



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Nov 17, 2019 – 07:55 PM EST

PDB ID : 6T59
EMDB ID: : EMD-10380
Title : Structure of rabbit 80S ribosome translating beta-tubulin in complex with tetratricopeptide protein 5 and nascent chain-associated complex
Authors : Lin, Z.; Gasic, I.; Chandrasekaran, V.; Peters, N.; Shao, S.; Ramakrishnan, V.; Mitchison, T.J.; Hegde, R.S.
Deposited on : 2019-10-15
Resolution : 3.11 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

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

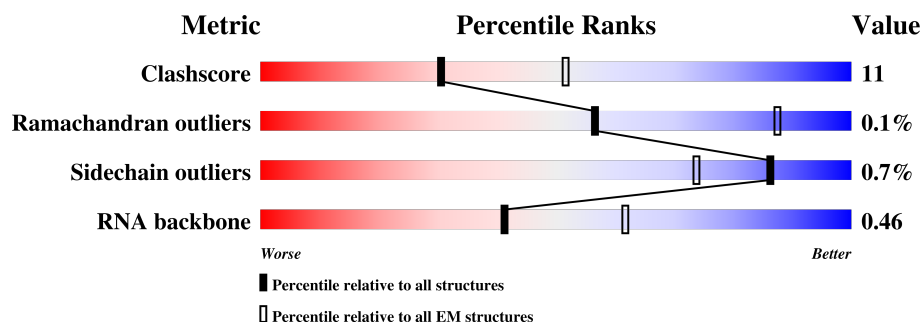
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.11 Å.

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
















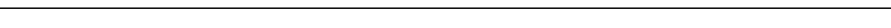




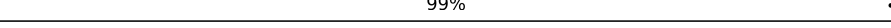



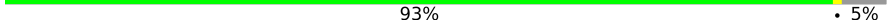
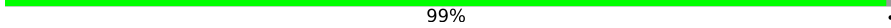
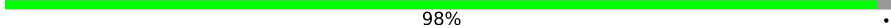
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 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	A3	257	69% 28% .
2	B3	403	69% 29% .
3	C3	425	63% 22% 15%
4	D3	297	75% 23% .
5	E3	291	53% 21% 26%
6	F3	247	68% 23% 9%
7	G3	319	54% 19% 27%
8	H3	192	68% 31% .

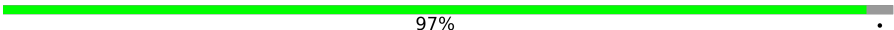

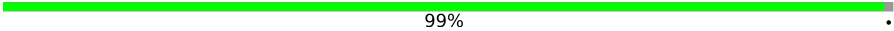
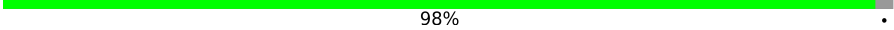

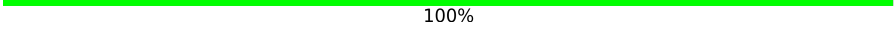
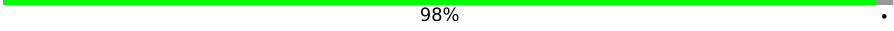
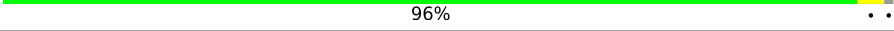



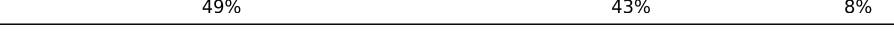

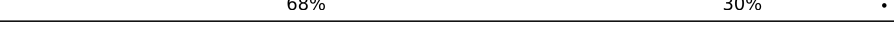






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Mol	Chain	Length	Quality of chain
9	I3	214	
10	J3	178	
11	L3	211	
12	M3	218	
13	N3	204	
14	O3	203	
15	P3	184	
16	Q3	188	
17	R3	196	
18	S3	176	
19	T3	160	
20	U3	128	
21	V3	140	
22	W3	157	
23	X3	156	
24	Y3	145	
25	Z3	136	
26	a3	148	
27	b3	226	
28	c3	115	
29	d3	125	
30	e3	135	
31	f3	110	
32	g3	116	
33	h3	123	

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Mol	Chain	Length	Quality of chain
34	i3	105	 97% .
35	j3	97	 86% . 11%
36	k3	70	 99% .
37	l3	51	 98% .
38	m3	102	 51% 49%
39	n3	25	 100%
40	o3	106	 98% .
41	p3	92	 96% . .
42	r3	137	 91% 9%
43	s3	318	 61% . 38%
44	t3	165	 91% . 7%
45	23	76	 49% 43% 8%
46	54	3543	 55% 34% 11%
47	74	120	 68% 30% .
48	84	156	 60% 26% 11% .
49	NI	29	 90% 10%
50	NA	215	 13% 12% 75%
51	NB	206	 15% 14% 72%
52	TT	440	 53% 43% .
53	1	64	 33% 16% 8% 44%

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 143047 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 Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A3	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	B3	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
B3	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C3	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	D3	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
D3	1	MET	-	initiating methionine	UNP G1SYJ6

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E3	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	F3	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
F3	61	ARG	GLY	conflict	UNP G1TUB1
F3	93	ARG	GLY	conflict	UNP G1TUB1
F3	131	MET	VAL	conflict	UNP G1TUB1
F3	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G3	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H3	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I3	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J3	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	L3	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 12 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M3	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	N3	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	O3	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	P3	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	Q3	187	Total	C	N	O	S	0	0
			1514	946	315	249	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R3	155	Total	C	N	O	S	0	0
			1294	808	278	199	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S3	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	T3	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	U3	102	Total	C	N	O	S	0	0
			834	534	146	152	2		

- Molecule 21 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V3	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	W3	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X3	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y3	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	Z3	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	a3	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
a3	1	MET	-	initiating methionine	UNP G1SNY0

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b3	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	c3	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	d3	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	e3	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	f3	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	g3	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	h3	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	i3	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	j3	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	k3	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k3	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l3	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	m3	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	n3	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	o3	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	p3	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	r3	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	s3	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t3	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	23	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 46 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	54	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 47 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	74	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 48 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	84	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 49 is a protein called Nascent polypeptide-associated complex subunit alpha N-terminal region.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	NI	29	Total	C	N	O	0	0
			150	92	29	29		

- Molecule 50 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	NA	54	Total	C	N	O	S	0	0
			420	270	71	78	1		

- Molecule 51 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	NB	58	Total	C	N	O	S	0	0
			444	278	76	88	2		

- Molecule 52 is a protein called Tetratricopeptide repeat protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	TT	426	Total	C	N	O	S	0	0
			3337	2097	580	647	13		

- Molecule 53 is a protein called Tubulin Beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	36	Total	C	N	O	S	0	0
			292	184	51	55	2		

- Molecule 54 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	g3	1	Total	Mg	0
			1	1	
54	54	201	Total	Mg	0
			201	201	
54	84	6	Total	Mg	0
			6	6	
54	P3	2	Total	Mg	0
			2	2	
54	74	7	Total	Mg	0
			7	7	
54	j3	1	Total	Mg	0
			1	1	
54	V3	1	Total	Mg	0
			1	1	
54	a3	1	Total	Mg	0
			1	1	

- Molecule 55 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	p3	1	Total	Zn	0
			1	1	
55	m3	1	Total	Zn	0
			1	1	

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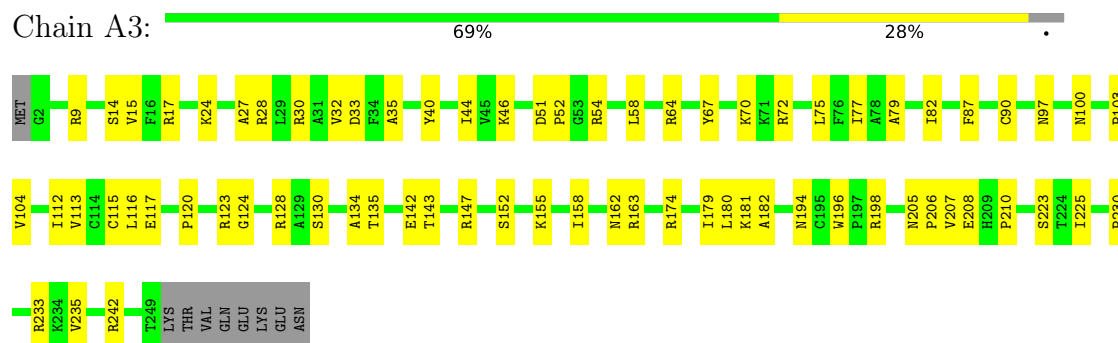
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Mol	Chain	Residues	Atoms		AltConf
55	o3	1	Total 1	Zn 1	0
55	j3	1	Total 1	Zn 1	0
55	g3	1	Total 1	Zn 1	0

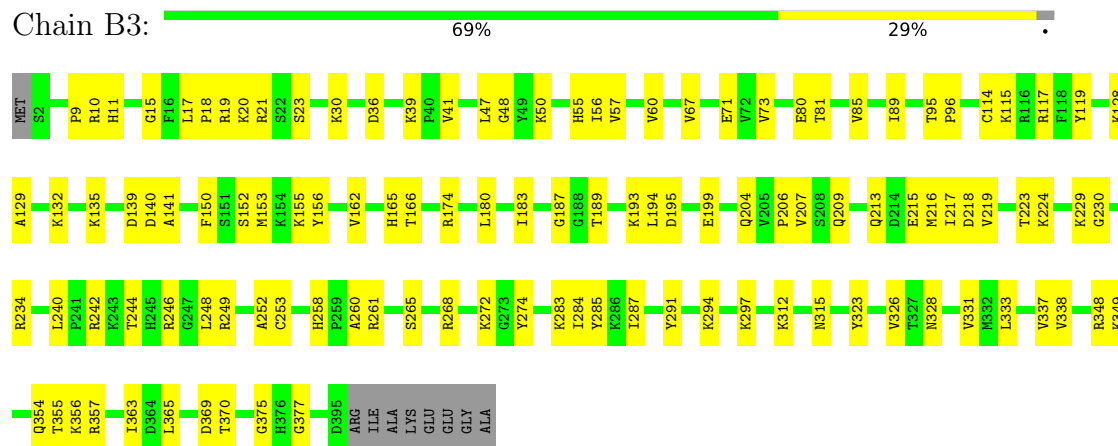
3 Residue-property plots

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

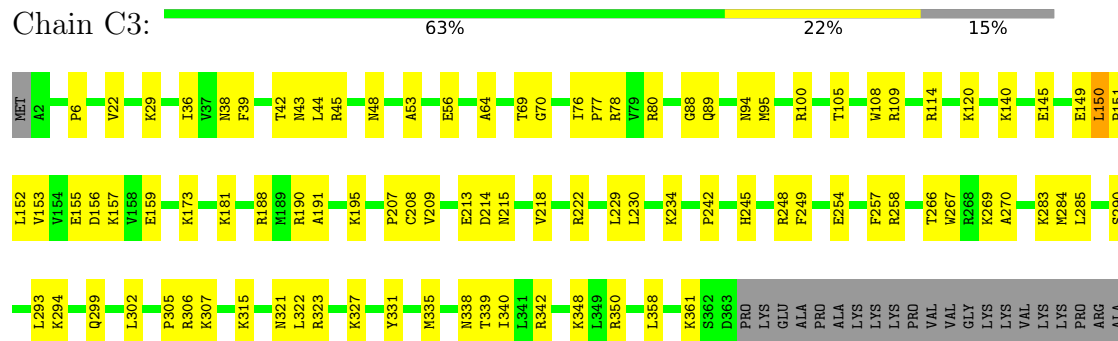
• Molecule 1: Ribosomal protein L8



• Molecule 2: uL3




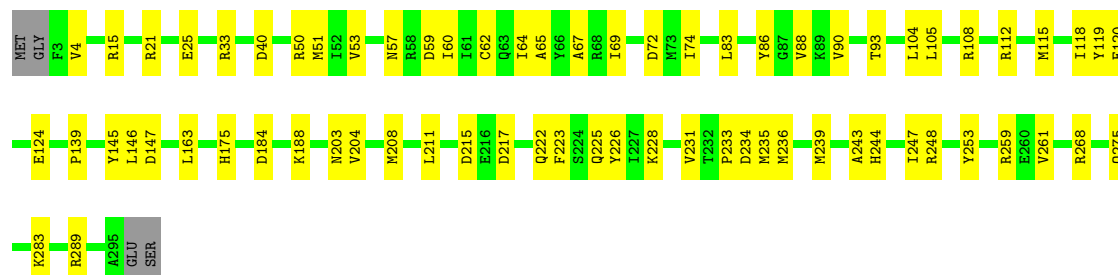
• Molecule 3: uL4



VAL
GLY
ILE
LYS
GLN
LYS
LYS
LYS
PRO
VAL
VAL
VAL
GLY
ARG
LYS
LYS
ALA
ALA
ALA
ALA
ALA
LYS
LYS
PRO
ALA
ALA
ALA
ASP
LYS
LYS
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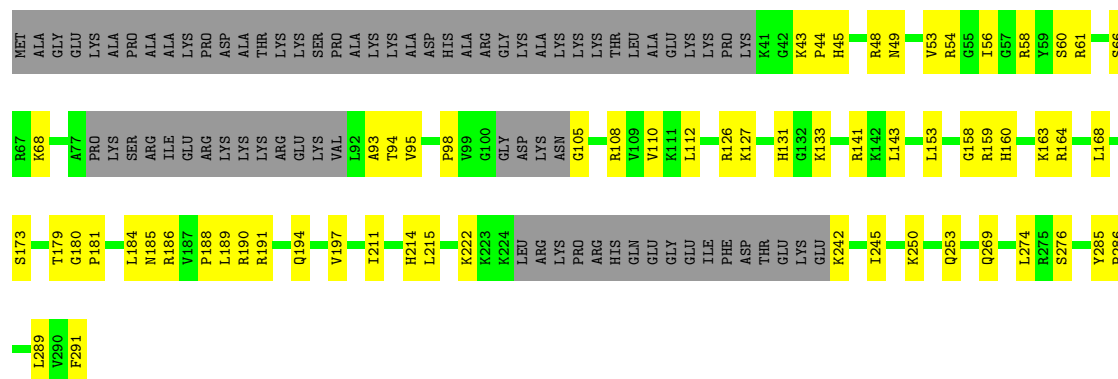
• Molecule 4: 60S ribosomal protein L5

Chain D3:  75% 23%



• Molecule 5: 60S ribosomal protein L6

Chain E3:  53% 21% 26%



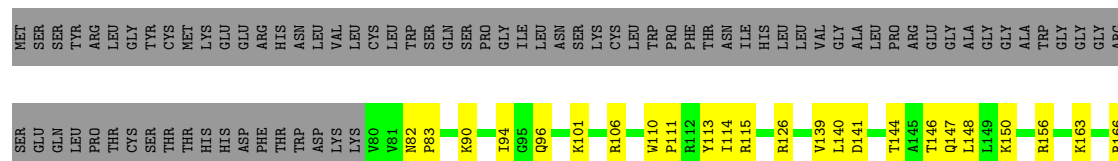
• Molecule 6: UI30

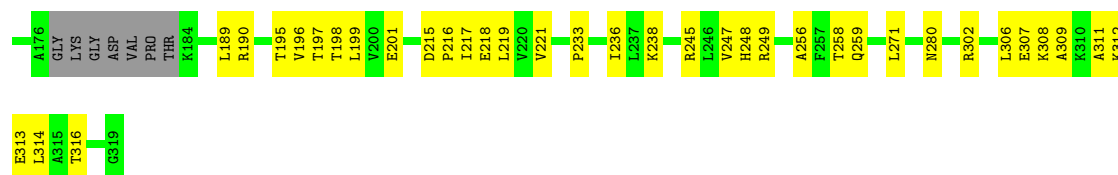
Chain F3:  68% 23% 9%



• Molecule 7: eL8

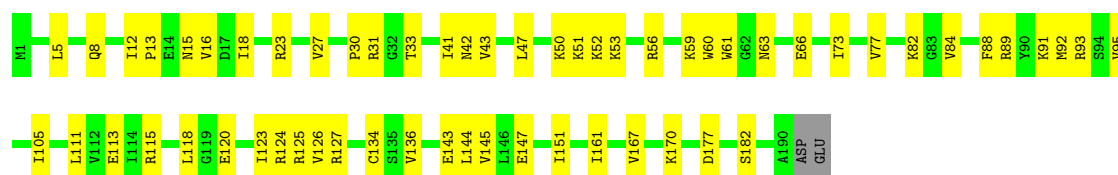
Chain G3:  54% 19% 27%





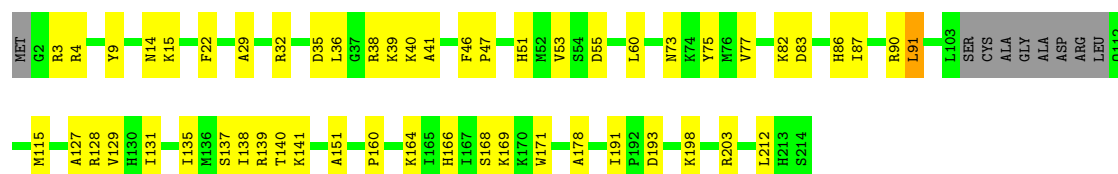
• Molecule 8: uL6

Chain H3: .



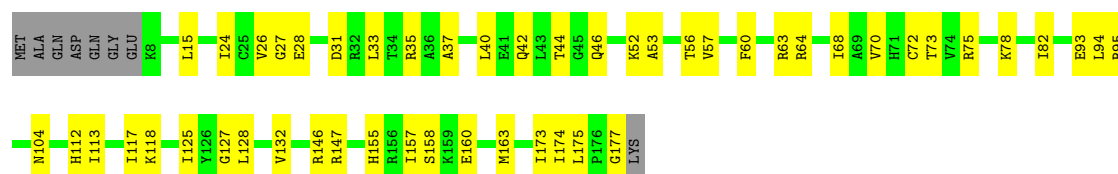
• Molecule 9: 60S ribosomal protein L10

Chain I3: .



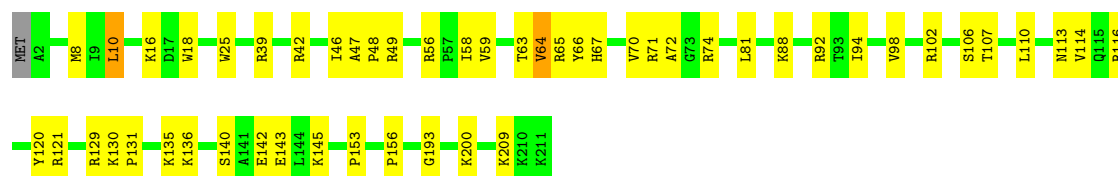
• Molecule 10: Ribosomal protein L11

Chain J3: .



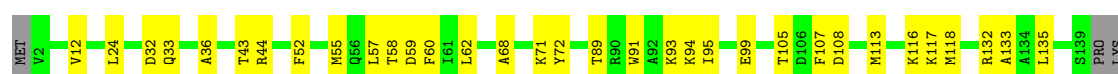
• Molecule 11: eL13

Chain L3: .



• Molecule 12: Ribosomal protein L14

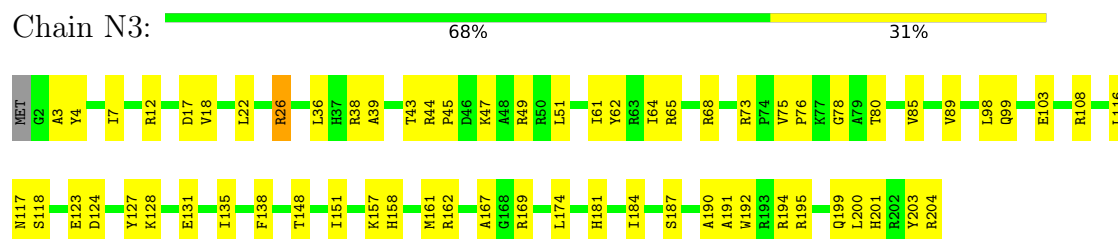
Chain M3: .



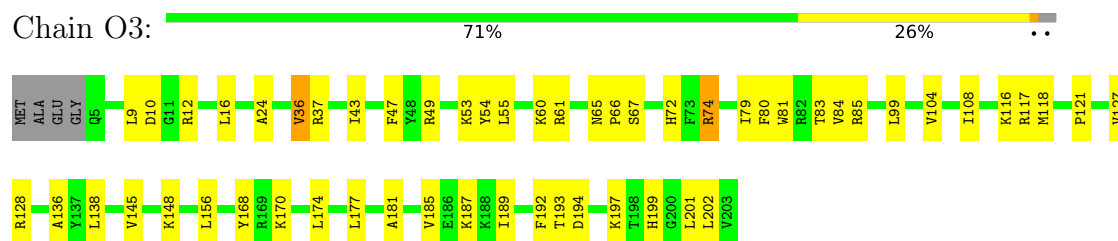
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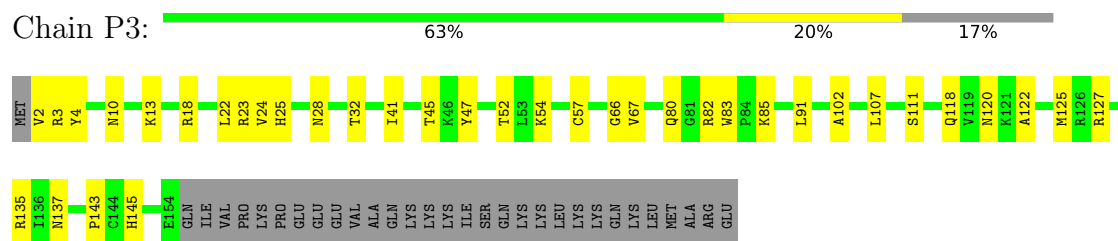
• Molecule 13: Ribosomal protein L15



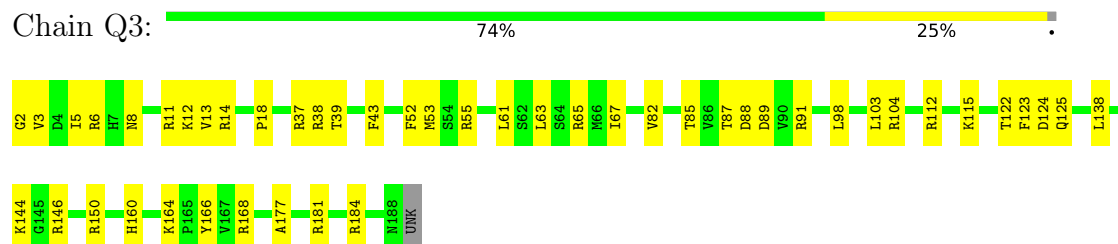
• Molecule 14: uL13



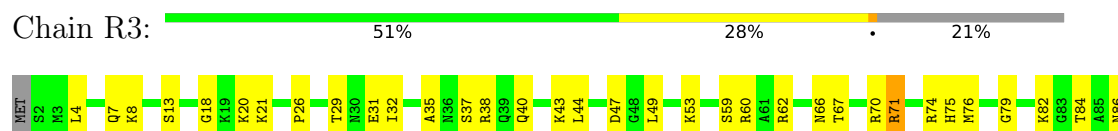
• Molecule 15: uL22

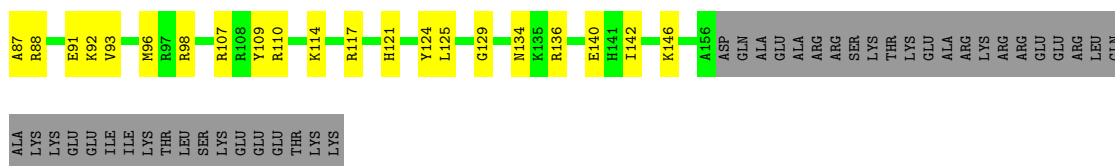


• Molecule 16: eL18



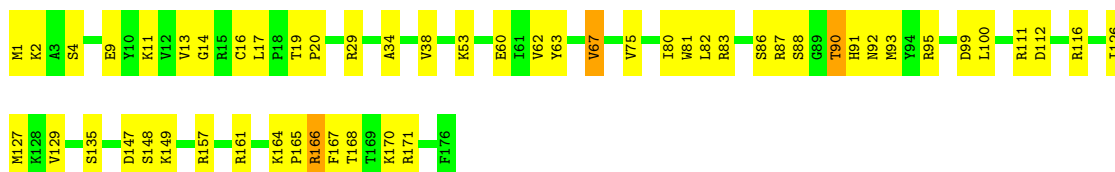
• Molecule 17: eL19





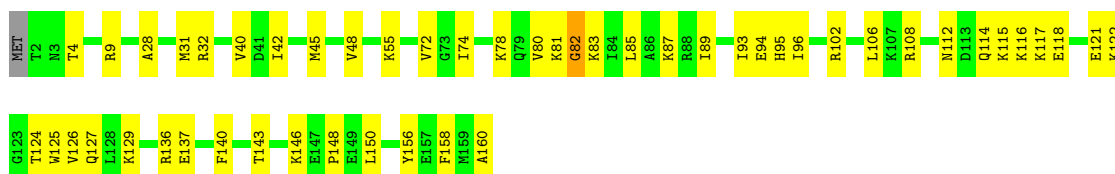
• Molecule 18: eL20

Chain S3: 70% 28% .



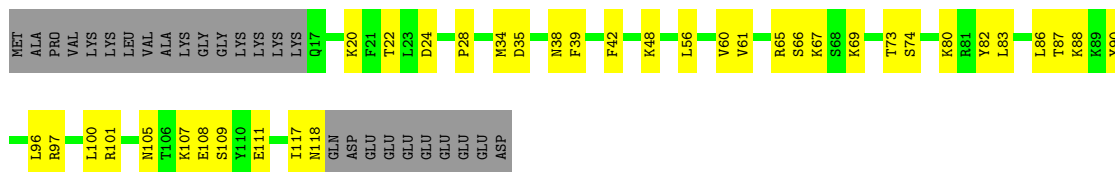
• Molecule 19: eL21

Chain T3: 68% 31% ..



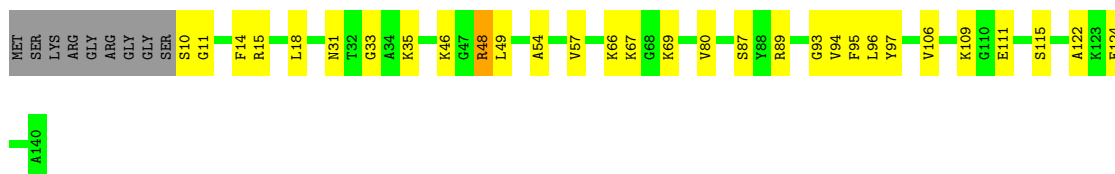
• Molecule 20: eL22

Chain U3: 51% 29% 20%



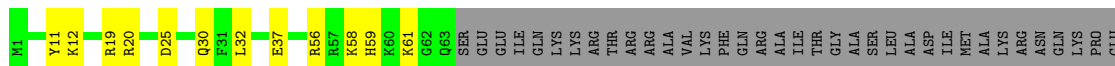
• Molecule 21: Ribosomal protein L23

Chain V3: 72% 21% 6%



• Molecule 22: eL24

Chain W3: 32% 8% 60%



VAL	ARG	LYS	ALA	GLN	ARG	GLU	GLN	ALA	ILE	ARG	ALA	ALA	LYS	GLU	ALA	LYS	GLN	ALA	LYS	SER	LYS	THR	ALA	MET	ALA	ALA	ALA	LYS	ALA	ALA	ALA	PRO	THR	LYS	LYS	GLN	LYS	ILE	VAL	LYS	VAL	PRO	ALA	ALA	ARG	VAL	GLY	LYS
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- Molecule 23: uL23

Chain X3: 

MET	ALA	PRO	PRO	LYS	ALA	LYS	GLU	ALA	PRO	ALA	PRO	PRO	VAL	GLU	LYS	ALA	LYS	ALA	LYS	ALA	LYS	LEU	LYS	ALA	LYS	LYS	VAL	VAL	LYS	GLY	VAL	HIS	SER	HIS	LYS	LYS	T81	T82	T83		I90	N93	J94	T95	L96
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	-----	-----	-----	-----	-----

D101	V102	H107	K110	Q111	K114	K115	I119	D120	R139	L140	A141	P142	D143	Y144	D145	A146	L147	D148	V149	A150	I155	I156
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- Molecule 24: Ribosomal protein L26

Chain Y3: 60% 32% 8%

M1	K2	V7	T8	S9	D10	R11	S12	K13	M14	R15	F19	H24	I25	R26	R27	R45	K51	D52	V55	Q56	V57	Q66	I67	V71	Y74	K77	V78	V79	I80	Y81	I82	R83	R84	V85	Q86	R87	S88	K89	A90	N91	G92	T93	P101	S102	K103	V104	V105	T106																																																																																																																																																																																																																																																																																																																																																																																																																																		
L109	K110	D114	R115	K116	K117	I118	L119	E120	R121	R126	K130	K134	T135	L136	G137	G138	T139	I140	L141	L142	L143	L144	L145	L146	L147	L148	L149	L150	L151	L152	L153	L154	L155	L156	L157	L158	L159	L160	L161	L162	L163	L164	L165	L166	L167	L168	L169	L170	L171	L172	L173	L174	L175	L176	L177	L178	L179	L180	L181	L182	L183	L184	L185	L186	L187	L188	L189	L190	L191	L192	L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L

- Molecule 25: 60S ribosomal protein L27

Chain Z3: 69% 29% .

- Molecule 26: uL15

Chain a3: 99%

MET P2 V122 A148


- Molecule 27: eL29

Chain b3: 46% 54%

[illegible][illegible]


PRO
LYS
ALA
GLN
ALA
THR
PRO
ALA

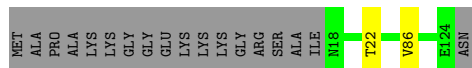
- Molecule 28: eL30

Chain c3:  84% 15%



- Molecule 29: eL31

Chain d3:  84% 14%



- Molecule 30: eL32

Chain e3:  93% 5%



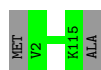
- Molecule 31: eL33

Chain f3:  99%



- Molecule 32: eL34

Chain g3:  98%



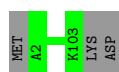
- Molecule 33: uL29

Chain h3:  99%




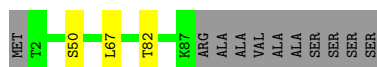
- Molecule 34: 60S ribosomal protein L36

Chain i3:  97%



- Molecule 35: Ribosomal protein L37

Chain j3:  86% 11%



- Molecule 36: eL38

Chain k3: 99%



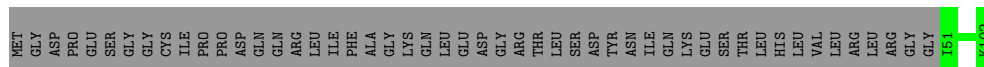
- Molecule 37: eL39

Chain l3: 98%



- Molecule 38: eL40

Chain m3: 51% 49%



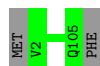
- Molecule 39: 60s ribosomal protein l41

Chain n3: 100%

There are no outlier residues recorded for this chain.

- Molecule 40: eL42

Chain o3: 98%



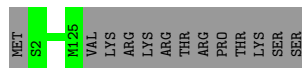
- Molecule 41: eL43

Chain p3: 96%



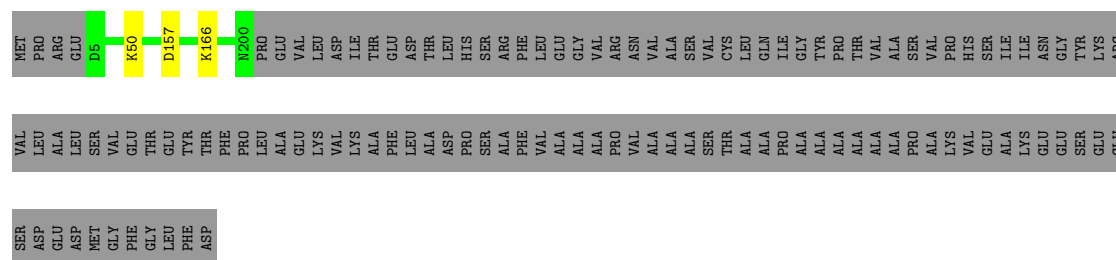
- Molecule 42: eL28

Chain r3: 91% 9%



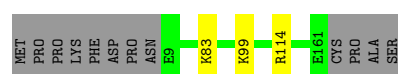
- Molecule 43: uL10

Chain s3:  61% . 38%



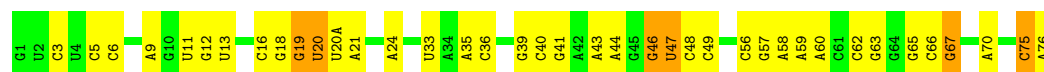
- Molecule 44: Ribosomal protein L12

Chain t3:  91% • 7%



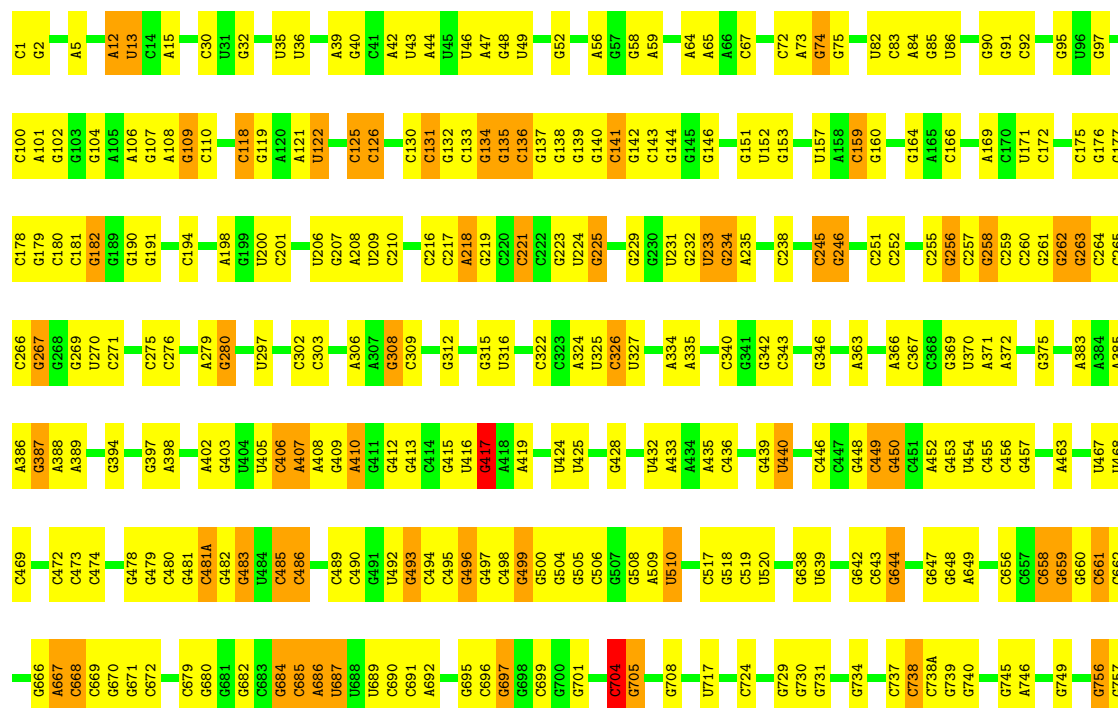
- Molecule 45: P-site tRNA

Chain 23:  49% 43% 8%



- Molecule 46: 28S ribosomal RNA

Chain 54: 55% 34% 11%

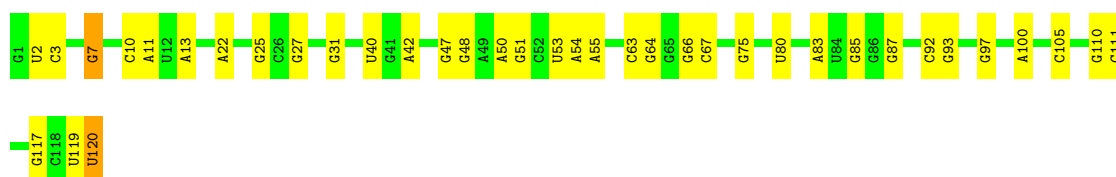





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U4923	C4924	U4925	C4926	G4927	C4928	G4931	C4935	G4936	C4937	A4938	C4939	C4940	C4941	C4942	A4943	C4944	C4945	U4946	U4947	C4948	U4949	G4951	G4954	A4955	A4956	C4957	C4958	U4959	C4960	G4963	C4964	U4965	A4966	A4967	U4971	U4976	A4977	G4981	U4985	U4988	U4989	C4990	U4991	G4992	G4993	G5000	U5001	U5002			
C4759	G4760	G4761	A4762	U4763	A4764	G4765	G4768	C4771	C4772	C4773	C4774	C4775	G4776	G4860	G4861	G4862	C4863	G4868	U4869	G4870	C4871	G4872	G4873	A4874	G4875	C4880	U4881	U4882	C4883	G4884	U4885	C4886	C4887	A4894	C4895	G4896	C4897	G4898	C4899	C4902	G4903	A4909	A4910	U4911	G4912	G4913	C4918	G4919	C4920	C4921	C4922
A4651	G4652	A4656	U4657	G4658	G4659	G4660	G4661	C4662	G4663	C4670	C4671	A4672	U4673	U4677	U4685	G4686	A4687	C4693	G4694	U4709	G4713	C4716	C4719	C4720	G4721	G4722	A4723	A4724	C4725	U4728	A4729	G4735	C4736	G4737	C4738	C4739	G4740	C4743	A4744	A4745	C4746	C4747	C4749	U4750	G4751	U4752	U4753	G4754	C4757	U4758	
G4554	U4555	C4560	C4561	C4562	G4567	A4568	U4569	G4570	A4571	U4572	G4573	U4574	G4575	U4579	U4580	A4584	U4585	G4586	G4587	A4590	C4596	U4597	A4605	G4606	A4607	G4614	C4615	U4618	U4619	U4620	A4626	U4627	G4631	G4632	U4633	U4634	A4635	U4636	G4637	U4638	U4639	C4640	U4641	U4642	U4646	G4647					
A4449	U4452	C4453	C4462	U4463	A4464	U4465	A4466	U4471	C4472	A4473	U4474	G4475	G4476	U4479	U4488	G4489	A4490	G4491	U4492	G4494	U4500	U4501	C4502	A4503	A4510	A4511	U4512	G4513	G4514	G4515	U4516	U4517	A4518	C4519	U4521	A4523	G4524	C4525	A4528	U4532	A4535	C4536	C4537	G4538	A4548	G4549					
G4330	U4331	C4332	U4339	U4340	C4341	C4349	C4350	U4354	C4355	G4356	G4357	G4364	G4371	U4372	G4373	G4377	A4378	A4379	A4380	C4387	A4388	C4389	A4390	G4391	G4392	G4393	A4394	U4395	C4398	G4401	C4413	U4419	U4420	C4421	A4422	U4423	C4429	U4430	U4431	U4437	U4438	C4444	U4445	G4448	U4449	G4454	G4459				
G4228	U4229	A4232	U4233	C4237	A4244	G4245	G4246	G4247	A4251	G4254	C4258	G4259	U4260	C4261	U4265	G4266	G4267	A4268	A4281	C4282	A4170	C4171	G4183	G4184	U4188	U4189	U4190	G4191	U4194	G4198	C4199	G4200	A4203	C4322	A4323	A4324	C4325	G4326	C4327	G4328	G4329										
G4124	C4125	C4126	A4127	A4128	G4131	C4132	C4133	C4134	G4135	C4136	C4137	C4138	G4146	G4147	C4148	G4151	C4152	G4153	C4154	C4155	C4156	A4157	C4158	C4162	U4163	G4166	G4167	C4168	C4169	A4170	C4171	G4183	G4184	U4188	U4189	U4190	G4191	U4194	G4198	C4199	G4200	A4203	C4322	A4323	A4324	C4325	G4326	C4327	G4328	G4329	
U3915	G3916	C3917	A3917	A3923	C3924	U3925	C3926	U3927	A3928	G3938	C3939	U3940	A3943	G3946	A3947	C4065	U4066	U4067	U4068	U4069	U4070	A4073	C4074	U4075	G4076	G4084	A4085	G4086	C4087	C4088	G4089	G4090	G4094	C4095	C4096	G4097	A4098	U4111	C4112	U4113	C4114	G4115	C4116	U4117	U4118	C4119	U4120	G4121	G4122	C4123	
G3809	C3810	G3811	G3811	U3814	G3815	G3816	A3817	U3818	G3819	U3822	G3823	A3824	U3838	G3839	U3840	C3843	U3844	A3845	C3855	A3856	G3859	A3860	A3861	C3864	A3867	A3872	A3876	A3877	C3878	G3879	G3880	C3887	G3888	G3889	C3893	A3894	G3895	G3896	C4114	G4115	C4116	U4117	U4118	C4119	U4120	G4121	G4122	C4123			
U3702	A3711	G3714	A3717	G3722	A3723	A3728	U3729	G3735	A3736	A3737	G3738	C3739	G3743	A3747	C3748	C3749	G3750	G3751	C3752	G3753	G3754	G3755	A3756	A3760	A3763	U3764	G3765	C3767	U3768	C3769	U3770	C3771	U3772	G3773	A3774	A3775	G3776	G3777	G3780	A3783	A3784	A3785	U3786	G3787	C3788	C3789	C3790	C3791			
G2809	U2810	G2811	A2812	C2814	C2814	G2822	U2826	G2827	U2828	U2829	C2834	G2842	U2843	A2844	A2845	G2848	C2849	A2850	C2855	C2856	G2862	C2867	C2868	U2869	C2875	A2879	U2880	A2881	A2882	A2894	A2895	G2896	C2899	A3599	C3600	C3601	G3603	A3604	U2803	C2804	C2805	A2806	A2807	C2808							
G3617	C3618	G3619	G3620	A3621	C3622	C3623	A3624	G3625	G3626	A3630	A3635	U3641	U3644	U3645	A3646	A3648	A3649	A3652	A3653	A3656	A3657	C3658	G3661	A3662	G3664	C3667	C3668	G3669	G3670	G3671	G3672	C3673	G3674	G3678	U3679	U3680	G3681	A3682	U3690	G3691	G3692	A3693	A3694	U3695	C3696	C3700	C3701				
U2708	C2709	G2710	G2711	G2714	U2718	C2719	G2720	G2721	U2725	G2726	U2740	U2741	G2742	A2743	A2744	G2752	C2753	G2754	A2755	G2758	G2759	G2760	U2761	G2762	U2763	A2764	A2765	G2768	U2769	C2772	C2779	A2783	A2787	U2788	A2789	U2790	G2793	C2794	A2798	U2803	C2804	C2805	A2806	A2807	C2808						

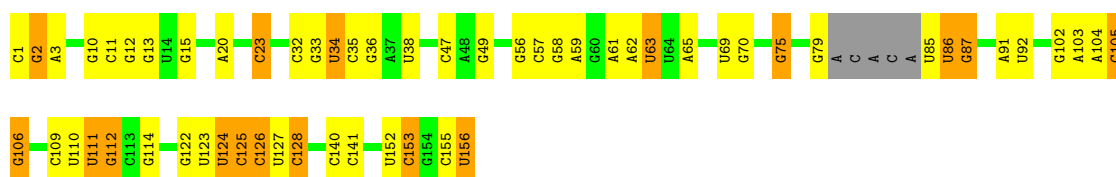
• Molecule 47: 5S ribosomal RNA

Chain 74:  68% 30% .



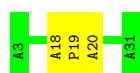
- Molecule 48: 5.8S ribosomal RNA

Chain 84: 60% 26% 11%



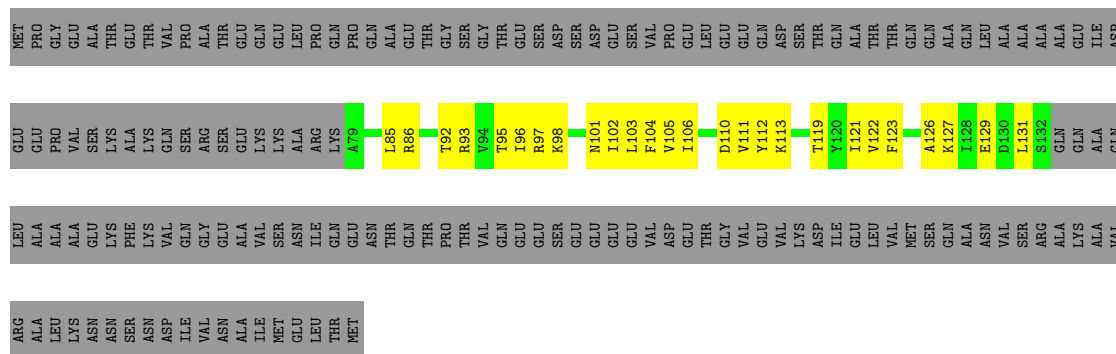
- Molecule 49: Nascent polypeptide-associated complex subunit alpha N-terminal region

Chain NI: 90% 10%



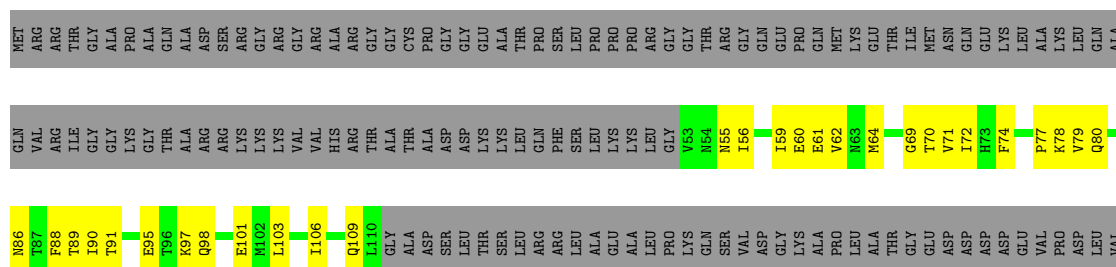
- Molecule 50: Nascent polypeptide-associated complex subunit alpha

Chain NA: 13% 12% 75%



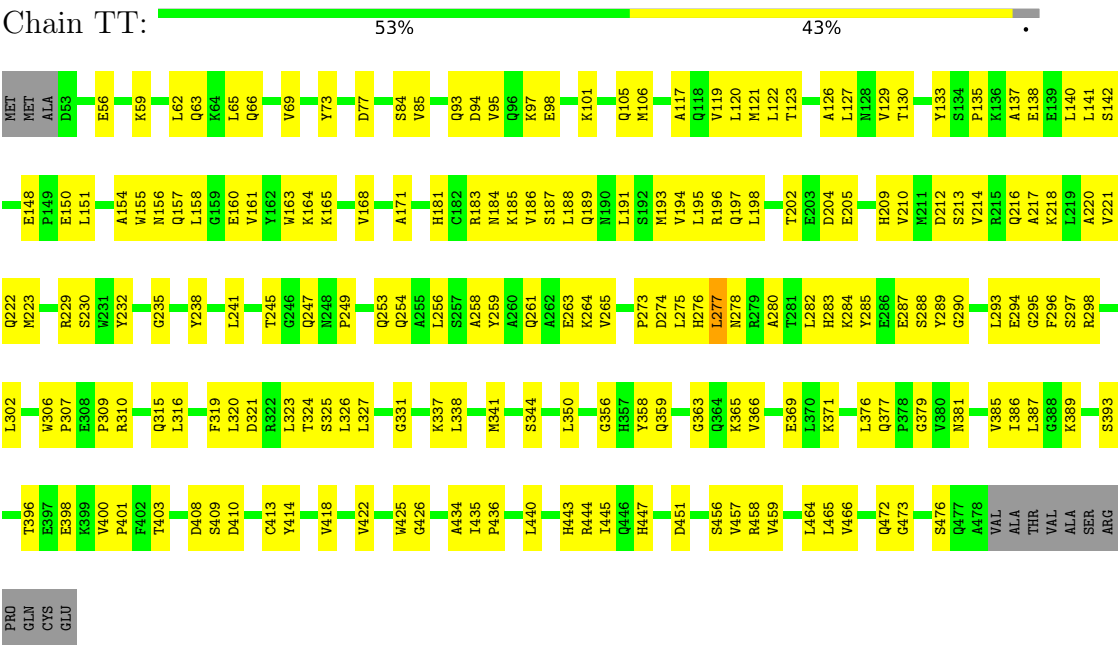
- Molecule 51: Transcription factor BTF3

Chain NB: 15% 14% 72%

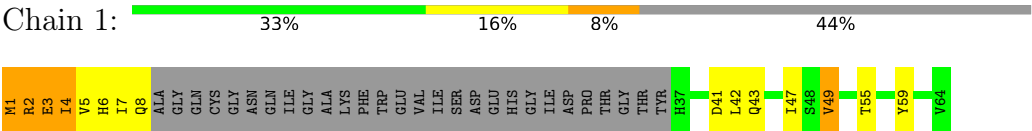


GLU
ASN
MET
PHE
ASP
GLU
ALA
SER
LYS
ASN
GLU
ALA
ASN

● Molecule 52: Tetratricopeptide repeat protein 5



● Molecule 53: Tubulin Beta



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	49626	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48.36	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	A3	0.63	0/1936	0.55	0/2596
10	J3	0.46	0/1385	0.52	0/1852
11	L3	0.54	0/1733	0.50	0/2316
12	M3	0.59	0/1158	0.49	0/1547
13	N3	0.70	0/1746	0.55	0/2338
14	O3	0.66	1/1662 (0.1%)	0.55	0/2222
15	P3	0.63	0/1268	0.55	1/1700 (0.1%)
16	Q3	0.64	0/1538	0.56	0/2054
17	R3	0.51	0/1310	0.52	0/1734
18	S3	0.69	0/1501	0.56	1/2012 (0.0%)
19	T3	0.64	0/1326	0.52	0/1770
2	B3	0.63	0/3240	0.56	0/4339
20	U3	0.52	0/848	0.55	0/1138
21	V3	0.60	0/993	0.55	0/1332
22	W3	0.61	0/541	0.50	0/720
23	X3	0.54	0/984	0.50	0/1323
24	Y3	0.59	0/1132	0.52	0/1504
25	Z3	0.57	0/1130	0.52	0/1507
26	a3	0.68	0/1191	0.55	0/1590
27	b3	0.45	0/861	0.47	0/1138
28	c3	0.56	0/771	0.52	0/1034
29	d3	0.60	0/903	0.52	0/1216
3	C3	0.61	0/2937	0.56	1/3946 (0.0%)
30	e3	0.64	0/1071	0.57	0/1429
31	f3	0.73	0/895	0.61	0/1198
32	g3	0.59	0/916	0.55	0/1220
33	h3	0.52	0/1021	0.48	0/1348
34	i3	0.46	0/841	0.48	0/1112
35	j3	0.70	1/720 (0.1%)	0.56	0/952
36	k3	0.51	0/575	0.53	0/761
37	l3	0.62	0/459	0.55	0/608
38	m3	0.57	0/435	0.59	0/575

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	n3	0.28	0/240	0.43	0/305
4	D3	0.60	0/2437	0.49	0/3264
40	o3	0.57	0/864	0.51	0/1140
41	p3	0.59	0/718	0.53	0/953
42	r3	0.61	0/1010	0.57	0/1354
43	s3	0.29	0/1530	0.49	0/2064
44	t3	0.27	0/1174	0.52	0/1582
45	23	0.41	0/1805	0.83	1/2809 (0.0%)
46	54	1.24	10/84976 (0.0%)	0.93	64/132520 (0.0%)
47	74	1.24	0/2858	0.87	0/4455
48	84	1.22	0/3581	0.87	0/5577
49	NI	0.31	0/150	0.63	0/209
5	E3	0.53	0/1762	0.55	0/2362
50	NA	0.28	0/425	0.53	0/572
51	NB	0.28	0/450	0.52	0/612
52	TT	0.30	0/3402	0.46	0/4603
53	1	0.47	0/295	0.57	0/394
6	F3	0.66	0/1911	0.50	0/2549
7	G3	0.51	0/1910	0.50	0/2569
8	H3	0.54	0/1535	0.54	0/2063
9	I3	0.60	0/1702	0.53	1/2272 (0.0%)
All	All	1.02	12/153762 (0.0%)	0.80	69/226359 (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
13	N3	0	2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	54	1890	G	N9-C4	-7.84	1.31	1.38
46	54	978	G	N9-C4	-6.37	1.32	1.38
35	j3	50	SER	CA-CB	-6.22	1.43	1.52
46	54	1896	A	N9-C4	-6.03	1.34	1.37
46	54	1337	A	N9-C4	-5.72	1.34	1.37

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	54	1890	G	N3-C4-C5	9.26	133.23	128.60
46	54	978	G	N3-C4-C5	8.94	133.07	128.60
46	54	1890	G	N3-C4-N9	-8.64	120.81	126.00
46	54	2638	G	N3-C4-N9	-8.53	120.88	126.00
46	54	2638	G	N3-C4-C5	8.28	132.74	128.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	N3	76	PRO	Peptide
13	N3	78	GLY	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	A3	1898	0	1993	61	0
2	B3	3172	0	3310	90	0
3	C3	2883	0	3053	77	0
4	D3	2391	0	2424	56	0
5	E3	1729	0	1887	47	0
6	F3	1875	0	1995	44	0
7	G3	1879	0	2027	47	0
8	H3	1516	0	1597	46	0
9	I3	1664	0	1712	37	0
10	J3	1362	0	1399	36	0
11	L3	1702	0	1820	44	0
12	M3	1137	0	1211	28	0
13	N3	1701	0	1749	50	0
14	O3	1630	0	1778	45	0
15	P3	1242	0	1274	30	0
16	Q3	1514	0	1634	46	0
17	R3	1294	0	1434	48	0
18	S3	1462	0	1508	44	0
19	T3	1298	0	1366	50	0
20	U3	834	0	858	23	0
21	V3	979	0	1039	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	W3	528	0	541	12	0
23	X3	967	0	1040	23	0
24	Y3	1115	0	1205	41	0
25	Z3	1107	0	1182	30	0
26	a3	1162	0	1209	0	0
27	b3	848	0	920	0	0
28	c3	761	0	794	0	0
29	d3	888	0	930	0	0
30	e3	1053	0	1147	0	0
31	f3	876	0	912	0	0
32	g3	906	0	999	0	0
33	h3	1013	0	1147	0	0
34	i3	830	0	916	0	0
35	j3	705	0	737	0	0
36	k3	569	0	637	0	0
37	l3	447	0	480	0	0
38	m3	429	0	465	0	0
39	n3	239	0	289	0	0
40	o3	851	0	920	0	0
41	p3	708	0	757	0	0
42	r3	994	0	1051	0	0
43	s3	1507	0	1564	0	0
44	t3	1160	0	1218	0	0
45	23	1616	0	823	18	0
46	54	75972	0	38385	969	0
47	74	2558	0	1296	22	0
48	84	3208	0	1629	35	0
49	NI	150	0	152	1	0
50	NA	420	0	450	27	0
51	NB	444	0	441	22	0
52	TT	3337	0	3318	144	0
53	1	292	0	291	28	0
54	54	201	0	0	0	0
54	74	7	0	0	0	0
54	84	6	0	0	0	0
54	P3	2	0	0	0	0
54	V3	1	0	0	0	0
54	a3	1	0	0	0	0
54	g3	1	0	0	0	0
54	j3	1	0	0	0	0
55	g3	1	0	0	0	0
55	j3	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	m3	1	0	0	0	0
55	o3	1	0	0	0	0
55	p3	1	0	0	0	0
All	All	143047	0	104913	2006	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 11.

The worst 5 of 2006 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)
46:54:973:G:N2	46:54:1282:G:N7	2.03	1.07
46:54:2638:G:N2	46:54:2697:A:N1	2.11	0.98
46:54:2486:G:H1	46:54:2492:C:H42	1.16	0.92
46:54:4751:G:H1	46:54:4948:C:H5	1.14	0.91
46:54:496:G:N1	46:54:658:C:N3	2.17	0.91

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A3	246/257 (96%)	218 (89%)	28 (11%)	0	100	100
2	B3	392/403 (97%)	358 (91%)	34 (9%)	0	100	100
3	C3	360/425 (85%)	331 (92%)	29 (8%)	0	100	100
4	D3	291/297 (98%)	265 (91%)	26 (9%)	0	100	100
5	E3	208/291 (72%)	185 (89%)	23 (11%)	0	100	100
6	F3	223/247 (90%)	206 (92%)	17 (8%)	0	100	100
7	G3	229/319 (72%)	212 (93%)	17 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H3	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
9	I3	201/214 (94%)	181 (90%)	20 (10%)	0	100	100
10	J3	168/178 (94%)	155 (92%)	13 (8%)	0	100	100
11	L3	208/211 (99%)	193 (93%)	14 (7%)	1 (0%)	31	67
12	M3	136/218 (62%)	125 (92%)	11 (8%)	0	100	100
13	N3	201/204 (98%)	185 (92%)	16 (8%)	0	100	100
14	O3	197/203 (97%)	185 (94%)	12 (6%)	0	100	100
15	P3	151/184 (82%)	142 (94%)	9 (6%)	0	100	100
16	Q3	185/188 (98%)	170 (92%)	15 (8%)	0	100	100
17	R3	153/196 (78%)	142 (93%)	11 (7%)	0	100	100
18	S3	174/176 (99%)	158 (91%)	15 (9%)	1 (1%)	27	64
19	T3	157/160 (98%)	138 (88%)	18 (12%)	1 (1%)	27	64
20	U3	100/128 (78%)	89 (89%)	11 (11%)	0	100	100
21	V3	129/140 (92%)	119 (92%)	10 (8%)	0	100	100
22	W3	61/157 (39%)	54 (88%)	7 (12%)	0	100	100
23	X3	116/156 (74%)	104 (90%)	12 (10%)	0	100	100
24	Y3	132/145 (91%)	122 (92%)	10 (8%)	0	100	100
25	Z3	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
26	a3	145/148 (98%)	131 (90%)	14 (10%)	0	100	100
27	b3	100/226 (44%)	94 (94%)	6 (6%)	0	100	100
28	c3	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
29	d3	105/125 (84%)	92 (88%)	13 (12%)	0	100	100
30	e3	126/135 (93%)	118 (94%)	7 (6%)	1 (1%)	21	58
31	f3	107/110 (97%)	98 (92%)	9 (8%)	0	100	100
32	g3	112/116 (97%)	106 (95%)	6 (5%)	0	100	100
33	h3	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
34	i3	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
35	j3	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
36	k3	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
37	l3	48/51 (94%)	38 (79%)	10 (21%)	0	100	100
38	m3	50/102 (49%)	46 (92%)	4 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	n3	23/25 (92%)	23 (100%)	0	0	100	100
40	o3	102/106 (96%)	90 (88%)	12 (12%)	0	100	100
41	p3	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
42	r3	122/137 (89%)	111 (91%)	11 (9%)	0	100	100
43	s3	194/318 (61%)	167 (86%)	27 (14%)	0	100	100
44	t3	151/165 (92%)	121 (80%)	30 (20%)	0	100	100
49	NI	27/29 (93%)	15 (56%)	11 (41%)	1 (4%)	4	21
50	NA	52/215 (24%)	42 (81%)	10 (19%)	0	100	100
51	NB	56/206 (27%)	50 (89%)	6 (11%)	0	100	100
52	TT	424/440 (96%)	395 (93%)	29 (7%)	0	100	100
53	1	32/64 (50%)	17 (53%)	13 (41%)	2 (6%)	1	9
All	All	7271/8745 (83%)	6614 (91%)	650 (9%)	7 (0%)	56	85

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
53	1	4	ILE
11	L3	64	VAL
18	S3	166	ARG
30	e3	127	ALA
49	NI	20	ALA

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	A3	190/199 (96%)	188 (99%)	2 (1%)	76	90
2	B3	342/348 (98%)	340 (99%)	2 (1%)	87	94
3	C3	302/347 (87%)	300 (99%)	2 (1%)	85	94
4	D3	247/250 (99%)	247 (100%)	0	100	100
5	E3	190/251 (76%)	187 (98%)	3 (2%)	65	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F3	196/215 (91%)	196 (100%)	0	100	100
7	G3	200/272 (74%)	200 (100%)	0	100	100
8	H3	169/171 (99%)	169 (100%)	0	100	100
9	I3	175/181 (97%)	175 (100%)	0	100	100
10	J3	143/149 (96%)	143 (100%)	0	100	100
11	L3	175/176 (99%)	173 (99%)	2 (1%)	76	90
12	M3	117/161 (73%)	117 (100%)	0	100	100
13	N3	171/172 (99%)	169 (99%)	2 (1%)	74	89
14	O3	171/173 (99%)	170 (99%)	1 (1%)	87	94
15	P3	134/163 (82%)	134 (100%)	0	100	100
16	Q3	164/164 (100%)	164 (100%)	0	100	100
17	R3	138/175 (79%)	137 (99%)	1 (1%)	85	94
18	S3	157/157 (100%)	155 (99%)	2 (1%)	71	88
19	T3	139/140 (99%)	139 (100%)	0	100	100
20	U3	92/114 (81%)	92 (100%)	0	100	100
21	V3	101/107 (94%)	100 (99%)	1 (1%)	78	91
22	W3	55/126 (44%)	55 (100%)	0	100	100
23	X3	106/134 (79%)	105 (99%)	1 (1%)	81	92
24	Y3	124/135 (92%)	122 (98%)	2 (2%)	65	86
25	Z3	117/118 (99%)	116 (99%)	1 (1%)	81	92
26	a3	119/120 (99%)	118 (99%)	1 (1%)	83	93
27	b3	84/172 (49%)	84 (100%)	0	100	100
28	c3	84/98 (86%)	83 (99%)	1 (1%)	74	89
29	d3	98/110 (89%)	96 (98%)	2 (2%)	58	83
30	e3	114/121 (94%)	113 (99%)	1 (1%)	81	92
31	f3	88/89 (99%)	88 (100%)	0	100	100
32	g3	98/99 (99%)	98 (100%)	0	100	100
33	h3	109/110 (99%)	109 (100%)	0	100	100
34	i3	86/89 (97%)	86 (100%)	0	100	100
35	j3	73/80 (91%)	71 (97%)	2 (3%)	48	78
36	k3	64/65 (98%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	l3	47/48 (98%)	47 (100%)	0	100	100
38	m3	48/90 (53%)	48 (100%)	0	100	100
39	n3	24/24 (100%)	24 (100%)	0	100	100
40	o3	92/94 (98%)	92 (100%)	0	100	100
41	p3	74/75 (99%)	71 (96%)	3 (4%)	33	68
42	r3	108/121 (89%)	108 (100%)	0	100	100
43	s3	164/258 (64%)	161 (98%)	3 (2%)	62	85
44	t3	126/137 (92%)	123 (98%)	3 (2%)	52	80
49	NI	2/2 (100%)	2 (100%)	0	100	100
50	NA	48/183 (26%)	48 (100%)	0	100	100
51	NB	51/165 (31%)	51 (100%)	0	100	100
52	TT	370/381 (97%)	367 (99%)	3 (1%)	83	93
53	1	32/53 (60%)	26 (81%)	6 (19%)	1	7
All	All	6318/7382 (86%)	6271 (99%)	47 (1%)	86	94

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	Z3	11	VAL
30	e3	48	ARG
53	1	3	GLU
28	c3	17	ARG
35	j3	67	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
15	P3	25	HIS
17	R3	39	GLN
52	TT	128	ASN
15	P3	56	GLN
16	Q3	8	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	23	74/76 (97%)	13 (17%)	0
46	54	3516/3543 (99%)	822 (23%)	58 (1%)
47	74	119/120 (99%)	14 (11%)	0
48	84	149/156 (95%)	32 (21%)	1 (0%)
All	All	3858/3895 (99%)	881 (22%)	59 (1%)

5 of 881 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	23	9	A
45	23	13	U
45	23	16	C
45	23	19	G
45	23	20(A)	U

5 of 59 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	54	1440	U
46	54	2046	G
46	54	4921	C
46	54	1445	U
46	54	1477	C

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 225 ligands modelled in this entry, 225 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	54	27
45	23	1

The worst 5 of 28 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	54	2113:G	O3'	2258:C	P	40.63
1	54	1252:C	O3'	1271:G	P	37.10
1	54	1219:G	O3'	1233:G	P	19.39
1	54	3948:C	O3'	4065:G	P	18.92
1	54	4138:C	O3'	4146:G	P	18.16