chain J:  89% 6% .



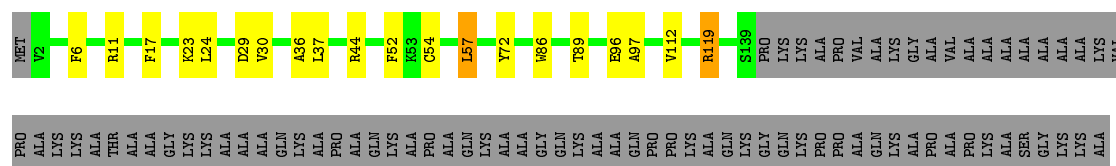
- Molecule 11: eL13

Chain L:  92% 7%



- Molecule 12: eL14

Chain M:  54% 8% 37%



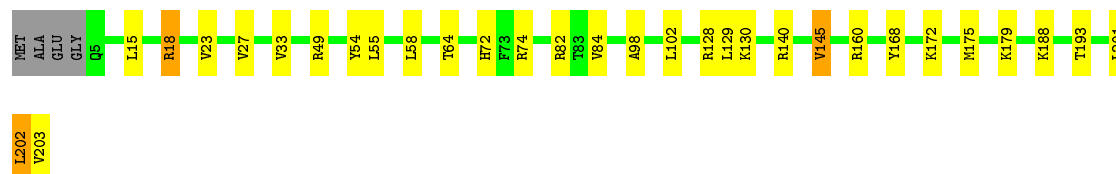
- Molecule 13: eL15

Chain N:  91% 8%



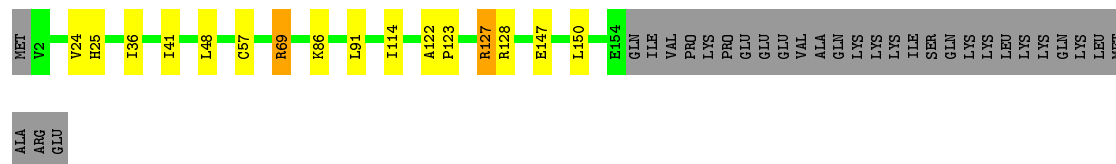
- Molecule 14: uL13

Chain O: 83% 14% ..




- Molecule 15: uL22

Chain P:  74% 8% • 17%




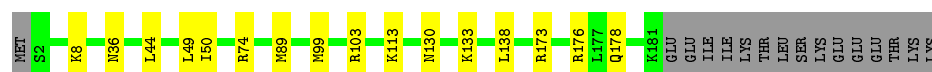
- Molecule 16: eL18

Chain Q:  86% 14% .




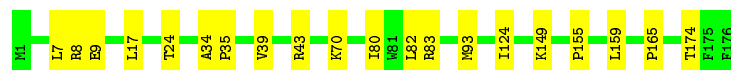
- Molecule 17: eL19

Chain R:  84% 8% 8%




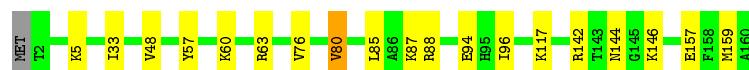
- Molecule 18: eL20

Chain S:  89% 11%



- Molecule 19: eL21

Chain T:  88% 11% ..




- Molecule 20: eL22

Chain U:  71% 6% 23%



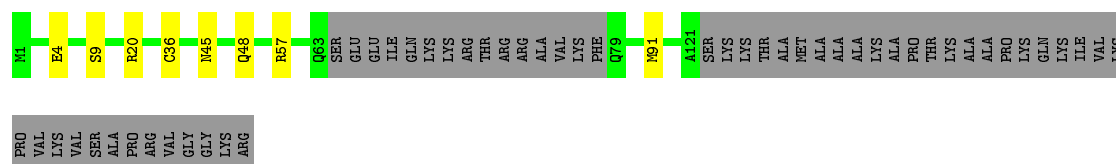
- Molecule 21: uL14

Chain V:  77% 16% 6%




- Molecule 22: eL24

Chain W:  62% 5% 32%



- Molecule 23: uL23

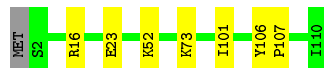
- Molecule 30: eL32

Chain e:  88% 7% 5%



- Molecule 31: eL33

Chain f:  93% 6% .



- Molecule 32: eL34

Chain g:  95% . .



- Molecule 33: uL29

Chain h:  96% . .




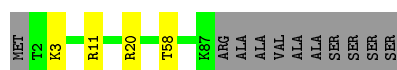
- Molecule 34: eL36

Chain i:  94% . .



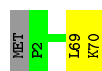
- Molecule 35: eL37

Chain j:  85% . 11%



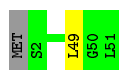
- Molecule 36: eL38

Chain k:  96% . .

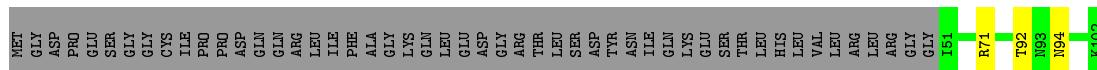


- Molecule 37: eL39

Chain l:  96% . .



- Molecule 38: eL40



- Molecule 39: eL41



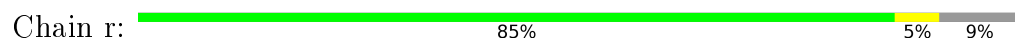
- Molecule 40: eL42



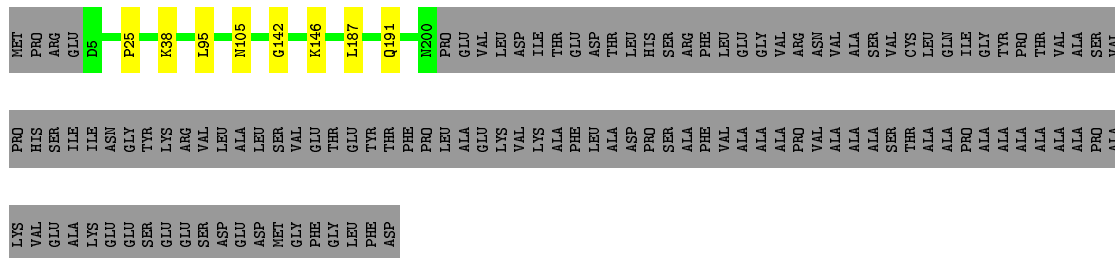
- Molecule 41: eL43




- Molecule 42: eL28



- Molecule 43: uL10



- Molecule 44: uL11

Chain t:  90% 7%




- Molecule 45: Nascent chain

Chain 1:  93% 7%



- Molecule 46: P-site tRNA

Chain 2:  79% 20%



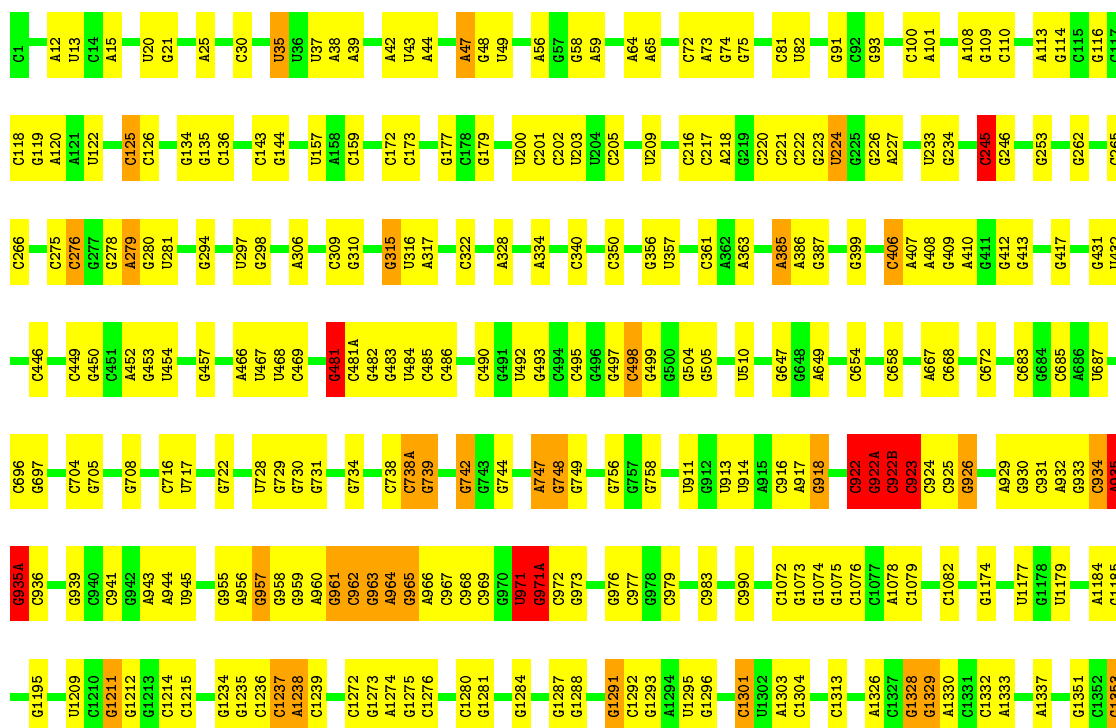
- Molecule 47: E-site tRNA

Chain 3:  64% 35%

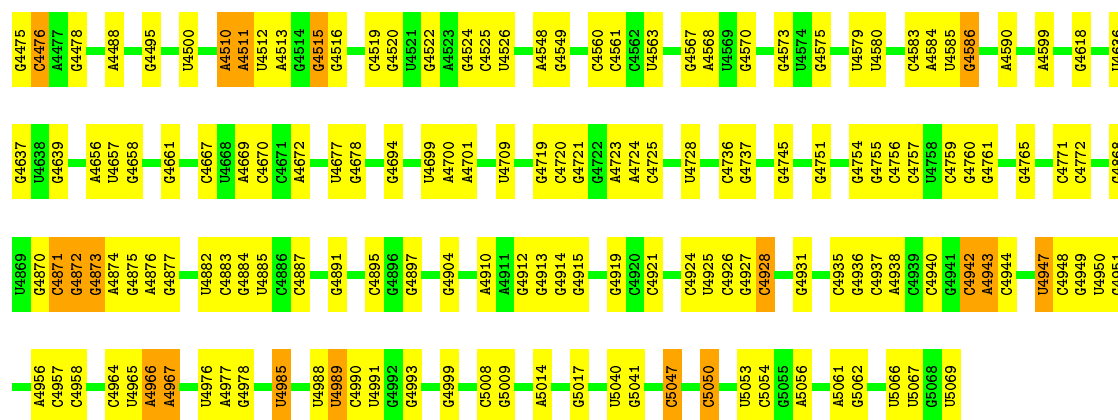


- Molecule 48: 28S ribosomal RNA

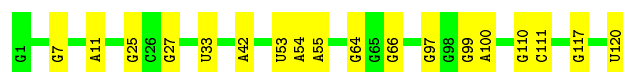
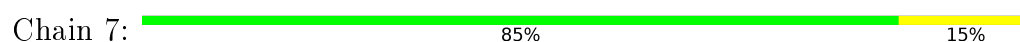
Chain 5:  70% 27%



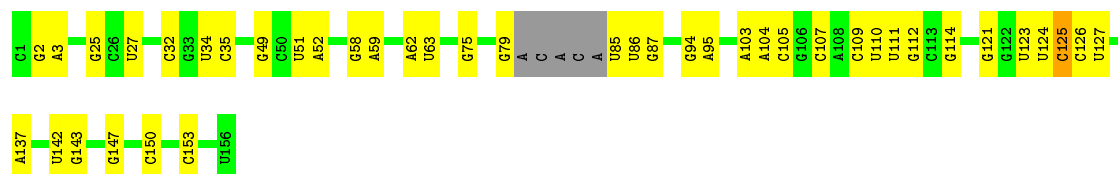
C4350	A4233	G4099	A3860	U3729	G2838	C2719	U2554	C2422	G2261	U2008	G1909	U1757	U1591	G1454	A1354
U4354	G4247	C4100	A3867	A3733	U2839	C2720	G2855	A2423	G2262	U2009	G1910	G1761	U1596	G1455	G1358
G4355	G4248	C4116	G3873	G3740	G2842	G2721	G2564	U2424	G2265	C2011	U1918	C1762	U1597	C1456	G1359
G4371	G4250	U4117	G3876	G3748	G2855	G2724	G2566	A2428	U2267	G2024	G1919	C1763	U1602	C1457	U1364
U4372	A4251	C4119	A3877	A3748	C2875	A2725	C2571	A2429	G2268	A2025	C1920	G1764	G1612	G1465	G1370
G4373	G4254	U4120	C3878	G3753	G2884	G2726	C2572	G2433	G2270	A2026	G1921	C1768	A1613	G1475	A1371
G4377	A4255	C4122	G3879	G3756	U2891	G2729	U2575	G2439	G2275	C2031	A1923	U1772	G1624	C1476	G1377
A4378	G4256	U4124	G3888	A3759	G2896	G2730	C2583	U2440	G2278	U2032	C1931	U1773	G1625	C1477	C1378
A4379	A4257	C4125	A3889	A3760	G2897	U2740	A2587	C2441	A2279	A2033	G1932	A1776	G1626	C1478	G1379
A4380	G4258	A4127	U3891	C3761	G2897	G2743	A2587	U2447	G2280	G2046	G1933	U1781	A1631	G1482	G1380
G4387	U4265	C4128	U3762	G3765	C3598	A2743	A2601	G2450	U2281	U2048	A1934	U1786	G1635	C1483	U1381
G4391	G4266	U4150	G3766	A3766	G3603	G2751	G2620	G2459	G2289	G2052	G1940	A1787	C1640	C1485	A1387
G4392	A4267	C4158	A3766	A3766	G3604	G2754	C2627	C2462	G2294	G2055	A1941	G1797	G1641	G1489	G1394
G4393	G4271	C4162	A3901	U3773	C3605	G2754	G2638	U2467	G2301	A2057	G1948	G1798	G1654	A1497	A1397
A4394	A4272	U4163	G3904	A3774	G3615	G2760	U2638	U2468	G2301	G2056	G1948	G1799	G1655	A1498	A1398
A4396	G4273	C4164	A3905	A3775	G3622	U2761	U2639	G2469	G2313	G2062	G1952	U1800	U1656	G1498	G1401
A4397	A4280	U4165	A3906	G3776	G3622	G2762	G2647	G2470	G2314	G2063	U1959	G1803	C1661	G1502	C1402
A4398	A4281	C4166	G3907	G3777	G3625	U2763	A2647	G2471	G2314	G2064	G1960	G1804	C1665	A1503	G1403
G4401	U4289	A4170	A3908	U3778	G3626	A2764	A2660	C2474	G2331	C2068	G1961	A1805	C1666	G1504	G1406
A4415	U4290	C4171	U3914	G3780	G3626	A2769	U2661	G2475	G2332	A2069	G1962	G1798	A1667	U1514	C1406A
U4419	G4297	U4177	U3915	A3784	G3630	U2782	G2662	G2476	G2333	U2070	C1963	G1818	G1670	A1515	C1406B
U4420	U4301	G4183	G3916	A3785	U3644	U2787	G2663	G2483	G2348	U2084	G1965	G1820	G1670	G1516	G1406C
A4421	U4301	A4184	A3917	U3786	U3644	U2788	G2663	G2488	G2349	G2085	C1966	G1821	G1677	G1517	C1411
U4423	A4304	C4187	C3919	U3798	A3648	U2789	G2673	U2490	U2352	A2088	C1967	U1822	C1678	A1518	G1411A
G4432	G4305	U4188	A3927	U3801	A3653	U2790	A2676	C2491	G2360	U2090	G1976	C1828	A1679	A1524	C1411C
U4440	A4310	G4191	G3928	U3814	C3658	C2794	G2681	G2492	A2367	G2091	C1977	G1833	G1684	A1525	G1416
G4444	A4311	C4201	G3939	G3810	C3658	A2795	G2681	G2493	G2367	G2092	C1978	G1834	A1684	A1533	C1417
G4448	C4314	U4202	A3943	G3811	G2686	G2796	G2686	U2494	A2367	G2093	A1979	U1835	G1684	A1534	C1418
A4449	G4314	A4203	A3943	G3812	G2686	C2797	G2687	U2495	G2364	C2094	G1981	G1836	C1690	C1535	G1419
U4450	G4317	U4210	U4067	A3813	G2688	A2798	G2688	A2502	A2367	G2096	A1983	A1837	G1691	A1420	A1420
G4453	C4318	G4211	U4068	U3814	C3673	C2802	G2689	G2503	A2367	A2097	A1984	G1842	G1724	A1547	G1421
G4454	C4319	A4212	U4069	A3817	G3674	A2806	G2693	C2504	A2370	G2098	G1985	G1855	U1725	A1554	C1429
A4523	A4323	A4214	A4073	G3819	A3692	A2807	G2694	G2506	G2380	G2100	C1987	G1869	U1726	A1563	G1432
G4526	G4326	C4215	G4074	U3822	C3696	C2814	A2696	A2513	A2395	G2102	A1990	G1872	G1734	A1564	G1435
U4459	U4459	U4218	U4075	U3822	G3698	A2815	A2696	G2521	A2396	A2103	A1991	G1872	G1734	A1565	G1436
U4460	G4329	A4219	G4076	U3831	G3710	G2826	U2707	G2530	G2397	A2104	U1992	G1882	C1740	C1566	C1437
U4463	G4330	C4221	A4085	U3838	A3711	G2827	G2709	U2530	U2398	A2106	C1993	U1882	G1741	U1567	U1438
A4464	C4335	G4225	G4086	G3839	A3712	U2828	C2710	A2537	G2399	A2107	G1997	A1888	A1742	C1568	U1440
G4467	A4336	G4225	G4087	U3840	G3722	U2829	G2712	A2537	U2408	G2108	U1997	A1889	G1750	G1574	U1441
U4471	A4339	U4229	G4088	C3843	G3722	G2713	G2715	G2546	U2409	A2109	G2001	G1890	G1750	G1577	U1442
	G4349	U4232	G4092	G3859	A3724	A2835	G2716	G2547	G2416	G2110	A2002	A1891	G1753	U1578	U1445
					G3725	A2837	G2716	A2553	A2417	C2260	G2003	A1892	U1754	U1578	C1446
											G2004	A1897	U1756	G1586	G1453



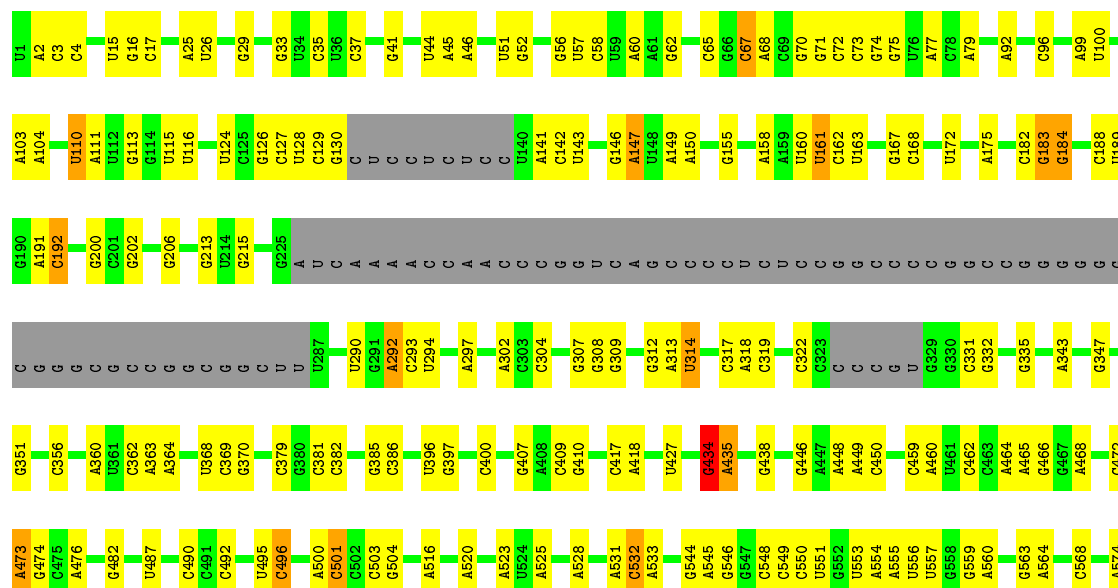
- Molecule 49: 5S ribosomal RNA

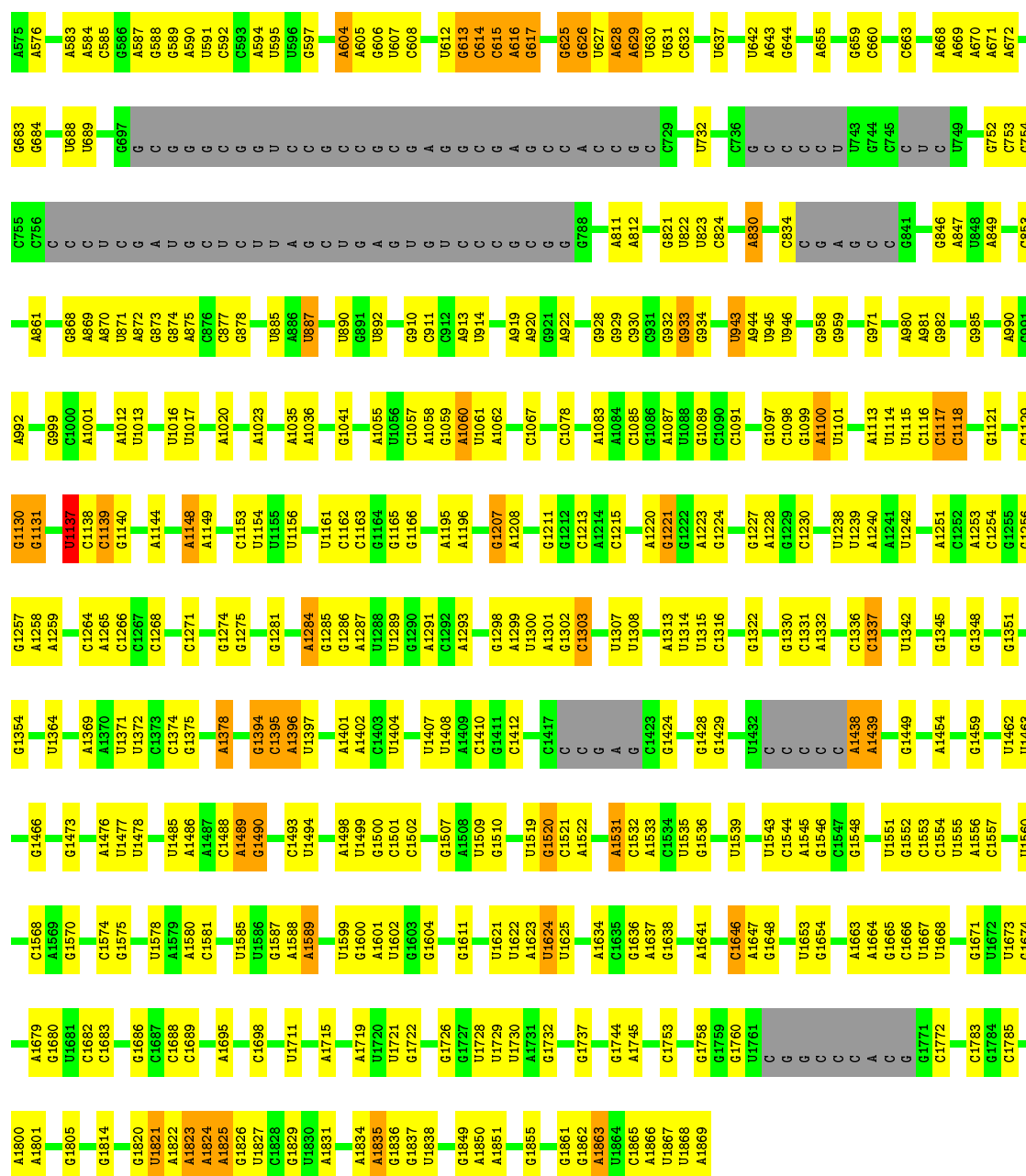


- Molecule 50: 5.8S ribosomal RNA



- Molecule 51: 18S ribosomal RNA

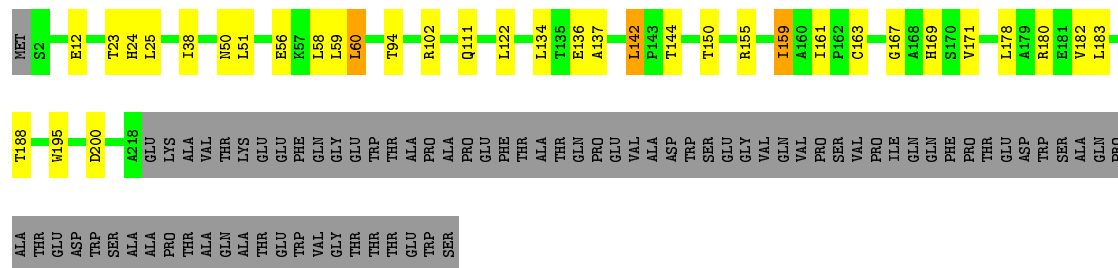




- Molecule 52: uS2

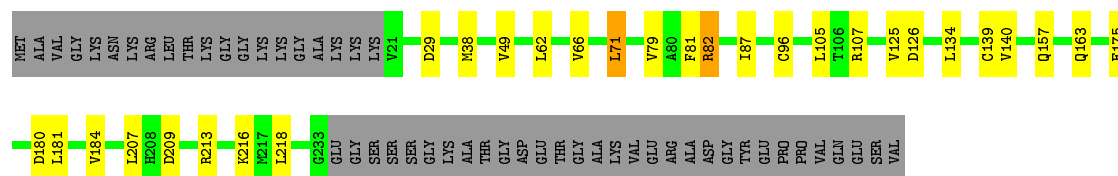
Chain AA:

62% 11% 26%



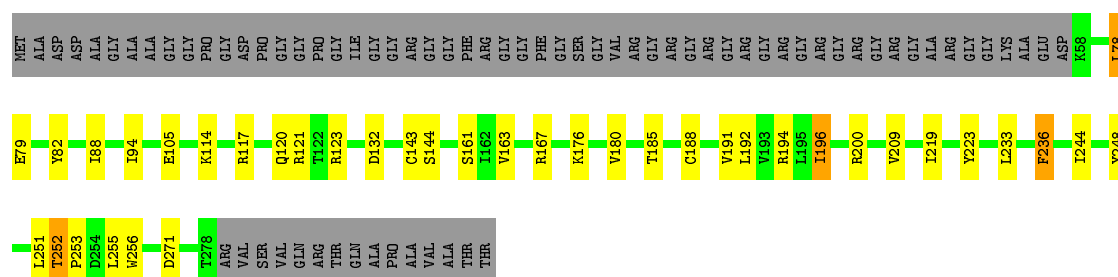
- Molecule 53: eS1

Chain BB:  70% 10% • 19%




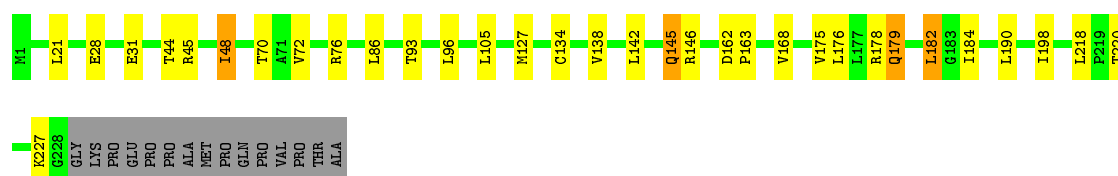
- Molecule 54: uS5

Chain CC:  62% 12% 25%

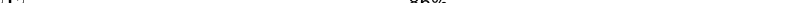


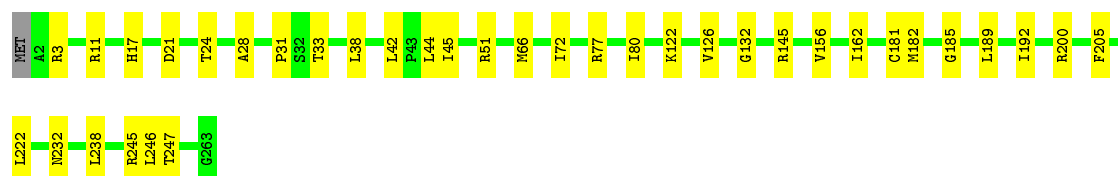
- Molecule 55: uS3

Chain DD:  80% 12% • 6%




- Molecule 56: eS4

Chain EE:  86% 14%



- Molecule 57: uS7

Chain FF: 




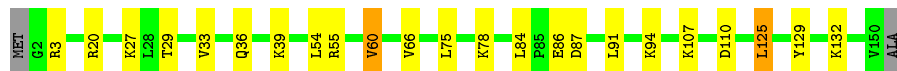
- Molecule 58: eS6

Chain GG:  84% 11% 5%



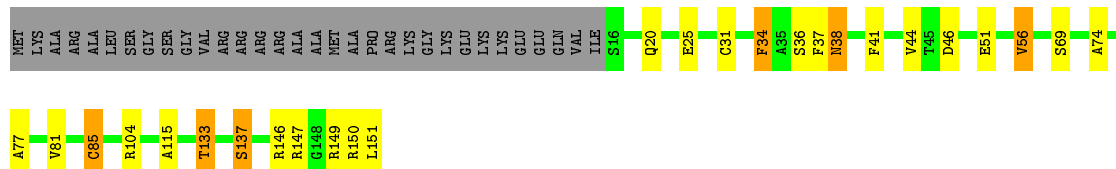
- Molecule 65: uS15

Chain NN:  83% 14% ..



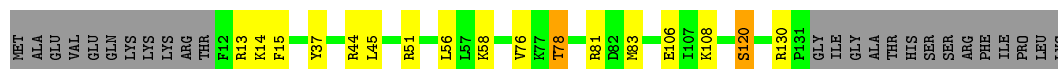
- Molecule 66: uS11

Chain OO:  65% 12% • 19%




- Molecule 67: uS19

Chain PP:  71% 10% • 17%




- Molecule 68: uS9

Chain QQ:  84% 14% •




- Molecule 69: eS17

Chain RR:  87% 10% ..




- Molecule 70: uS13

Chain SS:  81% 13% • 5%



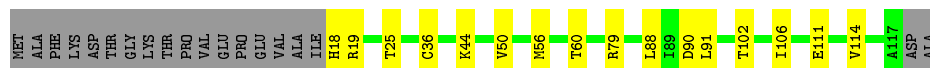
- Molecule 71: eS19

Chain TT:  84% 12% ..



- Molecule 72: uS10

Chain UU:  71% 13% 16%




- Molecule 73: eS21

Chain VV:  89% 10% .




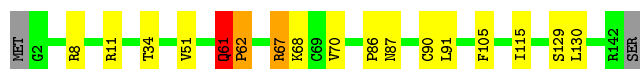
- Molecule 74: uS8

Chain WW:  85% 14% ..




- Molecule 75: uS12

Chain XX:  87% 10% ...



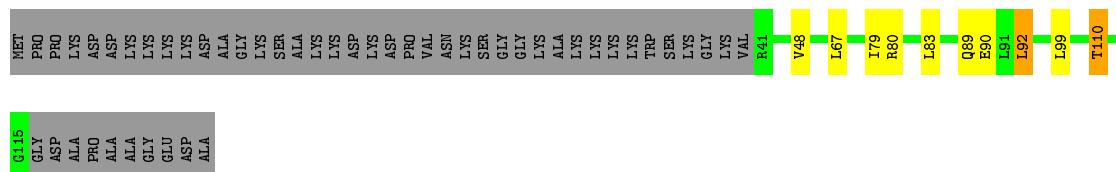
- Molecule 76: eS24

Chain YY:  81% 14% . 5%




- Molecule 77: eS25

Chain ZZ:  52% 6% . 40%



- Molecule 78: eS26

Chain aa:  78% 10% 12%



- Molecule 79: eS27

- Molecule 80: eS28

- Molecule 81: uS14

- Molecule 82: eS30

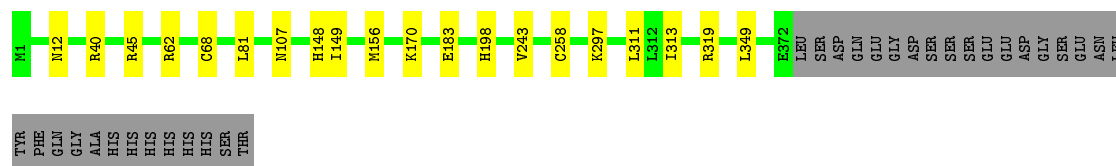
- Molecule 83: eS31

- Molecule 84: RACK1

- Molecule 85: mRNA (truncated)

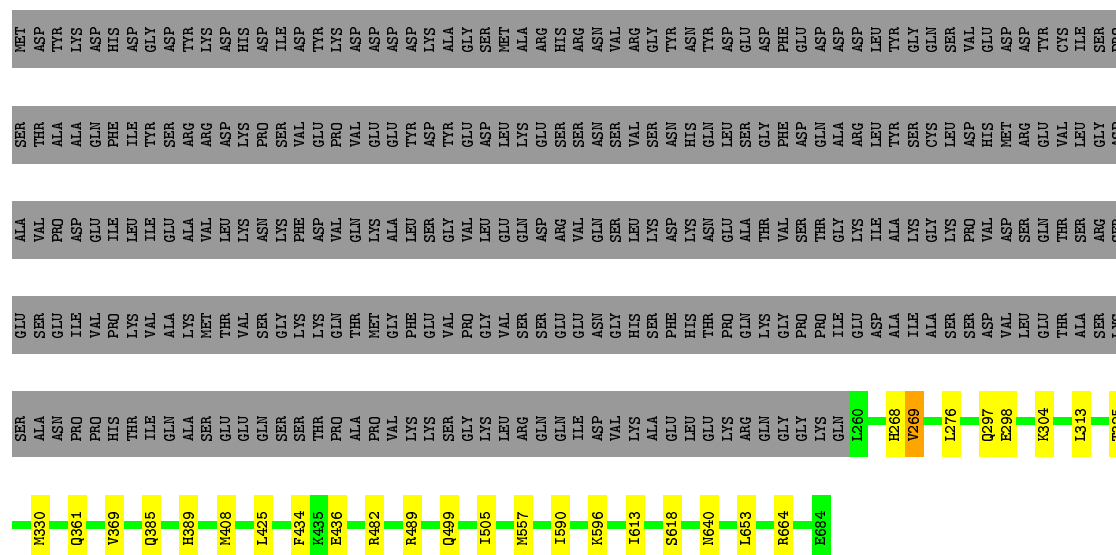
- Molecule 86: Pelota

Chain ii: 87% 5% 8%



- Molecule 87: Hbs11

Chain jj:  56% . 40%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	42011	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	104478	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.36	0/1936	0.71	0/2596
10	J	0.33	0/1385	0.60	0/1852
11	L	0.35	0/1733	0.66	0/2316
12	M	0.37	0/1158	0.68	0/1547
13	N	0.36	0/1746	0.69	0/2338
14	O	0.36	0/1662	0.67	0/2222
15	P	0.36	0/1268	0.65	0/1700
16	Q	0.36	0/1539	0.73	0/2054
17	R	0.35	0/1524	0.67	0/2013
18	S	0.35	0/1501	0.65	0/2012
19	T	0.37	0/1326	0.63	0/1770
2	B	0.34	0/3240	0.64	0/4339
20	U	0.36	0/823	0.56	0/1104
21	V	0.37	0/993	0.67	0/1332
22	W	0.35	0/873	0.57	0/1158
23	X	0.33	0/984	0.60	0/1323
24	Y	0.35	0/1132	0.64	0/1504
25	Z	0.35	0/1130	0.61	0/1507
26	a	0.34	0/1191	0.63	0/1590
27	b	0.33	0/861	0.58	0/1138
28	c	0.33	0/771	0.54	0/1034
29	d	0.35	0/903	0.67	0/1216
3	C	0.35	0/2937	0.67	0/3946
30	e	0.38	0/1071	0.68	0/1429
31	f	0.36	0/895	0.70	0/1198
32	g	0.34	0/916	0.70	0/1220
33	h	0.32	0/1021	0.59	0/1348
34	i	0.34	0/841	0.59	0/1112
35	j	0.35	0/720	0.70	0/952
36	k	0.32	0/575	0.54	0/761
37	l	0.34	0/459	0.62	0/608
38	m	0.35	0/435	0.63	0/575

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	n	0.35	0/240	0.68	0/305
4	D	0.34	0/2437	0.61	1/3264 (0.0%)
40	o	0.33	0/864	0.61	0/1140
41	p	0.33	0/718	0.60	0/953
42	r	0.36	0/1010	0.66	0/1354
43	s	0.36	0/1530	0.50	0/2064
44	t	0.36	0/1174	0.53	0/1582
45	1	0.44	0/129	0.61	0/173
46	2	0.21	0/1805	0.66	0/2809
47	3	0.21	0/1777	0.66	0/2763
48	5	0.74	31/84961 (0.0%)	0.78	72/132460 (0.1%)
49	7	0.26	0/2858	0.65	0/4455
5	E	0.34	0/1762	0.62	0/2362
50	8	0.26	0/3581	0.68	0/5577
51	9	0.27	0/40523	0.71	14/63130 (0.0%)
52	AA	0.36	0/1747	0.61	0/2374
53	BB	0.34	0/1756	0.59	0/2350
54	CC	0.36	0/1753	0.66	0/2369
55	DD	0.36	0/1796	0.63	0/2417
56	EE	0.36	0/2118	0.64	0/2849
57	FF	0.34	0/1492	0.60	0/2005
58	GG	0.36	0/1946	0.68	1/2590 (0.0%)
59	HH	0.36	0/1510	0.58	0/2022
6	F	0.36	0/1911	0.67	0/2549
60	II	0.36	0/1715	0.67	0/2287
61	JJ	0.35	0/1550	0.68	0/2069
62	KK	0.39	0/834	0.61	0/1125
63	LL	0.35	0/1195	0.68	0/1597
64	MM	0.37	0/918	0.59	0/1233
65	NN	0.36	0/1226	0.64	0/1649
66	OO	0.36	0/1029	0.73	0/1380
67	PP	0.38	0/1017	0.65	0/1358
68	QQ	0.35	0/1146	0.63	0/1534
69	RR	0.36	0/1082	0.61	0/1452
7	G	0.34	0/1910	0.61	0/2569
70	SS	0.37	0/1208	0.67	0/1618
71	TT	0.38	0/1115	0.65	0/1493
72	UU	0.35	0/805	0.65	0/1081
73	VV	0.38	0/643	0.66	0/860
74	WW	0.36	0/1051	0.71	0/1406
75	XX	0.33	0/1116	0.65	0/1490
76	YY	0.37	0/1028	0.64	0/1366
77	ZZ	0.36	0/604	0.60	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	aa	0.38	0/828	0.71	0/1109
79	bb	0.35	0/665	0.63	0/891
8	H	0.33	0/1535	0.62	0/2063
80	cc	0.38	0/490	0.73	1/656 (0.2%)
81	dd	0.39	0/470	0.65	0/623
82	ee	0.36	0/447	0.66	0/587
83	ff	0.38	0/567	0.55	0/753
84	gg	0.33	0/2493	0.55	0/3394
85	hh	0.29	0/188	0.82	0/290
86	ii	0.33	0/2996	0.56	0/4050
87	jj	0.34	0/3352	0.55	0/4523
9	I	0.35	0/1702	0.63	0/2272
All	All	0.52	31/237872 (0.0%)	0.71	89/348318 (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
2	B	0	2
48	5	0	3
6	F	0	1
75	XX	0	1
86	ii	0	2
All	All	0	9

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	5	935	A	C6-N6	192.84	2.88	1.33
48	5	935	A	C5-C6	-20.65	1.22	1.41
48	5	922(A)	G	O3'-P	17.07	1.81	1.61
48	5	481	G	C2-N3	-13.50	1.22	1.32
48	5	971	U	C2-O2	-13.31	1.10	1.22

The worst 5 of 89 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	5	481	G	C8-N9-C1'	-61.05	47.63	127.00
48	5	935	A	C6-N1-C2	-39.97	94.62	118.60
48	5	935	A	C5-C6-N6	-39.04	92.47	123.70

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
48	5	481	G	N1-C2-N2	-38.45	81.59	116.20
48	5	481	G	N3-C2-N2	-37.53	93.63	119.90

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
48	5	481	G	Sidechain
48	5	935	A	Sidechain
2	B	16	PHE	Peptide
2	B	258	HIS	Peptide
6	F	235	ARG	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	A	1898	0	1993	17	0
2	B	3172	0	3310	15	0
3	C	2883	0	3053	13	0
4	D	2391	0	2424	14	0
5	E	1729	0	1887	10	0
6	F	1875	0	1995	11	0
7	G	1879	0	2027	5	0
8	H	1516	0	1597	8	0
9	I	1664	0	1712	4	0
10	J	1362	0	1399	4	0
11	L	1702	0	1820	4	0
12	M	1137	0	1211	13	0
13	N	1701	0	1749	6	0
14	O	1630	0	1778	17	0
15	P	1242	0	1274	5	0
16	Q	1515	0	1634	10	0
17	R	1508	0	1664	3	0
18	S	1462	0	1508	7	0
19	T	1298	0	1366	6	0
20	U	809	0	833	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	V	979	0	1039	8	0
22	W	860	0	903	3	0
23	X	967	0	1040	1	0
24	Y	1115	0	1205	1	0
25	Z	1107	0	1182	5	0
26	a	1162	0	1209	0	0
27	b	848	0	920	0	0
28	c	761	0	794	0	0
29	d	888	0	930	0	0
30	e	1053	0	1147	0	0
31	f	876	0	912	0	0
32	g	906	0	1000	0	0
33	h	1013	0	1147	0	0
34	i	830	0	916	0	0
35	j	705	0	737	0	0
36	k	569	0	637	0	0
37	l	447	0	480	0	0
38	m	429	0	465	0	0
39	n	239	0	289	0	0
40	o	851	0	920	0	0
41	p	708	0	756	0	0
42	r	994	0	1051	0	0
43	s	1507	0	1564	0	0
44	t	1160	0	1218	0	0
45	1	125	0	117	1	0
46	2	1616	0	824	2	0
47	3	1593	0	811	1	0
48	5	75972	0	38402	283	0
49	7	2558	0	1296	3	0
50	8	3208	0	1629	5	0
51	9	36249	0	18314	186	0
52	AA	1710	0	1708	12	0
53	BB	1729	0	1803	8	0
54	CC	1716	0	1806	15	0
55	DD	1768	0	1866	26	0
56	EE	2076	0	2177	12	0
57	FF	1471	0	1522	7	0
58	GG	1923	0	2089	11	0
59	HH	1488	0	1582	12	0
60	II	1686	0	1772	10	0
61	JJ	1525	0	1640	7	0
62	KK	810	0	836	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	LL	1175	0	1249	3	0
64	MM	908	0	939	4	0
65	NN	1202	0	1289	6	0
66	OO	1016	0	1039	10	0
67	PP	997	0	1045	2	0
68	QQ	1128	0	1195	8	0
69	RR	1068	0	1121	3	0
70	SS	1190	0	1249	4	0
71	TT	1097	0	1132	5	0
72	UU	795	0	862	2	0
73	VV	636	0	637	3	0
74	WW	1034	0	1080	8	0
75	XX	1098	0	1167	7	0
76	YY	1011	0	1083	5	0
77	ZZ	598	0	656	5	0
78	aa	814	0	865	0	0
79	bb	651	0	672	0	0
80	cc	488	0	514	0	0
81	dd	459	0	449	0	0
82	ee	443	0	492	0	0
83	ff	555	0	567	0	0
84	gg	2436	0	2393	0	0
85	hh	169	0	86	0	0
86	ii	2947	0	2957	0	0
87	jj	3292	0	3371	0	0
88	5	188	0	0	0	0
88	7	5	0	0	0	0
88	8	6	0	0	0	0
88	9	71	0	0	0	0
88	B	1	0	0	0	0
88	I	1	0	0	0	0
88	P	2	0	0	0	0
88	Q	1	0	0	0	0
88	V	1	0	0	0	0
88	a	1	0	0	0	0
88	e	1	0	0	0	0
88	g	1	0	0	0	0
88	j	1	0	0	0	0
88	jj	1	0	0	0	0
89	aa	1	0	0	0	0
89	dd	1	0	0	0	0
89	ff	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	g	1	0	0	0	0
89	j	1	0	0	0	0
89	m	1	0	0	0	0
89	o	1	0	0	0	0
89	p	1	0	0	0	0
90	9	32	0	14	28	0
90	jj	32	0	14	0	0
All	All	222130	0	167026	791	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 791 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)
48:5:922:C:C5'	48:5:922(A):G:H3'	1.47	1.45
48:5:922:C:H5'	48:5:922(A):G:C3'	1.56	1.34
48:5:922:C:H2'	48:5:922(B):C:C2	1.62	1.33
51:9:1137:U:O4	51:9:1148:A:N1	1.64	1.29
51:9:614:C:C4'	51:9:626:G:H21	1.45	1.29

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	246/257 (96%)	222 (90%)	23 (9%)	1 (0%)	39	80
2	B	392/403 (97%)	363 (93%)	26 (7%)	3 (1%)	24	69
3	C	360/425 (85%)	339 (94%)	20 (6%)	1 (0%)	46	83
4	D	291/297 (98%)	276 (95%)	13 (4%)	2 (1%)	26	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	208/291 (72%)	190 (91%)	17 (8%)	1 (0%)	34	77
6	F	223/247 (90%)	209 (94%)	12 (5%)	2 (1%)	21	67
7	G	229/319 (72%)	222 (97%)	7 (3%)	0	100	100
8	H	188/192 (98%)	178 (95%)	10 (5%)	0	100	100
9	I	201/214 (94%)	182 (90%)	19 (10%)	0	100	100
10	J	168/178 (94%)	162 (96%)	6 (4%)	0	100	100
11	L	208/211 (99%)	200 (96%)	7 (3%)	1 (0%)	34	77
12	M	136/218 (62%)	126 (93%)	10 (7%)	0	100	100
13	N	201/204 (98%)	187 (93%)	13 (6%)	1 (0%)	34	77
14	O	197/203 (97%)	188 (95%)	9 (5%)	0	100	100
15	P	151/184 (82%)	143 (95%)	7 (5%)	1 (1%)	26	72
16	Q	185/188 (98%)	169 (91%)	15 (8%)	1 (0%)	34	77
17	R	178/196 (91%)	172 (97%)	6 (3%)	0	100	100
18	S	174/176 (99%)	164 (94%)	8 (5%)	2 (1%)	17	63
19	T	157/160 (98%)	145 (92%)	12 (8%)	0	100	100
20	U	97/128 (76%)	85 (88%)	12 (12%)	0	100	100
21	V	129/140 (92%)	114 (88%)	15 (12%)	0	100	100
22	W	102/157 (65%)	96 (94%)	6 (6%)	0	100	100
23	X	116/156 (74%)	110 (95%)	6 (5%)	0	100	100
24	Y	132/145 (91%)	122 (92%)	10 (8%)	0	100	100
25	Z	133/136 (98%)	127 (96%)	4 (3%)	2 (2%)	13	56
26	a	145/148 (98%)	130 (90%)	15 (10%)	0	100	100
27	b	100/245 (41%)	92 (92%)	7 (7%)	1 (1%)	19	65
28	c	96/115 (84%)	90 (94%)	5 (5%)	1 (1%)	19	65
29	d	105/125 (84%)	89 (85%)	15 (14%)	1 (1%)	19	65
30	e	126/135 (93%)	120 (95%)	6 (5%)	0	100	100
31	f	107/110 (97%)	99 (92%)	6 (6%)	2 (2%)	10	51
32	g	112/116 (97%)	105 (94%)	7 (6%)	0	100	100
33	h	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
34	i	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
35	j	84/97 (87%)	78 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	k	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
37	l	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
38	m	50/102 (49%)	49 (98%)	0	1 (2%)	9	50
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	96 (94%)	6 (6%)	0	100	100
41	p	89/92 (97%)	82 (92%)	6 (7%)	1 (1%)	17	63
42	r	122/137 (89%)	111 (91%)	10 (8%)	1 (1%)	24	69
43	s	194/318 (61%)	175 (90%)	17 (9%)	2 (1%)	19	65
44	t	151/165 (92%)	135 (89%)	14 (9%)	2 (1%)	15	59
45	1	13/15 (87%)	10 (77%)	3 (23%)	0	100	100
52	AA	215/295 (73%)	200 (93%)	13 (6%)	2 (1%)	21	67
53	BB	211/264 (80%)	197 (93%)	14 (7%)	0	100	100
54	CC	219/293 (75%)	206 (94%)	13 (6%)	0	100	100
55	DD	226/243 (93%)	209 (92%)	14 (6%)	3 (1%)	15	59
56	EE	260/263 (99%)	242 (93%)	18 (7%)	0	100	100
57	FF	181/204 (89%)	170 (94%)	11 (6%)	0	100	100
58	GG	235/249 (94%)	227 (97%)	7 (3%)	1 (0%)	39	80
59	HH	181/194 (93%)	170 (94%)	11 (6%)	0	100	100
60	II	204/208 (98%)	192 (94%)	12 (6%)	0	100	100
61	JJ	183/194 (94%)	173 (94%)	10 (6%)	0	100	100
62	KK	94/165 (57%)	85 (90%)	8 (8%)	1 (1%)	17	63
63	LL	139/158 (88%)	129 (93%)	10 (7%)	0	100	100
64	MM	115/132 (87%)	103 (90%)	12 (10%)	0	100	100
65	NN	147/151 (97%)	141 (96%)	6 (4%)	0	100	100
66	OO	134/168 (80%)	122 (91%)	10 (8%)	2 (2%)	13	56
67	PP	118/145 (81%)	106 (90%)	12 (10%)	0	100	100
68	QQ	140/146 (96%)	131 (94%)	9 (6%)	0	100	100
69	RR	130/135 (96%)	122 (94%)	7 (5%)	1 (1%)	24	69
70	SS	142/152 (93%)	135 (95%)	7 (5%)	0	100	100
71	TT	139/145 (96%)	130 (94%)	8 (6%)	1 (1%)	26	72
72	UU	98/119 (82%)	91 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	VV	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
74	WW	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	12	54
75	XX	139/143 (97%)	129 (93%)	7 (5%)	3 (2%)	8	48
76	YY	122/130 (94%)	112 (92%)	10 (8%)	0	100	100
77	ZZ	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
78	aa	99/115 (86%)	92 (93%)	6 (6%)	1 (1%)	19	65
79	bb	81/84 (96%)	74 (91%)	6 (7%)	1 (1%)	16	61
80	cc	60/69 (87%)	57 (95%)	3 (5%)	0	100	100
81	dd	53/56 (95%)	47 (89%)	5 (9%)	1 (2%)	10	51
82	ee	53/133 (40%)	51 (96%)	2 (4%)	0	100	100
83	ff	66/156 (42%)	60 (91%)	6 (9%)	0	100	100
84	gg	311/317 (98%)	285 (92%)	23 (7%)	3 (1%)	19	65
86	ii	370/403 (92%)	338 (91%)	31 (8%)	1 (0%)	46	83
87	jj	423/710 (60%)	387 (92%)	32 (8%)	4 (1%)	21	67
All	All	12325/14502 (85%)	11474 (93%)	794 (6%)	57 (0%)	38	77

5 of 57 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
75	XX	62	PRO
1	A	14	SER
3	C	83	GLY
11	L	63	THR
15	P	114	ILE

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	
1	A	190/199 (96%)	174 (92%)	16 (8%)	14	50
2	B	342/348 (98%)	324 (95%)	18 (5%)	28	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	302/347 (87%)	284 (94%)	18 (6%)	24	64
4	D	247/250 (99%)	235 (95%)	12 (5%)	31	70
5	E	190/251 (76%)	178 (94%)	12 (6%)	22	63
6	F	196/215 (91%)	183 (93%)	13 (7%)	21	61
7	G	200/272 (74%)	188 (94%)	12 (6%)	24	64
8	H	169/171 (99%)	157 (93%)	12 (7%)	18	58
9	I	175/181 (97%)	166 (95%)	9 (5%)	29	69
10	J	143/149 (96%)	138 (96%)	5 (4%)	43	78
11	L	175/176 (99%)	167 (95%)	8 (5%)	33	72
12	M	117/161 (73%)	112 (96%)	5 (4%)	35	74
13	N	171/172 (99%)	162 (95%)	9 (5%)	28	67
14	O	171/173 (99%)	159 (93%)	12 (7%)	19	59
15	P	134/163 (82%)	125 (93%)	9 (7%)	20	61
16	Q	164/165 (99%)	152 (93%)	12 (7%)	17	57
17	R	159/175 (91%)	147 (92%)	12 (8%)	17	56
18	S	157/157 (100%)	146 (93%)	11 (7%)	19	59
19	T	139/140 (99%)	126 (91%)	13 (9%)	11	45
20	U	89/114 (78%)	88 (99%)	1 (1%)	80	92
21	V	101/107 (94%)	92 (91%)	9 (9%)	12	48
22	W	86/126 (68%)	84 (98%)	2 (2%)	58	85
23	X	106/134 (79%)	100 (94%)	6 (6%)	25	66
24	Y	124/135 (92%)	118 (95%)	6 (5%)	31	71
25	Z	117/118 (99%)	114 (97%)	3 (3%)	54	83
26	a	119/120 (99%)	116 (98%)	3 (2%)	55	84
27	b	84/184 (46%)	81 (96%)	3 (4%)	42	78
28	c	84/98 (86%)	81 (96%)	3 (4%)	42	78
29	d	98/110 (89%)	87 (89%)	11 (11%)	7	35
30	e	114/121 (94%)	105 (92%)	9 (8%)	15	53
31	f	88/89 (99%)	83 (94%)	5 (6%)	25	66
32	g	98/99 (99%)	94 (96%)	4 (4%)	37	74
33	h	109/110 (99%)	105 (96%)	4 (4%)	41	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	i	86/89 (97%)	83 (96%)	3 (4%)	43	78
35	j	73/80 (91%)	69 (94%)	4 (6%)	27	67
36	k	64/65 (98%)	62 (97%)	2 (3%)	47	81
37	l	47/48 (98%)	46 (98%)	1 (2%)	61	86
38	m	48/90 (53%)	46 (96%)	2 (4%)	36	74
39	n	24/24 (100%)	22 (92%)	2 (8%)	14	50
40	o	92/94 (98%)	87 (95%)	5 (5%)	27	67
41	p	74/75 (99%)	73 (99%)	1 (1%)	74	91
42	r	108/121 (89%)	102 (94%)	6 (6%)	26	66
43	s	164/258 (64%)	158 (96%)	6 (4%)	41	76
44	t	126/137 (92%)	123 (98%)	3 (2%)	57	85
45	1	13/13 (100%)	13 (100%)	0	100	100
52	AA	180/245 (74%)	165 (92%)	15 (8%)	14	50
53	BB	194/231 (84%)	177 (91%)	17 (9%)	12	48
54	CC	187/225 (83%)	167 (89%)	20 (11%)	8	38
55	DD	190/202 (94%)	173 (91%)	17 (9%)	12	48
56	EE	224/225 (100%)	208 (93%)	16 (7%)	18	58
57	FF	158/170 (93%)	148 (94%)	10 (6%)	22	63
58	GG	207/218 (95%)	189 (91%)	18 (9%)	13	49
59	HH	165/174 (95%)	149 (90%)	16 (10%)	10	43
60	II	178/180 (99%)	164 (92%)	14 (8%)	15	53
61	JJ	161/168 (96%)	147 (91%)	14 (9%)	13	49
62	KK	87/136 (64%)	78 (90%)	9 (10%)	9	40
63	LL	130/142 (92%)	114 (88%)	16 (12%)	6	30
64	MM	99/108 (92%)	86 (87%)	13 (13%)	5	28
65	NN	130/131 (99%)	113 (87%)	17 (13%)	5	28
66	OO	106/130 (82%)	91 (86%)	15 (14%)	4	24
67	PP	109/130 (84%)	94 (86%)	15 (14%)	4	25
68	QQ	117/121 (97%)	108 (92%)	9 (8%)	16	55
69	RR	119/121 (98%)	108 (91%)	11 (9%)	11	46
70	SS	125/132 (95%)	108 (86%)	17 (14%)	5	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	TT	111/115 (96%)	100 (90%)	11 (10%)	10	42
72	UU	92/107 (86%)	80 (87%)	12 (13%)	5	28
73	VV	67/67 (100%)	62 (92%)	5 (8%)	17	56
74	WW	112/113 (99%)	105 (94%)	7 (6%)	22	63
75	XX	113/115 (98%)	106 (94%)	7 (6%)	23	63
76	YY	107/112 (96%)	94 (88%)	13 (12%)	6	31
77	ZZ	66/103 (64%)	61 (92%)	5 (8%)	16	55
78	aa	88/98 (90%)	78 (89%)	10 (11%)	7	34
79	bb	75/76 (99%)	69 (92%)	6 (8%)	15	53
80	cc	55/62 (89%)	50 (91%)	5 (9%)	12	46
81	dd	48/49 (98%)	46 (96%)	2 (4%)	36	74
82	ee	46/106 (43%)	41 (89%)	5 (11%)	8	37
83	ff	61/140 (44%)	55 (90%)	6 (10%)	10	42
84	gg	272/275 (99%)	261 (96%)	11 (4%)	38	75
86	ii	326/353 (92%)	309 (95%)	17 (5%)	29	68
87	jj	358/608 (59%)	332 (93%)	26 (7%)	17	57
All	All	10740/12312 (87%)	9991 (93%)	749 (7%)	23	59

5 of 749 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	BB	38	MET
58	GG	63	MET
83	ff	110	GLU
53	BB	180	ASP
55	DD	134	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
42	r	103	HIS
56	EE	67	GLN
87	jj	361	GLN
43	s	34	ASN
55	DD	4	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	2	74/76 (97%)	15 (20%)	0
47	3	72/75 (96%)	27 (37%)	2 (2%)
48	5	3506/3543 (98%)	868 (24%)	165 (4%)
49	7	119/120 (99%)	15 (12%)	0
50	8	150/156 (96%)	37 (24%)	7 (4%)
51	9	1680/1869 (89%)	434 (25%)	87 (5%)
85	hh	7/8 (87%)	4 (57%)	0
All	All	5608/5847 (95%)	1400 (24%)	261 (4%)

5 of 1400 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
46	2	8	U
46	2	9	A
46	2	13	U
46	2	16	C
46	2	19	G

5 of 261 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	5	2724	G
48	5	4266	G
51	9	1519	U
48	5	2789	A
48	5	3876	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 291 ligands modelled in this entry, 289 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
90	GCP	9	1972	-	29,34,34	2.57	8 (27%)	31,54,54	1.16	2 (6%)
90	GCP	jj	700	88	29,34,34	2.49	8 (27%)	31,54,54	1.12	2 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
90	GCP	9	1972	-	-	0/18/38/38	0/3/3/3
90	GCP	jj	700	88	-	0/18/38/38	0/3/3/3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	9	1972	GCP	C4-N9	-11.03	1.33	1.47
90	jj	700	GCP	C4-N9	-10.27	1.34	1.47
90	9	1972	GCP	C8-N9	-3.84	1.34	1.47
90	jj	700	GCP	C8-N9	-3.71	1.35	1.47
90	9	1972	GCP	C5-C6	-2.67	1.48	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
90	jj	700	GCP	C4-C5-N7	2.40	106.41	102.67
90	9	1972	GCP	C4-C5-N7	2.58	106.69	102.67
90	jj	700	GCP	C8-N9-C4	3.19	108.42	104.78
90	9	1972	GCP	C8-N9-C4	3.35	108.60	104.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
90	9	1972	GCP	28	0

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
48	5	44
51	9	8
47	3	2
46	2	1

The worst 5 of 55 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	40.78
1	5	1252:C	O3'	1271:G	P	35.85
1	5	1219:G	O3'	1233:G	P	22.84
1	5	1405:C	O3'	1406:G	P	22.78
1	5	3948:C	O3'	4065:G	P	19.74