



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:46 PM BST

PDB ID : 5APO  
EMDB ID: : 3151  
Title : Structure of the yeast 60S ribosomal subunit in complex with Arx1, Alb1 and C-terminally tagged Rei1  
Authors : Greber, B.J.; Gerhardy, S.; Leitner, A.; Leibundgut, M.; Salem, M.; Boehringer, D.; Leulliot, N.; Aebersold, R.; Panse, V.G.; Ban, N.  
Deposited on : 2015-09-17  
Resolution : 3.41 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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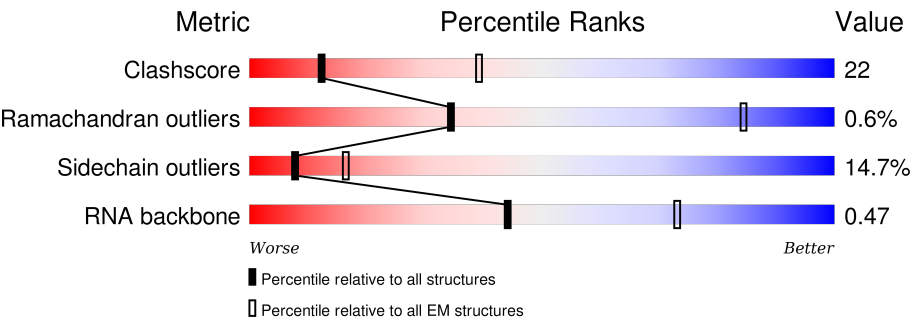
MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 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 3.41 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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	5	3396	<div><div>40%</div><div>38%</div><div>12%</div><div>8%</div></div>
2	7	121	<div><div>45%</div><div>49%</div><div>7%</div></div>
3	8	158	<div><div>47%</div><div>35%</div><div>16%</div><div>.</div></div>
4	A	254	<div><div>36%</div><div>38%</div><div>9%</div><div>17%</div></div>
5	B	387	<div><div>50%</div><div>40%</div><div>10%</div></div>
6	C	362	<div><div>49%</div><div>41%</div><div>10%</div><div>.</div></div>
7	D	297	<div><div>53%</div><div>38%</div><div>8%</div><div>.</div></div>
8	E	176	<div><div>55%</div><div>40%</div><div>5%</div><div>.</div></div>

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Mol	Chain	Length	Quality of chain
9	F	244	
10	G	256	
11	H	191	
12	I	221	
13	J	174	
14	L	199	
15	M	138	
16	N	204	
17	O	199	
18	P	184	
19	Q	186	
20	R	189	
21	S	172	
22	T	160	
23	U	121	
24	V	137	
25	W	155	
26	X	142	
27	Y	127	
28	Z	136	
29	a	149	
30	b	59	
31	c	105	
32	d	113	
33	e	130	

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Mol	Chain	Length	Quality of chain
34	f	107	 93% 6%
35	g	121	 83% 10% 7%
36	h	120	 83% 16%
37	i	100	 76% 23%
38	j	88	 86% 13%
39	k	78	 88% 10%
40	l	51	 78% 20%
41	m	128	 35% 5% 59%
42	o	106	 82% 17%
43	p	92	 80% 18%
44	q	312	 33% 6% 62%
45	x	616	 87% 6% 6%
46	y	401	 50% 46%
47	z	95	 89% 11%

## 2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 129386 atoms, of which 3 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3112	Total	C	N	O	P	0	0
			66537	29736	11996	21694	3111		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	212	Total	C	N	O	S	0	0
			1630	1021	325	283	1		

- Molecule 5 is a protein called 60S ribosomal protein L3.

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

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN EL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	175	Total	C	N	O	S	0	0
			1356	878	242	235	1		

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1722	1094	325	297	6		

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

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

- Molecule 14 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	L	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	P	183	Total	C	N	O	0	0
			1442	896	287	259		

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	R	156	Total	C	N	O	0	0
			1258	781	265	212		

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	102	Total	C	N	O		0	0
			808	524	132	152			

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 27 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 28 is a protein called 60S ribosomal protein L27-A.



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

- Molecule 29 is a protein called 60S ribosomal protein L28.

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

- Molecule 30 is a protein called 60S ribosomal protein L29.

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

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 32 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	129	Total	C	N	O	S	0	0
			1034	655	207	171	1		

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 35 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 37 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 38 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	k	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 42 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 44 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	120	Total	C	N	O	S	0	0
			962	618	169	172	3		

- Molecule 45 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	579	Total	C	N	O	S	0	0
			4477	2823	772	867	15		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	-22	MET	-	initiating methionine	UNP Q03862
x	-21	GLY	-	expression tag	UNP Q03862
x	-20	SER	-	expression tag	UNP Q03862
x	-19	SER	-	expression tag	UNP Q03862
x	-18	HIS	-	expression tag	UNP Q03862
x	-17	HIS	-	expression tag	UNP Q03862
x	-16	HIS	-	expression tag	UNP Q03862
x	-15	HIS	-	expression tag	UNP Q03862
x	-14	HIS	-	expression tag	UNP Q03862
x	-13	HIS	-	expression tag	UNP Q03862
x	-12	SER	-	expression tag	UNP Q03862
x	-11	SER	-	expression tag	UNP Q03862
x	-10	GLY	-	expression tag	UNP Q03862
x	-9	LEU	-	expression tag	UNP Q03862
x	-8	VAL	-	expression tag	UNP Q03862
x	-7	PRO	-	expression tag	UNP Q03862
x	-6	ARG	-	expression tag	UNP Q03862
x	-5	GLY	-	expression tag	UNP Q03862
x	-4	SER	-	expression tag	UNP Q03862

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Chain	Residue	Modelled	Actual	Comment	Reference
x	-3	HIS	-	expression tag	UNP Q03862
x	-2	MET	-	expression tag	UNP Q03862
x	-1	LEU	-	expression tag	UNP Q03862
x	0	GLU	-	expression tag	UNP Q03862

- Molecule 46 is a protein called CYTOPLASMIC 60S SUBUNIT BIOGENESIS FACTOR REI1.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	y	217	Total	C	H	N	O	S	0	0
			1788	1131	3	324	322	8		

- Molecule 47 is a protein called ALB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	z	85	Total	C	N	O	0	0
			510	340	85	85		

- Molecule 48 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	P	1	Total	Mg	0
			1	1	
48	B	2	Total	Mg	0
			2	2	
48	C	1	Total	Mg	0
			1	1	
48	V	1	Total	Mg	0
			1	1	
48	7	6	Total	Mg	0
			6	6	
48	N	1	Total	Mg	0
			1	1	
48	5	259	Total	Mg	0
			259	259	
48	8	7	Total	Mg	0
			7	7	
48	R	1	Total	Mg	0
			1	1	
48	y	1	Total	Mg	0
			1	1	

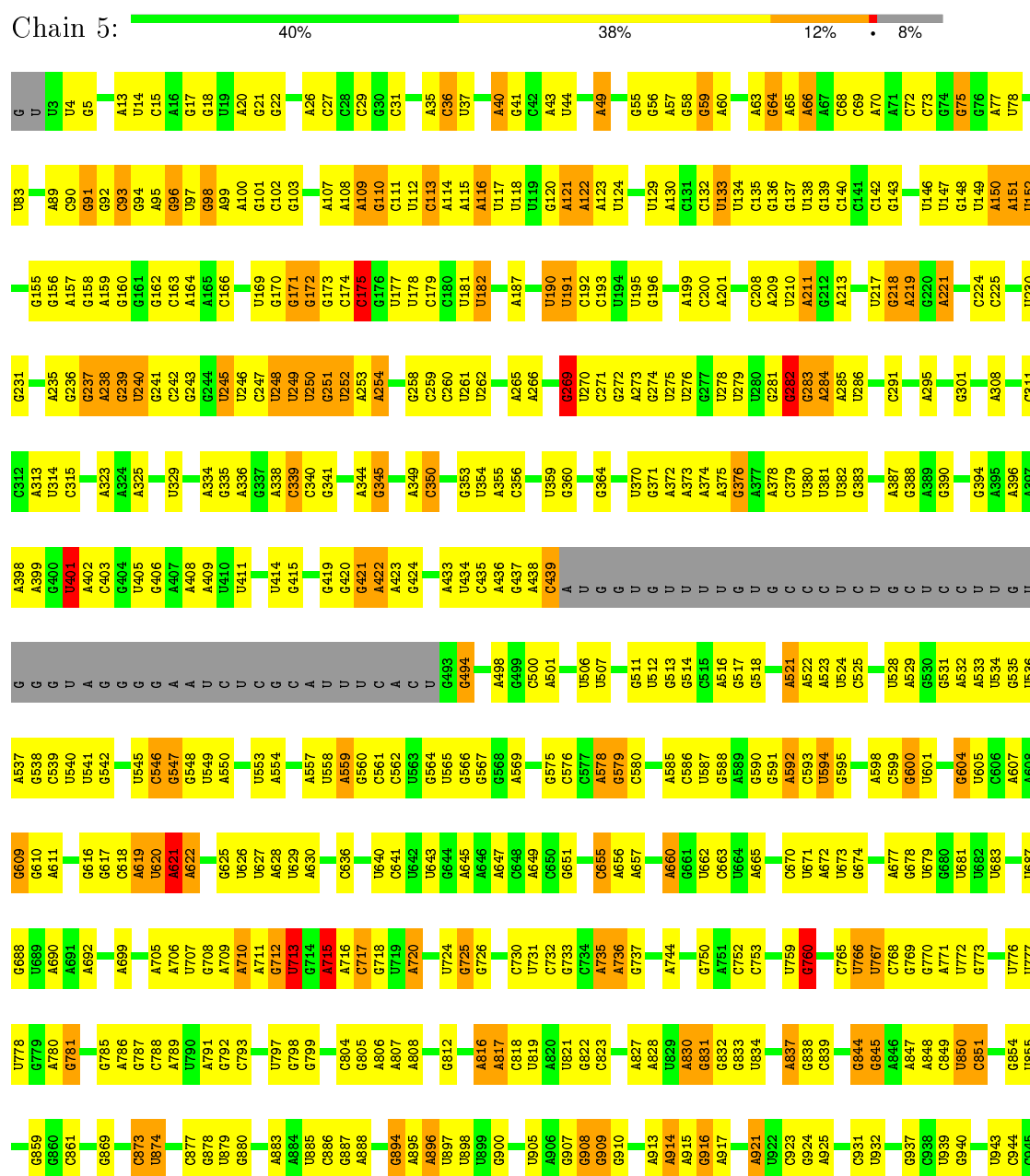
- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	p	1	Total 1	Zn 1	0
49	o	1	Total 1	Zn 1	0
49	j	1	Total 1	Zn 1	0
49	y	2	Total 2	Zn 2	0
49	m	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 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: 25S ribosomal RNA



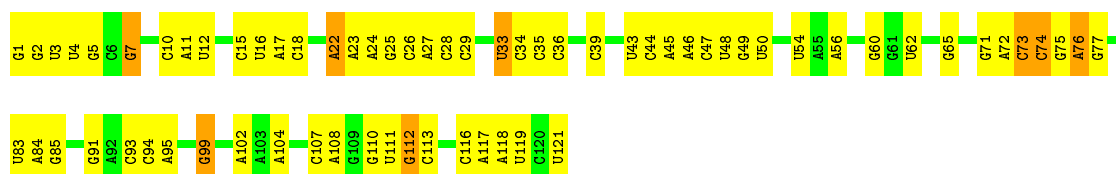
A2164	P5P	A1864	Y5P	G1666	C1578	G1493	A1394	U1315	G1243	G1171	G1088	G	U946
A2168	P5P	A1865	Y5P	G1778	C1579	U1494	G1395	C1316	A1244	G1172	G1090	G	G947
G2169	P5P	C1866	Y5P	G1779	A1580	U1495	G1396	A1317	G1245	U1173	C1091	G	C948
U2175	P5P	C1870	Y5P	G1784	C1581	U1496	C1397	A1318	G1246	U1174	C1092	U	C949
U2176	P5P	C1874	Y5P	G1785	C1582	U1501	G1398	G1319	U1247	C1175	A1093	C	G950
G2177	P5P	U1876	Y5P	G1786	C1583	U1502	A1399	C1320	G1248	A1180	U1094	G	A951
A2178	P5P	U1877	Y5P	G1787	U1584	A1503	G1400	G1321	C1248	A1181	U1095	A	A952
C2179	P5P	U1878	Y5P	G1788	A1587	A1506	G1408	U1322	A1251	U1182	U1096	A	G953
G2180	P5P	U1879	Y5P	G1789	A1588	C1507	U1415	G1323	A1252	C1183	G1097	A	U956
C2181	P5P	U1880	Y5P	G1794	A1589	C1508	G1416	U1324	U1253	A1184	U1098	U	U957
G2185	P5P	U1795	Y5P	G1795	A1593	G1510	U1417	C1327	G1257	G1101	G1101	A	C959
U2186	P5P	A1886	Y5P	G1796	C1596	G1514	G1418	C1328	A1258	G1185	A1102	C	U960
G2187	P5P	A1887	Y5P	G1797	C1597	C1509	G1419	U1329	A1259	G1186	A1103	C	C961
U2190	P5P	A1891	Y5P	C1803	G1598	G1521	A1420	A1330	G1260	C1187	G1104	U	G968
G2191	P5P	A1892	Y5P	A1804	A1603	U1522	G1421	C1331	G1261	U1188	U1108	G1035	C969
U2192	P5P	A1893	Y5P	C1701	A1603	U1523	G1422	A1332	A1262	C1189	U1109	A1036	A970
C2193	P5P	U1894	Y5P	G1700	A1603	U1524	C1426	C1333	G1263	U1191	U1110	C1037	G971
G2198	P5P	U1895	Y5P	G1704	A1603	U1525	U1430	C1334	G1264	C1192	U1111	C1038	A972
C2200	P5P	U1896	Y5P	G1705	A1603	U1526	G1431	C1342	U1267	C1196	U1039	U1039	G973
G2201	P5P	U1897	Y5P	G1706	A1603	U1527	G1432	A1343	G1268	A1197	A1040	A1040	G974
C2204	P5P	U1898	Y5P	G1707	A1603	U1528	G1433	C1344	U1269	C1198	A1047	A1047	C977
G2205	P5P	U1899	Y5P	G1708	A1603	U1529	G1434	G1345	A1270	C1199	A1048	C1049	G978
U2209	P5P	U1900	Y5P	G1709	A1603	U1530	G1435	G1346	A1271	A1200	C1049	C1049	U979
G2210	P5P	U1901	Y5P	G1710	A1603	U1531	G1436	G1347	A1272	C1201	U1050	A1050	A980
U2211	P5P	U1902	Y5P	G1711	A1603	U1532	G1437	C1348	A1273	A1202	U1051	U1051	A981
C2212	P5P	U1903	Y5P	G1712	A1603	U1533	G1438	G1349	A1274	A1203	C982	C982	C982
A2213	P5P	U1904	Y5P	G1713	A1603	U1534	G1439	C1350	A1275	A1204	U1052	U1052	C983
A2214	P5P	U1905	Y5P	G1714	A1603	U1535	G1440	C1351	A1276	U1208	A1053	A1053	A983
A2215	P5P	U1906	Y5P	G1715	A1603	U1536	G1441	U1352	A1277	U1209	G984	G984	U985
G2216	P5P	U1907	Y5P	G1716	A1603	U1537	G1442	A1353	A1278	U1210	C1133	C1133	U986
U2219	P5P	U1908	Y5P	G1717	A1603	U1538	G1443	C1354	A1279	U1211	A1133	A1133	U987
G2220	P5P	U1909	Y5P	G1718	A1603	U1539	G1444	G1355	A1280	C1213	G1134	G1134	U988
C2221	P5P	U1910	Y5P	G1719	A1603	U1540	G1445	C1356	G1281	U1138	U1138	U1138	G991
A2222	P5P	U1911	Y5P	G1720	A1603	U1541	G1446	C1357	G1282	A1216	C1141	C1141	A992
C2223	P5P	U1912	Y5P	G1721	A1603	U1542	G1447	C1358	A1283	A1217	G1142	G1142	A993
U2225	P5P	U1913	Y5P	G1722	A1603	U1543	G1448	C1359	G1284	U1220	A1143	A1143	G994
U2226	P5P	U1914	Y5P	G1723	A1603	U1544	G1449	C1360	A1285	A1221	U1144	U1144	U995
C2227	P5P	U1915	Y5P	G1724	A1603	U1545	G1450	C1361	A1286	A1222	G1147	G1147	A996
A2228	P5P	U1916	Y5P	G1725	A1603	U1546	G1451	C1362	A1287	A1223	U1151	U1151	A997
C2229	P5P	U1917	Y5P	G1726	A1603	U1547	G1452	C1363	A1288	A1224	C1152	C1152	A998
G2230	P5P	U1918	Y5P	G1727	A1603	U1548	G1453	C1364	A1289	C1224	A1153	A1153	G999
A2231	P5P	U1919	Y5P	G1728	A1603	U1549	G1454	G1377	A1290	A1225	C1154	C1154	G1000
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U3325	U3325	G3260										U2369	

• Molecule 2: 5S ribosomal RNA

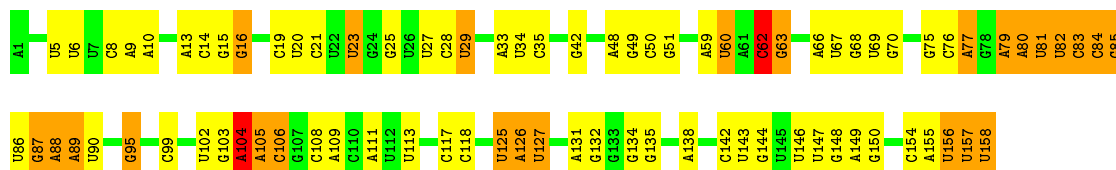
Chain 7:  45%  49%  7%





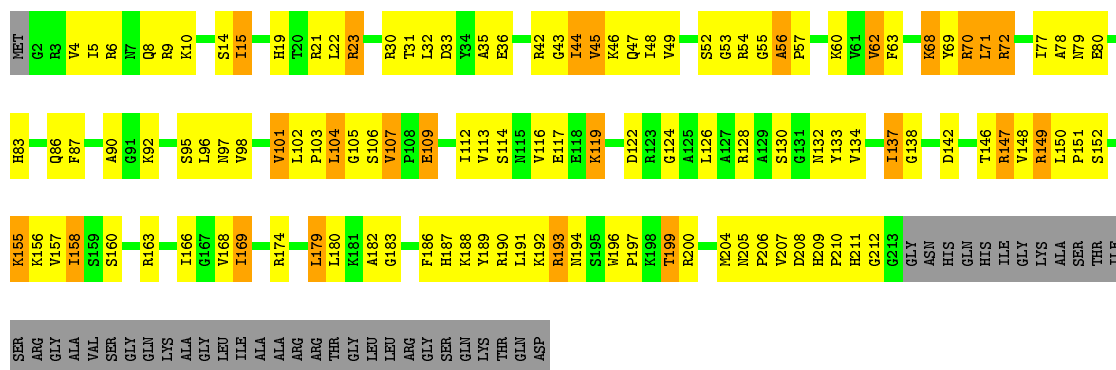
• Molecule 3: 5.8S ribosomal RNA

Chain 8: 47% 35% 16%



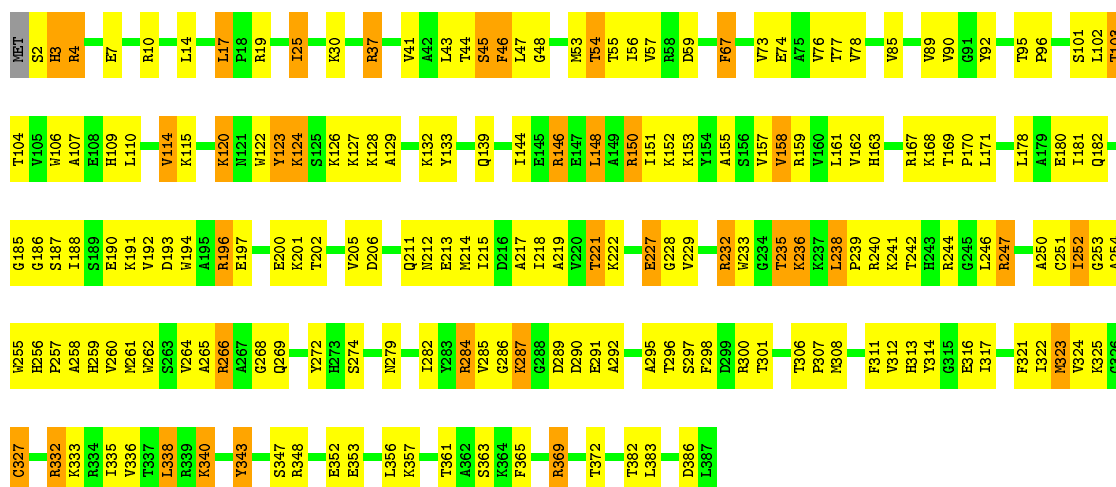
• Molecule 4: 60S ribosomal protein L2-A

Chain A: 36% 38% 9% 17%

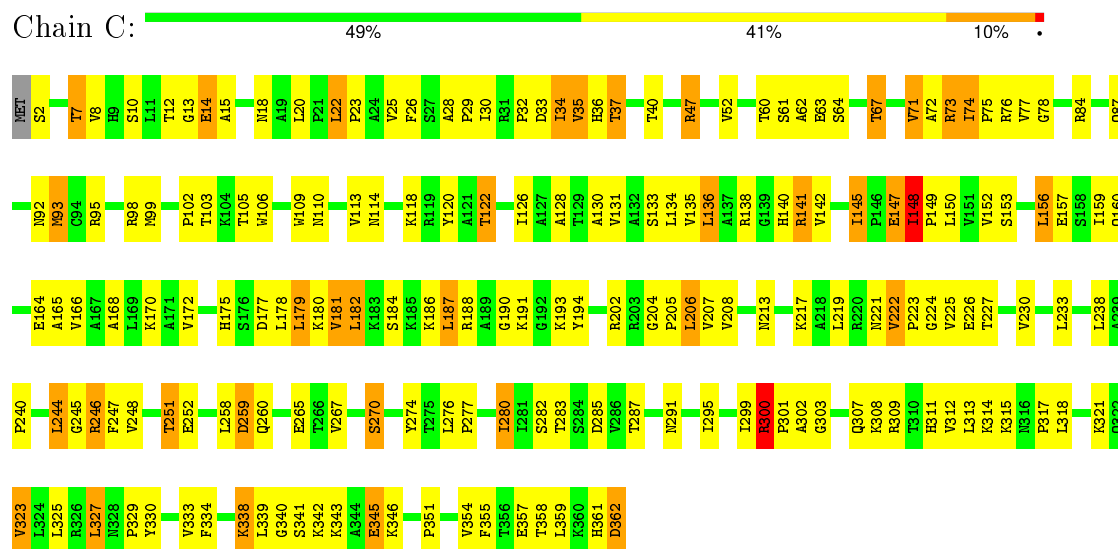


• Molecule 5: 60S ribosomal protein L3

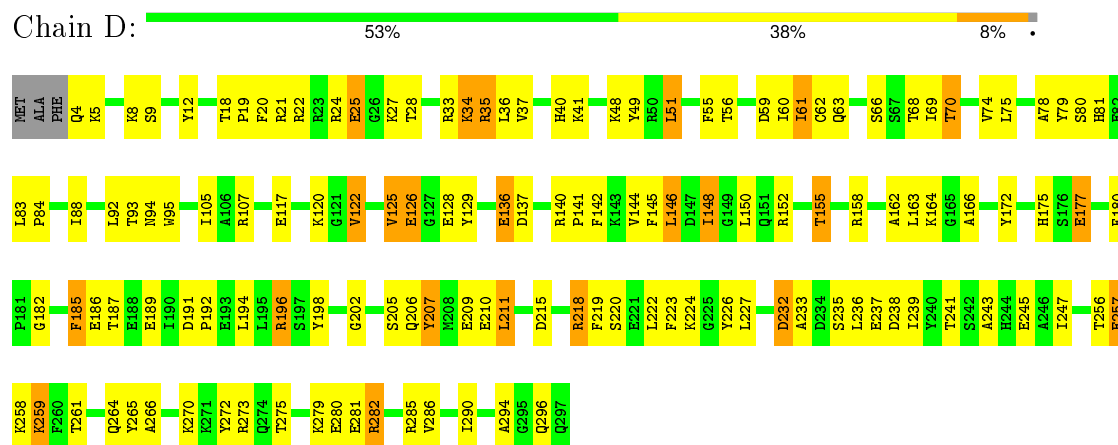
Chain B: 50% 40% 10%



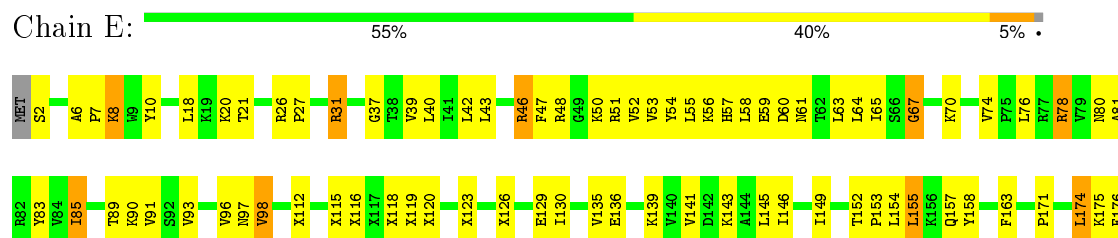
• Molecule 6: 60S ribosomal protein L4-A



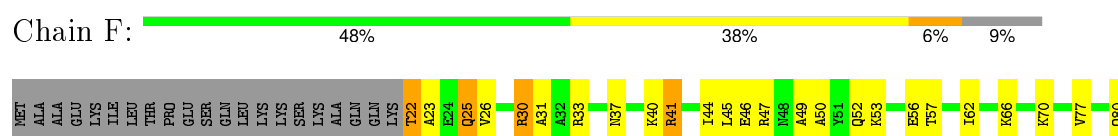
- Molecule 7: 60S ribosomal protein L5



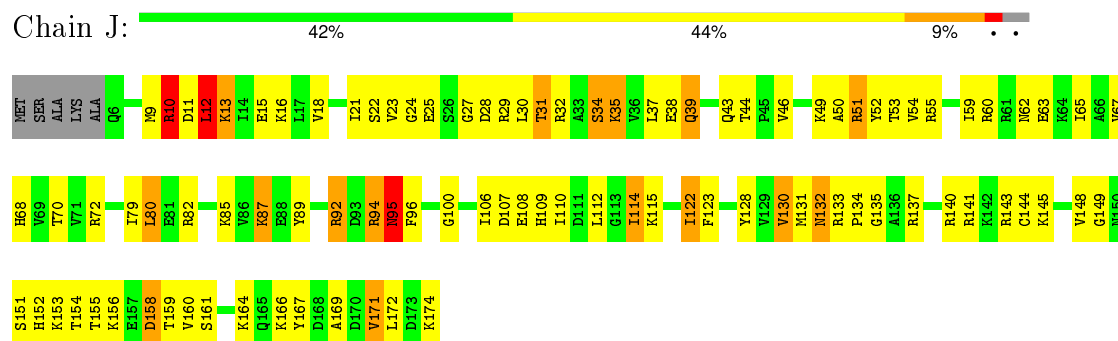
- Molecule 8: 60S RIBOSOMAL PROTEIN EL6



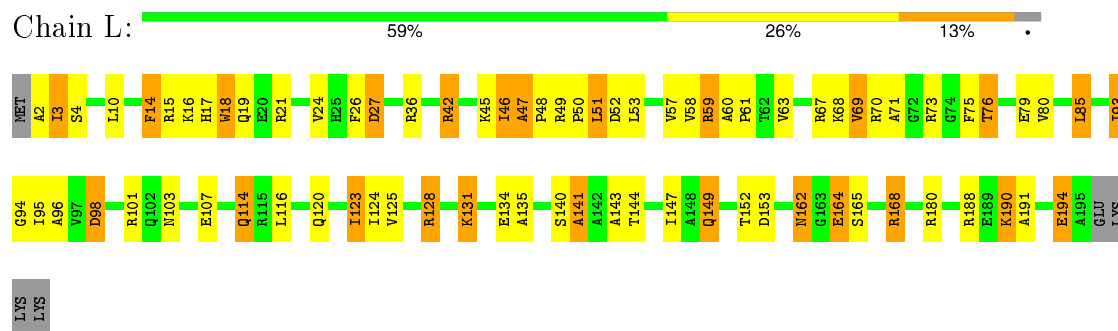
- Molecule 9: 60S ribosomal protein L7-A



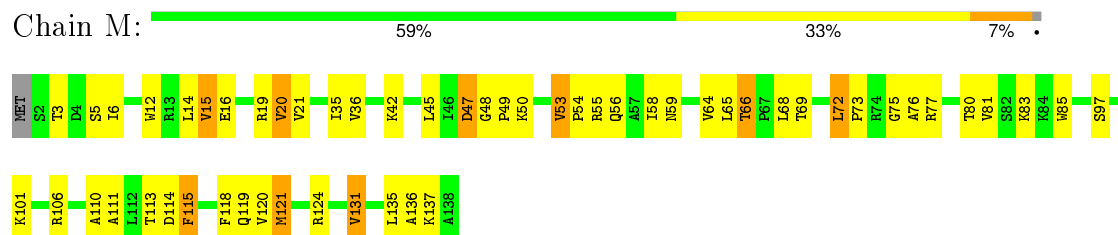




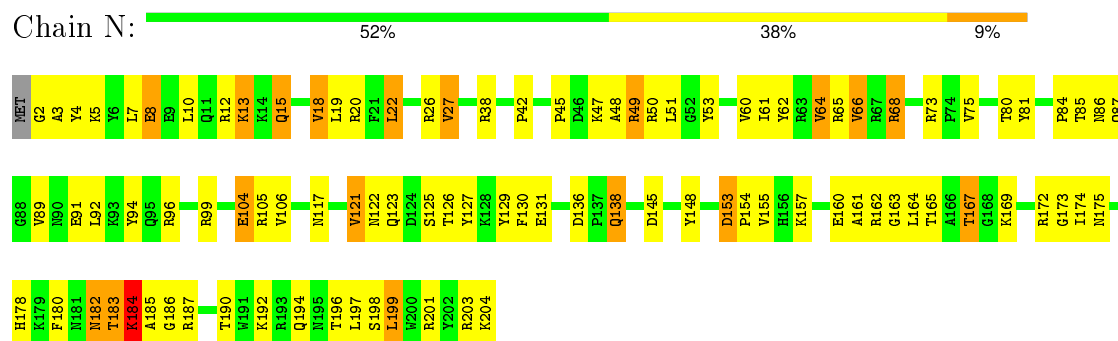
- Molecule 14: 60S ribosomal protein L13-A



- Molecule 15: 60S ribosomal protein L14-A

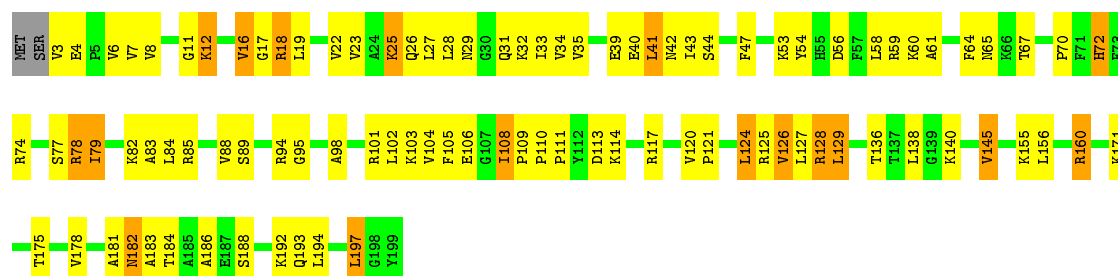


- Molecule 16: 60S ribosomal protein L15-A



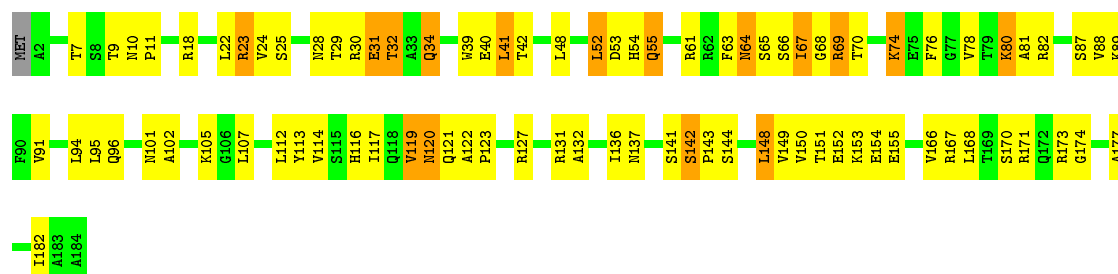
- Molecule 17: 60S ribosomal protein L16-A





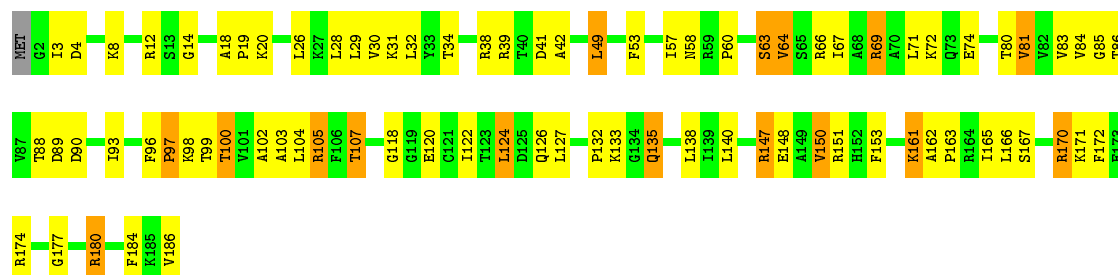
• Molecule 18: 60S ribosomal protein L17-A

Chain P: 53% 38% 9%



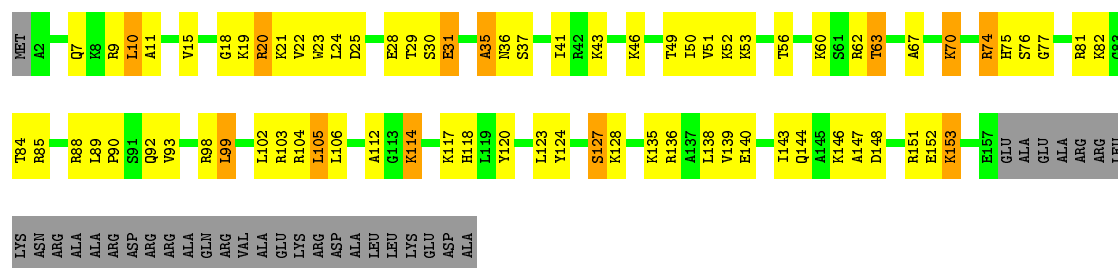
• Molecule 19: 60S ribosomal protein L18-A

Chain Q: 55% 35% 9%



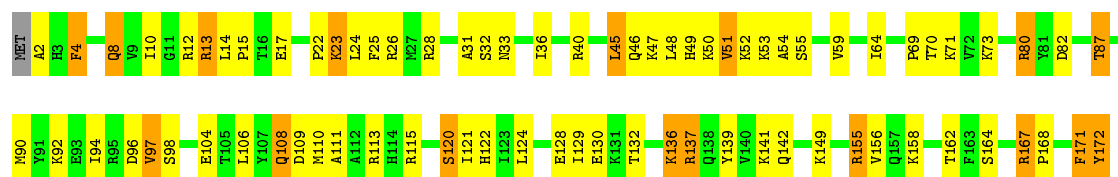
• Molecule 20: 60S ribosomal protein L19-A

Chain R: 42% 34% 6% 17%



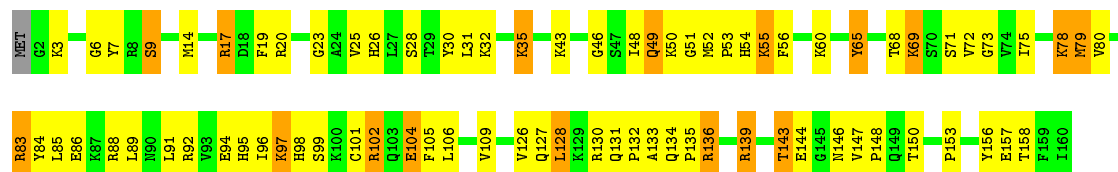
• Molecule 21: 60S ribosomal protein L20-A

Chain S: 55% 35% 10%



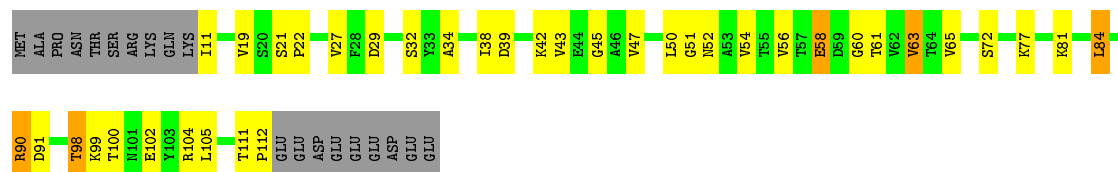
- Molecule 22: 60S ribosomal protein L21-A

Chain T: 50% 39% 11%



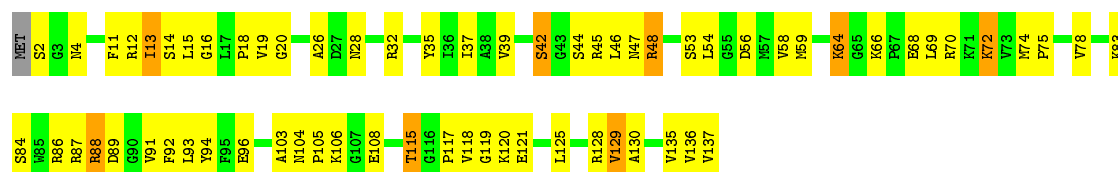
- Molecule 23: 60S ribosomal protein L22-A

Chain U: 53% 27% 16%



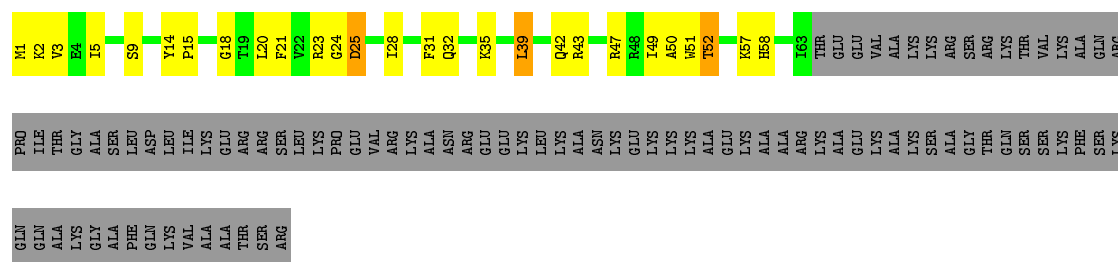
- Molecule 24: 60S ribosomal protein L23-A

Chain V: 51% 42% 6%



- Molecule 25: 60S ribosomal protein L24-A

Chain W: 23% 15% 59%



- Molecule 26: 60S ribosomal protein L25

Chain X: 40% 37% 8% 15%





- Molecule 33: 60S ribosomal protein L32

Chain e: 87% 12%



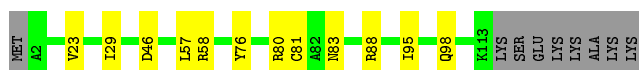
- Molecule 34: 60S ribosomal protein L33-A

Chain f: 93% 6%



- Molecule 35: 60S ribosomal protein L34-A

Chain g: 83% 10% 7%



- Molecule 36: 60S ribosomal protein L35-A

Chain h: 83% 16%



- Molecule 37: 60S ribosomal protein L36-A

Chain i: 76% 23%



- Molecule 38: 60S ribosomal protein L37-A

Chain j: 86% 13%



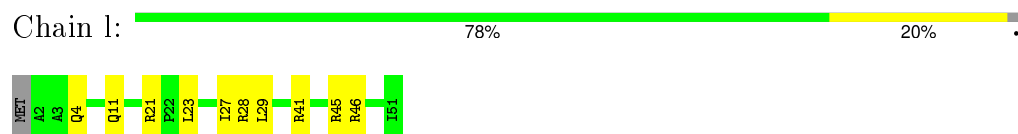
- Molecule 39: 60S ribosomal protein L38

Chain k: 88% 10%

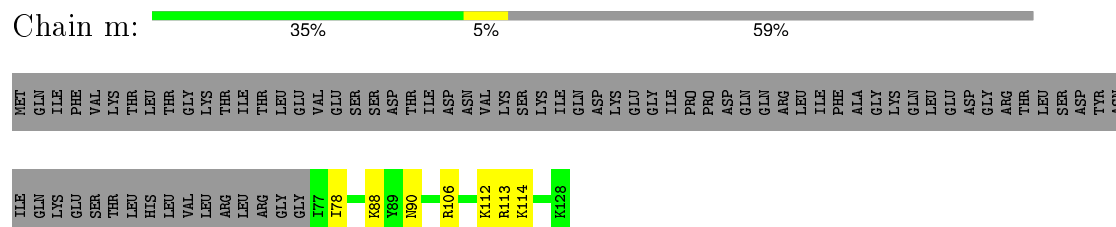




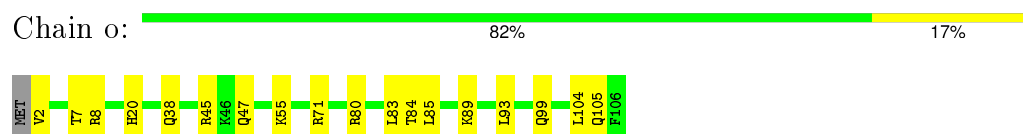
- Molecule 40: 60S ribosomal protein L39



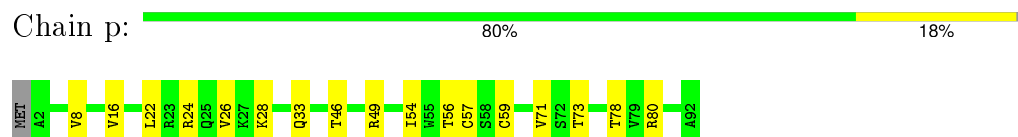
- Molecule 41: Ubiquitin-60S ribosomal protein L40



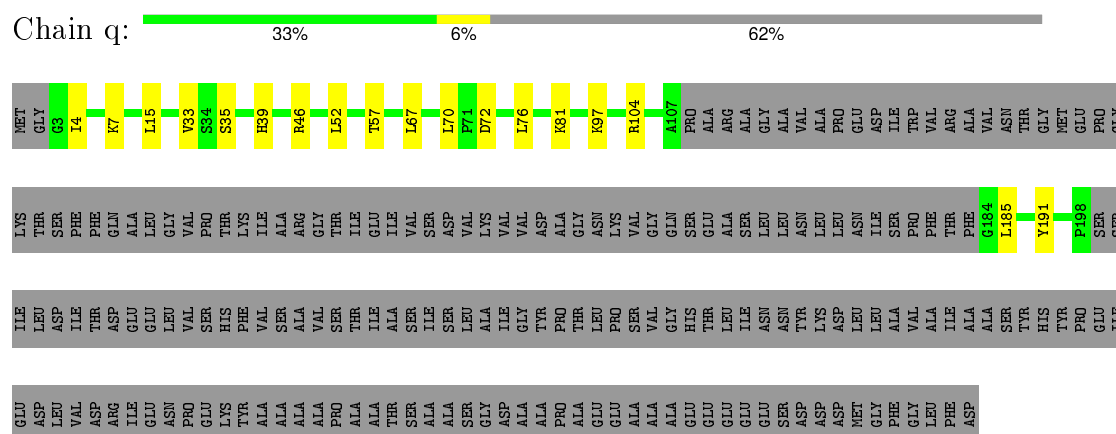
- Molecule 42: 60S ribosomal protein L42-A



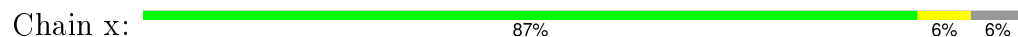
- Molecule 43: 60S ribosomal protein L43-A



- Molecule 44: 60S acidic ribosomal protein P0



- Molecule 45: Probable metalloprotease ARX1



[illegible]

- Molecule 47: ALB1

[illegible]

## 4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	PER DETECTOR FRAME	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	800.00	Depositor
Maximum defocus (nm)	3000.00	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: Y5P, ZN, P5P, 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	5	0.66	12/74039 (0.0%)	1.09	121/115426 (0.1%)
10	G	0.38	0/1795	0.58	0/2429
11	H	0.40	0/1539	0.54	0/2073
12	I	0.36	0/1758	0.57	0/2358
13	J	0.34	0/1374	0.55	0/1842
14	L	0.46	0/1573	0.61	0/2113
15	M	0.38	0/1074	0.55	0/1446
16	N	0.52	0/1757	0.65	0/2354
17	O	0.48	0/1585	0.63	1/2128 (0.0%)
18	P	0.50	0/1465	0.60	0/1968
19	Q	0.42	0/1465	0.61	0/1965
2	7	0.41	0/2883	0.90	1/4491 (0.0%)
20	R	0.39	0/1275	0.52	0/1702
21	S	0.45	0/1473	0.59	0/1980
22	T	0.42	0/1300	0.56	0/1743
23	U	0.36	0/825	0.56	0/1120
24	V	0.43	0/1018	0.60	0/1369
25	W	0.40	0/533	0.53	0/707
26	X	0.42	0/974	0.62	0/1314
27	Y	0.43	0/1004	0.62	0/1341
28	Z	0.38	0/1118	0.62	0/1497
29	a	0.47	0/1204	0.64	0/1612
3	8	0.69	0/3746	1.12	8/5832 (0.1%)
30	b	0.39	0/473	0.53	0/629
31	c	0.35	0/775	0.52	0/1040
32	d	0.46	0/897	0.62	0/1205
33	e	0.52	0/1055	0.63	0/1413
34	f	0.52	0/868	0.67	0/1168
35	g	0.43	0/890	0.63	0/1189
36	h	0.42	0/974	0.58	0/1297
37	i	0.35	0/777	0.55	0/1033
38	j	0.51	0/696	0.65	0/923

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	k	0.34	0/614	0.53	0/822
4	A	0.41	0/1662	0.60	0/2236
40	l	0.46	0/443	0.57	0/588
41	m	0.40	0/423	0.55	0/562
42	o	0.41	0/860	0.56	0/1136
43	p	0.46	0/701	0.62	0/934
44	q	0.58	0/977	0.61	0/1313
45	x	0.37	0/4557	0.57	0/6189
46	y	0.39	0/1746	0.54	0/2346
5	B	0.46	0/3146	0.59	0/4228
6	C	0.47	0/2800	0.67	1/3790 (0.0%)
7	D	0.34	0/2408	0.50	0/3248
8	E	0.39	0/1269	0.58	0/1705
9	F	0.46	0/1828	0.58	0/2461
All	All	0.57	12/137616 (0.0%)	0.93	132/202265 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
14	L	0	1
16	N	0	1
27	Y	0	1
28	Z	0	1
32	d	0	3
37	i	0	1
45	x	0	3
46	y	0	1
6	C	0	3
8	E	0	1
All	All	0	16

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1152	G	N9-C4	-7.14	1.32	1.38
1	5	2368	A	N9-C4	-6.55	1.33	1.37
1	5	336	A	N9-C4	-6.44	1.33	1.37
1	5	2392	C	N1-C6	-6.25	1.33	1.37
1	5	1446	A	N9-C4	-6.19	1.34	1.37

The worst 5 of 132 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1152	G	N3-C4-C5	10.03	133.61	128.60
1	5	408	A	N1-C6-N6	-8.94	113.24	118.60
1	5	1232	C	O4'-C1'-N1	8.59	115.07	108.20
1	5	2193	U	N1-C2-N3	8.32	119.89	114.90
3	8	62	C	C6-N1-C2	8.32	123.63	120.30

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	145	ILE	Peptide
6	C	148	ILE	Peptide
6	C	300	ARG	Peptide
8	E	67	GLY	Peptide
14	L	141	ALA	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	66537	0	33466	1532	0
2	7	2579	0	1304	66	0
3	8	3353	0	1695	81	0
4	A	1630	0	1682	124	0
5	B	3075	0	3142	185	0
6	C	2748	0	2859	171	0
7	D	2359	0	2311	131	0
8	E	1356	0	1448	98	0
9	F	1791	0	1869	114	0
10	G	1763	0	1819	117	0
11	H	1518	0	1587	77	0
12	I	1722	0	1755	101	0
13	J	1353	0	1383	89	0
14	L	1548	0	1613	91	0
15	M	1059	0	1154	55	0
16	N	1720	0	1779	90	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	O	1555	0	1659	96	0
18	P	1442	0	1485	72	0
19	Q	1441	0	1543	77	0
20	R	1258	0	1342	70	0
21	S	1437	0	1475	77	0
22	T	1276	0	1323	87	0
23	U	808	0	822	24	0
24	V	1003	0	1048	71	0
25	W	521	0	551	26	0
26	X	959	0	1023	64	0
27	Y	993	0	1081	81	0
28	Z	1092	0	1155	73	0
29	a	1173	0	1215	0	0
30	b	462	0	491	0	0
31	c	767	0	816	0	0
32	d	883	0	918	0	0
33	e	1034	0	1101	0	0
34	f	850	0	880	0	0
35	g	880	0	945	0	0
36	h	965	0	1067	0	0
37	i	770	0	846	0	0
38	j	681	0	683	0	0
39	k	608	0	671	0	0
40	l	436	0	475	0	0
41	m	417	0	455	0	0
42	o	847	0	914	0	0
43	p	694	0	734	0	0
44	q	962	0	989	0	0
45	x	4477	0	4559	0	0
46	y	1785	3	1755	0	0
47	z	510	0	517	0	0
48	5	259	0	0	0	0
48	7	6	0	0	0	0
48	8	7	0	0	0	0
48	B	2	0	0	0	0
48	C	1	0	0	0	0
48	N	1	0	0	0	0
48	P	1	0	0	0	0
48	R	1	0	0	0	0
48	V	1	0	0	0	0
48	y	1	0	0	0	0
49	j	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	m	1	0	0	0	0
49	o	1	0	0	0	0
49	p	1	0	0	0	0
49	y	2	0	0	0	0
All	All	129383	3	95404	3549	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 22.

The worst 5 of 3549 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)
15:M:48:GLY:HA3	15:M:53:VAL:HG13	1.25	1.18
4:A:149:ARG:HH12	4:A:155:LYS:HE3	1.06	1.18
8:E:78:ARG:HG3	8:E:78:ARG:HH11	1.03	1.14
5:B:4:ARG:HG3	5:B:4:ARG:HH11	1.03	1.12
10:G:44:ARG:HH11	10:G:44:ARG:HG3	1.15	1.11

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	
4	A	210/254 (83%)	195 (93%)	14 (7%)	1 (0%)	34	75
5	B	384/387 (99%)	367 (96%)	17 (4%)	0	100	100
6	C	359/362 (99%)	329 (92%)	28 (8%)	2 (1%)	30	73
7	D	292/297 (98%)	282 (97%)	8 (3%)	2 (1%)	26	70
8	E	155/176 (88%)	143 (92%)	9 (6%)	3 (2%)	10	50
9	F	221/244 (91%)	210 (95%)	10 (4%)	1 (0%)	34	75

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	G	229/256 (90%)	200 (87%)	28 (12%)	1 (0%)	39	79
11	H	189/191 (99%)	178 (94%)	10 (5%)	1 (0%)	34	75
12	I	209/221 (95%)	193 (92%)	16 (8%)	0	100	100
13	J	167/174 (96%)	143 (86%)	18 (11%)	6 (4%)	4	36
14	L	192/199 (96%)	170 (88%)	20 (10%)	2 (1%)	19	64
15	M	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
16	N	201/204 (98%)	187 (93%)	13 (6%)	1 (0%)	34	75
17	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
18	P	181/184 (98%)	176 (97%)	5 (3%)	0	100	100
19	Q	183/186 (98%)	174 (95%)	8 (4%)	1 (0%)	34	75
20	R	154/189 (82%)	148 (96%)	5 (3%)	1 (1%)	30	73
21	S	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
22	T	157/160 (98%)	151 (96%)	4 (2%)	2 (1%)	15	58
23	U	100/121 (83%)	95 (95%)	5 (5%)	0	100	100
24	V	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
25	W	61/155 (39%)	57 (93%)	3 (5%)	1 (2%)	12	53
26	X	118/142 (83%)	109 (92%)	9 (8%)	0	100	100
27	Y	124/127 (98%)	118 (95%)	5 (4%)	1 (1%)	24	68
28	Z	133/136 (98%)	112 (84%)	18 (14%)	3 (2%)	8	46
29	a	146/149 (98%)	132 (90%)	13 (9%)	1 (1%)	26	70
30	b	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
31	c	98/105 (93%)	92 (94%)	6 (6%)	0	100	100
32	d	107/113 (95%)	97 (91%)	8 (8%)	2 (2%)	10	50
33	e	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
34	f	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
35	g	110/121 (91%)	104 (94%)	5 (4%)	1 (1%)	21	66
36	h	117/120 (98%)	109 (93%)	8 (7%)	0	100	100
37	i	97/100 (97%)	86 (89%)	8 (8%)	3 (3%)	5	40
38	j	85/88 (97%)	77 (91%)	8 (9%)	0	100	100
39	k	75/78 (96%)	70 (93%)	4 (5%)	1 (1%)	15	58
40	l	48/51 (94%)	47 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	m	50/128 (39%)	46 (92%)	3 (6%)	1 (2%)	9	49
42	o	103/106 (97%)	94 (91%)	9 (9%)	0	100	100
43	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
44	q	116/312 (37%)	111 (96%)	4 (3%)	1 (1%)	21	66
45	x	577/616 (94%)	544 (94%)	32 (6%)	1 (0%)	52	87
46	y	201/401 (50%)	191 (95%)	10 (5%)	0	100	100
All	All	6958/7887 (88%)	6511 (94%)	407 (6%)	40 (1%)	34	73

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	98	VAL
13	J	10	ARG
13	J	95	ASN
16	N	184	LYS
25	W	25	ASP

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	166/196 (85%)	133 (80%)	33 (20%)	1	8
5	B	321/323 (99%)	260 (81%)	61 (19%)	2	9
6	C	288/289 (100%)	234 (81%)	54 (19%)	2	9
7	D	243/245 (99%)	209 (86%)	34 (14%)	4	23
8	E	135/136 (99%)	123 (91%)	12 (9%)	12	47
9	F	187/205 (91%)	168 (90%)	19 (10%)	9	39
10	G	177/208 (85%)	150 (85%)	27 (15%)	3	20
11	H	171/171 (100%)	148 (86%)	23 (14%)	5	25
12	I	179/187 (96%)	153 (86%)	26 (14%)	4	22
13	J	147/150 (98%)	122 (83%)	25 (17%)	2	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	L	154/159 (97%)	126 (82%)	28 (18%)	2	11
15	M	108/109 (99%)	95 (88%)	13 (12%)	6	30
16	N	175/176 (99%)	143 (82%)	32 (18%)	2	10
17	O	160/162 (99%)	129 (81%)	31 (19%)	2	8
18	P	145/146 (99%)	118 (81%)	27 (19%)	2	9
19	Q	150/151 (99%)	127 (85%)	23 (15%)	3	20
20	R	129/154 (84%)	106 (82%)	23 (18%)	2	12
21	S	155/156 (99%)	131 (84%)	24 (16%)	3	19
22	T	136/137 (99%)	113 (83%)	23 (17%)	2	14
23	U	89/107 (83%)	80 (90%)	9 (10%)	9	40
24	V	104/105 (99%)	93 (89%)	11 (11%)	8	37
25	W	55/129 (43%)	52 (94%)	3 (6%)	27	67
26	X	104/118 (88%)	86 (83%)	18 (17%)	2	13
27	Y	109/110 (99%)	96 (88%)	13 (12%)	6	30
28	Z	115/116 (99%)	92 (80%)	23 (20%)	1	7
29	a	118/119 (99%)	106 (90%)	12 (10%)	9	39
30	b	46/47 (98%)	38 (83%)	8 (17%)	2	13
31	c	84/88 (96%)	70 (83%)	14 (17%)	3	15
32	d	94/97 (97%)	85 (90%)	9 (10%)	10	42
33	e	110/111 (99%)	94 (86%)	16 (14%)	4	22
34	f	90/91 (99%)	84 (93%)	6 (7%)	20	61
35	g	95/103 (92%)	84 (88%)	11 (12%)	7	32
36	h	103/105 (98%)	84 (82%)	19 (18%)	2	10
37	i	80/82 (98%)	61 (76%)	19 (24%)	1	4
38	j	70/71 (99%)	59 (84%)	11 (16%)	3	18
39	k	67/69 (97%)	60 (90%)	7 (10%)	9	38
40	l	45/46 (98%)	35 (78%)	10 (22%)	1	5
41	m	47/116 (40%)	41 (87%)	6 (13%)	5	27
42	o	90/91 (99%)	72 (80%)	18 (20%)	1	7
43	p	71/72 (99%)	54 (76%)	17 (24%)	1	4
44	q	105/254 (41%)	88 (84%)	17 (16%)	3	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	x	508/540 (94%)	469 (92%)	39 (8%)	16	54
46	y	187/355 (53%)	171 (91%)	16 (9%)	13	49
All	All	5912/6602 (90%)	5042 (85%)	870 (15%)	8	21

5 of 870 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	O	41	LEU
20	R	114	LYS
44	q	52	LEU
17	O	108	ILE
18	P	127	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 107 such sidechains are listed below:

Mol	Chain	Res	Type
17	O	122	GLN
22	T	77	ASN
45	x	377	GLN
18	P	55	GLN
20	R	58	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3084/3396 (90%)	669 (21%)	73 (2%)
2	7	120/121 (99%)	14 (11%)	0
3	8	157/158 (99%)	36 (22%)	5 (3%)
All	All	3361/3675 (91%)	719 (21%)	78 (2%)

5 of 719 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	14	U
1	5	15	C
1	5	22	G
1	5	26	A
1	5	40	A

5 of 78 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	1816	A
1	5	2418	G
1	5	3357	U
1	5	1819	U
1	5	2204	C

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

20 non-standard protein/DNA/RNA residues are 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	$\# Z  > 2$
1	Y5P	5	1986	1	14,19,20	3.23	2 (14%)	18,26,29	3.04	2 (11%)
1	Y5P	5	1987	1	14,19,20	3.26	2 (14%)	18,26,29	2.89	2 (11%)
1	Y5P	5	1988	1	14,19,20	3.23	2 (14%)	18,26,29	2.98	2 (11%)
1	Y5P	5	1989	1	14,19,20	3.25	2 (14%)	18,26,29	2.88	2 (11%)
1	Y5P	5	1990	1	14,19,20	3.23	2 (14%)	18,26,29	3.01	2 (11%)
1	Y5P	5	1991	1	14,19,20	3.30	2 (14%)	18,26,29	2.81	2 (11%)
1	Y5P	5	1992	1	14,19,20	3.18	2 (14%)	18,26,29	3.01	2 (11%)
1	Y5P	5	1993	1	14,19,20	3.30	2 (14%)	18,26,29	2.90	2 (11%)
1	Y5P	5	1994	1	14,19,20	3.26	2 (14%)	18,26,29	3.05	2 (11%)
1	Y5P	5	1995	1	14,19,20	3.25	2 (14%)	18,26,29	2.87	2 (11%)
1	P5P	5	2016	1	16,23,24	0.71	0	15,33,36	0.78	0
1	P5P	5	2017	1	16,23,24	0.71	0	15,33,36	0.75	0
1	P5P	5	2018	1	16,23,24	0.72	0	15,33,36	0.79	0
1	P5P	5	2019	1	16,23,24	0.72	0	15,33,36	0.81	0
1	P5P	5	2020	1	16,23,24	0.71	0	15,33,36	0.81	0
1	P5P	5	2021	1	16,23,24	0.71	0	15,33,36	0.72	0
1	P5P	5	2022	1	16,23,24	0.72	0	15,33,36	0.82	0
1	P5P	5	2023	1	16,23,24	0.73	0	15,33,36	0.83	0
1	P5P	5	2024	1	16,23,24	0.70	0	15,33,36	0.79	0
1	P5P	5	2025	1	16,23,24	0.70	0	15,33,36	0.74	0

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
1	Y5P	5	1986	1	-	0/7/33/34	0/2/2/2
1	Y5P	5	1987	1	-	0/7/33/34	0/2/2/2
1	Y5P	5	1988	1	-	0/7/33/34	0/2/2/2
1	Y5P	5	1989	1	-	0/7/33/34	0/2/2/2
1	Y5P	5	1990	1	-	0/7/33/34	0/2/2/2
1	Y5P	5	1991	1	-	0/7/33/34	0/2/2/2
1	Y5P	5	1992	1	-	0/7/33/34	0/2/2/2
1	Y5P	5	1993	1	-	0/7/33/34	0/2/2/2
1	Y5P	5	1994	1	-	0/7/33/34	0/2/2/2
1	Y5P	5	1995	1	-	0/7/33/34	0/2/2/2
1	P5P	5	2016	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2017	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2018	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2019	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2020	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2021	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2022	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2023	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2024	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2025	1	-	0/3/25/26	0/3/3/3

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1991	Y5P	C4-N3	-11.56	1.38	1.46
1	5	1993	Y5P	C4-N3	-11.45	1.38	1.46
1	5	1987	Y5P	C4-N3	-11.41	1.38	1.46
1	5	1995	Y5P	C4-N3	-11.36	1.38	1.46
1	5	1989	Y5P	C4-N3	-11.34	1.38	1.46

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1986	Y5P	N1-C2-N3	-12.11	114.34	125.85
1	5	1994	Y5P	N1-C2-N3	-12.07	114.37	125.85
1	5	1992	Y5P	N1-C2-N3	-11.93	114.50	125.85
1	5	1990	Y5P	N1-C2-N3	-11.90	114.53	125.85
1	5	1988	Y5P	N1-C2-N3	-11.82	114.61	125.85

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	5	1987	Y5P	1	0
1	5	1988	Y5P	1	0
1	5	1989	Y5P	2	0
1	5	1990	Y5P	2	0
1	5	1991	Y5P	1	0
1	5	1992	Y5P	1	0
1	5	1993	Y5P	1	0
1	5	1994	Y5P	1	0
1	5	2017	P5P	1	0
1	5	2018	P5P	1	0
1	5	2023	P5P	1	0
1	5	2024	P5P	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 286 ligands modelled in this entry, 286 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 [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
47	<i>z</i>	2
1	<i>5</i>	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	<i>z</i>	107:UNK	C	115:UNK	N	20.22
1	<i>5</i>	1995:Y5P	O3'	2016:P5P	P	17.42
1	<i>z</i>	127:UNK	C	131:UNK	N	9.67