



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jul 24, 2017 – 10:46 AM EDT

PDB ID : 5APN
EMDB ID: : EMD-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 : unknown
Resolution : 3.91 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

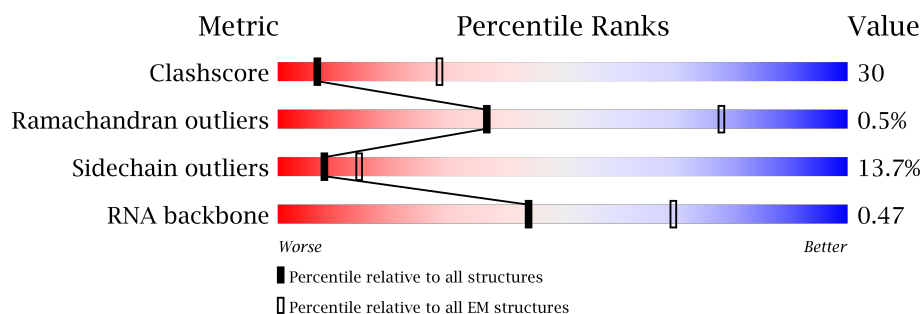
1 Overall quality at a glance

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.



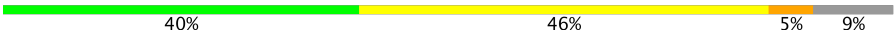


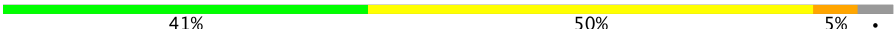
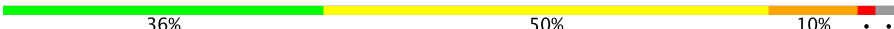
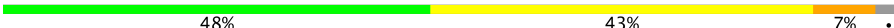
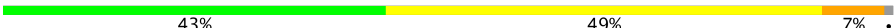


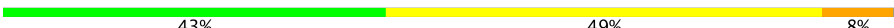
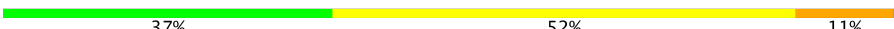
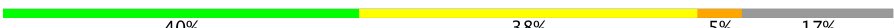





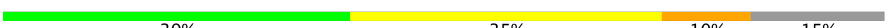

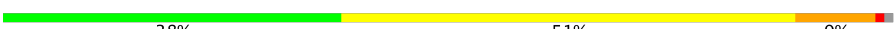





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	31% 47% 14% 8%
2	7	121	35% 56% 9%
3	8	158	28% 50% 21% .
4	A	254	36% 39% 9% 17%
5	B	387	38% 53% 9%
6	C	362	41% 50% 9%
7	D	297	45% 47% 7% .
8	E	176	46% 44% 9% ..

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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	S	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	S	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

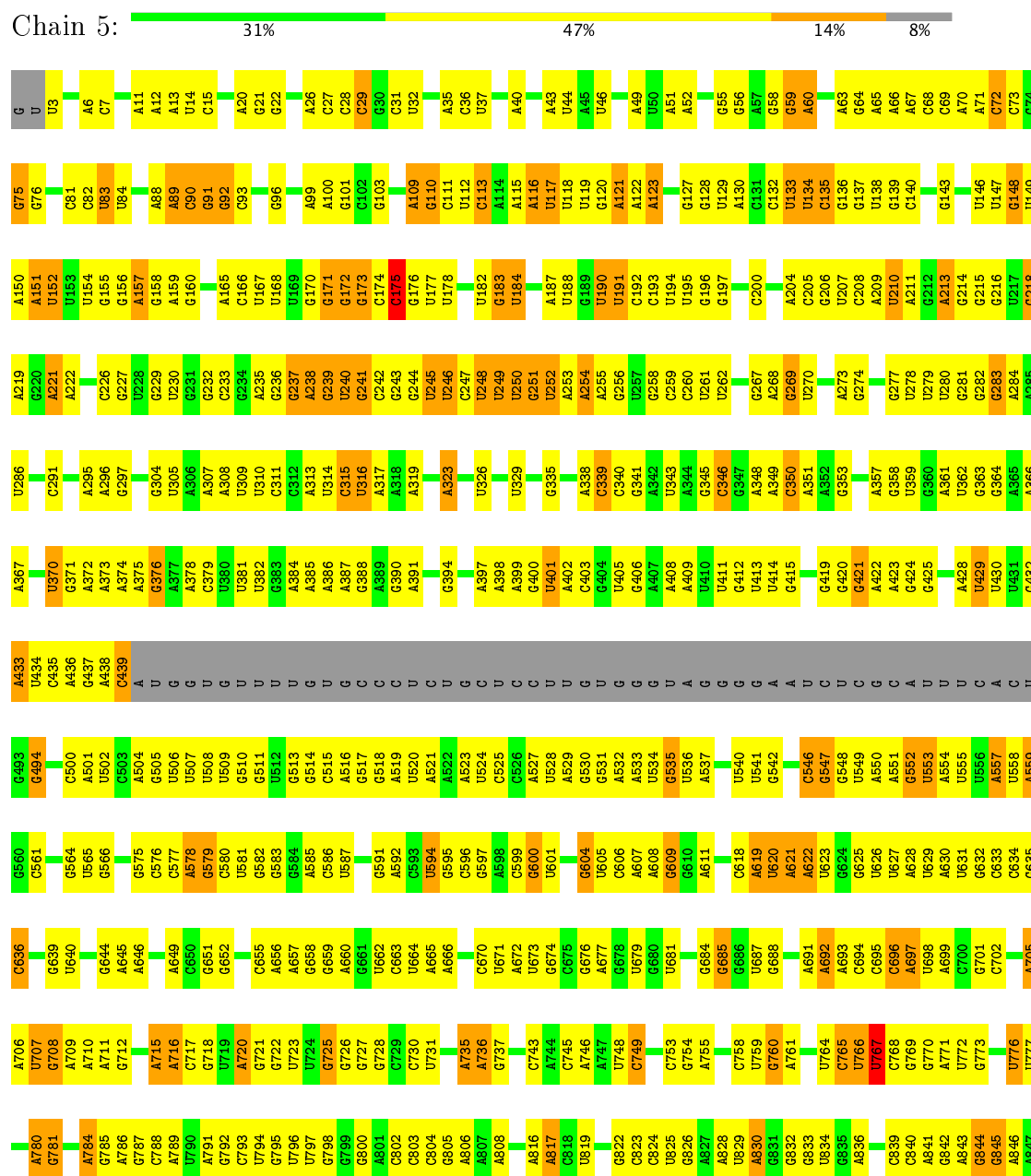
- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

3 Residue-property plots

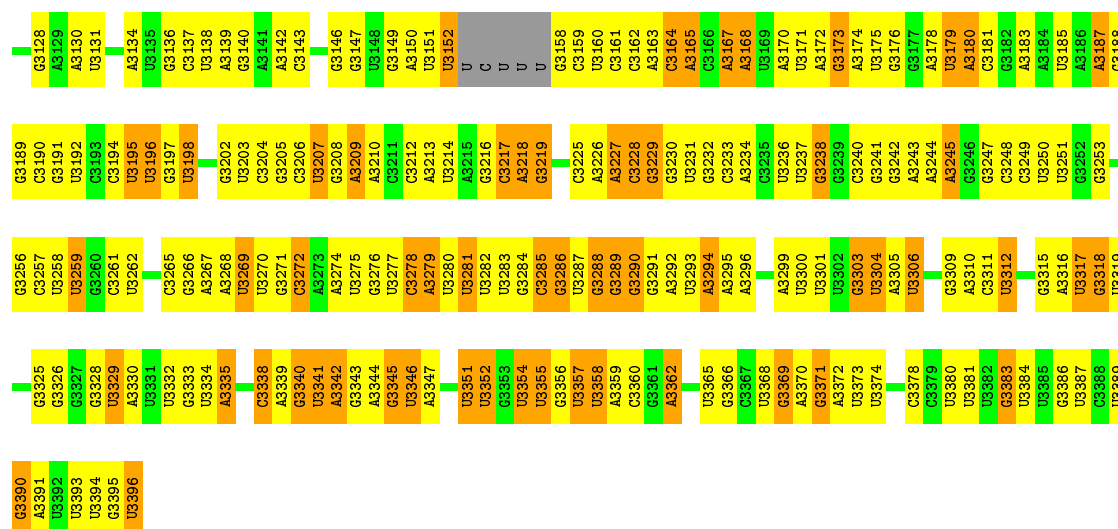
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according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

• Molecule 1: 25S rRNA



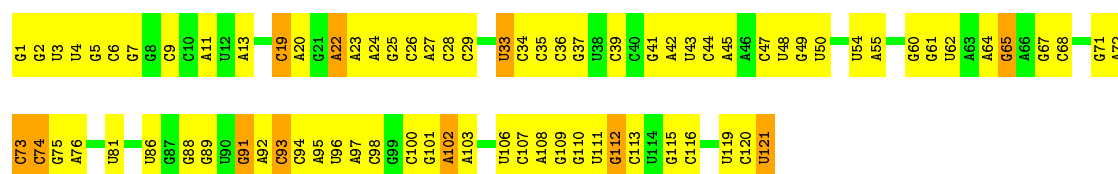
A1946	C1856	G1780	U1702	U1629	G1560	A1477	C1397	C1328	U1258	G1119	U1051	G984	C918	A848
G1947	C1857	G1781	U1703	U1630	G1561	C1478	U1398	U1329	A1259	A1120	U1052	G985	C918	C849
G1948	A1858	U1782	C1710	A1632	C1562	U1479	A1399	A1330	A1260	U1121	A1053	U986	A921	U850
U1950	G1860	U1783	C1711	G1633	U1564	G1480	G1400	U1331	G1261	U1122	A1054	U987	U922	C851
C1951	G1861	G1784	G1712	G1634	G1565	U1484	U1405	C1333	A1263	U1125	U1056	U988	G923	U852
	U1862	G1785	G1713	G1635	A1566		A1406	U1334	G1264	G1126	A1057	U990	A925	G853
	G1863	U1786	A1714	U1636	U1567		A1407	C1335	U1265	G1127	U1058	G991	A926	G856
	A1864	A1787	G1715	A1637	U1568		G1417	U1336	A1200	G1128	U1059	A992	C927	G857
	C1866	G1788	U1716	U1638	U1569		U1418	A1337	G993	A1129		G994	C928	A858
		G1789	U1717	U1639	U1570		U1494	C1338	A1205	A1130	A1062	U995	C929	A859
		G1790	G1718	G1640	A1571		U1495	C1339	G1206	G1132	A1064	A996	U930	G860
		G1791	G1719	U1641	U1572		C1496	G1340	A1271	A1133	A1065	A997		G861
		U1720	U1720	A1642	G1573		C1497	U1341	C1272	G1134	A1066	A998	G934	G869
	U1873	C1793	U1721	A1643	C1574		A1498		U1208		G1067	U999	G937	G870
	A1874	G1794	U1722	A1644	A1575		C1499		G1209		C1068	G1000	C938	G871
	G1875	U1795	U1723	U1645	G1576		G1500	U1346	U1276	U1138		G1001	U939	C873
	U1876	G1796	A1724	U1646	U1577		U1501	U1347	C1277	G1139		A1002	G940	U874
	G1877	A1797	U1725	A1647	G1578		C1502	U1348	A1278	G1140		A1003	G941	
	A1878	U1798	C1726	A1648	C1579		A1503	G1349	C1279			U1004	U942	C877
	U1880	A1799	G1727	U1649	U1580		U1504	A1350	C1280		U1074	U1005	U943	U878
	A1881	A1800	U1728	G1650	C1582		C1432	U1351	G1281		A1075	A1006	C944	U879
	G1882	U1801	G1729	U1651	U1583		A1433	G1352	G1282		C1076	U1007	C945	G880
	Y5P	C1805	G1730		A1584		G1434	U1353	C1283		U1077	U1008	U946	C881
	A1884	A1883		A1654	U1585		U1435	G1354	C1284		G1147	A1009	C947	A882
	U1886	G1807		G1656	C1586		U1436	A1355	G1285		A1078	G1010	C948	A883
	A1887	A1808	G1736	U1657	U1587		C1437	U1356	A1286		U1080	A1011	C949	C886
	Y5P	U1809	U1737	G1658	A1589		U1438	C1357	A1290		U1081	U1014	U951	C887
	Y5P	A1810	A1741	U1659	U1590		U1439	C1358	A1291		G1082	U1015	A952	A888
	Y5P	G1811	U1742	G1660	G1591		G1440	G1360	A1292		A1084	C	G953	U889
	Y5P	G1812	G1743	G1661	U1592		G1443	U1361	A1294		A1085	C	U956	C890
	Y5P	A1813		G1662	A1593		G1444	G1362	G1295		C1086	C	U957	G891
	Y5P	U1814	U1746	C1663	U1594		U1445	C1363	C1296		G1089	G	U958	U892
	Y5P	A1815	G1747		U1595		U1446	A1364	C1297		G1090	G	C959	C893
	Y5P	U1816	C1596		C1596		A1447	G1365	C1298			G	U960	G894
	Y5P	G1817	C1597		U1598		U1448	A1366	U1299		A1093	U	C961	A895
	Y5P	U1818	G1598		C1599		U1449		G1300		U1094	C	A962	A896
	Y5P	U1819	G1599		U1600		A1452	A1369	A1301		U1095	G	G963	U897
	Y5P	U1820			G1604		U1458	G1370	A1302		U1096	A	G964	U898
	Y5P	G1829	G1756		A1605		C1459	G1371	C1297		U1097	A	A965	U899
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	A3046	G2901	G2751	G2751		G2607	U2541	C	U2350	A2279	A2279	C2132	P5P
C3120	A2967	U2902	G2828	U2752	A2680	C2607	U2540	C	U2351	G2279	G2279	U2211	P5P
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A3048	G2753	G2753	G2753	G2753	C2682	U2681	U2543	C	G2352	A2281	A2281	U2137	P5P
U3050	G2972	U2905	G2834	G2754	U2683	G2610	U2544	G	C2353	C2282	C2282	A2143	P5P
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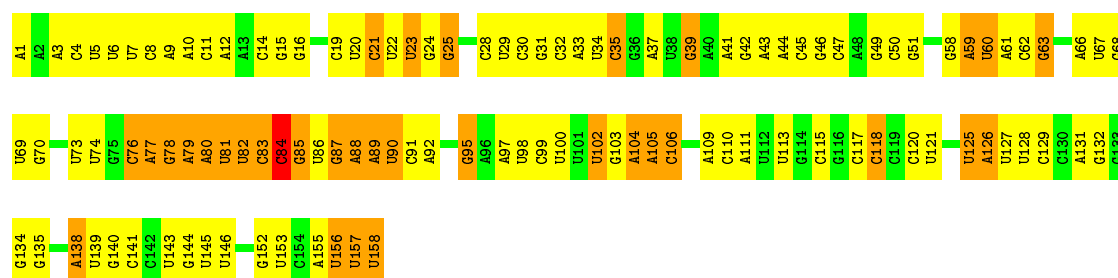
• Molecule 2: 5S rRNA

Chain 7: 35% 56% 9%



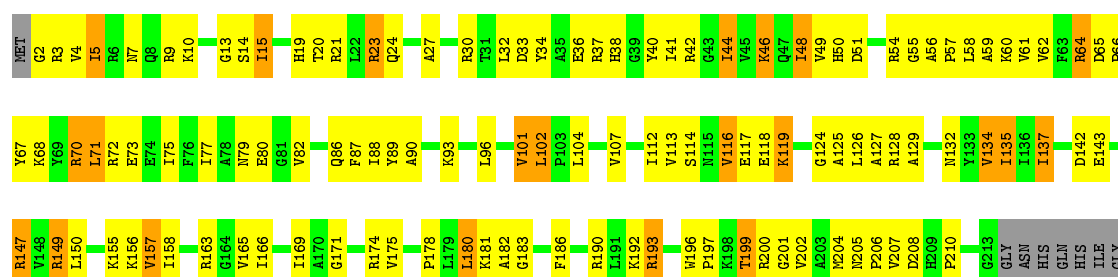
• Molecule 3: 5.8S rRNA

Chain 8: 28% 50% 21%



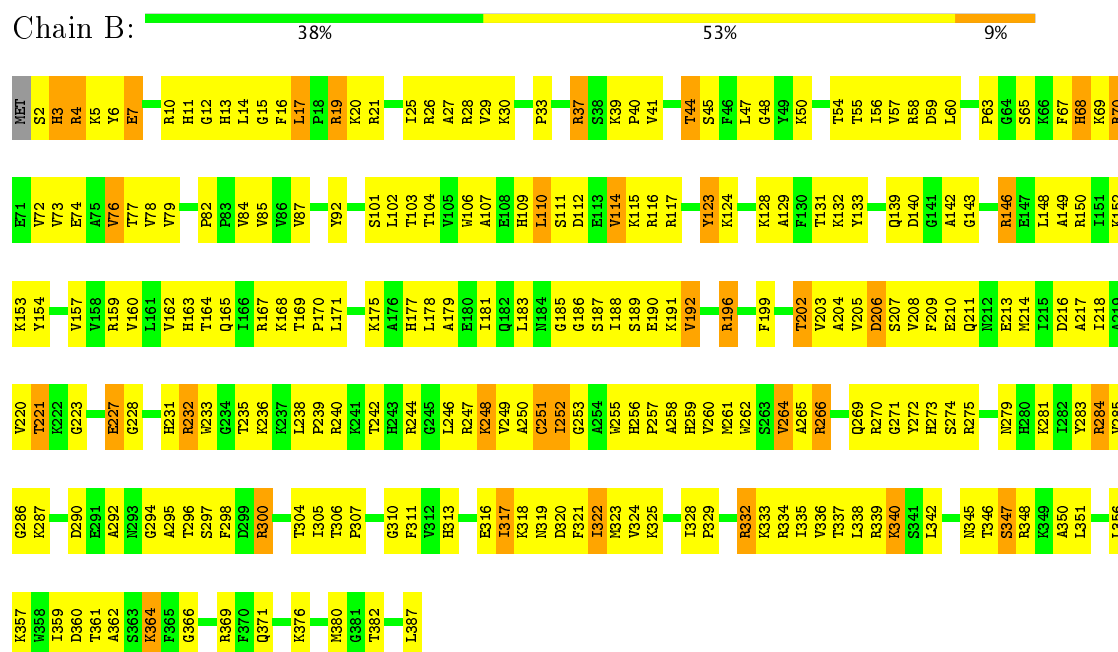
• Molecule 4: 60S ribosomal protein L2-A

Chain A: 36% 39% 9% 17%

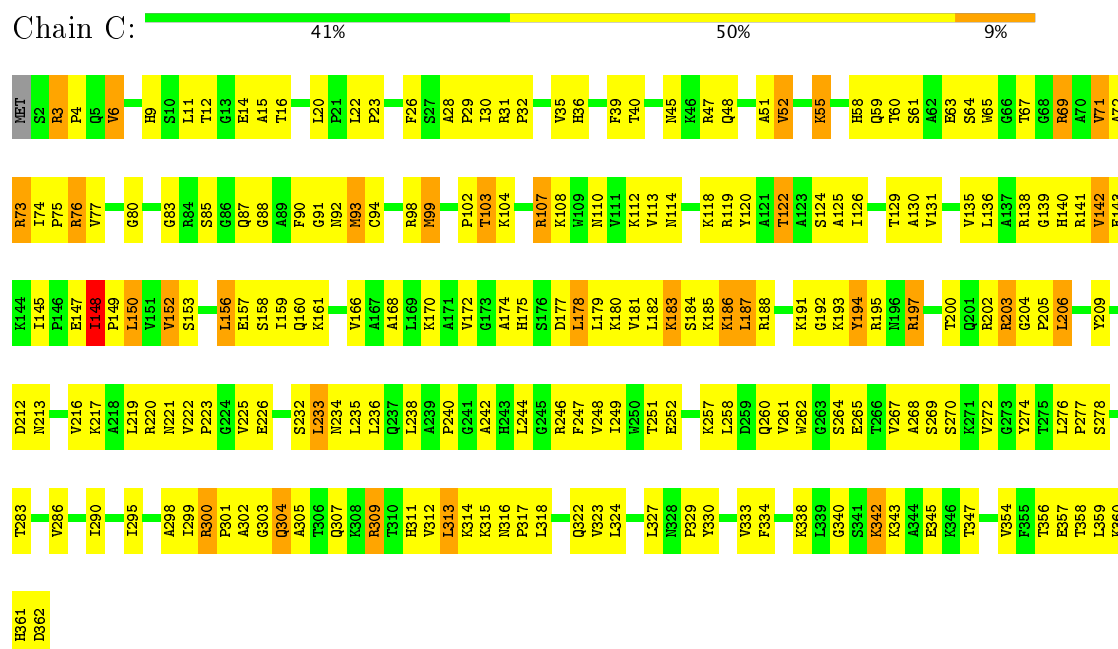


LYS
ALA
SER
THR
R4
ILE
SER
ARG
GLY
VAL
SER
GLY
GLN
LYS
ALA
GLY
LEU
ILE
ALA
ALA
ARG
ARG
THR
GLY
LEU
LEU
ARG
GLY
SER
GLN
LYS
THR
GLN
ASP

• Molecule 5: 60S ribosomal protein L3

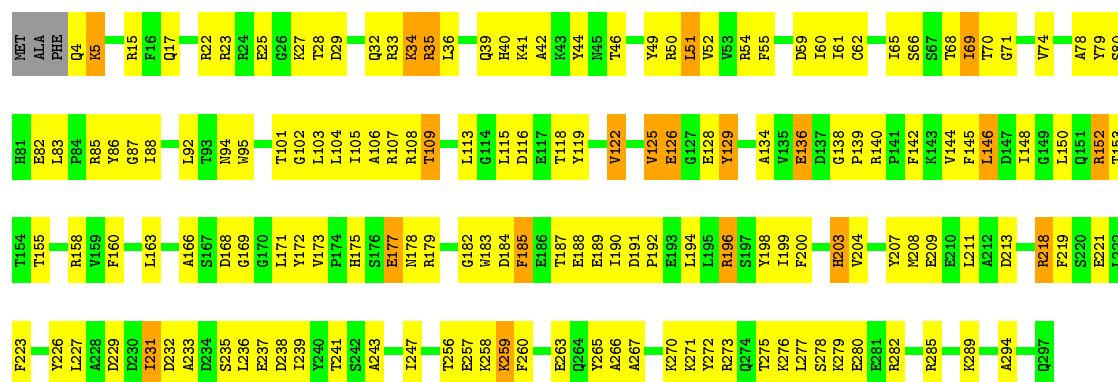


• Molecule 6: 60S ribosomal protein L4-A



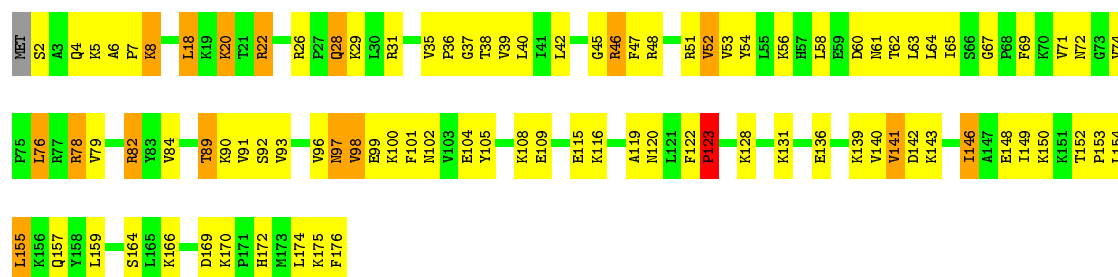
• Molecule 7: 60S ribosomal protein L5





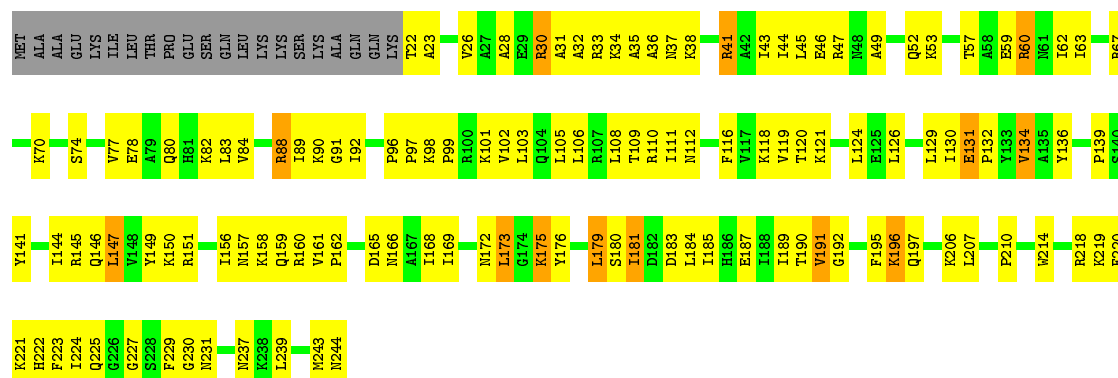
• Molecule 8: 60S ribosomal protein L6-A

Chain E: 46% 44% 9% ..



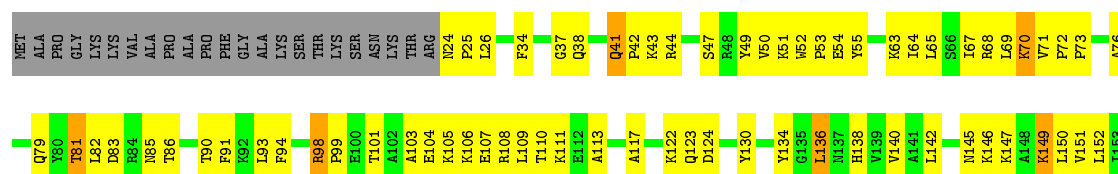
• Molecule 9: 60S ribosomal protein L7-A

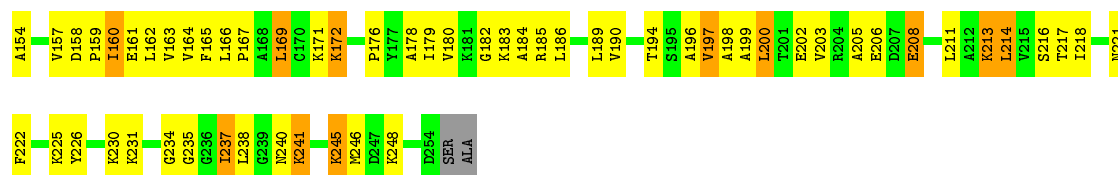
Chain F: 40% 46% 5% 9%



• Molecule 10: 60S ribosomal protein L8-A

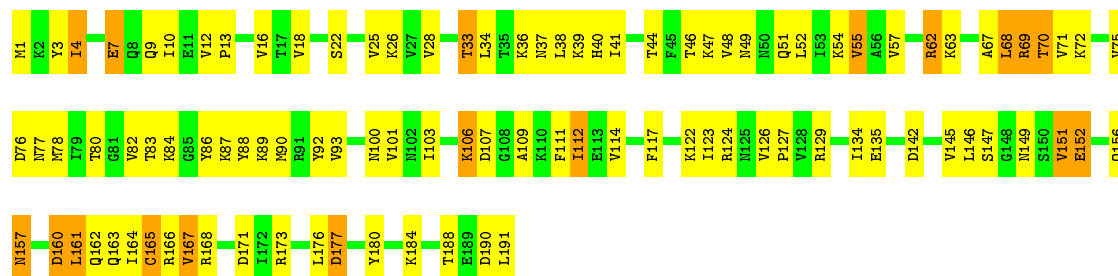
Chain G: 41% 43% 7% 10%





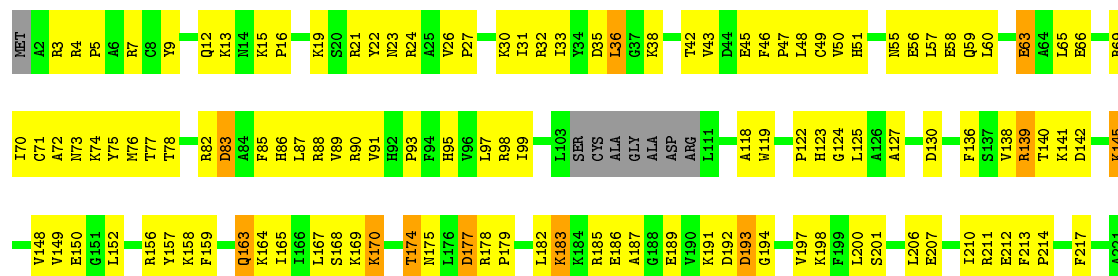
• Molecule 11: 60S ribosomal protein L9-A

Chain H: 48% 43% 9%



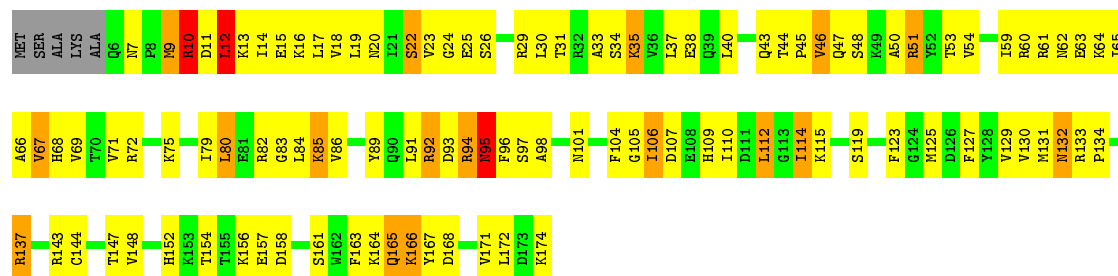
• Molecule 12: 60S ribosomal protein L10

Chain I: 41% 50% 5%



• Molecule 13: 60S ribosomal protein L11-A

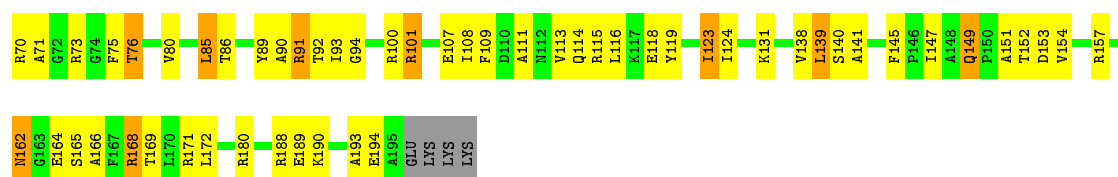
Chain J: 36% 50% 10%



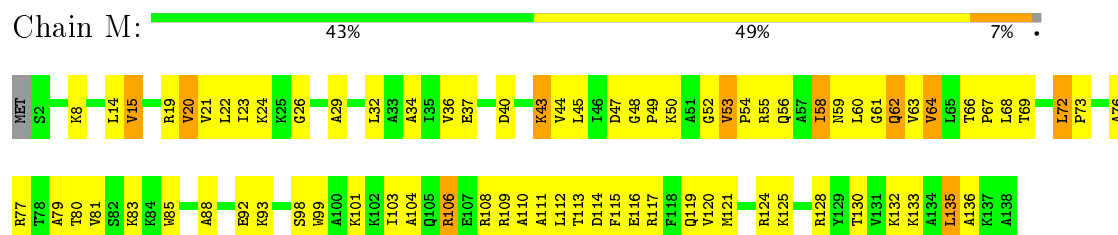
• Molecule 14: 60S ribosomal protein L13-A

Chain L: 48% 43% 7%





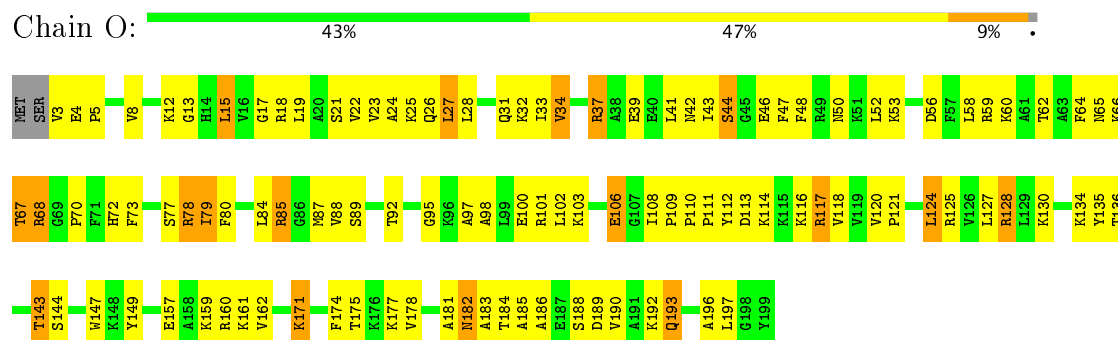
• Molecule 15: 60S ribosomal protein L14-A



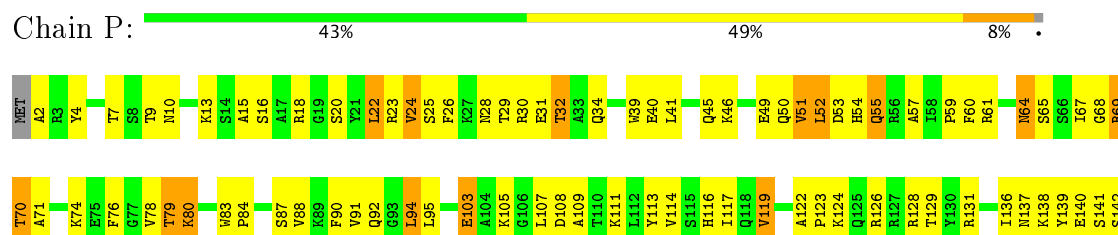
• Molecule 16: 60S ribosomal protein L15-A

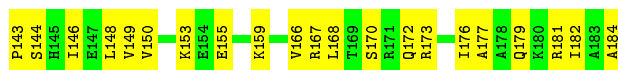


• Molecule 17: 60S ribosomal protein L16-A



• Molecule 18: 60S ribosomal protein L17-A





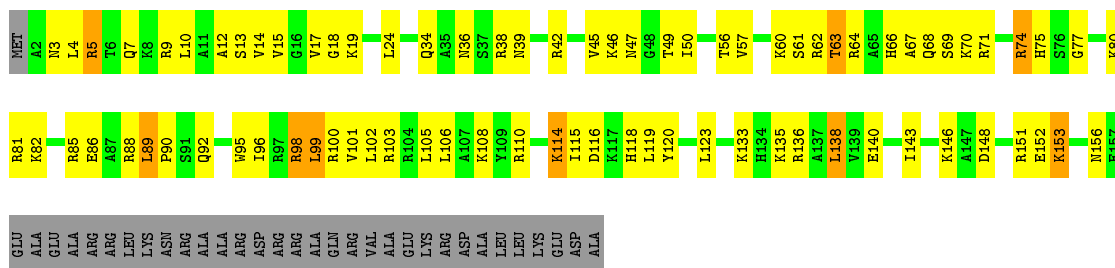
• Molecule 19: 60S ribosomal protein L18-A

Chain Q: 37% 52% 11% .



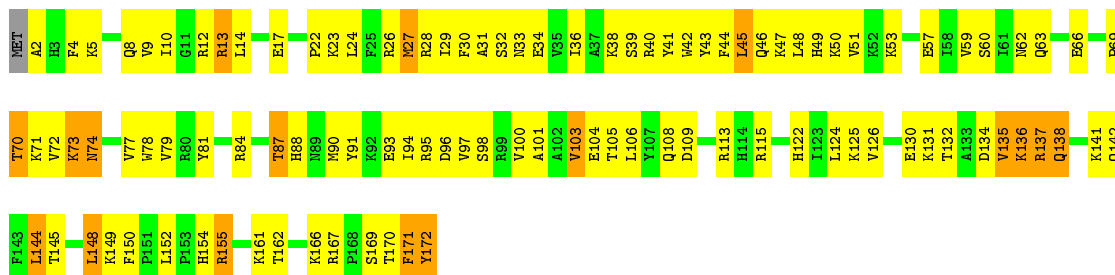
• Molecule 20: 60S ribosomal protein L19-A

Chain R: 40% 38% 5% 17% .



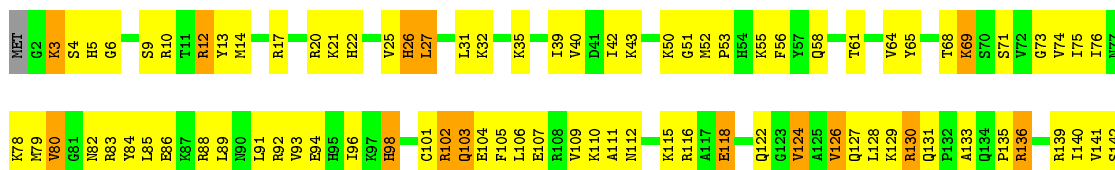
• Molecule 21: 60S ribosomal protein L20-A

Chain S: 38% 51% 10% .



• Molecule 22: 60S ribosomal protein L21-A

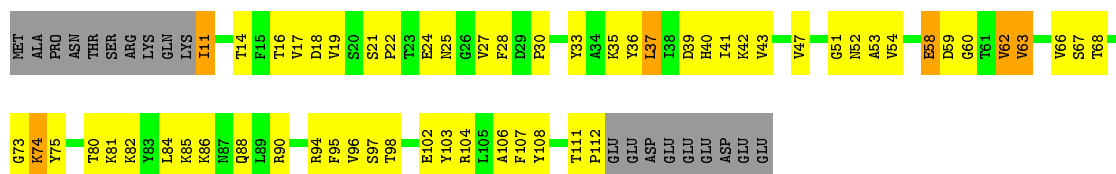
Chain T: 41% 49% 9% .





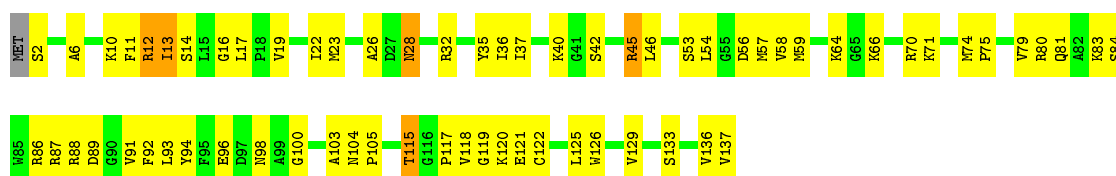
• Molecule 23: 60S ribosomal protein L22-A

Chain U: 36% 44% 5% 16%



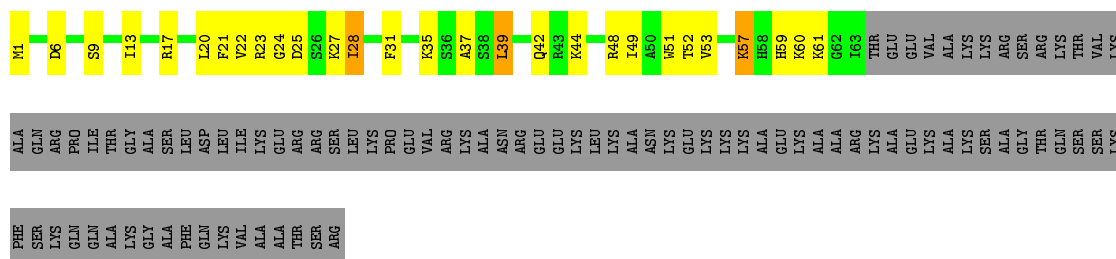
• Molecule 24: 60S ribosomal protein L23-A

Chain V: 51% 45%



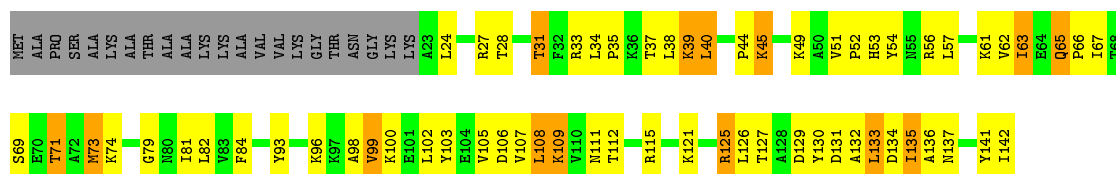
• Molecule 25: 60S ribosomal protein L24-A

Chain W: 23% 16% 59%



• Molecule 26: 60S ribosomal protein L25

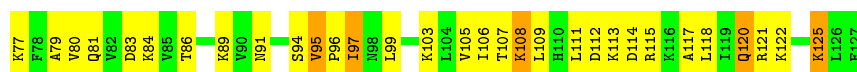
Chain X: 39% 35% 10% 15%



• Molecule 27: 60S ribosomal protein L26-A

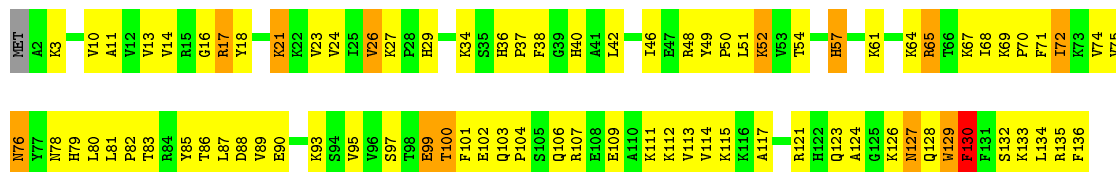
Chain Y: 43% 46% 10%





- 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% .



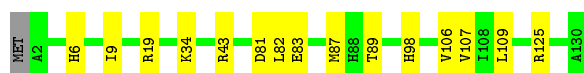
- Molecule 32: 60S ribosomal protein L31-A

Chain d: 84% 12% .



- Molecule 33: 60S ribosomal protein L32

Chain e: 88% 12% .



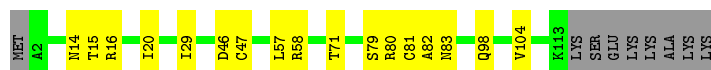
- Molecule 34: 60S ribosomal protein L33-A

Chain f: 92% 7% .



- Molecule 35: 60S ribosomal protein L34-A

Chain g: 79% 14% 7%



- Molecule 36: 60S ribosomal protein L35-A

Chain h: 84% 15%



- Molecule 37: 60S ribosomal protein L36-A

Chain i: 76% 22%



- Molecule 38: 60S ribosomal protein L37-A

Chain j: 86% 13%



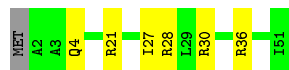
- Molecule 39: 60S ribosomal protein L38

Chain k: 83% 15%



- Molecule 40: 60S ribosomal protein L39

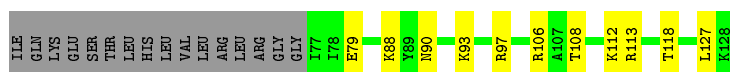
Chain l: 86% 12%



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain m: 32% 9% 59%





- Molecule 42: 60S ribosomal protein L42-A

Chain o: 88% 11% .



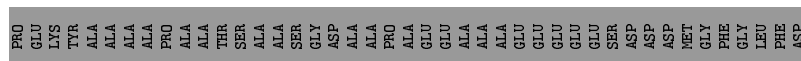
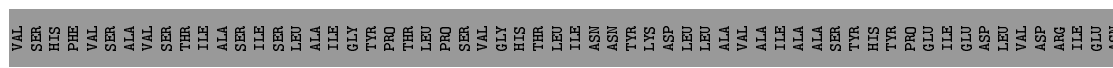
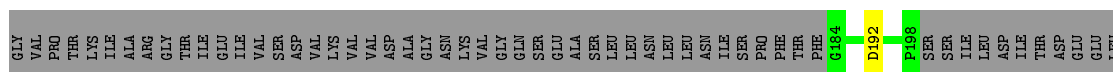
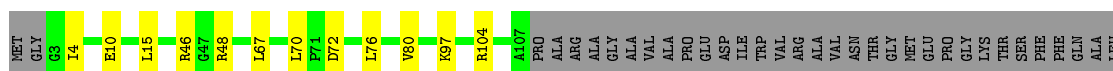
- Molecule 43: 60S ribosomal protein L43-A

Chain p: 93% 5% .



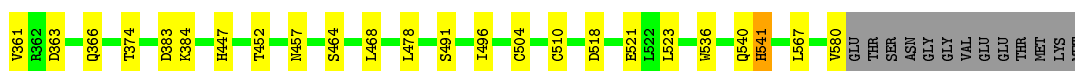
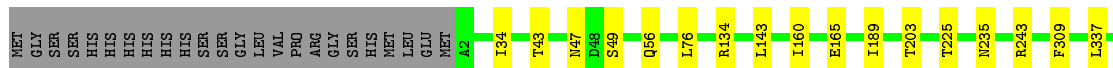
- Molecule 44: 60S acidic ribosomal protein P0

Chain q: 34% 62% .



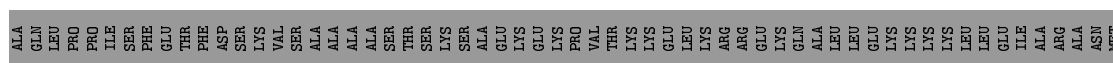
- Molecule 45: Probable metalloprotease ARX1

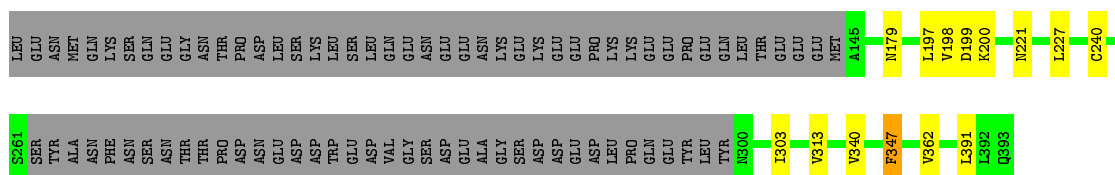
Chain x: 87% 6% 6% .



- Molecule 46: Cytoplasmic 60S subunit biogenesis factor REI1

Chain y: 48% 49% .





- Molecule 47: ALB1

Chain z:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	22040	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)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	100720	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	2242	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	4989	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 4989 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%)	28	70
7	D	292/297 (98%)	283 (97%)	7 (2%)	2 (1%)	25	67
8	E	173/176 (98%)	160 (92%)	10 (6%)	3 (2%)	11	52
9	F	221/244 (91%)	211 (96%)	9 (4%)	1 (0%)	32	73
10	G	229/256 (90%)	201 (88%)	26 (11%)	2 (1%)	20	63
11	H	189/191 (99%)	178 (94%)	10 (5%)	1 (0%)	32	73
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	41
14	L	192/199 (96%)	169 (88%)	21 (11%)	2 (1%)	18	61
15	M	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
16	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	18	61
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%)	32	73
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%)	14	57
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%)	22	65
28	Z	133/136 (98%)	114 (86%)	16 (12%)	3 (2%)	7	46
29	a	146/149 (98%)	131 (90%)	14 (10%)	1 (1%)	25	67
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%)	20	63
33	e	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	22	65
34	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
35	g	110/121 (91%)	100 (91%)	8 (7%)	2 (2%)	10	51
36	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
37	i	97/100 (97%)	87 (90%)	7 (7%)	3 (3%)	5	40
38	j	85/88 (97%)	78 (92%)	7 (8%)	0	100	100
39	k	75/78 (96%)	68 (91%)	6 (8%)	1 (1%)	14	57
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%)	37	73

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	20
5	B	319/323 (99%)	269 (84%)	50 (16%)	3	22
6	C	288/289 (100%)	240 (83%)	48 (17%)	2	19
7	D	243/245 (99%)	216 (89%)	27 (11%)	7	35
8	E	136/153 (89%)	119 (88%)	17 (12%)	5	30
9	F	187/205 (91%)	166 (89%)	21 (11%)	7	35
10	G	177/208 (85%)	154 (87%)	23 (13%)	5	29
11	H	171/171 (100%)	144 (84%)	27 (16%)	3	22
12	I	179/187 (96%)	157 (88%)	22 (12%)	5	30
13	J	147/150 (98%)	122 (83%)	25 (17%)	2	18
14	L	154/159 (97%)	136 (88%)	18 (12%)	6	33
15	M	108/109 (99%)	93 (86%)	15 (14%)	4	27
16	N	175/176 (99%)	147 (84%)	28 (16%)	3	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	O	160/162 (99%)	136 (85%)	24 (15%)	3	23
18	P	145/146 (99%)	128 (88%)	17 (12%)	6	33
19	Q	150/151 (99%)	124 (83%)	26 (17%)	2	17
20	R	129/154 (84%)	111 (86%)	18 (14%)	4	27
21	S	155/156 (99%)	129 (83%)	26 (17%)	2	19
22	T	136/137 (99%)	112 (82%)	24 (18%)	2	17
23	U	89/107 (83%)	76 (85%)	13 (15%)	3	24
24	V	104/105 (99%)	95 (91%)	9 (9%)	12	45
25	W	55/129 (43%)	50 (91%)	5 (9%)	11	43
26	X	104/118 (88%)	85 (82%)	19 (18%)	2	14
27	Y	109/110 (99%)	90 (83%)	19 (17%)	2	17
28	Z	115/116 (99%)	98 (85%)	17 (15%)	3	24
29	a	118/119 (99%)	103 (87%)	15 (13%)	5	29
30	b	46/47 (98%)	38 (83%)	8 (17%)	2	17
31	c	84/88 (96%)	71 (84%)	13 (16%)	3	22
32	d	94/97 (97%)	83 (88%)	11 (12%)	6	33
33	e	110/111 (99%)	96 (87%)	14 (13%)	5	29
34	f	90/91 (99%)	82 (91%)	8 (9%)	11	44
35	g	95/103 (92%)	81 (85%)	14 (15%)	3	24
36	h	103/105 (98%)	85 (82%)	18 (18%)	2	17
37	i	80/82 (98%)	59 (74%)	21 (26%)	0	5
38	j	70/71 (99%)	59 (84%)	11 (16%)	3	22
39	k	67/69 (97%)	56 (84%)	11 (16%)	2	20
40	l	45/46 (98%)	39 (87%)	6 (13%)	4	28
41	m	47/116 (40%)	36 (77%)	11 (23%)	1	7
42	o	90/91 (99%)	78 (87%)	12 (13%)	4	28
43	p	71/72 (99%)	66 (93%)	5 (7%)	18	54
44	q	105/254 (41%)	92 (88%)	13 (12%)	5	30
45	x	508/540 (94%)	468 (92%)	40 (8%)	14	50
46	y	182/378 (48%)	168 (92%)	14 (8%)	15	51
All	All	5906/6642 (89%)	5096 (86%)	810 (14%)	8	27

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	15,19,20	2.50	2 (13%)	19,26,29	1.52	2 (10%)
1	Y5P	5	1987	1	15,19,20	2.53	2 (13%)	19,26,29	1.51	2 (10%)
1	Y5P	5	1988	1	15,19,20	2.52	2 (13%)	19,26,29	1.50	2 (10%)
1	Y5P	5	1989	1	15,19,20	2.54	2 (13%)	19,26,29	1.46	2 (10%)
1	Y5P	5	1990	1	15,19,20	2.52	2 (13%)	19,26,29	1.53	2 (10%)
1	Y5P	5	1991	1	15,19,20	2.57	2 (13%)	19,26,29	1.49	2 (10%)
1	Y5P	5	1992	1	15,19,20	2.52	2 (13%)	19,26,29	1.53	2 (10%)
1	Y5P	5	1993	1	15,19,20	2.60	2 (13%)	19,26,29	1.47	2 (10%)
1	Y5P	5	1994	1	15,19,20	2.55	2 (13%)	19,26,29	1.55	2 (10%)
1	Y5P	5	1995	1	15,19,20	2.52	2 (13%)	19,26,29	1.48	2 (10%)
1	P5P	5	2016	1	16,23,24	0.83	0	14,33,36	0.86	0
1	P5P	5	2017	1	16,23,24	0.83	0	14,33,36	0.86	0
1	P5P	5	2018	1	16,23,24	0.84	0	14,33,36	0.88	0
1	P5P	5	2019	1	16,23,24	0.85	0	14,33,36	0.90	0
1	P5P	5	2020	1	16,23,24	0.83	0	14,33,36	0.87	0
1	P5P	5	2021	1	16,23,24	0.82	0	14,33,36	0.84	0
1	P5P	5	2022	1	16,23,24	0.84	0	14,33,36	0.88	0
1	P5P	5	2023	1	16,23,24	0.86	0	14,33,36	0.92	0
1	P5P	5	2024	1	16,23,24	0.84	0	14,33,36	0.86	0
1	P5P	5	2025	1	16,23,24	0.83	0	14,33,36	0.84	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	-8.82	1.38	1.46
1	5	1993	Y5P	C4-N3	-8.81	1.38	1.46
1	5	1987	Y5P	C4-N3	-8.69	1.38	1.46
1	5	1989	Y5P	C4-N3	-8.67	1.38	1.46
1	5	1994	Y5P	C4-N3	-8.64	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	-3.98	114.34	125.46
1	5	1986	Y5P	N1-C2-N3	-3.96	114.38	125.46
1	5	1992	Y5P	N1-C2-N3	-3.93	114.47	125.46
1	5	1990	Y5P	N1-C2-N3	-3.91	114.52	125.46
1	5	1988	Y5P	N1-C2-N3	-3.86	114.67	125.46

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