



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Nov 22, 2016 – 02:16 PM EST

PDB ID : 5LZS
EMDB ID: : EMD-4130
Title : Structure of the mammalian ribosomal elongation complex with aminoacyl-tRNA, eEF1A, and didemnin B
Authors : Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.
Deposited on : 2016-10-02
Resolution : 3.31 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.

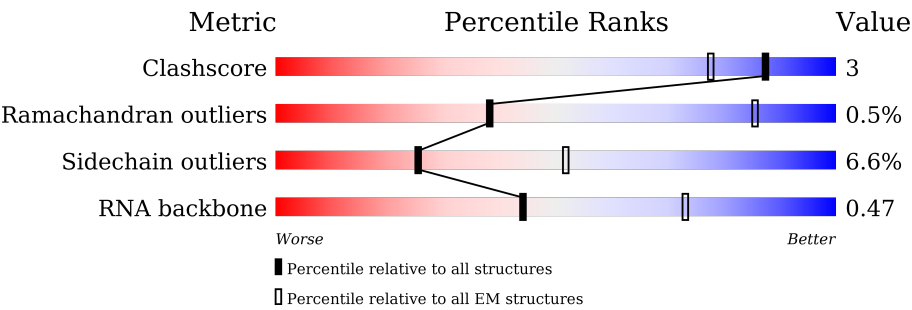
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
EM map analysis : **NOT EXECUTED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.31 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.




















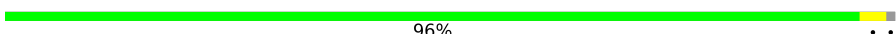






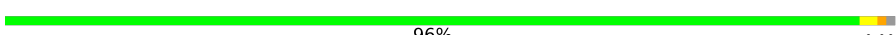
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	
2	B	403	
3	C	425	
4	D	297	
5	E	291	
6	F	247	
7	G	319	
8	H	192	

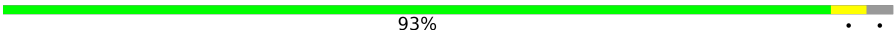

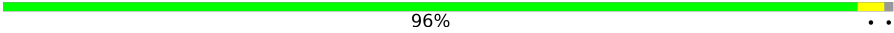
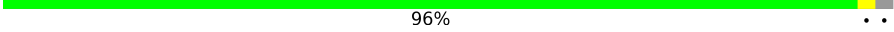


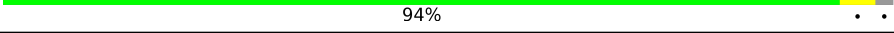
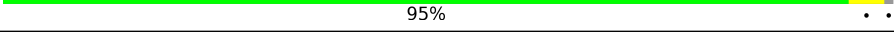


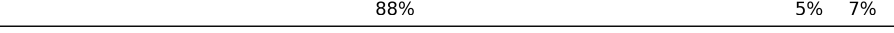
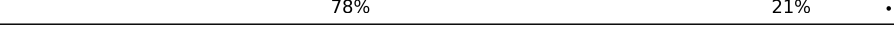
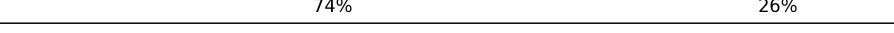


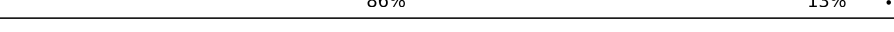









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Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	218	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	245	
28	c	115	
29	d	125	
30	e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




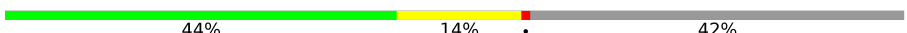





















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Mol	Chain	Length	Quality of chain
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	102	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	318	
44	t	165	
45	2	76	
45	ii	76	
46	3	75	
47	5	3543	
48	7	120	
49	8	156	
50	9	1869	
51	AA	295	
52	BB	264	
53	CC	293	
54	DD	243	
55	EE	263	
56	FF	204	
57	GG	249	

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Mol	Chain	Length	Quality of chain
58	HH	194	 85% 10% 5%
59	II	208	 89% 10% .
60	JJ	194	 83% 10% 5%
61	KK	165	 44% 14% . 42%
62	LL	158	 79% 11% 9%
63	MM	132	 77% 12% 11%
64	NN	151	 89% 9% ..
65	OO	168	 69% 10% . 19%
66	PP	145	 79% 10% . 11%
67	QQ	146	 86% 12% .
68	RR	135	 86% 10% ..
69	SS	152	 82% 13% 5%
70	TT	145	 89% 8% ..
71	UU	119	 73% 10% . 16%
72	VV	83	 90% 10%
73	WW	130	 82% 17% ..
74	XX	143	 87% 10% ..
75	YY	130	 84% 11% . 5%
76	ZZ	125	 50% 8% . 40%
77	aa	115	 82% 6% 12%
78	bb	84	 92% 6% ..
79	cc	69	 81% 9% 10%
80	dd	56	 93% 5% .
81	ee	133	 41% . 57%
82	ff	156	 38% 5% 56%

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Mol	Chain	Length	Quality of chain
83	gg	317	<div><div></div><div>96%</div><div></div><div>.</div><div>.</div></div>
84	hh	10	<div><div></div><div>90%</div><div>10%</div></div>
85	jj	462	<div><div></div><div>93%</div><div></div><div>•</div><div>5%</div></div>

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 220934 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 Uncharacterized protein.

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 Uncharacterized protein.

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 Uncharacterized protein,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 60S ribosomal protein L5.

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	-	initiating methionine	UNP G1SYJ6

- Molecule 5 is a protein called 60S ribosomal protein L6.

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 Uncharacterized protein.

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,Uncharacterized protein.

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 Uncharacterized protein.

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 Ribosomal protein L10 (Predicted).

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 Uncharacterized protein.

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 Uncharacterized protein.

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 Ribosomal protein L15.

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 Uncharacterized protein.

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 Uncharacterized protein.

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 Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 22 is a protein called Uncharacterized protein.

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 Uncharacterized protein.

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 Uncharacterized protein.

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 60S ribosomal protein L27.

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 Uncharacterized protein.

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 Uncharacterized protein,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 Uncharacterized protein.

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 Uncharacterized protein.

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 Uncharacterized protein.

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 Uncharacterized protein.

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 Uncharacterized protein.

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 Uncharacterized protein.

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 60S ribosomal protein L36.

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 Ribosomal protein L37.

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 Uncharacterized protein.

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 60s ribosomal protein l41.

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 Uncharacterized protein.

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 Uncharacterized protein.

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 Uncharacterized protein.

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 Uncharacterized protein.

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 RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		
45	ii	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	3	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 47 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 48 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 49 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 50 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	9	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 51 is a protein called uS2.

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

- Molecule 52 is a protein called 40S ribosomal protein S3a.

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

- Molecule 53 is a protein called uS5.

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

- Molecule 54 is a protein called Uncharacterized protein.

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

- Molecule 55 is a protein called 40S ribosomal protein S4.

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

- Molecule 56 is a protein called Uncharacterized protein.

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

- Molecule 57 is a protein called 40S ribosomal protein S6.

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

- Molecule 58 is a protein called Uncharacterized protein.

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

- Molecule 59 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	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 60 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 61 is a protein called Uncharacterized protein.

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

- Molecule 62 is a protein called Uncharacterized protein.

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

- Molecule 63 is a protein called 40S ribosomal protein S12.

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

- Molecule 64 is a protein called Uncharacterized protein.

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

- Molecule 65 is a protein called uS11,Uncharacterized protein.

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

- Molecule 66 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	PP	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 67 is a protein called Uncharacterized protein.

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

- Molecule 68 is a protein called Uncharacterized protein.

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

- Molecule 69 is a protein called Uncharacterized protein.

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

- Molecule 70 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	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 71 is a protein called Uncharacterized protein.

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

- Molecule 72 is a protein called eS21.

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

- Molecule 73 is a protein called Uncharacterized protein.

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

- Molecule 74 is a protein called uS12.

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

- Molecule 75 is a protein called eS24.

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

- Molecule 76 is a protein called Uncharacterized protein.

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

- Molecule 77 is a protein called eS26.

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

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

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

- Molecule 79 is a protein called Uncharacterized protein.

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

- Molecule 80 is a protein called Uncharacterized protein.

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

- Molecule 81 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	ee	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 82 is a protein called Uncharacterized protein.

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

- Molecule 83 is a protein called Uncharacterized protein.

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

- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	hh	10	Total	C	N	O	P	0	0
			210	94	33	73	10		

- Molecule 85 is a protein called Elongation factor 1-alpha 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
85	jj	441	Total	C	N	O	P	S	0	0
			3383	2148	581	636	1	17		

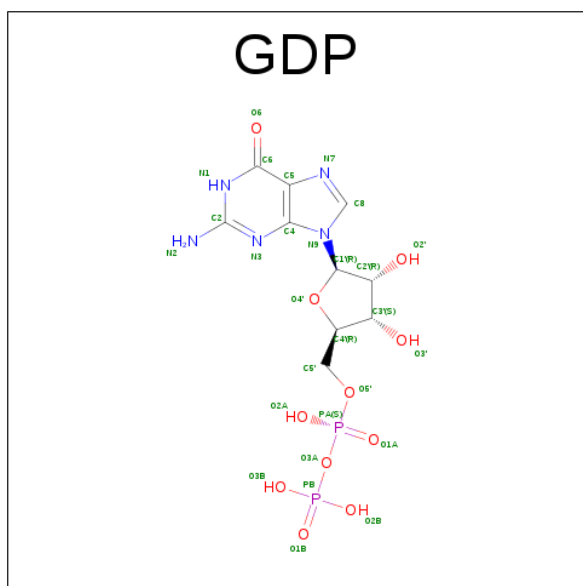
- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	P	1	Total	Mg	0
			1	1	
86	g	1	Total	Mg	0
			1	1	
86	j	1	Total	Mg	0
			1	1	
86	Q	1	Total	Mg	0
			1	1	
86	jj	1	Total	Mg	0
			1	1	
86	B	1	Total	Mg	0
			1	1	
86	I	1	Total	Mg	0
			1	1	
86	V	1	Total	Mg	0
			1	1	
86	7	6	Total	Mg	0
			6	6	
86	a	2	Total	Mg	0
			2	2	
86	5	185	Total	Mg	0
			185	185	
86	8	5	Total	Mg	0
			5	5	
86	9	70	Total	Mg	0
			70	70	

- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

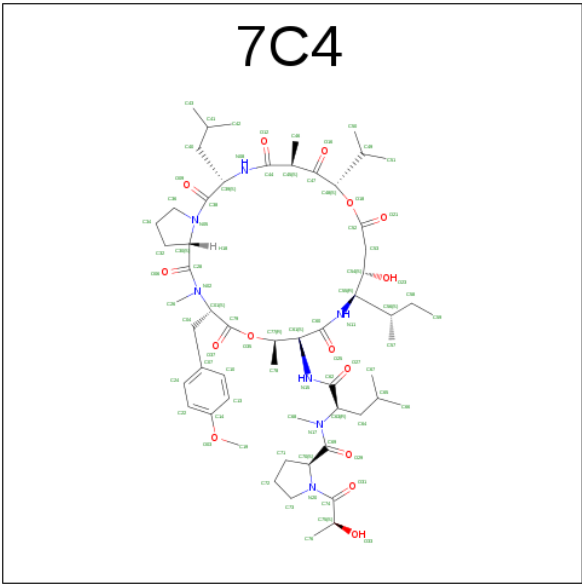
- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
88	jj	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 89 is (2 {S})- {N}-[(2 {R})-1-[(3 {S},6 {S},8 {S},12 {S},13 {R},16 {S},17 {R},20 {S},23 {S})-13-[(2 {S})-butan-2-yl]-20-[(4-methoxyphenyl)methyl]-6,17,21-trimethyl-3-(2-m ethylpropyl)-12-oxidanyl-2,5,7,10,15,19,22-heptakis(oxidanylidene)-8-propan-2-yl-9,18-diox a-1,4,14,21-tetrazabicyclo[21.3.0]hexacosan-16-yl]amino]-4-methyl-1-oxidanylidene-pentan

-2-yl]- {N}-methyl-1-[(2 {S})-2-oxidanylpropanoyl]pyrrolidine-2-carboxamide (three-letter code: 7C4) (formula: C₅₇H₈₉N₇O₁₅).

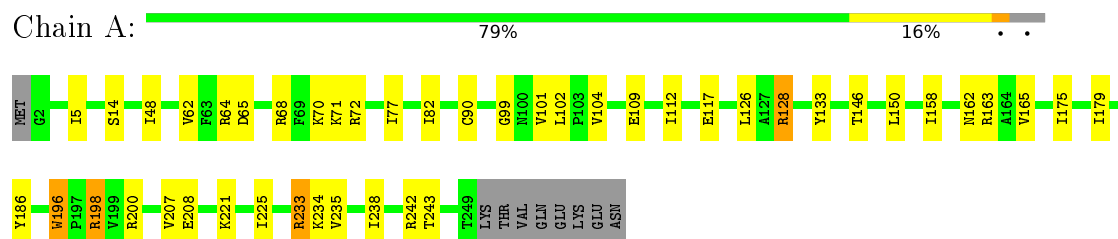


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
89	jj	1	79	57	7	15	0

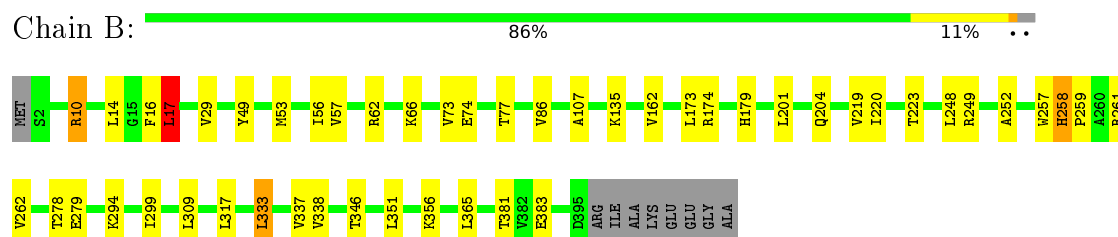
3 Residue-property plots

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.

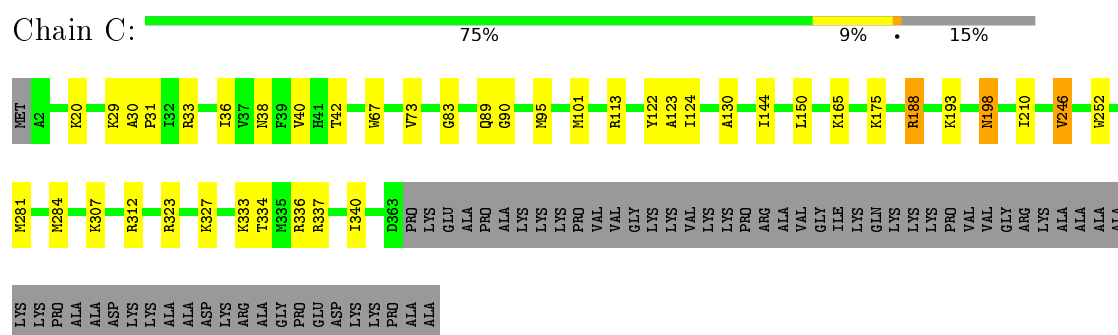
- Molecule 1: Uncharacterized protein



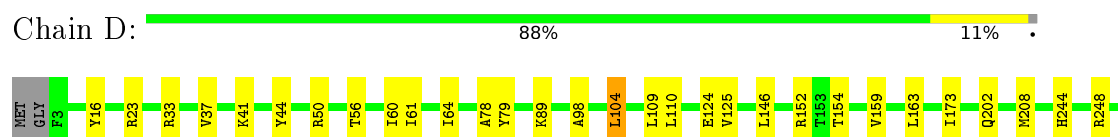
- Molecule 2: Uncharacterized protein



- Molecule 3: Uncharacterized protein,uL4



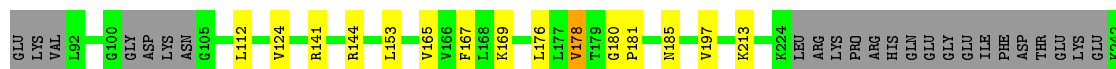
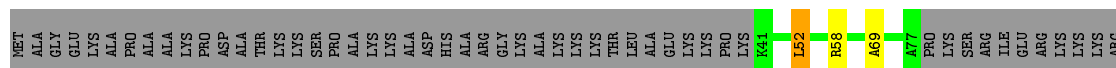
- Molecule 4: 60S ribosomal protein L5





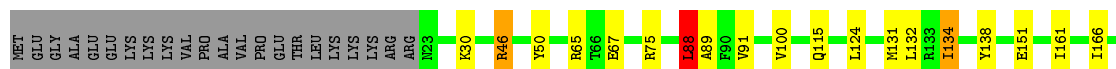
- Molecule 5: 60S ribosomal protein L6

Chain E: 66% 7% 26%



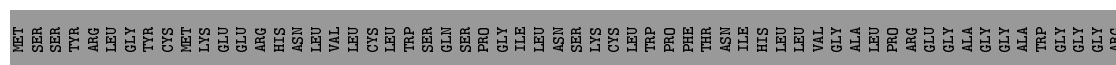
- Molecule 6: Uncharacterized protein

Chain F: 79% 11% 9%



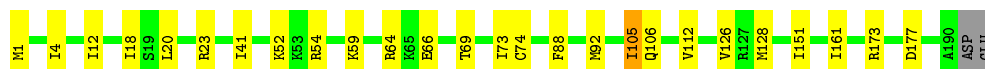
- Molecule 7: eL8, Uncharacterized protein

Chain G: 62% 11% 27%



- Molecule 8: Uncharacterized protein

Chain H: 85% 13% 2%



- Molecule 9: Ribosomal protein L10 (Predicted)

Chain I: 82% 11% 7%



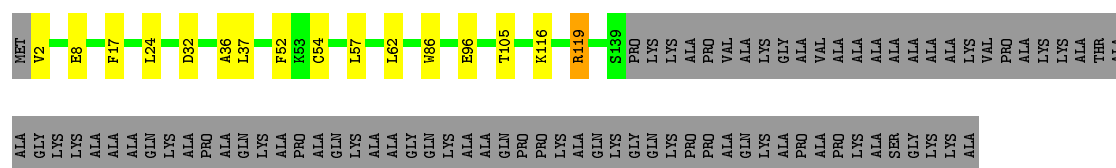
- Molecule 10: Uncharacterized protein



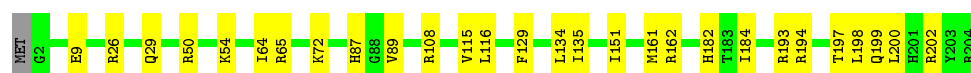
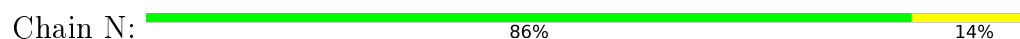
- Molecule 11: eL13



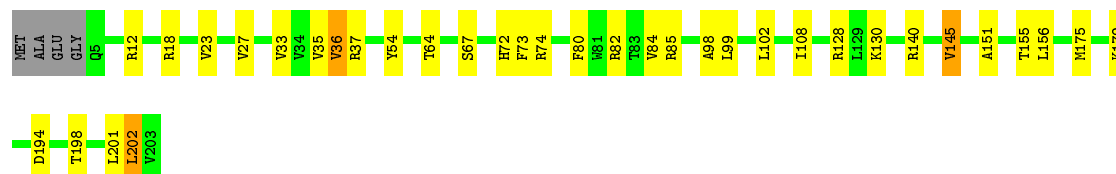
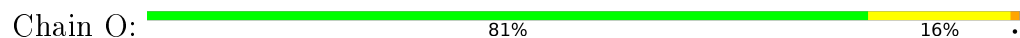
- Molecule 12: Uncharacterized protein



- Molecule 13: Ribosomal protein L15

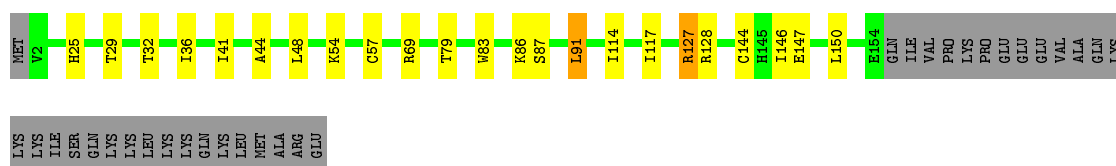


- Molecule 14: uL13



- Molecule 15: Uncharacterized protein





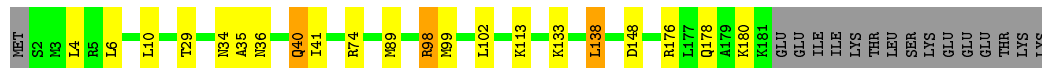
- Molecule 16: eL18

Chain Q: 88% 11% ..



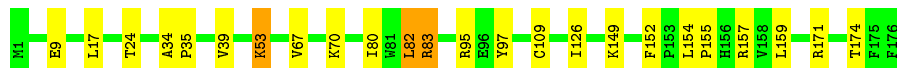
- Molecule 17: eL19

Chain R: 81% 9% 8%



- Molecule 18: eL20

Chain S: 86% 12% .



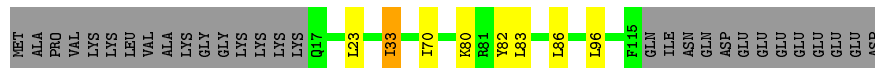
- Molecule 19: Uncharacterized protein

Chain T: 88% 11% ..



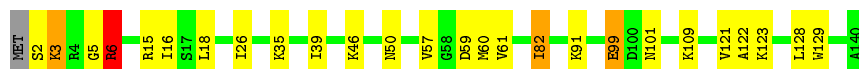
- Molecule 20: eL22

Chain U: 71% 5% 23%



- Molecule 21: Uncharacterized protein

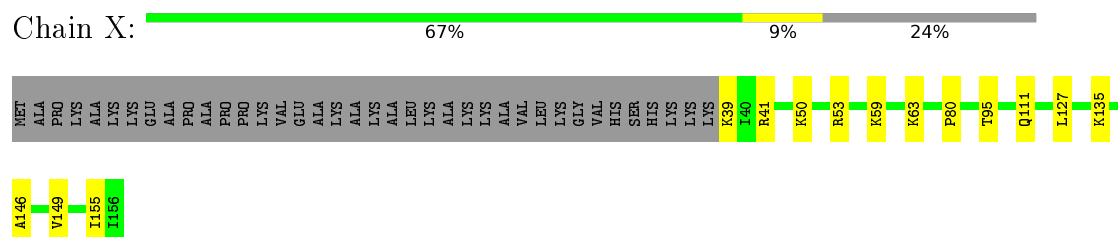
Chain V: 81% 16% ..



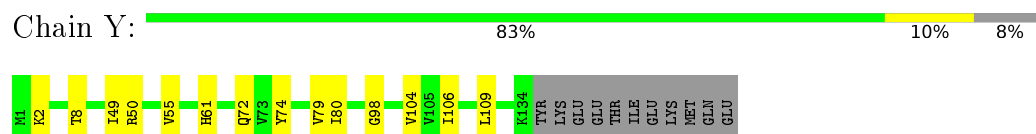
- Molecule 22: Uncharacterized protein

Chain W: 62% 32%

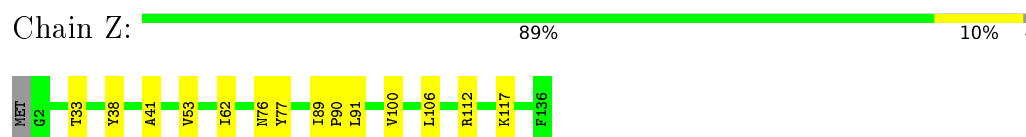
- Molecule 23: Uncharacterized protein



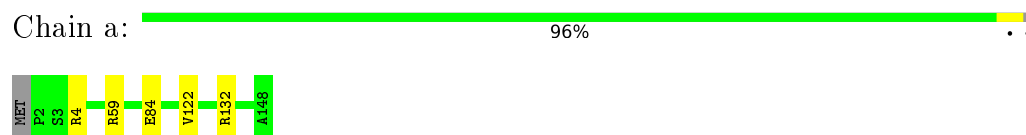
- Molecule 24: Uncharacterized protein



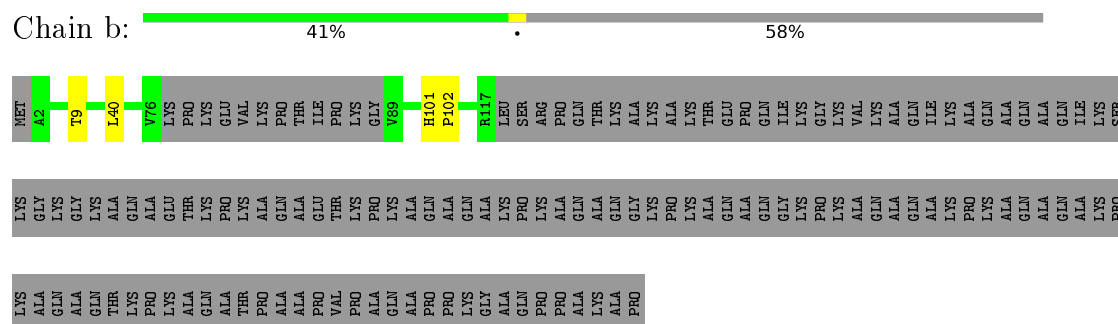
- Molecule 25: 60S ribosomal protein L27




- Molecule 26: Uncharacterized protein



- Molecule 27: Uncharacterized protein,eL29




- Molecule 28: Uncharacterized protein

Chain c:  82% 15%




- Molecule 29: Uncharacterized protein

Chain d:  77% 9% 14%




- Molecule 30: Uncharacterized protein

Chain e:  88% 7% 5%



- Molecule 31: Uncharacterized protein

Chain f:  92% 6% ..



- Molecule 32: Uncharacterized protein

Chain g:  93% 5% .



- Molecule 33: Uncharacterized protein

Chain h:  96% ..




- Molecule 34: 60S ribosomal protein L36

Chain i:  93% . .



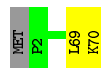
- Molecule 35: Ribosomal protein L37

Chain j:  82% 6% 11%



- Molecule 36: eL38

Chain k: 96% ..



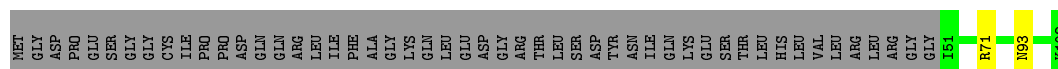
- Molecule 37: Uncharacterized protein

Chain l: 96% ..



- Molecule 38: eL40

Chain m: 49% . 49%



- Molecule 39: 60s ribosomal protein l41

Chain n: 88% 12%



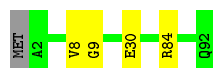
- Molecule 40: Uncharacterized protein

Chain o: 94% ..



- Molecule 41: Uncharacterized protein

Chain p: 95% ..

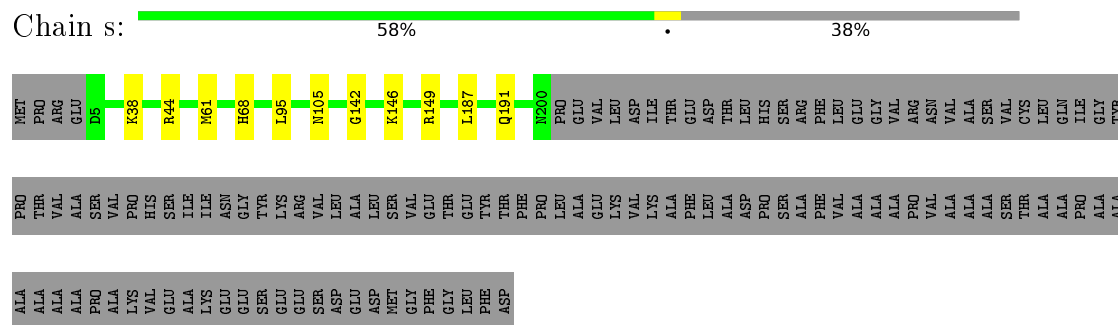


- Molecule 42: Uncharacterized protein

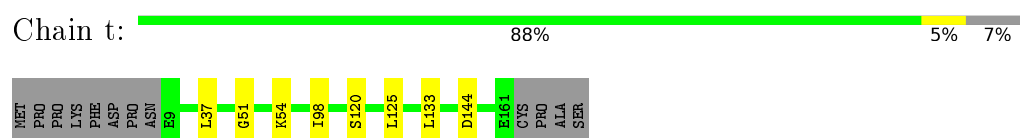
Chain r: 84% 7% 9%



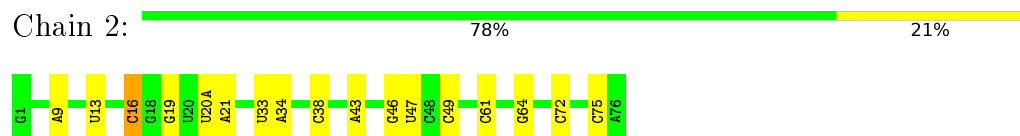
- Molecule 43: uL10



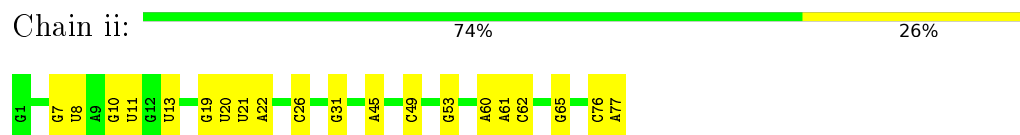
- Molecule 44: Uncharacterized protein



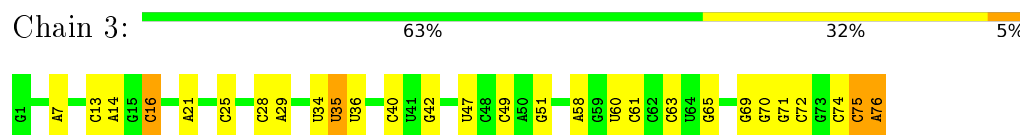
- Molecule 45: tRNA



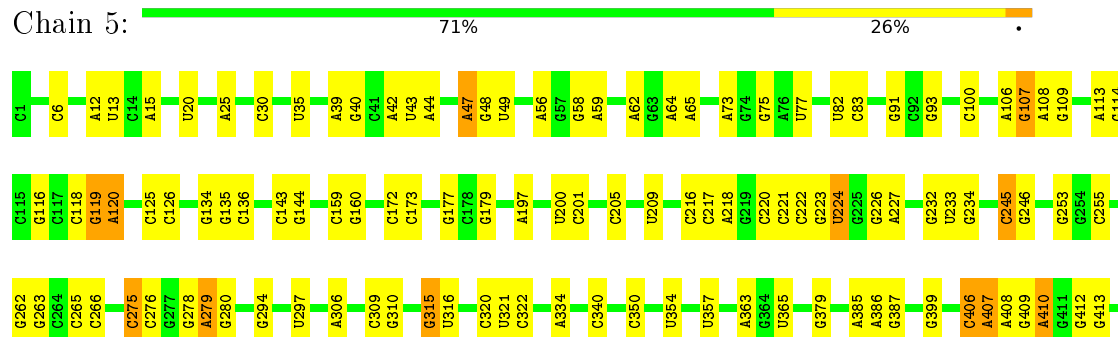
- Molecule 45: tRNA



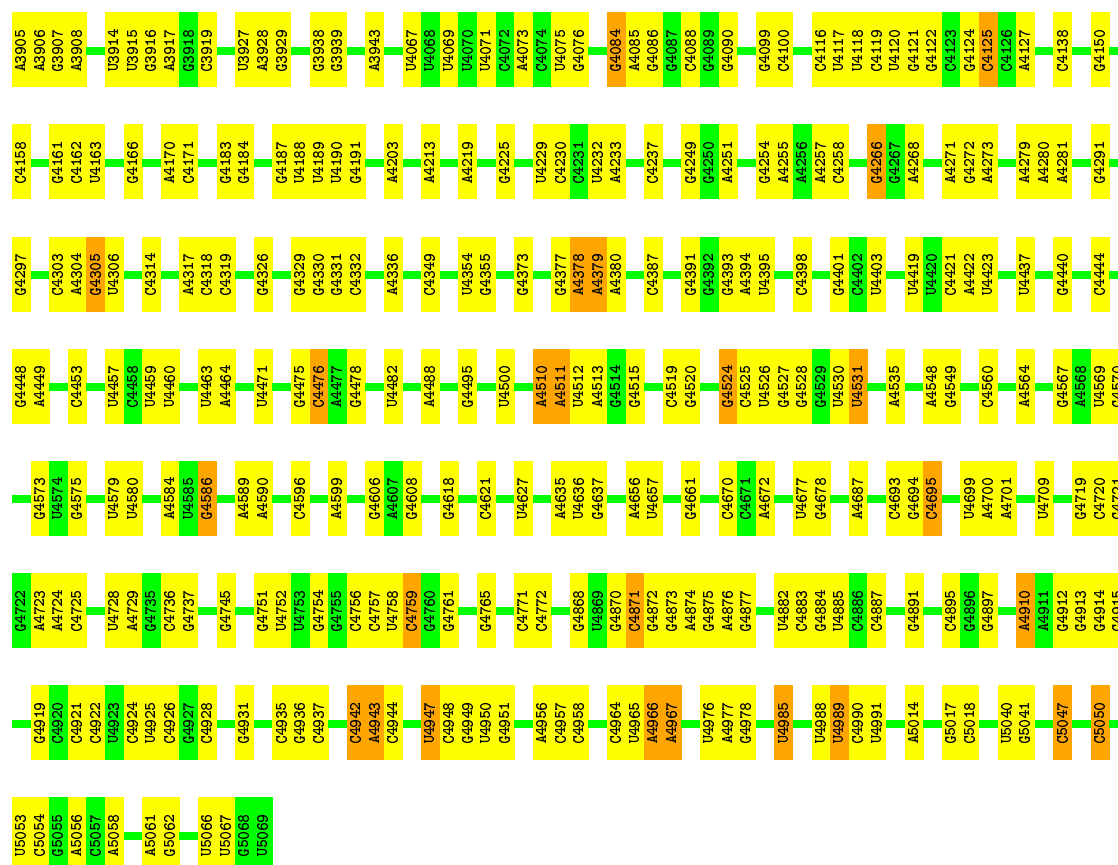
- Molecule 46: E-site tRNA



- Molecule 47: 28S ribosomal RNA

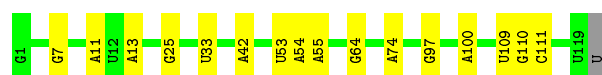


U3773	U3774	U3775	U3776	U3777	U3778	A2764	G2640	G2483	G2316	C2068	A1979	G1833	A1667	C1485	A1354	C1180	C931	G683	G417																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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A3784	A3785	A3786	A3787	A3788	A3789	A3790	A3791	A3792	A3793	A3794	A3795	A3796	A3797	A3798	A3799	A3800	A3801	A3802	A3803	A3804	A3805	A3806	A3807	A3808	A3809	A3810	A3811	A3812	A3813	A3814	A3815	A3816	A3817	A3818	A3819	A3820	A3821	A3822	A3823	A3824	A3825	A3826	A3827	A3828	A3829	A3830	A3831	A3832	A3833	A3834	A3835	A3836	A3837	A3838	A3839	A3840	A3841	A3842	A3843	A3844	A3845	A3846	A3847	A3848	A3849	A3850	A3851	A3852	A3853	A3854	A3855	A3856	A3857	A3858	A3859	A3860	A3861	A3862	A3863	A3864	A3865	A3866	A3867	A3868	A3869	A3870	A3871	A3872	A3873	A3874	A3875	A3876	A3877	A3878	A3879	A3880	A3881	A3882	A3883	A3884	A3885	A3886	A3887	A3888	A3889	A3890	A3891	A3892	A3893	A3894	A3895	A3896	A3897	A3898	A3899	A3900	A3901	A3902	A3903	A3904	A3905	A3906	A3907	A3908	A3909	A3910	A3911	A3912	A3913	A3914	A3915	A3916	A3917	A3918	A3919	A3920	A3921	A3922	A3923	A3924	A3925	A3926	A3927	A3928	A3929	A3930	A3931	A3932	A3933	A3934	A3935	A3936	A3937	A3938	A3939	A3940	A3941	A3942	A3943	A3944	A3945	A3946	A3947	A3948	A3949	A3950	A3951	A3952	A3953	A3954	A3955	A3956	A3957	A3958	A3959	A3960	A3961	A3962	A3963	A3964	A3965	A3966	A3967	A3968	A3969	A3970	A3971	A3972	A3973	A3974	A3975	A3976	A3977	A3978	A3979	A3980	A3981	A3982	A3983	A3984	A3985	A3986	A3987	A3988	A3989	A3990	A3991	A3992	A3993	A3994	A3995	A3996	A3997	A3998	A3999	A4000	A4001	A4002	A4003	A4004	A4005	A4006	A4007	A4008	A4009	A4010	A4011	A4012	A4013	A4014	A4015	A4016	A4017	A4018	A4019	A4020	A4021	A4022	A4023	A4024	A4025	A4026	A4027	A4028	A4029	A4030	A4031	A4032	A4033	A4034	A4035	A4036	A4037	A4038	A4039	A4040	A4041	A4042	A4043	A4044	A4045	A4046	A4047	A4048	A4049	A4050	A4051	A4052	A4053	A4054	A4055	A4056	A4057	A4058	A4059	A4060	A4061	A4062	A4063	A4064	A4065	A4066	A4067	A4068	A4069	A4070	A4071	A4072	A4073	A4074	A4075	A4076	A4077	A4078	A4079	A4080	A4081	A4082	A4083	A4084	A4085	A4086	A4087	A4088	A4089	A4090	A4091	A4092	A4093	A4094	A4095	A4096	A4097	A4098	A4099	A4100	A4101	A4102	A4103	A4104	A4105	A4106	A4107	A4108	A4109	A4110	A4111	A4112	A4113	A4114	A4115	A4116	A4117	A4118	A4119	A4120	A4121	A4122	A4123	A4124	A4125	A4126	A4127	A4128	A4129	A4130	A4131	A4132	A4133	A4134	A4135	A4136	A4137	A4138	A4139	A4140	A4141	A4142	A4143	A4144	A4145	A4146	A4147	A4148	A4149	A4150	A4151	A4152	A4153	A4154	A4155	A4156	A4157	A4158	A4159	A4160	A4161	A4162	A4163	A4164	A4165	A4166	A4167	A4168	A4169	A4170	A4171	A4172	A4173	A4174	A4175	A4176	A4177	A4178	A4179	A4180	A4181	A4182	A4183	A4184	A4185	A4186	A4187	A4188	A4189	A4190	A4191	A4192	A4193	A4194	A4195	A4196	A4197	A4198	A4199	A4200	A4201	A4202	A4203	A4204	A4205	A4206	A4207	A4208	A4209	A4210	A4211	A4212	A4213	A4214	A4215	A4216	A4217	A4218	A4219	A4220	A4221	A4222	A4223	A4224	A4225	A4226	A4227	A4228	A4229	A4230	A4231	A4232	A4233	A4234	A4235	A4236	A4237	A4238	A4239	A4240	A4241	A4242	A4243	A4244	A4245	A4246	A4247	A4248	A4249	A4250	A4251	A4252	A4253	A4254	A4255	A4256	A4257	A4258	A4259	A4260	A4261	A4262	A4263	A4264	A4265	A4266	A4267	A4268	A4269	A4270	A4271	A4272	A4273	A4274	A4275	A4276	A4277	A4278	A4279	A4280	A4281	A4282	A4283	A4284	A4285	A4286	A4287	A4288	A4289	A4290	A4291	A4292	A4293	A4294	A4295	A4296	A4297	A4298	A4299	A4300	A4301	A4302	A4303	A4304	A4305	A4306	A4307	A4308	A4309	A4310	A4311	A4312	A4313	A4314	A4315	A4316	A4317	A4318	A4319	A4320	A4321	A4322	A4323	A4324	A4325	A4326	A4327	A4328	A4329	A4330	A4331	A4332	A4333	A4334	A4335	A4336	A4337	A4338	A4339	A4340	A4341	A4342	A4343	A4344	A4345	A4346	A4347	A4348	A4349	A4350	A4351	A4352	A4353	A4354	A4355	A4356	A4357	A4358	A4359	A4360	A4361	A4362	A4363	A4364	A4365	A4366	A4367	A4368	A4369	A4370	A4371	A4372	A4373	A4374	A4375	A4376	A4377	A4378	A4379	A4380	A4381	A4382	A4383	A4384	A4385	A4386	A4387	A4388	A4389	A4390	A4391	A4392	A4393	A4394	A4395	A4396	A4397	A4398	A4399	A4400	A4401	A4402	A4403	A4404	A4405	A4406	A4407	A4408	A4409	A4410	A4411	A4412	A4413	A4414	A4415	A4416	A4417	A4418	A4419	A4420	A4421	A4422	A4423	A4424	A4425	A4426	A4427	A4428	A4429	A4430	A4431	A4432	A4433	A4434	A4435	A4436	A4437	A4438	A4439	A4440	A4441	A4442	A4443	A4444	A4445	A4446	A4447	A4448	A4449	A4450	A4451	A4452	A4453	A4454	A4455	A4456	A4457	A4458	A4459	A4460	A4461	A4462	A4463	A4464	A4465	A4466	A4467	A4468	A4469	A4470	A4471	A4472	A4473	A4474	A4475	A4476	A4477	A4478	A4479	A4480	A4481	A4482	A4483	A4484	A4485	A4486	A4487	A4488	A4489	A4490	A4491	A4492	A4493	A4494	A4495	A4496	A4497	A4498	A4499	A4500	A4501	A4502	A4503	A4504	A4505	A4506	A4507	A4508	A4509	A4510	A4511	A4512	A4513	A4514	A4515	A4516	A4517	A4518	A4519	A4520	A4521	A4522	A4523	A4524	A4525	A4526	A4527	A4528	A4529	A4530	A4531	A4532	A4533	A4534	A4535	A4536	A4537	A4538	A4539	A4540	A4541	A4542	A4543	A4544	A4545	A4546	A4547	A4548	A4549	A4550	A4551	A4552	A4553	A4554	A4555	A4556	A4557	A4558	A4559	A4560	A4561	A4562	A4563	A4564	A4565	A4566	A4567	A4568	A4569	A4570	A4571	A4572	A4573	A4574	A4575	A4576	A4577	A4578	A4579	A4580	A



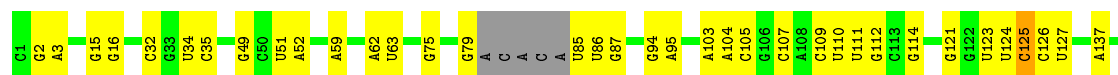
- Molecule 48: 5S ribosomal RNA

Chain 7: 86% 13% .



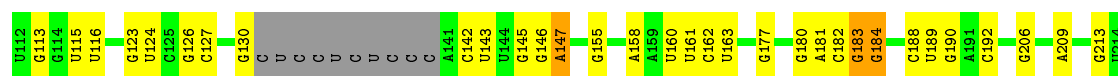
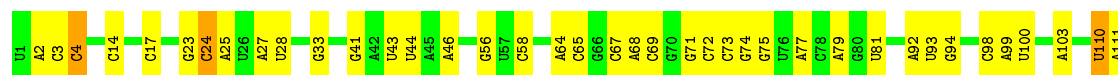
- Molecule 49: 5.8S ribosomal RNA

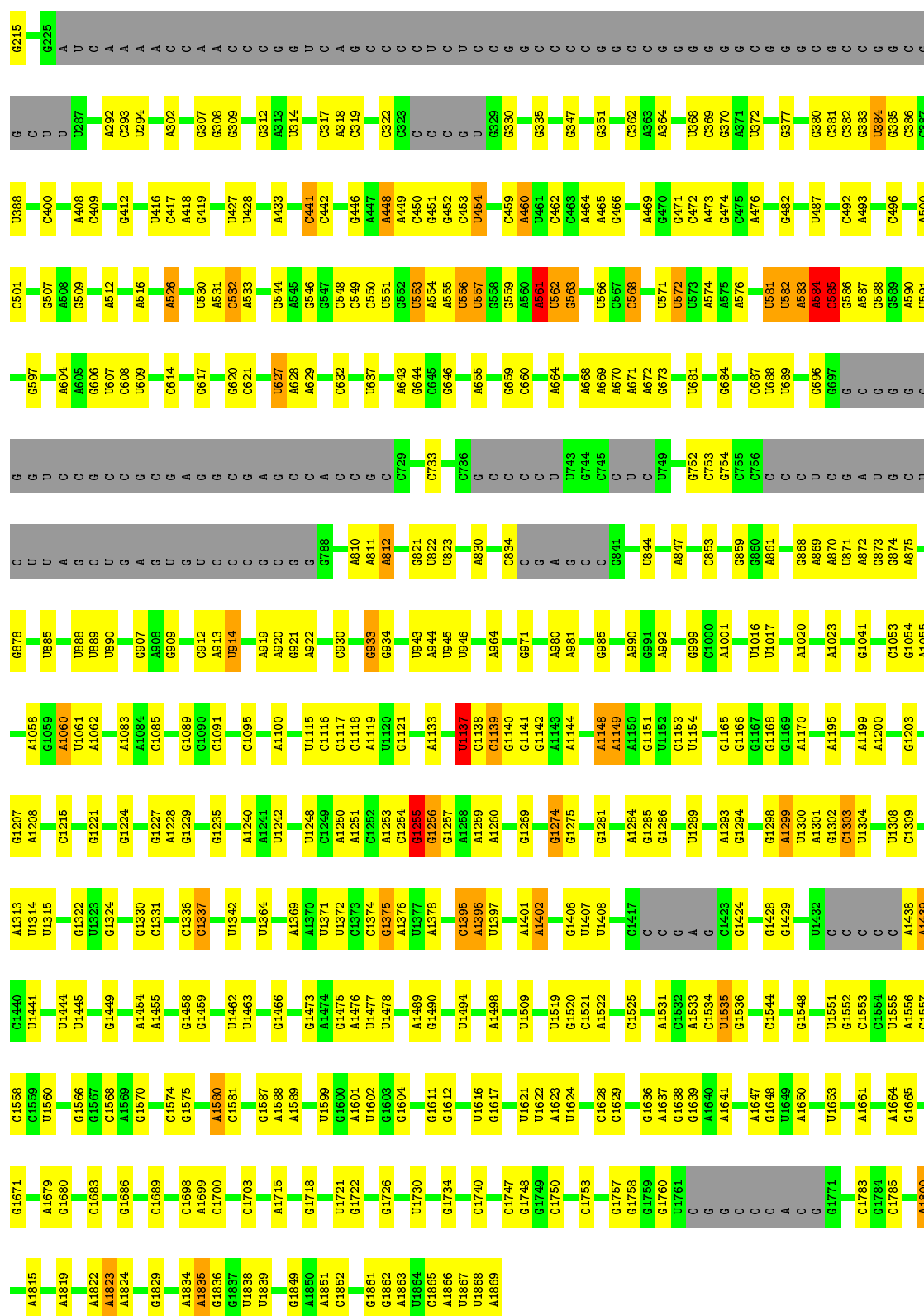
Chain 8: 73% 23% . .



- Molecule 50: 18S ribosomal RNA

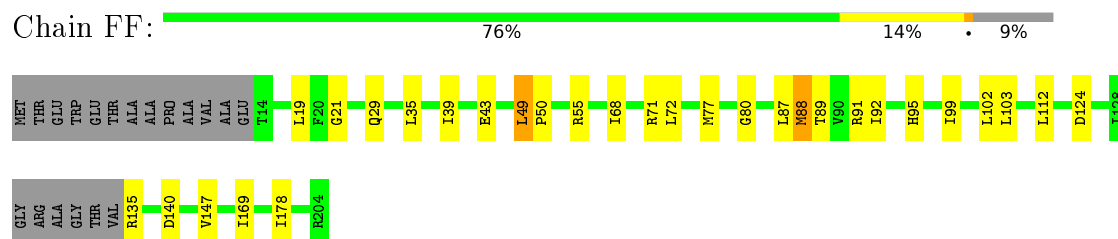
Chain 9: 63% 25% . 9%



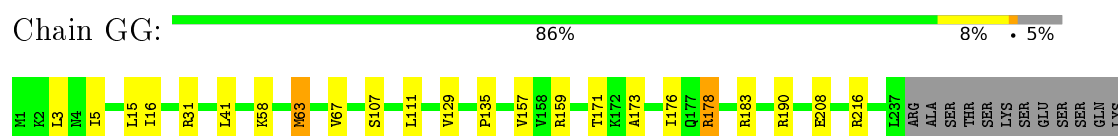




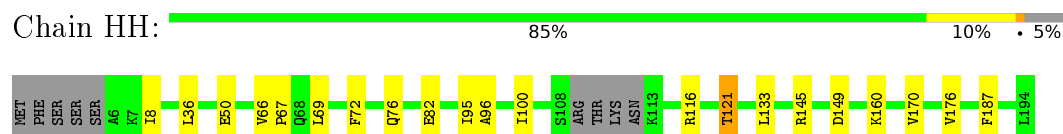
- Molecule 56: Uncharacterized protein



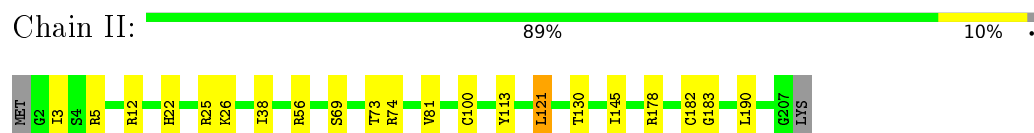
- Molecule 57: 40S ribosomal protein S6



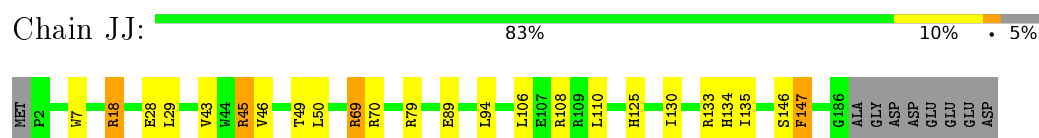
- Molecule 58: Uncharacterized protein



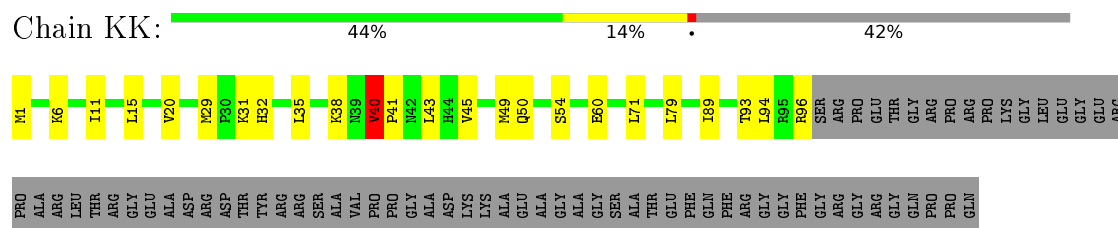
- Molecule 59: 40S ribosomal protein S8



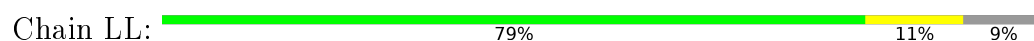
- Molecule 60: Ribosomal protein S9 (Predicted)



- Molecule 61: Uncharacterized protein



- Molecule 62: Uncharacterized protein





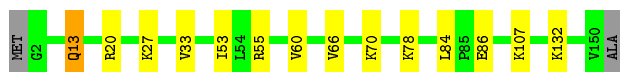
- Molecule 63: 40S ribosomal protein S12

Chain MM: 77% 12% 11%



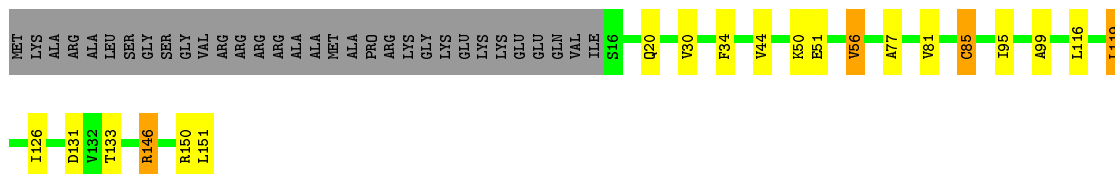
- Molecule 64: Uncharacterized protein

Chain NN: 89% 9% ..



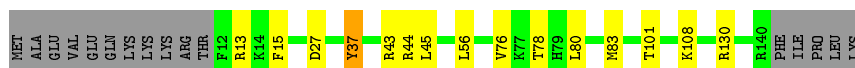
- Molecule 65: uS11, Uncharacterized protein

Chain OO: 69% 10% 19%



- Molecule 66: Uncharacterized protein

Chain PP: 79% 10% 11%



- Molecule 67: Uncharacterized protein

Chain QQ: 86% 12% .



- Molecule 68: Uncharacterized protein

Chain RR: 86% 10% ..



- Molecule 69: Uncharacterized protein

Chain SS: 82% 13% 5%



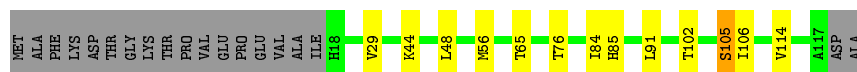
- Molecule 70: Uncharacterized protein

Chain TT: 89% 8% ..



- Molecule 71: Uncharacterized protein

Chain UU: 73% 10% 16%



- Molecule 72: eS21

Chain VV: 90% 10%



- Molecule 73: Uncharacterized protein

Chain WW: 82% 17% ..



- Molecule 74: uS12

Chain XX: 87% 10% ..



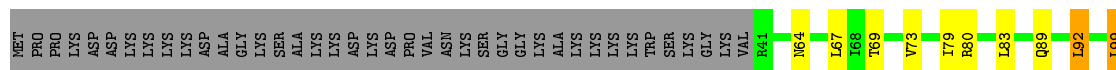
- Molecule 75: eS24

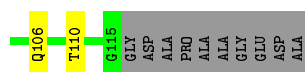
Chain YY: 84% 11% 5%



- Molecule 76: Uncharacterized protein

Chain ZZ: 50% 8% 40%





- Molecule 77: eS26

Chain aa: 82% 6% 12%



- Molecule 78: 40S ribosomal protein S27

Chain bb: 92% 6% ..



- Molecule 79: Uncharacterized protein

Chain cc: 81% 9% 10%



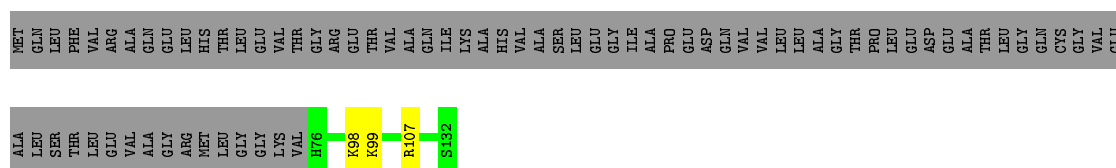
- Molecule 80: Uncharacterized protein

Chain dd: 93% 5% .



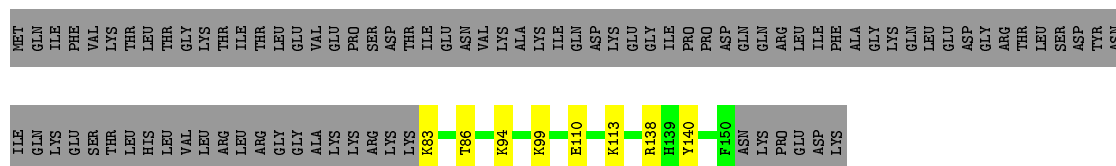
- Molecule 81: Uncharacterized protein

Chain ee: 41% . 57%



- Molecule 82: Uncharacterized protein

Chain ff: 38% 5% 56%



- Molecule 83: Uncharacterized protein

Chain gg:

96%

..



● Molecule 84: mRNA

Chain hh:

90%

10%



● Molecule 85: Elongation factor 1-alpha 1

Chain jj:

93%

5%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	40347	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	134615	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: GDP, MG, SEP, ZN, 7C4

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	0.38	0/1936	0.71	0/2596
10	J	0.33	0/1385	0.60	0/1852
11	L	0.43	0/1733	0.77	0/2316
12	M	0.43	0/1158	0.74	0/1547
13	N	0.43	0/1746	0.75	0/2338
14	O	0.47	0/1662	0.79	0/2222
15	P	0.41	0/1268	0.67	0/1700
16	Q	0.39	0/1539	0.77	0/2054
17	R	0.49	0/1524	0.82	0/2013
18	S	0.38	0/1501	0.69	0/2012
19	T	0.35	0/1326	0.62	0/1770
2	B	0.38	0/3240	0.68	0/4339
20	U	0.36	0/823	0.56	0/1104
21	V	0.38	0/1048	0.67	0/1402
22	W	0.36	0/873	0.61	0/1158
23	X	0.36	0/984	0.63	0/1323
24	Y	0.36	0/1132	0.65	0/1504
25	Z	0.38	0/1130	0.65	0/1507
26	a	0.39	0/1191	0.67	0/1590
27	b	0.40	0/861	0.67	0/1138
28	c	0.35	0/771	0.58	0/1034
29	d	0.38	0/903	0.68	0/1216
3	C	0.42	0/2937	0.73	0/3946
30	e	0.38	0/1071	0.68	0/1429
31	f	0.41	0/895	0.73	0/1198
32	g	0.35	0/916	0.72	0/1220
33	h	0.51	0/1021	0.78	0/1348
34	i	0.50	0/841	0.77	0/1112
35	j	0.42	0/720	0.76	0/952
36	k	0.41	0/575	0.65	0/761
37	l	0.46	0/459	0.72	0/608
38	m	0.40	0/435	0.66	0/575

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	n	0.59	0/240	0.94	0/305
4	D	0.39	0/2437	0.63	0/3264
40	o	0.38	0/864	0.65	0/1140
41	p	0.44	0/718	0.72	0/953
42	r	0.44	0/1010	0.76	0/1354
43	s	0.44	0/1530	0.64	0/2064
44	t	0.47	0/1174	0.68	0/1582
45	2	0.23	0/1803	0.67	0/2801
45	ii	0.21	0/1805	0.71	0/2809
46	3	0.21	0/1777	0.65	0/2763
47	5	0.33	1/84973 (0.0%)	0.70	19/132508 (0.0%)
48	7	0.26	0/2836	0.65	0/4421
49	8	0.31	0/3581	0.68	0/5577
5	E	0.35	0/1762	0.65	0/2362
50	9	0.26	0/40502	0.70	15/63100 (0.0%)
51	AA	0.33	0/1747	0.58	0/2374
52	BB	0.33	0/1756	0.60	0/2350
53	CC	0.34	0/1753	0.62	0/2369
54	DD	0.36	0/1796	0.64	0/2417
55	EE	0.34	0/2118	0.63	0/2849
56	FF	0.34	0/1492	0.61	0/2005
57	GG	0.34	0/1946	0.66	0/2590
58	HH	0.34	0/1510	0.59	0/2022
59	II	0.34	0/1715	0.64	0/2287
6	F	0.44	0/1911	0.74	1/2549 (0.0%)
60	JJ	0.36	0/1550	0.68	0/2069
61	KK	0.34	0/834	0.65	1/1125 (0.1%)
62	LL	0.35	0/1195	0.62	0/1597
63	MM	0.35	0/918	0.58	0/1233
64	NN	0.33	0/1226	0.63	0/1649
65	OO	0.35	0/1029	0.74	2/1380 (0.1%)
66	PP	0.35	0/1079	0.63	0/1441
67	QQ	0.33	0/1146	0.60	0/1534
68	RR	0.34	0/1082	0.58	0/1452
69	SS	0.35	0/1208	0.66	0/1618
7	G	0.42	0/1910	0.72	0/2569
70	TT	0.37	0/1115	0.62	1/1493 (0.1%)
71	UU	0.34	0/805	0.64	0/1081
72	VV	0.34	0/643	0.65	0/860
73	WW	0.37	0/1051	0.71	0/1406
74	XX	0.35	0/1116	0.67	0/1490
75	YY	0.36	0/1028	0.63	0/1366
76	ZZ	0.34	0/604	0.60	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
77	aa	0.37	0/828	0.70	0/1109
78	bb	0.37	0/665	0.62	0/891
79	cc	0.35	0/490	0.68	0/656
8	H	0.34	0/1535	0.63	0/2063
80	dd	0.39	0/470	0.70	0/623
81	ee	0.35	0/462	0.68	0/607
82	ff	0.36	0/567	0.56	0/753
83	gg	0.33	0/2493	0.55	0/3394
84	hh	0.25	0/233	0.69	0/360
85	jj	0.35	0/3442	0.51	0/4656
9	I	0.36	0/1702	0.61	0/2272
All	All	0.34	1/236786 (0.0%)	0.68	39/347256 (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	3
21	V	0	1
31	f	0	1
74	XX	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	5	2025	A	O3'-P	-30.56	1.24	1.61

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	5	2025	A	OP1-P-O3'	-39.69	17.89	105.20
47	5	2025	A	P-O3'-C3'	-17.17	99.09	119.70
61	KK	40	VAL	C-N-CD	-10.98	96.44	120.60
50	9	581	U	N1-C1'-C2'	-10.17	100.77	114.00
50	9	582	U	N1-C1'-C2'	-9.01	102.09	112.00

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	16	PHE	Peptide
2	B	257	TRP	Peptide
2	B	258	HIS	Peptide
21	V	6	ARG	Sidechain
31	f	106	TYR	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	28	0
2	B	3172	0	3310	20	0
3	C	2883	0	3053	15	0
4	D	2391	0	2424	13	0
5	E	1729	0	1887	10	0
6	F	1875	0	1995	17	0
7	G	1879	0	2027	18	0
8	H	1516	0	1597	9	0
9	I	1664	0	1712	17	0
10	J	1362	0	1399	5	0
11	L	1702	0	1820	9	0
12	M	1137	0	1211	6	0
13	N	1701	0	1749	15	0
14	O	1630	0	1778	20	0
15	P	1242	0	1274	10	0
16	Q	1515	0	1634	6	0
17	R	1508	0	1664	6	0
18	S	1462	0	1508	12	0
19	T	1298	0	1366	17	0
20	U	809	0	833	5	0
21	V	1034	0	1097	17	0
22	W	860	0	903	6	0
23	X	967	0	1040	4	0
24	Y	1115	0	1205	5	0
25	Z	1107	0	1182	6	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	738	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	921	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	2	1616	0	826	3	0
45	ii	1616	0	824	0	0
46	3	1593	0	811	4	0
47	5	75972	0	38391	191	0
48	7	2538	0	1286	5	0
49	8	3208	0	1629	2	0
50	9	36229	0	18306	102	0
51	AA	1710	0	1708	30	0
52	BB	1729	0	1803	7	0
53	CC	1716	0	1806	11	0
54	DD	1768	0	1866	10	0
55	EE	2076	0	2177	13	0
56	FF	1471	0	1522	13	0
57	GG	1923	0	2089	7	0
58	HH	1488	0	1582	7	0
59	II	1686	0	1772	7	0
60	JJ	1525	0	1640	12	0
61	KK	810	0	836	14	0
62	LL	1175	0	1249	1	0
63	MM	908	0	939	4	0
64	NN	1202	0	1289	4	0
65	OO	1016	0	1039	7	0
66	PP	1058	0	1104	3	0
67	QQ	1128	0	1195	7	0
68	RR	1068	0	1121	5	0
69	SS	1190	0	1249	4	0
70	TT	1097	0	1132	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	UU	795	0	862	6	0
72	VV	636	0	637	6	0
73	WW	1034	0	1080	9	0
74	XX	1098	0	1167	7	0
75	YY	1011	0	1083	5	0
76	ZZ	598	0	656	6	0
77	aa	814	0	864	0	0
78	bb	651	0	672	0	0
79	cc	488	0	514	0	0
80	dd	459	0	449	0	0
81	ee	457	0	502	0	0
82	ff	555	0	565	0	0
83	gg	2436	0	2393	0	0
84	hh	210	0	106	0	0
85	jj	3383	0	3431	0	0
86	5	185	0	0	0	0
86	7	6	0	0	0	0
86	8	5	0	0	0	0
86	9	70	0	0	0	0
86	B	1	0	0	0	0
86	I	1	0	0	0	0
86	P	1	0	0	0	0
86	Q	1	0	0	0	0
86	V	1	0	0	0	0
86	a	2	0	0	0	0
86	g	1	0	0	0	0
86	j	1	0	0	0	0
86	jj	1	0	0	0	0
87	aa	1	0	0	0	0
87	dd	1	0	0	0	0
87	ff	1	0	0	0	0
87	g	1	0	0	0	0
87	j	1	0	0	0	0
87	m	1	0	0	0	0
87	o	1	0	0	0	0
87	p	1	0	0	0	0
88	jj	28	0	12	0	0
89	jj	79	0	0	0	0
All	All	220934	0	164939	707	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 707 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)
47:5:1962:A:H2	47:5:2026:A:N3	1.15	1.38
47:5:3914:U:O4	47:5:4378:A:N1	1.62	1.32
47:5:1962:A:C2	47:5:2026:A:N3	1.97	1.32
47:5:1979:A:C2	47:5:1980:U:O2	1.84	1.28
47:5:1962:A:N1	47:5:2026:A:H1'	1.48	1.26

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%)	225 (92%)	19 (8%)	2 (1%)	24	63
2	B	392/403 (97%)	364 (93%)	25 (6%)	3 (1%)	24	63
3	C	360/425 (85%)	337 (94%)	21 (6%)	2 (1%)	30	69
4	D	291/297 (98%)	275 (94%)	14 (5%)	2 (1%)	26	66
5	E	208/291 (72%)	189 (91%)	18 (9%)	1 (0%)	34	72
6	F	223/247 (90%)	211 (95%)	11 (5%)	1 (0%)	39	76
7	G	229/319 (72%)	217 (95%)	12 (5%)	0	100	100
8	H	188/192 (98%)	173 (92%)	15 (8%)	0	100	100
9	I	201/214 (94%)	185 (92%)	16 (8%)	0	100	100
10	J	168/178 (94%)	158 (94%)	10 (6%)	0	100	100
11	L	208/211 (99%)	198 (95%)	10 (5%)	0	100	100
12	M	136/218 (62%)	126 (93%)	10 (7%)	0	100	100
13	N	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
14	O	197/203 (97%)	189 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	P	151/184 (82%)	145 (96%)	6 (4%)	0	100	100
16	Q	185/188 (98%)	175 (95%)	9 (5%)	1 (0%)	34	72
17	R	178/196 (91%)	172 (97%)	6 (3%)	0	100	100
18	S	174/176 (99%)	160 (92%)	12 (7%)	2 (1%)	17	57
19	T	157/160 (98%)	146 (93%)	10 (6%)	1 (1%)	30	69
20	U	97/128 (76%)	86 (89%)	11 (11%)	0	100	100
21	V	137/140 (98%)	125 (91%)	12 (9%)	0	100	100
22	W	102/157 (65%)	98 (96%)	3 (3%)	1 (1%)	19	59
23	X	116/156 (74%)	113 (97%)	3 (3%)	0	100	100
24	Y	132/145 (91%)	125 (95%)	7 (5%)	0	100	100
25	Z	133/136 (98%)	126 (95%)	5 (4%)	2 (2%)	13	49
26	a	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
27	b	100/245 (41%)	93 (93%)	6 (6%)	1 (1%)	19	59
28	c	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
29	d	105/125 (84%)	94 (90%)	10 (10%)	1 (1%)	19	59
30	e	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
31	f	107/110 (97%)	101 (94%)	4 (4%)	2 (2%)	10	45
32	g	112/116 (97%)	106 (95%)	6 (5%)	0	100	100
33	h	120/123 (98%)	118 (98%)	1 (1%)	1 (1%)	24	63
34	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
35	j	84/97 (87%)	78 (93%)	6 (7%)	0	100	100
36	k	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
37	l	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
38	m	50/102 (49%)	47 (94%)	3 (6%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	99 (97%)	3 (3%)	0	100	100
41	p	89/92 (97%)	80 (90%)	8 (9%)	1 (1%)	17	57
42	r	122/137 (89%)	110 (90%)	11 (9%)	1 (1%)	24	63
43	s	194/318 (61%)	171 (88%)	22 (11%)	1 (0%)	34	72
44	t	151/165 (92%)	134 (89%)	13 (9%)	4 (3%)	7	37
51	AA	215/295 (73%)	204 (95%)	10 (5%)	1 (0%)	34	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	BB	211/264 (80%)	199 (94%)	11 (5%)	1 (0%)	34	72
53	CC	219/293 (75%)	205 (94%)	13 (6%)	1 (0%)	34	72
54	DD	226/243 (93%)	214 (95%)	9 (4%)	3 (1%)	15	53
55	EE	260/263 (99%)	246 (95%)	14 (5%)	0	100	100
56	FF	181/204 (89%)	166 (92%)	11 (6%)	4 (2%)	8	41
57	GG	235/249 (94%)	224 (95%)	10 (4%)	1 (0%)	39	76
58	HH	181/194 (93%)	171 (94%)	10 (6%)	0	100	100
59	II	204/208 (98%)	192 (94%)	11 (5%)	1 (0%)	34	72
60	JJ	183/194 (94%)	177 (97%)	5 (3%)	1 (0%)	34	72
61	KK	94/165 (57%)	88 (94%)	5 (5%)	1 (1%)	17	57
62	LL	139/158 (88%)	129 (93%)	10 (7%)	0	100	100
63	MM	115/132 (87%)	103 (90%)	12 (10%)	0	100	100
64	NN	147/151 (97%)	141 (96%)	6 (4%)	0	100	100
65	OO	134/168 (80%)	122 (91%)	10 (8%)	2 (2%)	13	49
66	PP	127/145 (88%)	117 (92%)	9 (7%)	1 (1%)	24	63
67	QQ	140/146 (96%)	130 (93%)	10 (7%)	0	100	100
68	RR	130/135 (96%)	118 (91%)	11 (8%)	1 (1%)	24	63
69	SS	142/152 (93%)	134 (94%)	8 (6%)	0	100	100
70	TT	139/145 (96%)	132 (95%)	7 (5%)	0	100	100
71	UU	98/119 (82%)	89 (91%)	9 (9%)	0	100	100
72	VV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
73	WW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
74	XX	139/143 (97%)	129 (93%)	8 (6%)	2 (1%)	14	50
75	YY	122/130 (94%)	116 (95%)	5 (4%)	1 (1%)	24	63
76	ZZ	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
77	aa	99/115 (86%)	90 (91%)	8 (8%)	1 (1%)	19	59
78	bb	81/84 (96%)	75 (93%)	5 (6%)	1 (1%)	16	54
79	cc	60/69 (87%)	59 (98%)	1 (2%)	0	100	100
80	dd	53/56 (95%)	49 (92%)	3 (6%)	1 (2%)	10	45
81	ee	55/133 (41%)	52 (94%)	3 (6%)	0	100	100
82	ff	66/156 (42%)	61 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
83	gg	311/317 (98%)	282 (91%)	28 (9%)	1 (0%)	46	81
85	jj	438/462 (95%)	419 (96%)	18 (4%)	1 (0%)	52	85
All	All	11976/13836 (87%)	11207 (94%)	713 (6%)	56 (0%)	38	72

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
44	t	120	SER
44	t	125	LEU
74	XX	62	PRO
74	XX	86	PRO
3	C	83	GLY

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%)	176 (93%)	14 (7%)	17	52
2	B	342/348 (98%)	324 (95%)	18 (5%)	28	66
3	C	302/347 (87%)	281 (93%)	21 (7%)	19	56
4	D	247/250 (99%)	234 (95%)	13 (5%)	28	66
5	E	190/251 (76%)	180 (95%)	10 (5%)	28	66
6	F	196/215 (91%)	184 (94%)	12 (6%)	23	61
7	G	200/272 (74%)	189 (94%)	11 (6%)	27	65
8	H	169/171 (99%)	156 (92%)	13 (8%)	16	51
9	I	175/181 (97%)	161 (92%)	14 (8%)	15	49
10	J	143/149 (96%)	137 (96%)	6 (4%)	36	73
11	L	175/176 (99%)	166 (95%)	9 (5%)	29	67
12	M	117/161 (73%)	108 (92%)	9 (8%)	16	51
13	N	171/172 (99%)	161 (94%)	10 (6%)	25	63
14	O	171/173 (99%)	159 (93%)	12 (7%)	19	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	P	134/163 (82%)	125 (93%)	9 (7%)	20	58
16	Q	164/165 (99%)	151 (92%)	13 (8%)	15	49
17	R	159/175 (91%)	145 (91%)	14 (9%)	12	43
18	S	157/157 (100%)	147 (94%)	10 (6%)	22	59
19	T	139/140 (99%)	130 (94%)	9 (6%)	21	59
20	U	89/114 (78%)	87 (98%)	2 (2%)	60	84
21	V	106/107 (99%)	92 (87%)	14 (13%)	5	22
22	W	86/126 (68%)	85 (99%)	1 (1%)	78	90
23	X	106/134 (79%)	99 (93%)	7 (7%)	21	58
24	Y	124/135 (92%)	118 (95%)	6 (5%)	31	69
25	Z	117/118 (99%)	115 (98%)	2 (2%)	68	86
26	a	119/120 (99%)	114 (96%)	5 (4%)	36	73
27	b	84/184 (46%)	81 (96%)	3 (4%)	42	76
28	c	84/98 (86%)	80 (95%)	4 (5%)	31	69
29	d	98/110 (89%)	88 (90%)	10 (10%)	9	35
30	e	114/121 (94%)	105 (92%)	9 (8%)	15	49
31	f	88/89 (99%)	82 (93%)	6 (7%)	20	57
32	g	98/99 (99%)	92 (94%)	6 (6%)	23	61
33	h	109/110 (99%)	105 (96%)	4 (4%)	41	75
34	i	86/89 (97%)	82 (95%)	4 (5%)	32	70
35	j	73/80 (91%)	67 (92%)	6 (8%)	14	48
36	k	64/65 (98%)	62 (97%)	2 (3%)	47	79
37	l	47/48 (98%)	46 (98%)	1 (2%)	61	84
38	m	48/90 (53%)	46 (96%)	2 (4%)	36	73
39	n	24/24 (100%)	21 (88%)	3 (12%)	6	24
40	o	92/94 (98%)	88 (96%)	4 (4%)	35	72
41	p	74/75 (99%)	71 (96%)	3 (4%)	37	73
42	r	108/121 (89%)	100 (93%)	8 (7%)	17	52
43	s	164/258 (64%)	154 (94%)	10 (6%)	23	61
44	t	126/137 (92%)	122 (97%)	4 (3%)	46	79
51	AA	180/245 (74%)	167 (93%)	13 (7%)	18	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	BB	194/231 (84%)	173 (89%)	21 (11%)	8	32
53	CC	187/225 (83%)	175 (94%)	12 (6%)	22	59
54	DD	190/202 (94%)	175 (92%)	15 (8%)	15	49
55	EE	224/225 (100%)	205 (92%)	19 (8%)	13	46
56	FF	158/170 (93%)	146 (92%)	12 (8%)	16	51
57	GG	207/218 (95%)	195 (94%)	12 (6%)	25	63
58	HH	165/174 (95%)	154 (93%)	11 (7%)	20	58
59	II	178/180 (99%)	167 (94%)	11 (6%)	23	60
60	JJ	161/168 (96%)	149 (92%)	12 (8%)	17	52
61	KK	87/136 (64%)	78 (90%)	9 (10%)	9	34
62	LL	130/142 (92%)	114 (88%)	16 (12%)	6	25
63	MM	99/108 (92%)	87 (88%)	12 (12%)	6	26
64	NN	130/131 (99%)	118 (91%)	12 (9%)	11	40
65	OO	106/130 (82%)	96 (91%)	10 (9%)	11	39
66	PP	115/130 (88%)	104 (90%)	11 (10%)	10	38
67	QQ	117/121 (97%)	108 (92%)	9 (8%)	16	51
68	RR	119/121 (98%)	109 (92%)	10 (8%)	14	46
69	SS	125/132 (95%)	112 (90%)	13 (10%)	9	33
70	TT	111/115 (96%)	101 (91%)	10 (9%)	12	42
71	UU	92/107 (86%)	87 (95%)	5 (5%)	27	66
72	VV	67/67 (100%)	63 (94%)	4 (6%)	24	62
73	WW	112/113 (99%)	104 (93%)	8 (7%)	18	55
74	XX	113/115 (98%)	110 (97%)	3 (3%)	52	81
75	YY	107/112 (96%)	98 (92%)	9 (8%)	14	46
76	ZZ	66/103 (64%)	59 (89%)	7 (11%)	8	32
77	aa	88/98 (90%)	82 (93%)	6 (7%)	20	57
78	bb	75/76 (99%)	69 (92%)	6 (8%)	15	49
79	cc	55/62 (89%)	49 (89%)	6 (11%)	8	31
80	dd	48/49 (98%)	46 (96%)	2 (4%)	36	73
81	ee	47/106 (44%)	44 (94%)	3 (6%)	22	59
82	ff	61/140 (44%)	53 (87%)	8 (13%)	5	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
83	gg	272/275 (99%)	264 (97%)	8 (3%)	50 80
85	jj	365/378 (97%)	353 (97%)	12 (3%)	45 78
All	All	10420/11716 (89%)	9730 (93%)	690 (7%)	25 58

5 of 690 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	j	20	ARG
52	BB	231	LEU
76	ZZ	99	LEU
39	n	1	MET
44	t	98	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
19	T	144	ASN
83	gg	14	HIS
85	jj	343	GLN
85	jj	367	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	2	73/76 (96%)	14 (19%)	1 (1%)
45	ii	74/76 (97%)	20 (27%)	0
46	3	72/75 (96%)	28 (38%)	2 (2%)
47	5	3514/3543 (99%)	869 (24%)	171 (4%)
48	7	118/120 (98%)	12 (10%)	1 (0%)
49	8	150/156 (96%)	34 (22%)	7 (4%)
50	9	1678/1869 (89%)	420 (25%)	65 (3%)
84	hh	9/10 (90%)	1 (11%)	0
All	All	5688/5925 (96%)	1398 (24%)	247 (4%)

5 of 1398 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	2	9	A
45	2	13	U

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Mol	Chain	Res	Type
45	2	16	C
45	2	19	G
45	2	21	A

5 of 247 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	5	2370	A
47	5	3809	G
50	9	1313	A
47	5	2467	U
47	5	2587	A

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

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	$\# Z > 2$
85	SEP	jj	163	85	7,9,10	0.69	0	8,12,14	1.54	1 (12%)

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
85	SEP	jj	163	85	-	0/5/8/10	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	jj	163	SEP	OG-CB-CA	2.63	110.55	108.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 286 ligands modelled in this entry, 284 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
88	GDP	jj	501	86	24,30,30	1.22	2 (8%)	26,47,47	1.90	5 (19%)
89	7C4	jj	503	-	80,82,82	1.02	5 (6%)	109,117,117	1.21	14 (12%)

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
88	GDP	jj	501	86	-	0/12/32/32	0/3/3/3
89	7C4	jj	503	-	-	0/120/140/140	0/3/4/4

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	jj	503	7C4	C72-C71	-4.47	1.32	1.51
89	jj	503	7C4	C54-C55	-2.95	1.50	1.53
89	jj	503	7C4	C45-C47	2.12	1.55	1.53
89	jj	503	7C4	C53-C54	2.18	1.56	1.53
89	jj	503	7C4	C48-C47	2.44	1.54	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	jj	501	GDP	C5-C6-N1	-3.93	118.39	123.52
88	jj	501	GDP	N3-C2-N1	-3.71	122.51	127.56
88	jj	501	GDP	C6-C5-C4	-3.54	116.81	120.86
89	jj	503	7C4	C36-N05-C30	-3.19	107.19	112.00
89	jj	503	7C4	C73-N20-C70	-2.83	107.73	112.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
47	5	31
50	9	7
45	2	3
46	3	2
45	ii	1

The worst 5 of 44 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	41.26
1	5	1252:C	O3'	1271:G	P	36.28

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1219:G	O3'	1233:G	P	22.71
1	5	3948:C	O3'	4065:G	P	19.70
1	5	1406(C):G	O3'	1411:C	P	18.70