



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:46 PM BST

PDB ID : 5APN
EMDB ID: : 3152
Title : Structure of the yeast 60S ribosomal subunit in complex with Arx1, Alb1 and N-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, V.
Deposited on : 2015-09-17
Resolution : 3.91 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

A user guide is available at

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

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

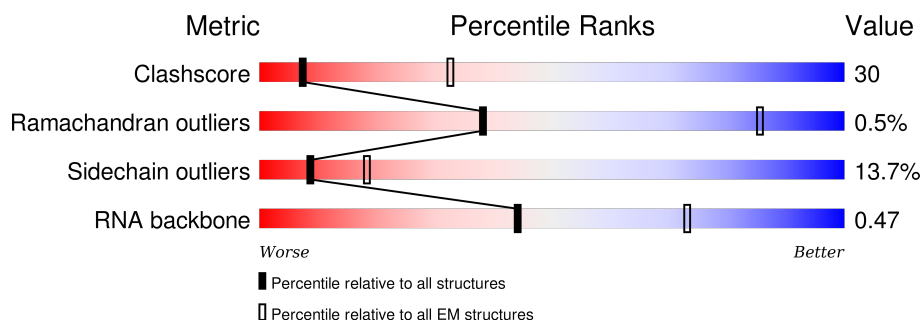
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.91 Å.

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



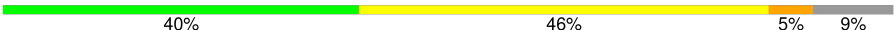

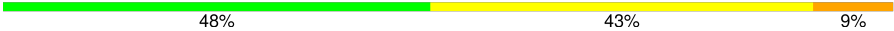








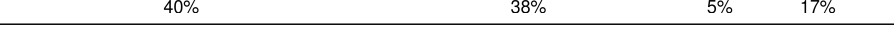







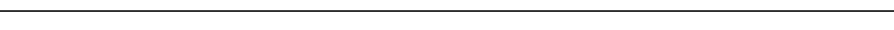

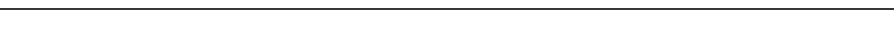
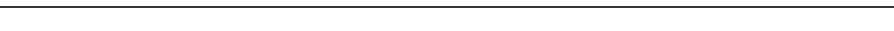


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	5	3396	
2	7	121	
3	8	158	
4	A	254	
5	B	387	
6	C	362	
7	D	297	
8	E	176	





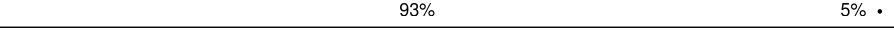

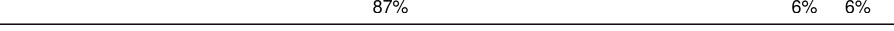
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Mol	Chain	Length	Quality of chain
9	F	244	
10	G	256	
11	H	191	
12	I	221	
13	J	174	
14	L	199	
15	M	138	
16	N	204	
17	O	199	
18	P	184	
19	Q	186	
20	R	189	
21	S	172	
22	T	160	
23	U	121	
24	V	137	
25	W	155	
26	X	142	
27	Y	127	
28	Z	136	
29	a	149	
30	b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

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Mol	Chain	Length	Quality of chain
34	f	107	 92% 7% .
35	g	121	 79% 14% 7%
36	h	120	 84% 15% .
37	i	100	 76% 22% ..
38	j	88	 86% 13% .
39	k	78	 83% 15% .
40	l	51	 86% 12% .
41	m	128	 32% 9% 59%
42	o	106	 88% 11% .
43	p	92	 93% 5% .
44	q	312	 34% . 62%
45	x	616	 87% 6% 6%
46	y	414	 48% . 49%
47	z	85	 100%

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 129324 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 rRNA.

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 rRNA.

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 rRNA.

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 L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	175	Total	C	N	O	S	0	0
			1355	877	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	211	Total	C	H	N	O	S	0	0
			1727	1095	3	307	314	8		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	-20	HIS	-	expression tag	UNP P38344
y	-19	HIS	-	expression tag	UNP P38344
y	-18	HIS	-	expression tag	UNP P38344
y	-17	HIS	-	expression tag	UNP P38344
y	-16	HIS	-	expression tag	UNP P38344
y	-15	HIS	-	expression tag	UNP P38344
y	-14	ASP	-	expression tag	UNP P38344
y	-13	TYR	-	expression tag	UNP P38344
y	-12	ASP	-	expression tag	UNP P38344
y	-11	ILE	-	expression tag	UNP P38344
y	-10	PRO	-	expression tag	UNP P38344
y	-9	THR	-	expression tag	UNP P38344
y	-8	THR	-	expression tag	UNP P38344
y	-7	GLU	-	expression tag	UNP P38344
y	-6	ASN	-	expression tag	UNP P38344
y	-5	LEU	-	expression tag	UNP P38344
y	-4	TYR	-	expression tag	UNP P38344
y	-3	PHE	-	expression tag	UNP P38344
y	-2	GLN	-	expression tag	UNP P38344
y	-1	GLY	-	expression tag	UNP P38344
y	0	ALA	-	expression tag	UNP P38344

- 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 1	Mg 1	0
48	B	1	Total 1	Mg 1	0
48	C	2	Total 2	Mg 2	0
48	V	1	Total 1	Mg 1	0
48	7	6	Total 6	Mg 6	0
48	a	2	Total 2	Mg 2	0
48	N	1	Total 1	Mg 1	0
48	5	259	Total 259	Mg 259	0
48	8	7	Total 7	Mg 7	0

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

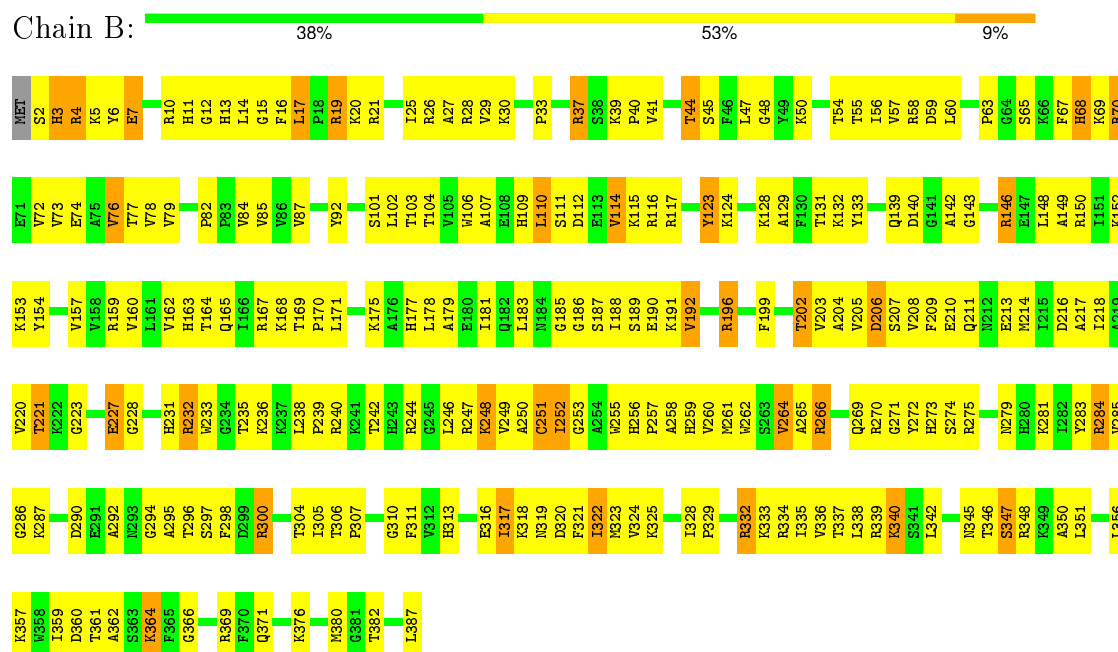
Mol	Chain	Residues	Atoms		AltConf
49	p	1	Total 1	Zn 1	0
49	o	1	Total 1	Zn 1	0
49	j	1	Total 1	Zn 1	0
49	y	2	Total 2	Zn 2	0
49	m	1	Total 1	Zn 1	0

A1946	C1856	G1780	U1702	U1629	G1560	A1477	C1397	C1328	U1258	U1191	C1119	U1051	G984	C918	A848
G1947	C1857	G1781	U1703	U1630	G1561	C1478	U1398	U1329	A1259	C1192	A1120	U1052	G985	C918	C849
G1948	A1858	U1781	C1710	A1631	C1562	U1479	A1399	A1330	A1260	A1193	U1121	A1053	U986	A921	U850
G1949	U1859	U1782	C1711	A1632	C1563	G1480	G1400	U1331	G1261	G1194	U1122	A1054	U987	U922	C851
U1950	G1860	U1783	C1711	C1633	U1564			A1332	A1262	A1195	U1055	U988	U988	G923	U852
C1951	G1861	G1784	G1712	G1634	G1565	U1484	U1405	C1333	A1263	C1196	U1125	U1056	U989	G924	G853
	U1862	U1785	G1713	G1635	A1566		A1406	U1334	G1264		G1126	A1057	U990	A925	
	G1863	U1786	G1714	U1636	U1567		A1407	C1335	U1265		G1127	U1058	G991	A926	G856
	A1864	A1787	A1715	A1637	U1568	A1491	U1417	U1336	G1266	A1200	U1128	U1059	G992	C927	G857
	G1865	G1788	U1716	A1638	U1569	G1492	G1418	A1337			A1130		G993	C928	A858
	C1866	G1789	U1717	C1639	U1570	U1494	A1418	C1338			G1131		G994	C929	A859
			G1718	G1640	U1571	U1495	A1419	C1339			G1132	A1064	A996	U930	G860
			G1719	U1641	U1572	C1496		G1340			A1133	A1065	A997		G861
			U1720	A1642	G1573	C1497	C1423	U1341			G1134	A1066	A998	G934	
	U1873	C1793	U1721	A1643	C1574	A1498	C1424					A1067	A999	G937	G869
	A1874	G1794	U1722	A1644	A1575	C1499						U1067	G999	C938	G870
	G1875	U1795	G1723	U1645	G1576	G1500	U1427	G1346	C1275		U1138	C1068	G1001	U939	C873
	U1876	G1796	A1724	G1646	A1577	U1501	A1428	U1347	C1276		G1139		G1002	G940	U874
	U1877	A1797	U1725	A1647	G1578	C1502	G1429	U1348	A1278		G1140		A1003		
	G1878	A1798	C1726	A1648	C1579	A1503	U1430	G1349	C1279				A1004	G941	
	A1879	U1799	G1727	U1649	U1580	A1504	G1431	A1350	C1280			U1073	U1004	U942	C877
	U1880	A1800	U1728	G1650	C1581		C1432	U1351	G1281			U1074	G1005	U943	G878
	G1881	U1801	G1729	U1651	C1582	C1508	A1433	A1352	G1282			A1075	A1006	C944	U879
	A1882		U1730		U1583	A1509	G1434	U1353	C1283			U1077	U1007	C945	G880
	U1883	C1805		A1654	U1584	G1510	U1435	G1354	C1284			G1147	U1008	U946	C881
	A1884	G1807		G1655	C1585	U1511	U1436	A1355	G1285			A1079	A1009	C947	A882
	A1886	A1808	G1736	A1656	G1586	U1512	C1437	U1356	A1286			U1080	G1010	C948	A883
	U1887	A1809	U1737	C1657		G1513	U1438	A1357				U1081	A1011	C949	
	U1888	G1810	A1741	G1658	U1589	G1519	U1439	C1358	A1290			U1082	G1014	U951	C886
	G1889	A1811	U1742	U1659	C1590	U1520	G1440	C1359	A1291			G1083	U1015	A952	G887
	U1890	G1812	G1743	C1660	U1591	G1521		G1360	A1292			A1084	C	G953	A888
	A1891	A1813		G1661	A1593	U1522	G1443	U1361	A1294			A1085	C		U889
	G1892	U1814	U1746	G1662	A1594	U1523	G1444	G1362	G1295			C1086	C	U956	C890
	U1893	A1815	G1747	C1663	U1595	U1524	U1445	C1363	C1296			G1089	G		G891
	A1894	A1816			C1596	A1524	A1446	A1364	C1297			G1090	G		U892
	U1895	G1817	U1750	G1668	C1597		U1447	G1365	C1298				G	C959	C893
	A1896	U1818	G1751	C1669	U1598	C1532	U1448	A1366	U1299			A1093	G	U960	G894
	G1897	U1819		C1670	G1599	U1533	U1449		G1300			A1094	U	C961	A895
	U1898	U1820		C1671	U1600	A1534		A1369	A1301			U1095	C	A962	A896
	G1899	A1821	G1756	A1676	G1604	A1535	A1452	G1370	A1302			U1096	G	A963	U897
		G1829	U1759	G1677	A1605	U1536		G1371				U1097	A	G964	U898
	U1906	G1830	A1760	A1678	U1606	U1539	U1458	C1372				U1098	A	A965	U899
	A1909		C1761	A1679	U1607	G1541	A1461	G1373	U1305			A1098	A	U966	G900
	G1919	A1839	U1762	U1682	C1609	G1542	U1462	A1374	G1306			A1099	U	A967	G901
	U1920	U1840	U1763	U1683	G1610	G1543	A1463	G1380	G1307			U1100	G	G968	G902
	U1921	A1841	U1764	U1684			U1464	A1381	A1308			U1109	C	C969	U903
	U1922	A1842	U1765	C1685			G1465	G1382	U1309			U1110	A	A970	A904
	G1928	C1843	G1766	U1686	G1614	A1546	A1466	G1383				G1104	C	G971	U905
	U1929	G1844	U1767	U1687	C1615	G1547	U1467	U1384	C1312			A1105	U	A972	A906
		U1846	C1768	U1688	U1616	C1548	A1467	C1385	G1313			U1108	U	A973	G907
	G1935	A1847	G1769	U1689	G1617	U1549	U1468	C1386	C1314			U1109	G1035	G974	G908
	U1939	U1848	U1770	C1690	A1619	U1553	U1469	U1387	U1315			U1110	A1036	C975	G909
	G1940	G1848	C1771	U1691	U1620	U1554	U1471	U1388	G1316			U1111	C1037	U976	G910
	U1941	C1849	U1772	A1621	U1622	U1555	U1472		U1317			U1181	C1038	C977	C911
	G1942	A1850	C1773	U1622	C1693	C1556	U1473		C1248			A1112	U1039	G978	G912
	P1943	G1851	G1774			A1557	A1475					G1115	A1047	U979	G913
	P1944	U1944	G1775	C1698	U1626	U1558	U1476		U1263			G1116	A1048	A980	A914
	A1945		G1776			A1559	G1476		C1257			G1117	C1049	U981	A915
													U1050	A983	G916
															A917

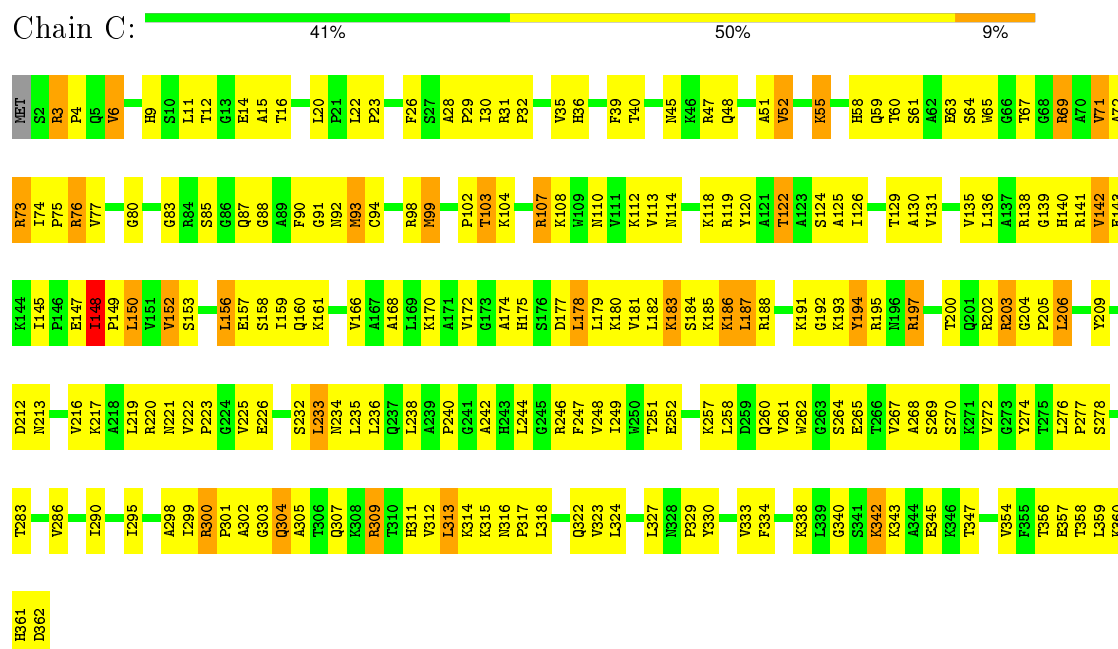



LYS
ALA
SER
THR
R4
H3
ILE
SER
ARG
GLY
VAL
SER
GLY
GLN
LYS
ALA
GLY
LEU
ILE
ALA
ALA
ARG
ARG
THR
GLY
LEU
LEU
ARG
GLY
SER
GLN
LYS
THR
GLN
ASP

• Molecule 5: 60S ribosomal protein L3

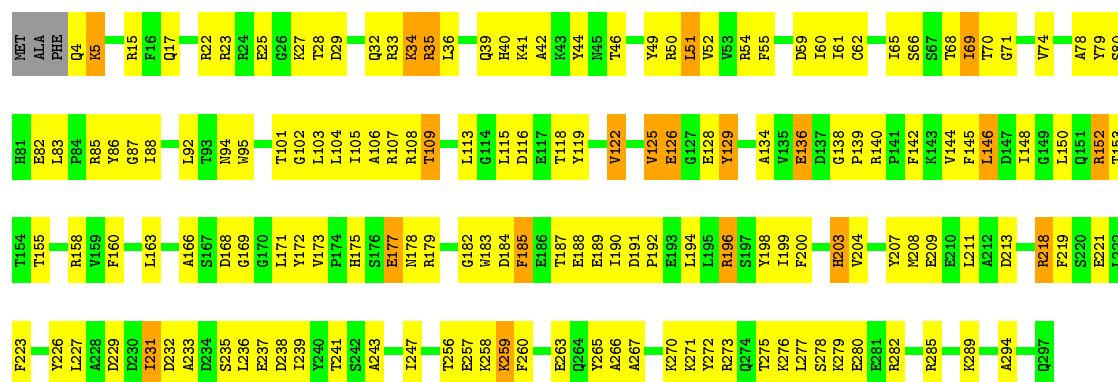


• Molecule 6: 60S ribosomal protein L4-A



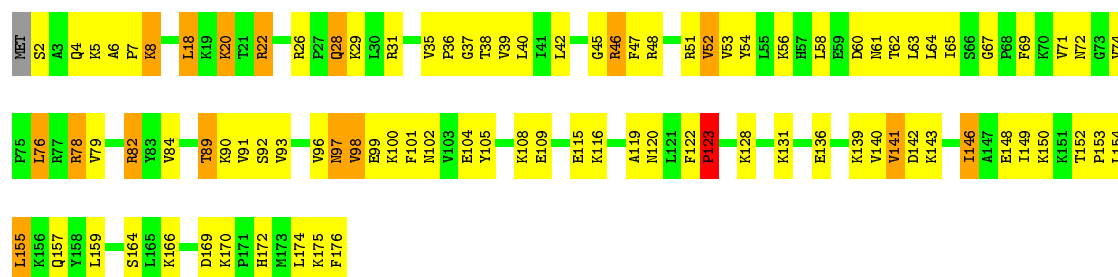
• Molecule 7: 60S ribosomal protein L5





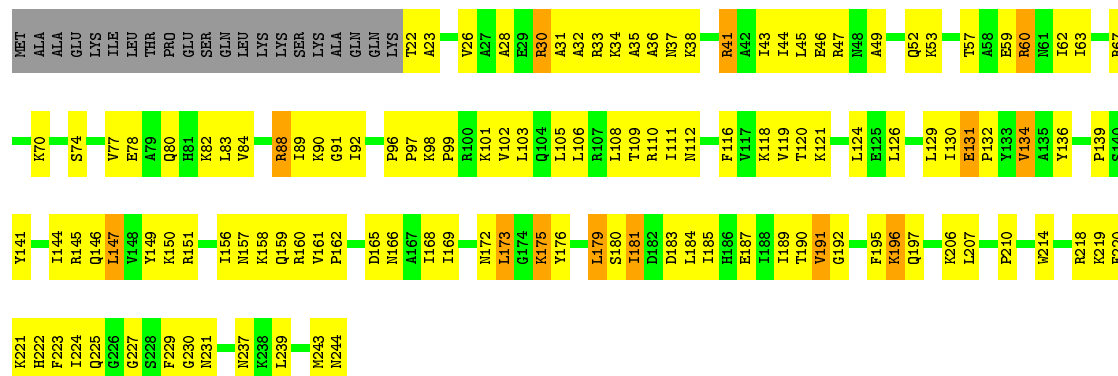
• Molecule 8: 60S ribosomal protein L6-A

Chain E: 46% 44% 9% ..



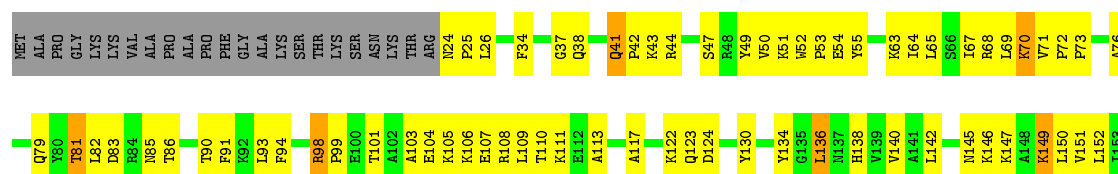
• Molecule 9: 60S ribosomal protein L7-A

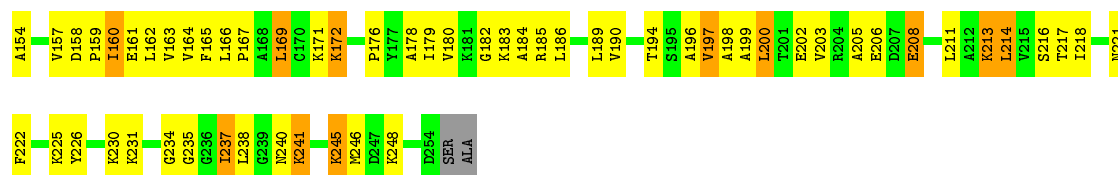
Chain F: 40% 46% 5% 9%



• Molecule 10: 60S ribosomal protein L8-A

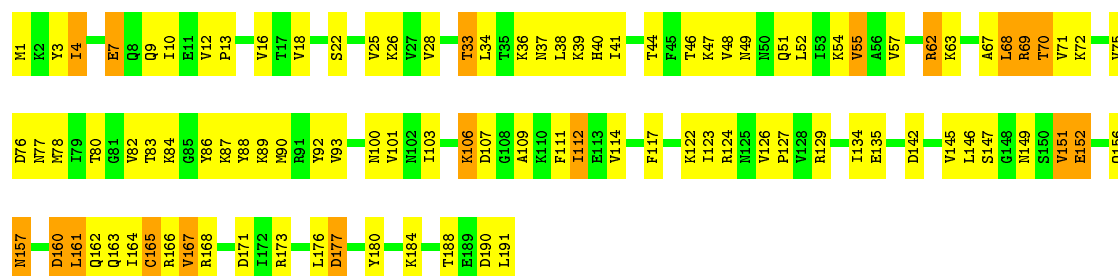
Chain G: 41% 43% 7% 10%





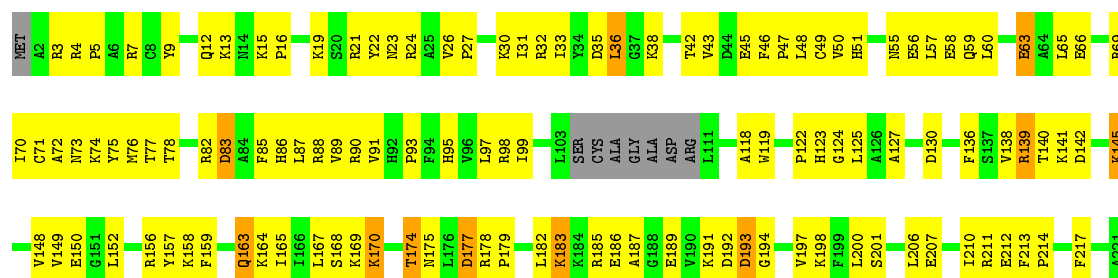
• Molecule 11: 60S ribosomal protein L9-A

Chain H: 48% 43% 9%



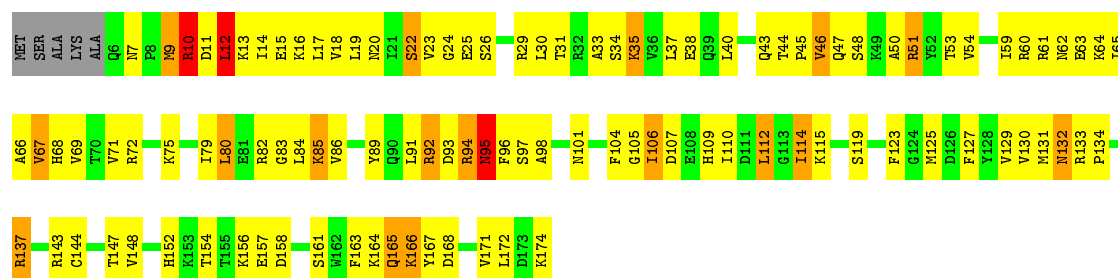
• Molecule 12: 60S ribosomal protein L10

Chain I: 41% 50% 5%



• Molecule 13: 60S ribosomal protein L11-A

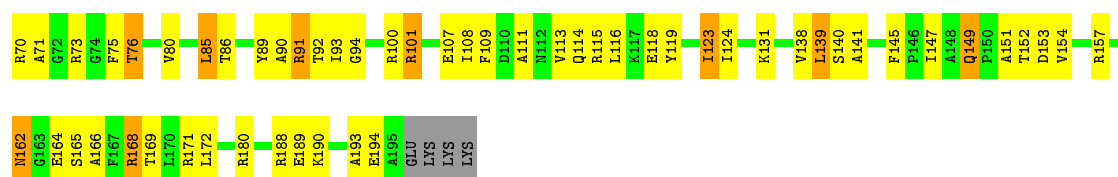
Chain J: 36% 50% 10%



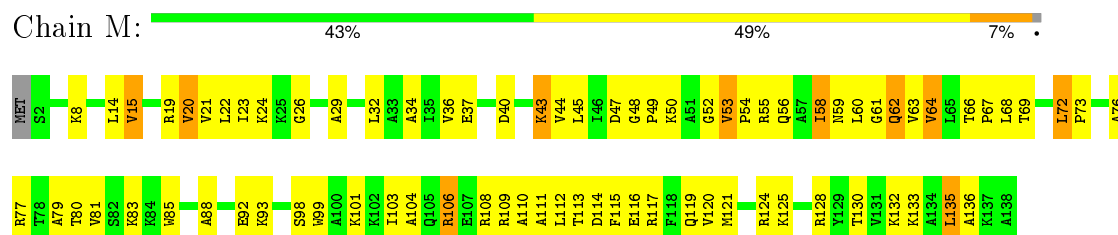
• Molecule 14: 60S ribosomal protein L13-A

Chain L: 48% 43% 7%

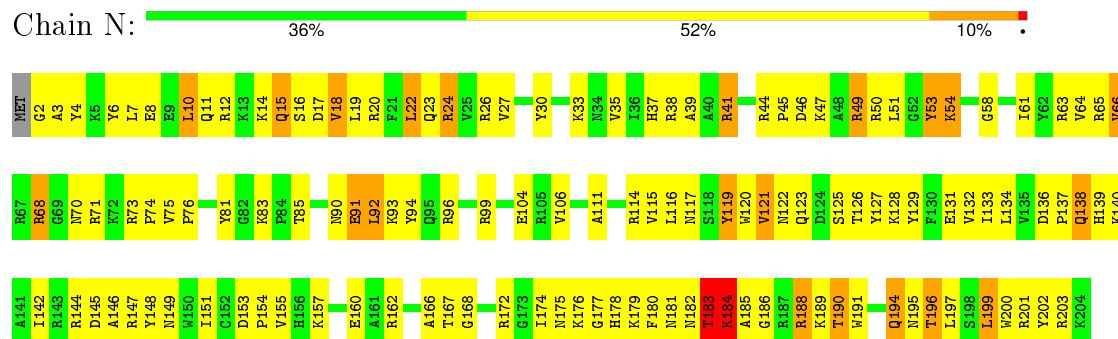




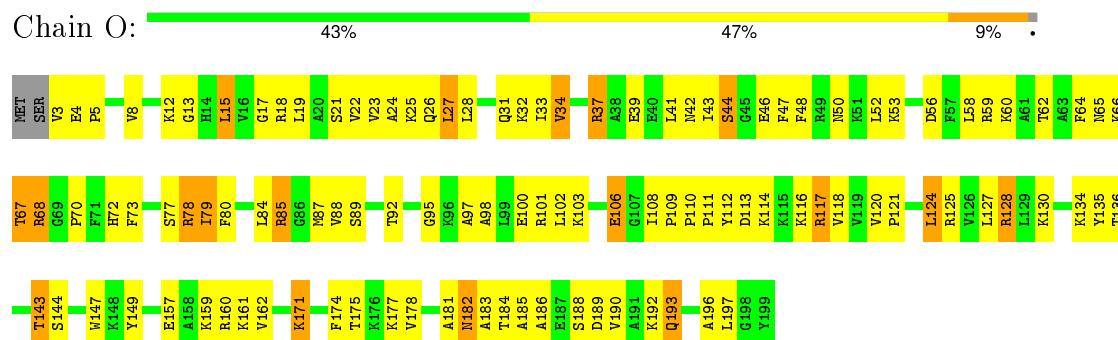
• Molecule 15: 60S ribosomal protein L14-A



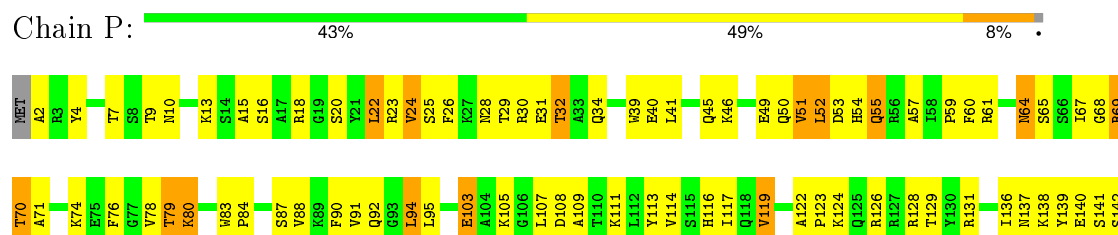
• Molecule 16: 60S ribosomal protein L15-A

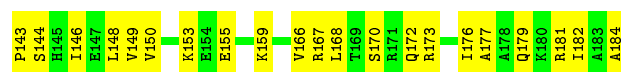


• Molecule 17: 60S ribosomal protein L16-A



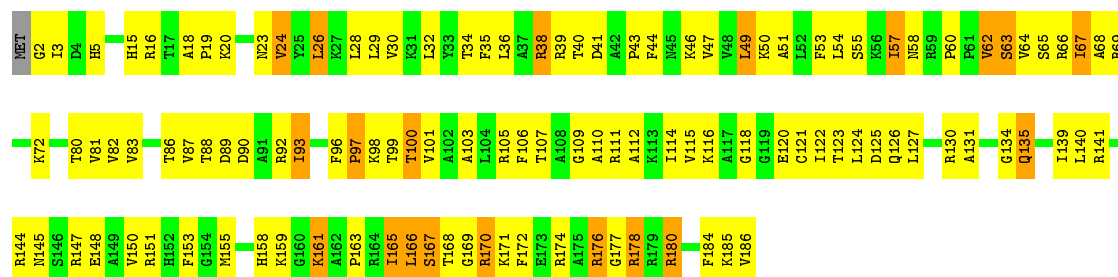
• Molecule 18: 60S ribosomal protein L17-A





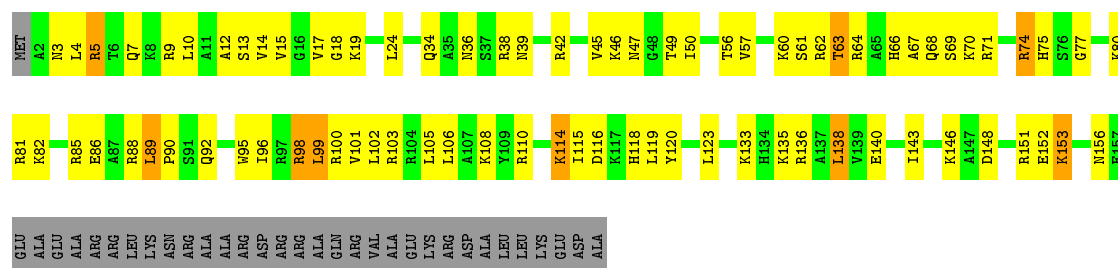
• Molecule 19: 60S ribosomal protein L18-A

Chain Q: 37% 52% 11%



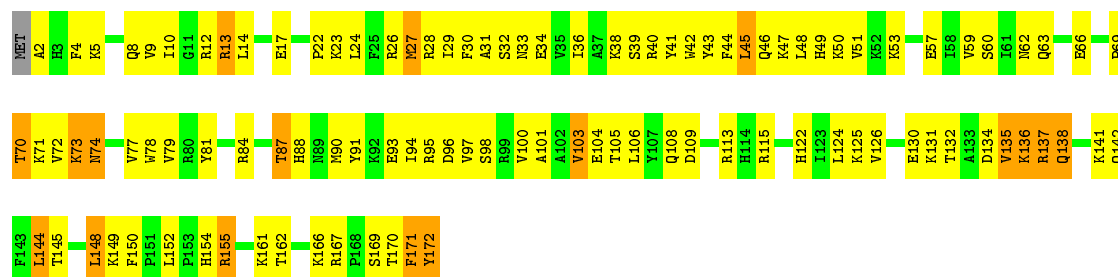
• Molecule 20: 60S ribosomal protein L19-A

Chain R: 40% 38% 5% 17%



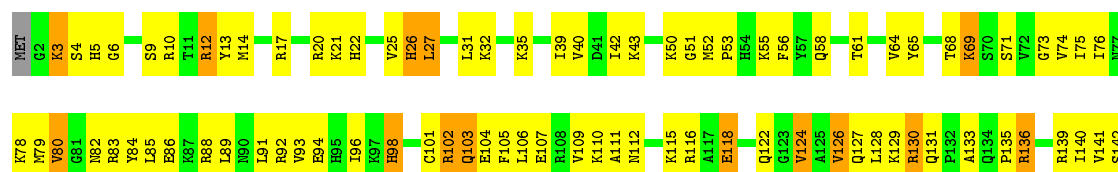
• Molecule 21: 60S ribosomal protein L20-A

Chain S: 38% 51% 10%



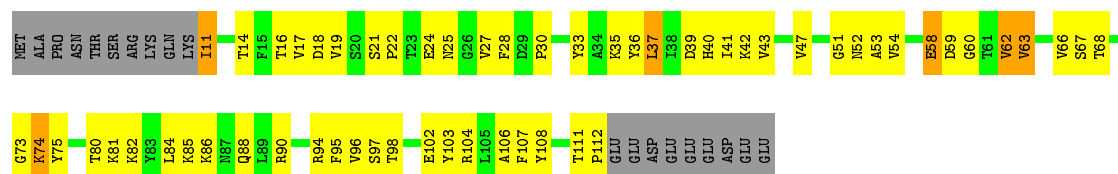
• Molecule 22: 60S ribosomal protein L21-A

Chain T: 41% 49% 9%

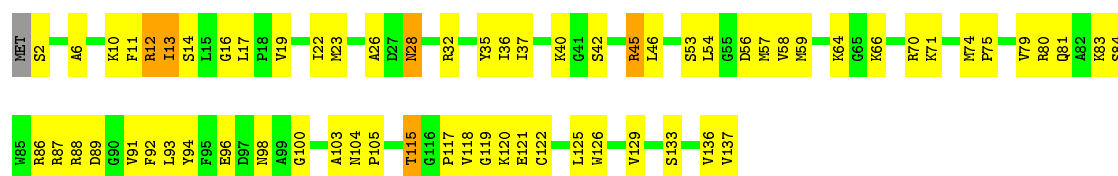




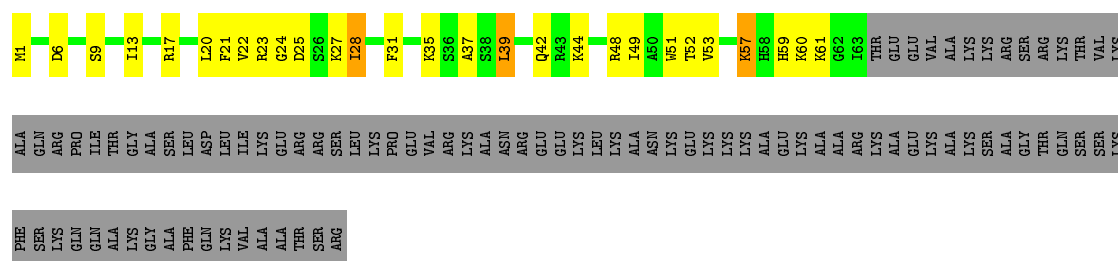
• Molecule 23: 60S ribosomal protein L22-A



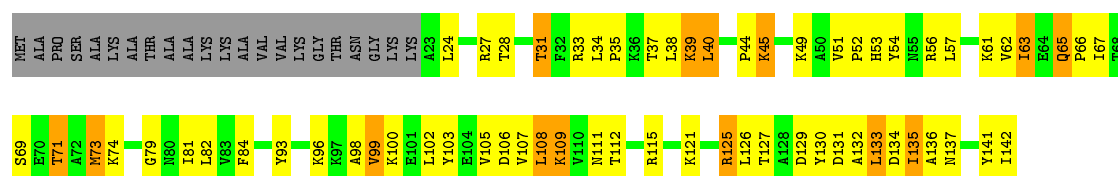
• Molecule 24: 60S ribosomal protein L23-A



• Molecule 25: 60S ribosomal protein L24-A

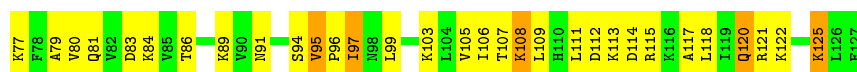


• Molecule 26: 60S ribosomal protein L25



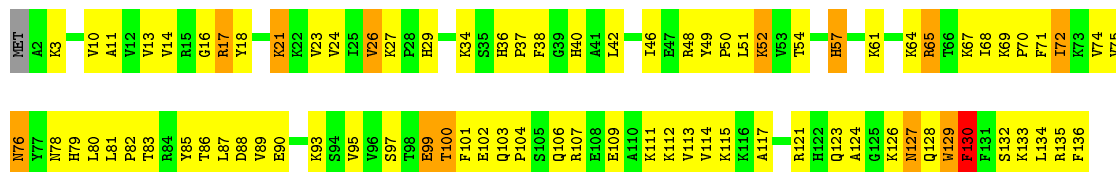
• Molecule 27: 60S ribosomal protein L26-A





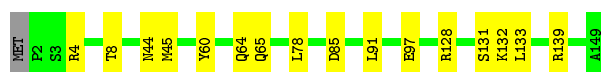
- Molecule 28: 60S ribosomal protein L27-A

Chain Z: 38% 51% 9% ..



- Molecule 29: 60S ribosomal protein L28

Chain a: 89% 11% .



- Molecule 30: 60S ribosomal protein L29

Chain b: 85% 14% .



- Molecule 31: 60S ribosomal protein L30

Chain c: 83% 12% 5%



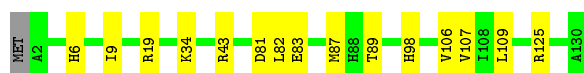
- Molecule 32: 60S ribosomal protein L31-A

Chain d: 84% 12% .



- Molecule 33: 60S ribosomal protein L32

Chain e: 88% 12% .

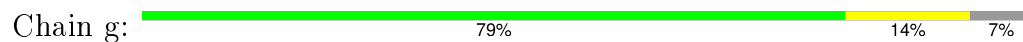


- Molecule 34: 60S ribosomal protein L33-A

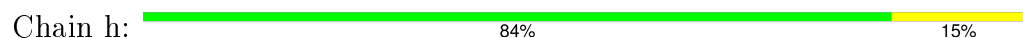
Chain f: 92% 7% .



- Molecule 35: 60S ribosomal protein L34-A



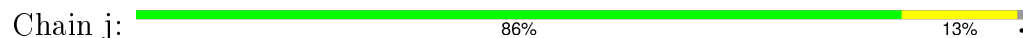
- Molecule 36: 60S ribosomal protein L35-A



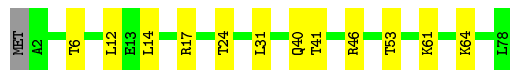
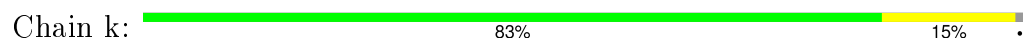
- Molecule 37: 60S ribosomal protein L36-A



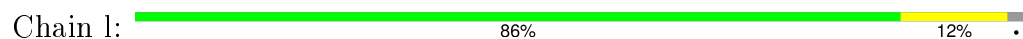
- Molecule 38: 60S ribosomal protein L37-A



- Molecule 39: 60S ribosomal protein L38

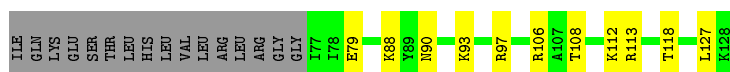


- Molecule 40: 60S ribosomal protein L39

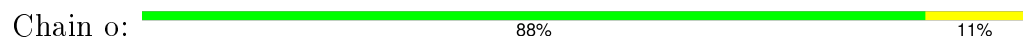


- Molecule 41: Ubiquitin-60S ribosomal protein L40





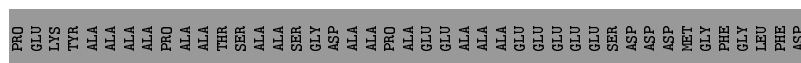
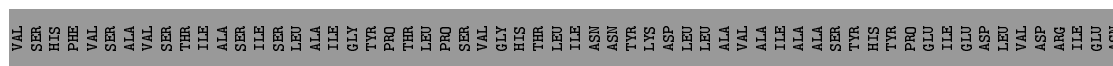
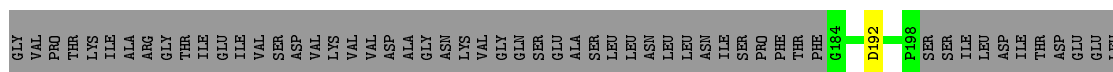
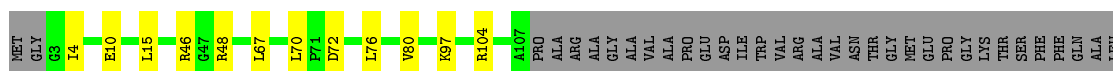
- Molecule 42: 60S ribosomal protein L42-A



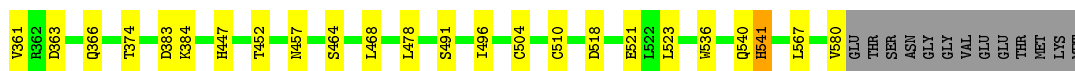
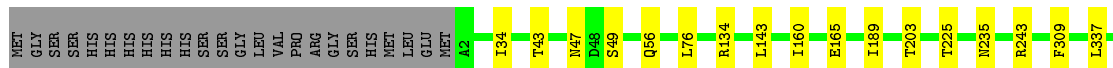
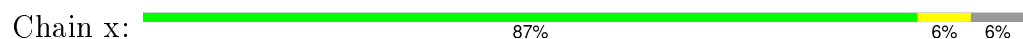
- Molecule 43: 60S ribosomal protein L43-A



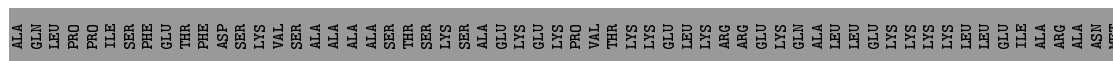
- Molecule 44: 60S acidic ribosomal protein P0

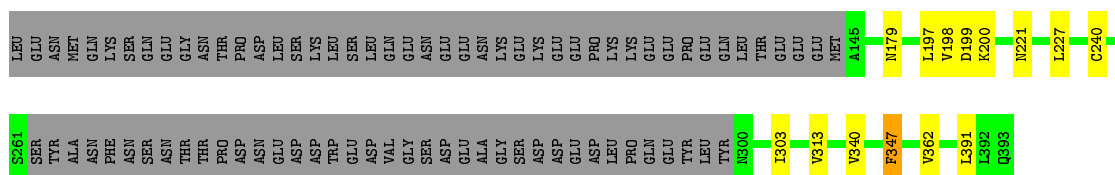


- Molecule 45: Probable metalloprotease ARX1



- Molecule 46: Cytoplasmic 60S subunit biogenesis factor REI1





- Molecule 47: ALB1

Chain z:  100%

There are no outlier residues recorded for this chain.

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 ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	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	0.45	1/74039 (0.0%)	0.94	44/115426 (0.0%)
10	G	0.34	0/1795	0.55	0/2429
11	H	0.34	0/1539	0.50	0/2073
12	I	0.34	0/1758	0.57	0/2358
13	J	0.33	0/1374	0.54	0/1842
14	L	0.35	0/1573	0.59	0/2113
15	M	0.34	0/1074	0.54	0/1446
16	N	0.43	0/1757	0.57	0/2354
17	O	0.37	0/1585	0.52	0/2128
18	P	0.39	0/1465	0.55	0/1968
19	Q	0.35	0/1465	0.56	0/1965
2	7	0.33	0/2883	0.85	0/4491
20	R	0.34	0/1275	0.48	0/1702
21	S	0.37	0/1473	0.54	0/1980
22	T	0.36	0/1300	0.51	0/1743
23	U	0.34	0/825	0.54	0/1120
24	V	0.33	0/1018	0.52	0/1369
25	W	0.36	0/533	0.47	0/707
26	X	0.35	0/974	0.60	0/1314
27	Y	0.33	0/1004	0.52	0/1341
28	Z	0.36	0/1118	0.59	0/1497
29	a	0.38	0/1204	0.57	0/1612
3	8	0.47	0/3746	0.97	1/5832 (0.0%)
30	b	0.33	0/473	0.53	0/629
31	c	0.35	0/775	0.53	0/1040
32	d	0.38	0/897	0.58	0/1205
33	e	0.37	0/1055	0.54	0/1413
34	f	0.39	0/868	0.55	0/1168
35	g	0.35	0/890	0.57	0/1189
36	h	0.37	0/974	0.55	0/1297
37	i	0.33	0/777	0.53	0/1033
38	j	0.39	0/696	0.58	0/923

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	k	0.35	0/614	0.58	0/822
4	A	0.34	0/1662	0.55	0/2236
40	l	0.37	0/443	0.53	0/588
41	m	0.33	0/423	0.53	0/562
42	o	0.38	0/860	0.59	0/1136
43	p	0.34	0/701	0.53	0/934
44	q	0.55	0/977	0.63	0/1313
45	x	0.37	0/4557	0.57	0/6189
46	y	0.41	0/1759	0.55	0/2363
5	B	0.36	0/3146	0.55	0/4228
6	C	0.37	0/2800	0.58	0/3790
7	D	0.34	0/2408	0.51	0/3248
8	E	0.34	0/1377	0.58	0/1851
9	F	0.36	0/1828	0.54	0/2461
All	All	0.41	1/137737 (0.0%)	0.82	45/202428 (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	J	0	1
16	N	0	2
28	Z	0	1
32	d	0	2
35	g	0	1
45	x	0	2
46	y	0	1
6	C	0	2
All	All	0	12

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1394	A	N9-C4	-5.33	1.34	1.37

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	2307	G	C4-N9-C1'	-8.80	115.06	126.50
1	5	2307	G	C8-N9-C1'	8.09	137.51	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1555	U	N3-C2-O2	-8.00	116.60	122.20
1	5	1812	G	N3-C4-N9	-7.42	121.55	126.00
1	5	2309	A	C8-N9-C4	-6.81	103.08	105.80

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	148	ILE	Peptide
6	C	197	ARG	Peptide
13	J	9	MET	Peptide
16	N	183	THR	Peptide
16	N	184	LYS	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	5	66537	0	33464	2243	0
2	7	2579	0	1303	103	0
3	8	3353	0	1695	131	0
4	A	1630	0	1682	143	0
5	B	3075	0	3142	281	0
6	C	2748	0	2859	266	0
7	D	2359	0	2311	166	0
8	E	1355	0	1413	111	0
9	F	1791	0	1869	148	0
10	G	1763	0	1819	156	0
11	H	1518	0	1587	118	0
12	I	1722	0	1755	134	0
13	J	1353	0	1383	140	0
14	L	1548	0	1613	138	0
15	M	1059	0	1154	84	0
16	N	1720	0	1779	169	0
17	O	1555	0	1659	126	0
18	P	1442	0	1485	117	0
19	Q	1441	0	1543	133	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	R	1258	0	1342	93	0
21	S	1437	0	1475	110	0
22	T	1276	0	1323	99	0
23	U	808	0	822	54	0
24	V	1003	0	1048	86	0
25	W	521	0	551	23	0
26	X	959	0	1023	67	0
27	Y	993	0	1081	79	0
28	Z	1092	0	1155	81	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	1724	3	1681	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	1	0	0	0	0
48	C	2	0	0	0	0
48	N	1	0	0	0	0
48	P	1	0	0	0	0
48	V	1	0	0	0	0
48	a	2	0	0	0	0
49	j	1	0	0	0	0
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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	129321	3	95292	4990	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 30.

The worst 5 of 4990 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)
17:O:128:ARG:HG3	17:O:128:ARG:HH11	1.11	1.14
10:G:162:LEU:HD23	16:N:7:LEU:HD11	1.30	1.13
14:L:91:ARG:HH11	14:L:91:ARG:HG3	1.15	1.11
1:5:2158:A:H4'	1:5:2159:U:H5''	1.27	1.11
11:H:87:LYS:HD3	11:H:191:LEU:HD21	1.33	1.09

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%)	193 (92%)	17 (8%)	0	100	100
5	B	384/387 (99%)	359 (94%)	25 (6%)	0	100	100
6	C	359/362 (99%)	330 (92%)	27 (8%)	2 (1%)	30	73
7	D	292/297 (98%)	283 (97%)	7 (2%)	2 (1%)	26	71
8	E	173/176 (98%)	160 (92%)	10 (6%)	3 (2%)	11	55
9	F	221/244 (91%)	211 (96%)	9 (4%)	1 (0%)	34	77
10	G	229/256 (90%)	201 (88%)	26 (11%)	2 (1%)	21	66
11	H	189/191 (99%)	178 (94%)	10 (5%)	1 (0%)	34	77
12	I	209/221 (95%)	193 (92%)	16 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	J	167/174 (96%)	143 (86%)	19 (11%)	5 (3%)	5	44
14	L	192/199 (96%)	169 (88%)	21 (11%)	2 (1%)	19	65
15	M	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
16	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	19	65
17	O	195/199 (98%)	190 (97%)	5 (3%)	0	100	100
18	P	181/184 (98%)	176 (97%)	5 (3%)	0	100	100
19	Q	183/186 (98%)	173 (94%)	9 (5%)	1 (0%)	34	77
20	R	154/189 (82%)	148 (96%)	6 (4%)	0	100	100
21	S	169/172 (98%)	161 (95%)	8 (5%)	0	100	100
22	T	157/160 (98%)	153 (98%)	2 (1%)	2 (1%)	15	60
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%)	4 (7%)	0	100	100
26	X	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
27	Y	124/127 (98%)	118 (95%)	5 (4%)	1 (1%)	24	69
28	Z	133/136 (98%)	114 (86%)	16 (12%)	3 (2%)	8	50
29	a	146/149 (98%)	131 (90%)	14 (10%)	1 (1%)	26	71
30	b	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
31	c	98/105 (93%)	91 (93%)	7 (7%)	0	100	100
32	d	107/113 (95%)	97 (91%)	9 (8%)	1 (1%)	21	66
33	e	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
34	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
35	g	110/121 (91%)	100 (91%)	8 (7%)	2 (2%)	11	54
36	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
37	i	97/100 (97%)	87 (90%)	7 (7%)	3 (3%)	5	44
38	j	85/88 (97%)	78 (92%)	7 (8%)	0	100	100
39	k	75/78 (96%)	68 (91%)	6 (8%)	1 (1%)	15	60
40	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	m	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
42	o	103/106 (97%)	96 (93%)	7 (7%)	0	100	100
43	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	q	116/312 (37%)	109 (94%)	7 (6%)	0	100	100
45	x	577/616 (94%)	540 (94%)	37 (6%)	0	100	100
46	y	207/414 (50%)	192 (93%)	15 (7%)	0	100	100
All	All	6982/7900 (88%)	6509 (93%)	437 (6%)	36 (0%)	38	77

5 of 36 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
13	J	115	LYS

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%)	139 (84%)	27 (16%)	3	21
5	B	319/323 (99%)	269 (84%)	50 (16%)	3	23
6	C	288/289 (100%)	240 (83%)	48 (17%)	3	20
7	D	243/245 (99%)	216 (89%)	27 (11%)	8	38
8	E	136/153 (89%)	119 (88%)	17 (12%)	6	32
9	F	187/205 (91%)	166 (89%)	21 (11%)	7	37
10	G	177/208 (85%)	154 (87%)	23 (13%)	5	31
11	H	171/171 (100%)	144 (84%)	27 (16%)	3	23
12	I	179/187 (96%)	157 (88%)	22 (12%)	6	32
13	J	147/150 (98%)	122 (83%)	25 (17%)	2	20
14	L	154/159 (97%)	136 (88%)	18 (12%)	7	35
15	M	108/109 (99%)	93 (86%)	15 (14%)	4	29
16	N	175/176 (99%)	147 (84%)	28 (16%)	3	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	O	160/162 (99%)	136 (85%)	24 (15%)	3	25
18	P	145/146 (99%)	128 (88%)	17 (12%)	7	35
19	Q	150/151 (99%)	124 (83%)	26 (17%)	2	18
20	R	129/154 (84%)	111 (86%)	18 (14%)	4	28
21	S	155/156 (99%)	129 (83%)	26 (17%)	2	20
22	T	136/137 (99%)	112 (82%)	24 (18%)	2	18
23	U	89/107 (83%)	76 (85%)	13 (15%)	4	26
24	V	104/105 (99%)	95 (91%)	9 (9%)	13	49
25	W	55/129 (43%)	50 (91%)	5 (9%)	12	47
26	X	104/118 (88%)	85 (82%)	19 (18%)	2	16
27	Y	109/110 (99%)	90 (83%)	19 (17%)	2	18
28	Z	115/116 (99%)	98 (85%)	17 (15%)	4	26
29	a	118/119 (99%)	103 (87%)	15 (13%)	5	31
30	b	46/47 (98%)	38 (83%)	8 (17%)	2	18
31	c	84/88 (96%)	71 (84%)	13 (16%)	3	24
32	d	94/97 (97%)	83 (88%)	11 (12%)	7	35
33	e	110/111 (99%)	96 (87%)	14 (13%)	5	31
34	f	90/91 (99%)	82 (91%)	8 (9%)	12	48
35	g	95/103 (92%)	81 (85%)	14 (15%)	4	26
36	h	103/105 (98%)	85 (82%)	18 (18%)	2	18
37	i	80/82 (98%)	59 (74%)	21 (26%)	0	6
38	j	70/71 (99%)	59 (84%)	11 (16%)	3	23
39	k	67/69 (97%)	56 (84%)	11 (16%)	3	21
40	l	45/46 (98%)	39 (87%)	6 (13%)	5	30
41	m	47/116 (40%)	36 (77%)	11 (23%)	1	8
42	o	90/91 (99%)	78 (87%)	12 (13%)	5	30
43	p	71/72 (99%)	66 (93%)	5 (7%)	19	58
44	q	105/254 (41%)	92 (88%)	13 (12%)	6	32
45	x	508/540 (94%)	468 (92%)	40 (8%)	15	54
46	y	182/378 (48%)	168 (92%)	14 (8%)	16	55
All	All	5906/6642 (89%)	5096 (86%)	810 (14%)	9	29

5 of 810 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	O	160	ARG
21	S	144	LEU
44	q	67	LEU
18	P	55	GLN
19	Q	170	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
18	P	64	ASN
22	T	131	GLN
45	x	429	ASN
18	P	125	GLN
20	R	47	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3084/3396 (90%)	666 (21%)	79 (2%)
2	7	120/121 (99%)	13 (10%)	0
3	8	157/158 (99%)	42 (26%)	6 (3%)
All	All	3361/3675 (91%)	721 (21%)	85 (2%)

5 of 721 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	14	U
1	5	15	C
1	5	21	G
1	5	22	G
1	5	26	A

5 of 85 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	1724	U
1	5	2418	G
1	5	3357	U
1	5	1816	A

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Mol	Chain	Res	Type
1	5	2112	U

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	3.19	2 (14%)	18,26,29	3.03	2 (11%)
1	Y5P	5	1987	1	14,19,20	3.25	2 (14%)	18,26,29	2.88	2 (11%)
1	Y5P	5	1988	1	14,19,20	3.21	2 (14%)	18,26,29	2.97	2 (11%)
1	Y5P	5	1989	1	14,19,20	3.25	2 (14%)	18,26,29	2.86	2 (11%)
1	Y5P	5	1990	1	14,19,20	3.22	2 (14%)	18,26,29	3.01	2 (11%)
1	Y5P	5	1991	1	14,19,20	3.30	2 (14%)	18,26,29	2.82	2 (11%)
1	Y5P	5	1992	1	14,19,20	3.20	2 (14%)	18,26,29	3.02	2 (11%)
1	Y5P	5	1993	1	14,19,20	3.33	2 (14%)	18,26,29	2.89	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	3.23	2 (14%)	18,26,29	2.87	2 (11%)
1	P5P	5	2016	1	16,23,24	0.72	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	0.80	0
1	P5P	5	2019	1	16,23,24	0.73	0	15,33,36	0.81	0
1	P5P	5	2020	1	16,23,24	0.72	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	0.73	0	15,33,36	0.81	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	0.72	0	15,33,36	0.78	0
1	P5P	5	2025	1	16,23,24	0.71	0	15,33,36	0.73	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	-11.55	1.38	1.46
1	5	1993	Y5P	C4-N3	-11.54	1.38	1.46
1	5	1987	Y5P	C4-N3	-11.38	1.38	1.46
1	5	1989	Y5P	C4-N3	-11.36	1.38	1.46
1	5	1994	Y5P	C4-N3	-11.32	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	1994	Y5P	N1-C2-N3	-12.10	114.34	125.85
1	5	1986	Y5P	N1-C2-N3	-12.06	114.38	125.85
1	5	1992	Y5P	N1-C2-N3	-11.97	114.47	125.85
1	5	1990	Y5P	N1-C2-N3	-11.91	114.52	125.85
1	5	1988	Y5P	N1-C2-N3	-11.76	114.67	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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
47	z	2
1	5	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1953:G	O3'	1986:Y5P	P	107.33
1	5	2025:P5P	O3'	2093:A	P	105.65
1	z	107:UNK	C	115:UNK	N	20.22
1	z	127:UNK	C	131:UNK	N	9.70