



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 11:51 am GMT

PDB ID : 3JAP  
EMDB ID: : EMD-3048  
Title : Structure of a partial yeast 48S preinitiation complex in closed conformation  
Authors : Llacer, J.L.; Hussain, T.; Ramakrishnan, V.  
Deposited on : 2015-06-18  
Resolution : 4.90 Å(reported)  
Based on PDB ID : 2D74, 3J81, 4U1C, 3CW2, 4U1D, 4U1E

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](mailto: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.

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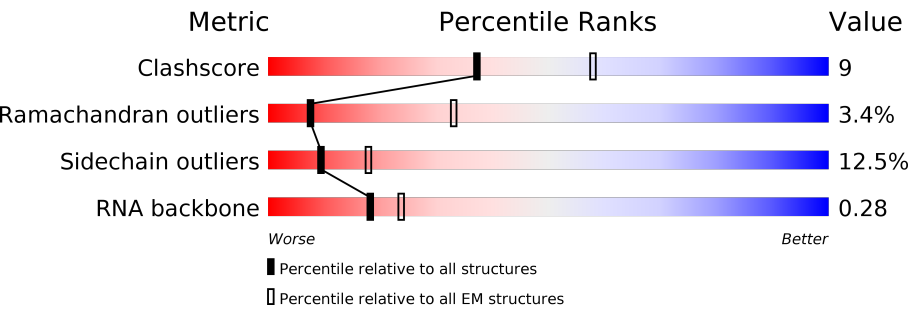
MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc29047

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 4.90 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.

















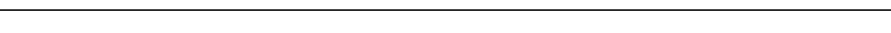




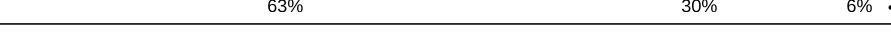





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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

Mol	Chain	Length	Quality of chain
1	1	75	<div><div>31%</div><div>45%</div><div>24%</div></div>
2	2	1781	<div><div>27%</div><div>50%</div><div>23%</div></div>
3	3	25	<div><div>52%</div><div>44%</div></div>
4	A	254	<div><div>59%</div><div>19%</div><div>18%</div></div>
5	B	255	<div><div>66%</div><div>20%</div><div>13%</div></div>
6	C	259	<div><div>59%</div><div>23%</div><div>16%</div></div>
7	D	237	<div><div>65%</div><div>24%</div><div>6%</div></div>
8	E	261	<div><div>70%</div><div>27%</div></div>

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Mol	Chain	Length	Quality of chain
9	F	227	
10	G	236	
11	H	190	
12	I	201	
13	J	188	
14	K	106	
15	L	156	
16	M	134	
17	N	151	
18	O	137	
19	P	142	
20	Q	143	
21	R	136	
22	S	146	
23	T	144	
24	U	117	
25	V	87	
26	W	130	
27	X	145	
28	Y	135	
29	Z	108	
30	a	119	
31	b	82	
32	c	67	
33	d	56	

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Mol	Chain	Length	Quality of chain
34	e	63	
35	f	150	
36	g	326	
37	h	25	
38	i	153	
39	j	304	
40	k	527	
41	l	285	
42	m	108	
43	o	588	
44	p	652	
45	q	347	
46	r	31	
47	s	52	

## 2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 98333 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called Met-tRNAi (U31:A39 variant).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	75	Total	C	N	O	P	0	0
			1607	716	296	520	75		

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1780	Total	C	N	O	P	0	0
			37797	16892	6658	12467	1780		

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	14	Total	C	N	O	P	0	0
			287	129	42	102	14		

- Molecule 4 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	208	Total	C	N	O	S	0	0
			1626	1040	286	298	2		

- Molecule 5 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	222	Total	C	N	O	S	0	0
			1769	1117	324	325	3		

- Molecule 6 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	217	Total	C	N	O	S	0	0
			1629	1041	287	297	4		

- Molecule 7 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	223	Total	C	N	O	S	0	0
			1744	1108	313	318	5		

- Molecule 8 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	260	Total	C	N	O	S	0	0
			2078	1322	393	359	4		

- Molecule 9 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	206	Total	C	N	O	S	0	0
			1609	1008	298	300	3		

- Molecule 10 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	226	Total	C	N	O	S	0	0
			1812	1134	348	326	4		

- Molecule 11 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	184	Total	C	N	O	S	0	0
			1483	950	270	263			

- Molecule 12 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	188	Total	C	N	O	S	0	0
			1489	923	300	265	1		

- Molecule 13 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	182	Total	C	N	O	S	0	0
			1471	929	287	254	1		

- Molecule 14 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	96	Total	C	N	O	S	0	0
			809	533	129	146	1		

- Molecule 15 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	155	Total	C	N	O	S	0	0
			1248	798	237	210	3		

- Molecule 16 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	117	Total	C	N	O	S	0	0
			885	553	161	171			

- Molecule 17 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	150	Total	C	N	O	S	0	0
			1187	756	223	206	2		

- Molecule 18 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	127	Total	C	N	O	S	0	0
			942	578	188	173	3		

- Molecule 19 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	117	Total	C	N	O	S	0	0
			927	595	166	161	5		

- Molecule 20 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	141	Total	C	N	O	S	0	0
			1105	709	204	192			

- Molecule 21 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	120	Total	C	N	O	S	0	0
			959	598	178	180	3		

- Molecule 22 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	145	Total	C	N	O	S	0	0
			1193	741	240	210	2		

- Molecule 23 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	143	Total	C	N	O	S	0	0
			1110	693	210	207			

- Molecule 24 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	106	Total	C	N	O	S	0	0
			845	540	152	152	1		

- Molecule 25 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	87	Total	C	N	O	S	0	0
			687	424	126	135	2		

- Molecule 26 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	129	Total	C	N	O	S	0	0
			1021	651	187	180	3		

- Molecule 27 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	144	Total	C	N	O	S	0	0
			1119	708	218	191	2		

- Molecule 28 is a protein called eS24.



Mol	Chain	Residues	Atoms				AltConf	Trace
28	Y	134	Total	C	N	O		
			1061	665	207	189	0	0

- Molecule 29 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	70	Total	C	N	O	S		
			558	355	104	98	1	0	0

- Molecule 30 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	98	Total	C	N	O	S		
			779	480	165	129	5	0	0

- Molecule 31 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	81	Total	C	N	O	S		
			609	379	112	113	5	0	0

- Molecule 32 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	62	Total	C	N	O	S		
			487	301	97	88	1	0	0

- Molecule 33 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	53	Total	C	N	O	S		
			446	280	89	76	1	0	0

- Molecule 34 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	e	54	Total	C	N	O	S		
			433	271	88	73	1	0	0

- Molecule 35 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	69	Total	C	N	O	S	0	0
			546	351	101	90	4		

- Molecule 36 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	318	Total	C	N	O	S	0	0
			2466	1561	430	470	5		

- Molecule 37 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 38 is a protein called eIF1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	111	Total	C	N	O	S	0	0
			884	542	170	167	5		

- Molecule 39 is a protein called eIF2 alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	249	Total	C	N	O	S	0	0
			2006	1283	333	382	8		

- Molecule 40 is a protein called eIF2 gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	396	Total	C	N	O	S	0	0
			3034	1932	542	544	16		

- Molecule 41 is a protein called eIF2 beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	128	Total	C	N	O	S	0	0
			1036	661	186	182	7		

- Molecule 42 is a protein called eIF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	90	Total	C	N	O	S	0	0
			716	452	132	128	4		

- Molecule 43 is a protein called eIF3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	550	Total	C	N	O	S	0	0
			4189	2667	721	794	7		

- Molecule 44 is a protein called eIF3c.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	634	Total	C	N	O	S	0	0
			4899	3121	826	940	12		

- Molecule 45 is a protein called eIF3i.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	342	Total	C	N	O	S	0	0
			2693	1711	443	530	9		

- Molecule 46 is a protein called eIF3b.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	r	31	Total	C	N	O	S	0	0
			277	177	48	50	2		

- Molecule 47 is a protein called eIF3g.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	s	52	Total	C	N	O	0	0
			418	257	82	79		

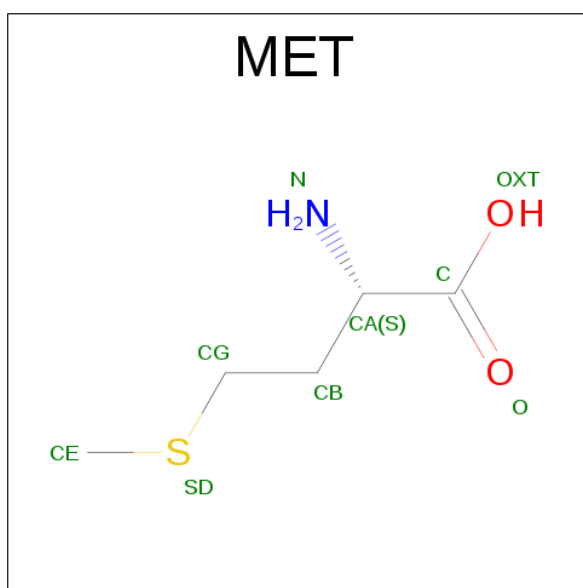
- Molecule 48 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	2	80	Total	Mg	0
			80	80	
48	k	1	Total	Mg	0
			1	1	

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

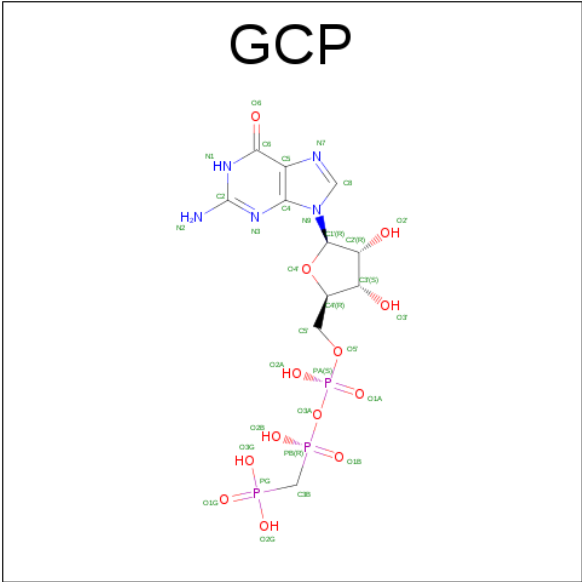
Mol	Chain	Residues	Atoms		AltConf
49	b	1	Total	Zn	0
			1	1	
49	a	1	Total	Zn	0
			1	1	
49	l	1	Total	Zn	0
			1	1	
49	f	1	Total	Zn	0
			1	1	

- Molecule 50 is METHIONINE (three-letter code: MET) (formula:  $C_5H_{11}NO_2S$ ).



Mol	Chain	Residues	Atoms					AltConf
50	k	1	Total	C	N	O	S	0
			8	5	1	1	1	

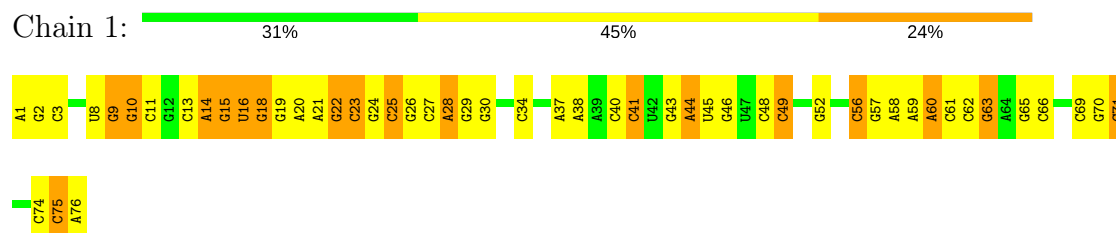
- Molecule 51 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula:  $C_{11}H_{18}N_5O_{13}P_3$ ).



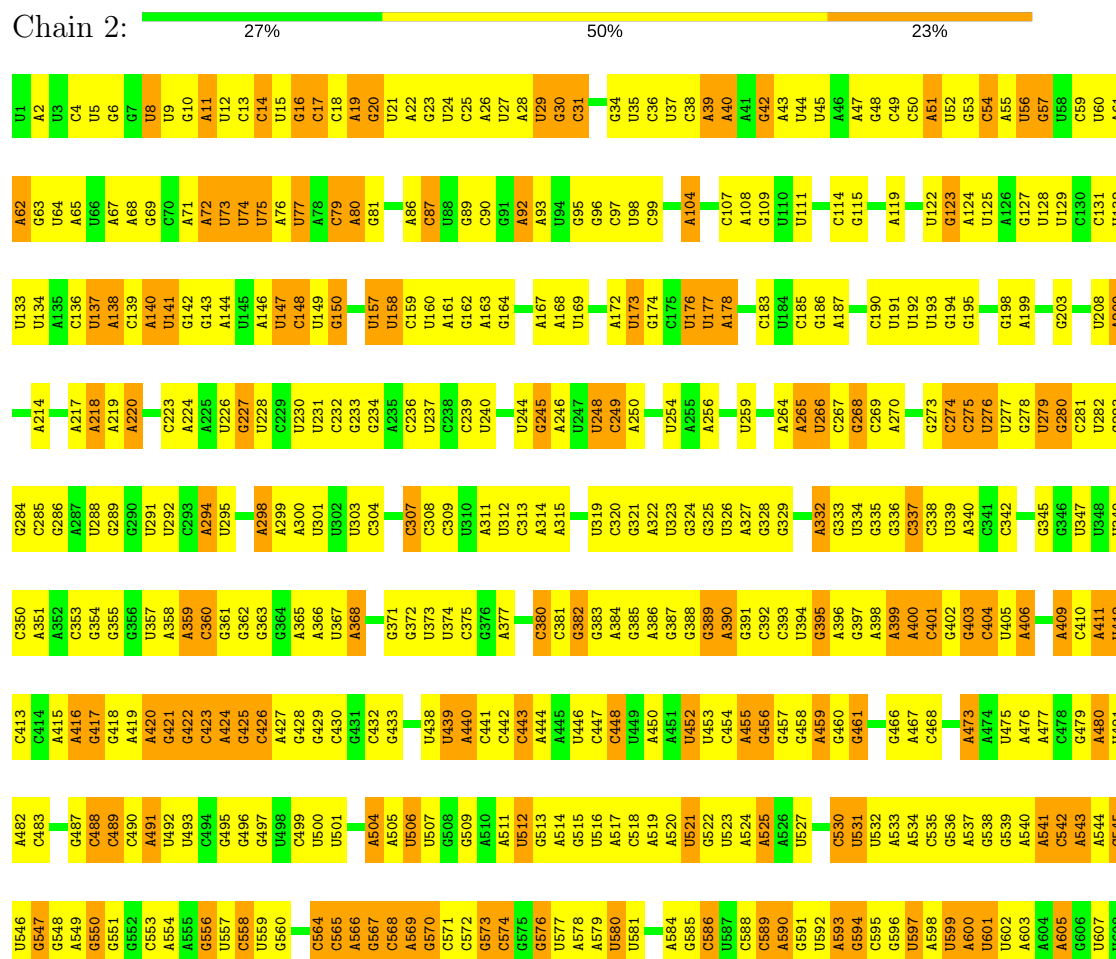
### 3 Residue-property plots

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: Met-tRNAi (U31:A39 variant)



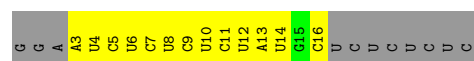
#### • Molecule 2: 18S rRNA



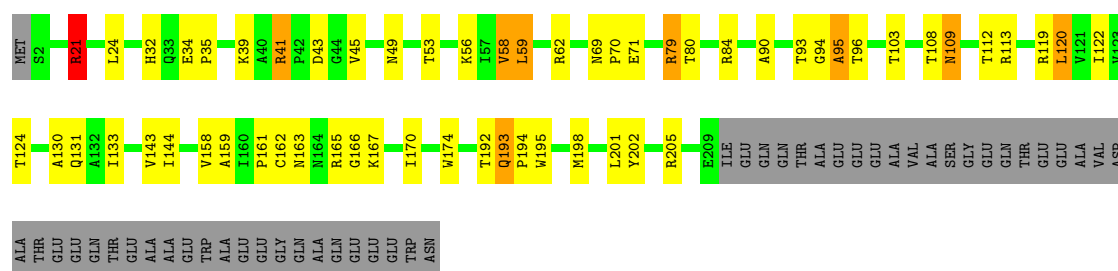
U1625	C1563	G1486	G1426	G1363	G1294	G1227	A1165	G1100	G1040	G971	A906	U831	G765	U694	G609
U1626	U1487	U1487	G1427	C1364	A1295	G1228	G1166	G1101	G1041	G971	U907	U832	U766	U695	U610
G1627	A1488	A1488	U1428	C1365	G1296	U1229	U1167	U1102	A1042	C974	C909	U833	U767	C996	U611
U1628	C1489	C1489	G1429	G1366	U1297	U1230	G1168	U1103	G1043	G975	C909	U834	C768	C697	U612
A1629	A1490	A1490	G1430	G1367	G1298	U1231	G1169	U1104	G1044	A976	U910	U835	A771	U699	C613
C1630	A1568	A1491	G1431	U1368	A1299	G1232	A1170	G1106	G1045	A977	U911	U836	G772	A614	A614
A1631	C1492	C1492	U1432	U1369	U1300	G1236	G1171	G1107	G1046	A978	U912	U837	G773	C700	G615
C1632	C1493	C1493	G1433	G1370	U1301	A1237	C1172	G1108	G1047	A978	U913	U838	G774	U701	G616
A1633	U1494	U1494	A1434	A1371	U1302	A1237	C1173	U1109	U1048	U981	A914	U839	A774	G702	U617
C1634	G1495	G1495	G1435	G1303	G1303	U1240	G1174	G1110	G1049	A982	U915	U840	G775	G703	A618
G1635	U1496	U1496	U1436	U1304	U1304	G1240	G1175	G1111	G1050	G983	U916	U841	G776	C704	A619
G1636	G1497	G1497	C1437	C1305	C1305	G1243	C1176	G1112	U1051	G984	U919	U842	C777	U705	A620
C1637	C1498	C1498	U1438	U1376	U1306	A1243	G1177	G1113	G1052	A987	U920	U843	G778	A706	A621
C1638	C1499	C1499	G1439	C1377	G1307	G1244	G1178	U1114	U1053	A987	U921	U844	A779	A622	A622
G1639	U1500	U1500	U1440	U1378	C1308	C1245	G1179	U1115	U1054	A987	U922	U845	A780	G709	G623
C1640	A1501	A1501	U1441	U1379	U1246	C1247	C1179	U1116	U1055	A991	A922	U846	A781	U710	G624
G1643	G1502	G1502	A1442	G1380	U1310	G1254	A1182	G1117	U1056	A992	A923	U847	G782	G711	U712
C1644	A1503	A1503	G1443	G1381	A1311	A1255	A1183	G1118	U1057	A993	A924	C848	G783	A713	U631
G1648	U1504	U1504	A1444	A1382	A1312	U1256	U1184	U1119	G1058	A994	A925	C849	U784	A714	U632
U1648	G1505	G1505	G1445	G1383	U1313	C1251	U1185	G1120	U1059	U995	C926	C851	G785	G715	U633
C1651	U1506	U1506	G1446	G1384	U1314	G1263	U1186	C1121	U1060	U996	U927	C852	U786	G716	U634
C1652	C1507	C1507	U1447	G1385	G1315	G1254	G1187	A1123	A1061	A997	C930	U855	A787	C717	A635
U1655	U1511	U1511	U1448	A1386	C1316	A1255	A1188	G1124	U1062	U998	C931	U856	U788	U718	A635
G1656	G1512	G1512	C1449	G1387	G1317	U1256	C1189	G1125	G1063	C999	U931	U857	U789	U719	U638
C1657	U1450	U1450	U1388	A1318	U1257	U1257	U1190	G1126	A1064	A1000	A932	C858	A790	G720	U639
U1658	G1451	G1451	U1451	U1389	U1258	U1258	C1191	C1127	G1065	U1003	U934	U859	U793	U721	G640
C1659	A1514	A1514	G1452	U1390	A1320	U1259	A1192	U1128	C1066	U1004	U935	U860	U794	G722	G641
U1659	G1453	G1453	C1454	C1321	G1261	U1261	C1194	A1068	A1068	C1005	C936	A861	A795	G723	U642
G1660	U1515	U1515	G1454	G1392	C1322	U1262	A1195	C1069	C1069	C1006	G937	A862	G796	G724	U643
G1661	C1393	C1393	G1393	G1393	G1262	U1262	C1196	U1070	C1070	G1007	A938	U863	C797	U725	U644
C1662	U1396	U1396	U1324	A1324	G1263	G1263	C1197	U1134	G1071	U1008	A939	A864	A798	G726	U645
U1667	C1397	C1397	A1328	A1328	G1266	G1266	G1198	U1135	G1072	C1009	A940	U865	A728	G727	G646
G1670	A1398	A1398	C1332	C1332	U1267	U1267	G1199	A1136	G1073	G1010	C941	U866	U803	A729	U647
C1671	U1399	U1399	U1333	U1333	G1269	G1269	G1200	A1137	C1074	U1011	C942	U867	U804	G730	U649
U1672	G1400	G1400	U1334	U1334	U1270	U1270	A1201	A1075	A1012	A943	U944	U872	A805	C731	G650
C1673	C1401	C1401	G1462	A1335	U1271	U1271	A1202	G1139	C1076	G1013	U945	C873	A806	G732	U651
U1674	C1402	C1402	C1463	A1336	U1272	U1272	C1204	G1140	C1077	U1014	U946	C874	U809	A733	C652
G1675	G1403	G1403	U1464	C1337	G1273	G1273	U1205	A1141	U1078	C1015	U947	C875	A810	A734	C653
U1676	U1405	U1405	U1465	C1338	A1274	U1274	C1206	A1142	A1080	U1017	C948	C876	U811	C735	G654
G1677	C1337	C1337	C1466	C1337	U1275	U1275	U1143	U1143	C1081	A1018	C949	C877	U812	C736	G655
C1678	A1408	A1408	A1468	A1340	G1277	G1277	C1208	G1145	G1082	A1019	A950	C878	A813	A737	U656
A1679	U1409	U1409	G1470	A1341	C1278	C1278	C1209	A1146	A1083	C1020	A953	C879	G814	G738	C657
U1680	U1410	U1410	U1411	A1344	C1279	C1279	A1210	G1149	G1084	C1021	G952	U883	G815	C	G
C1681	G1412	G1412	U1413	A1345	G1280	G1280	G1211	A1085	A1022	G953	G953	A884	A816	C741	G676
U1682	U1413	U1413	G1473	U1346	U1281	U1281	G1212	A1086	U1023	C917	G956	U885	C817	U742	G677
G1683	G1414	G1414	C1474	A1347	U1282	U1282	U1213	A1087	A1024	A1025	U957	U886	G818	U743	U678
C1684	U1415	U1415	G1475	G1348	C1283	C1283	C1214	U1088	A1026	U958	U958	U887	U819	U744	U679
U1685	G1416	G1416	G1476	U1352	U1284	U1284	C1215	C1089	A1026	C1027	U959	U888	U820	U745	U680
G1686	U1417	U1417	U1477	U1352	U1285	U1285	A1216	A1090	C1027	C1027	U959	U889	G822	U745	U681
A1687	C1418	C1418	C1478	G1353	A1286	A1286	C1217	A1156	A1091	U1030	A962	U894	G823	A753	A684
U1688	A1419	A1419	C1479	U1353	G1287	G1287	A1218	C1157	A1092	U1031	A965	U895	U824	A755	A685
C1689	U1420	U1420	C1480	G1357	U1288	U1288	G1221	A1159	U1094	C1032	A966	C896	U825	A760	C686
U1692	A1481	A1481	U1481	C1358	U1289	U1289	A1222	C1160	C1095	C1033	A967	C897	C826	G761	C687
G1693	U1482	U1482	G1482	A1359	G1290	G1290	C1161	U1096	U1096	G1034	U967	C898	U827	G762	G688
C1694	C1483	C1483	C1483	C1360	U1291	U1291	U1224	U1097	U1097	A1038	C968	A904	A828	A762	C692
G1695	U1424	U1424	C1424	C1424	U1292	U1292	G1163	U1098	U1098	A1038	A969	U829	U829	G763	C692
U1696	A1425	A1425	U1425	U1362	G1293	G1293	A1226	G1164	G1099	G1039	A970	U830	U830	U764	U693



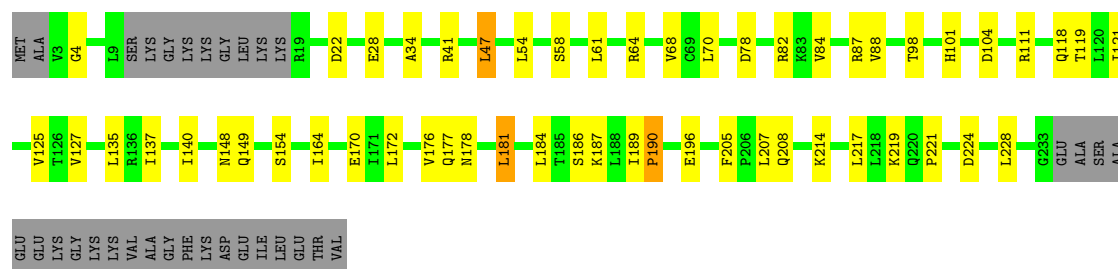
• Molecule 3: mRNA



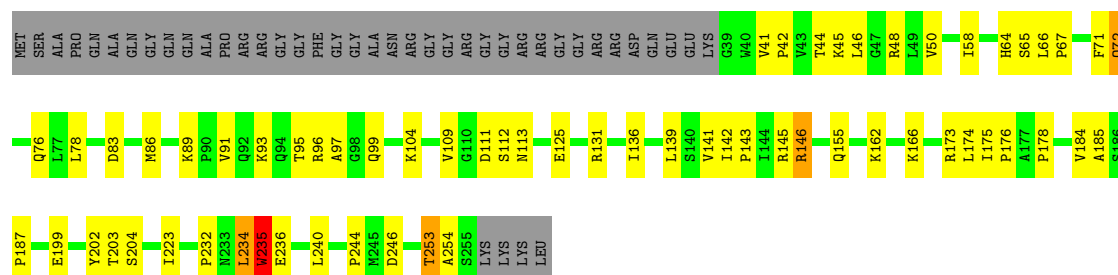
• Molecule 4: uS2



• Molecule 5: eS1

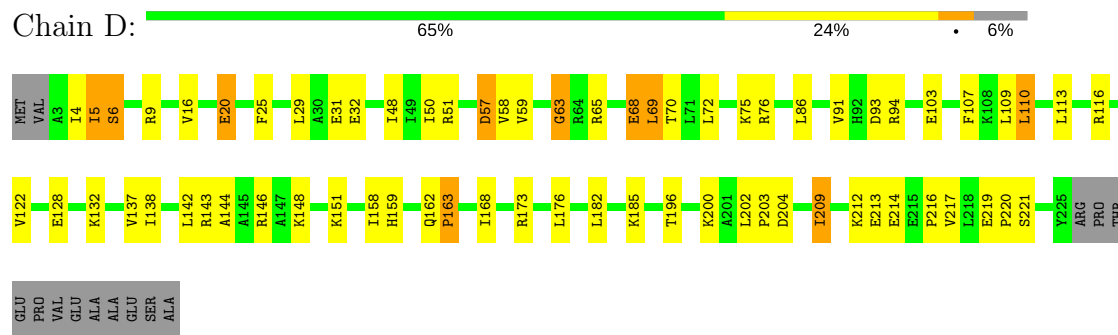


• Molecule 6: uS5

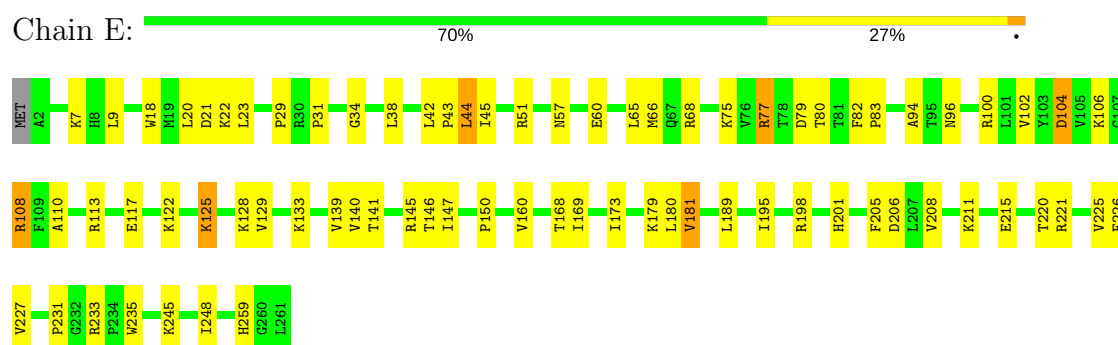




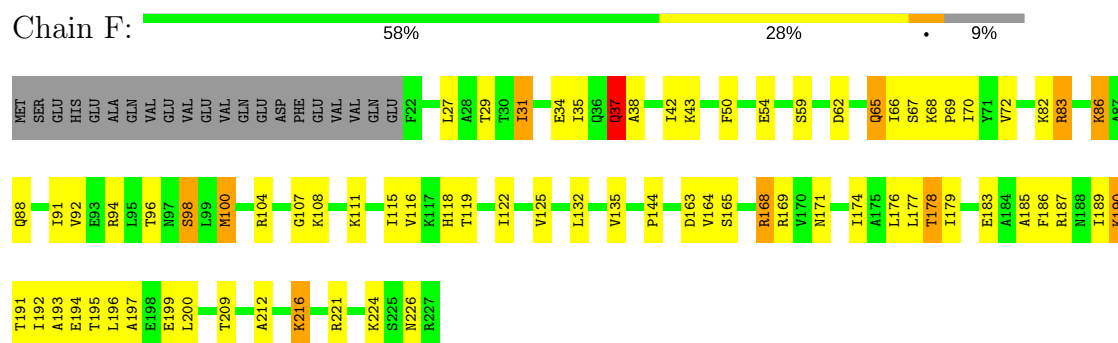
- Molecule 7: uS3



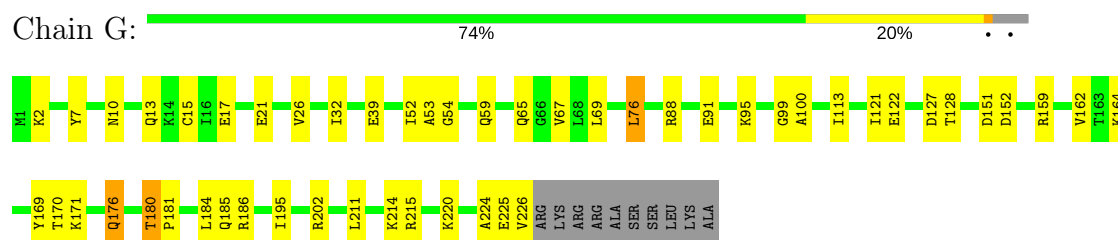
- Molecule 8: eS4



- Molecule 9: uS7

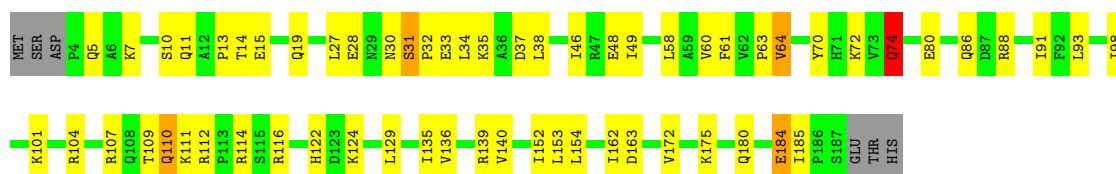


- Molecule 10: eS6



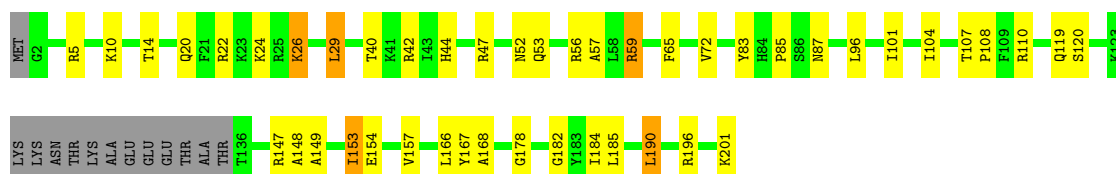
- Molecule 11: eS7





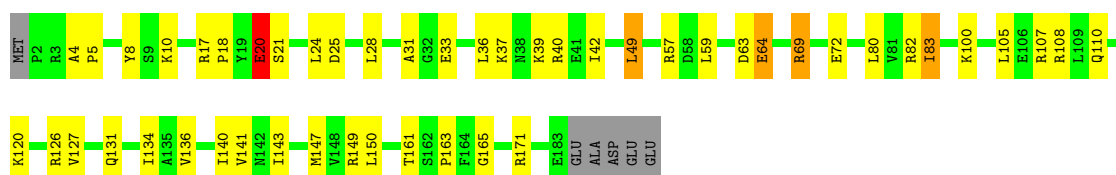
• Molecule 12: eS8

Chain I: 71% 20% 6%



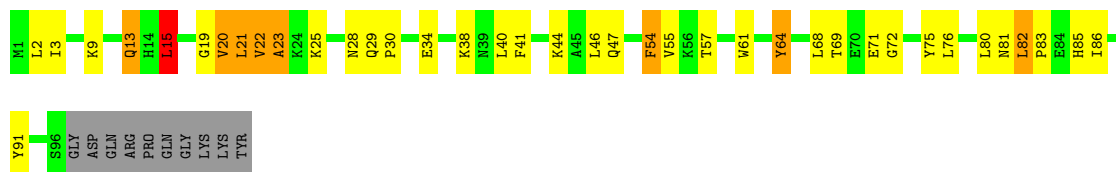
• Molecule 13: uS4

Chain J: 71% 23% 6%



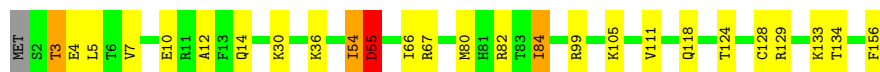
• Molecule 14: eS10

Chain K: 54% 28% 8% 9%



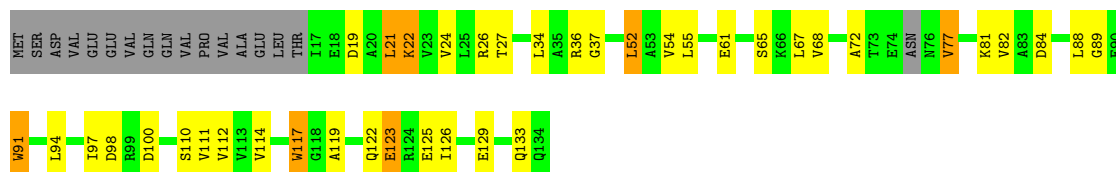
• Molecule 15: uS17

Chain L: 83% 14% 3%



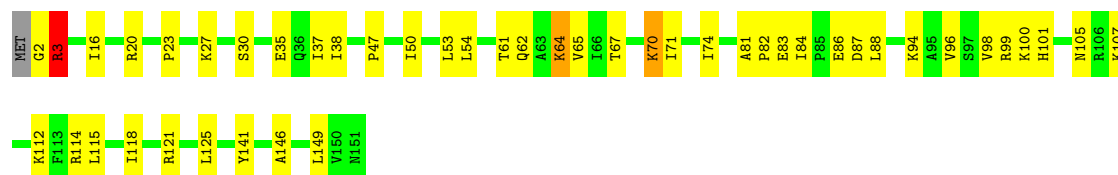
• Molecule 16: eS12

Chain M: 57% 25% 5% 13%



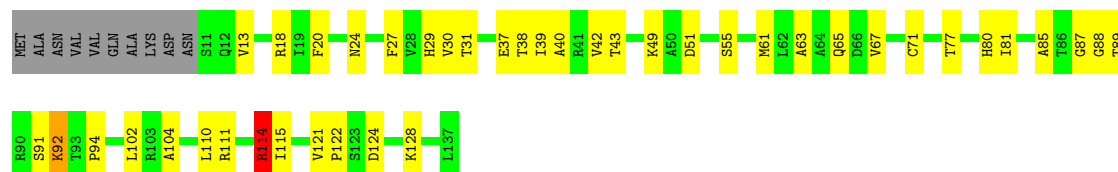
- Molecule 17: uS15

Chain N:  69% 28% ...



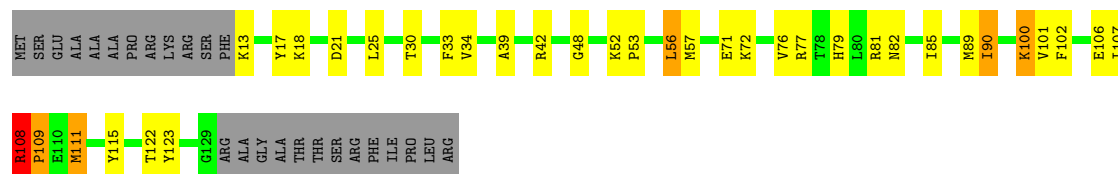
- Molecule 18: uS11

Chain 0:  62% 29% .. 7%



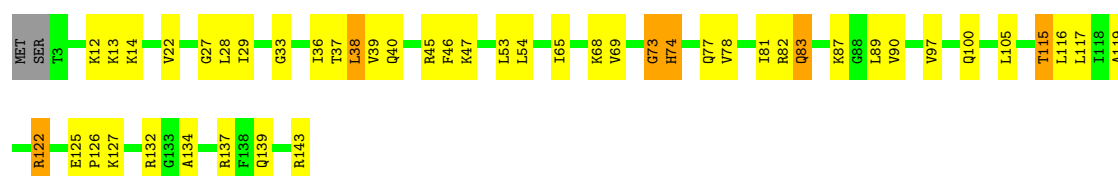
- Molecule 19: uS19

Chain P:  57% 21% 2% 1% 19%



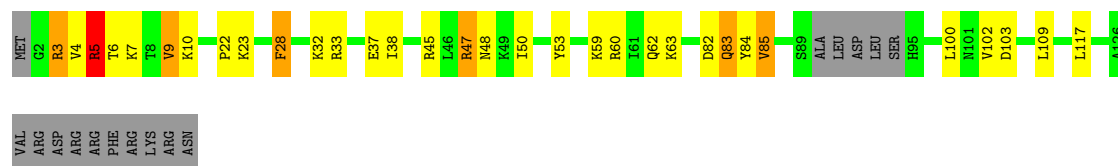
- Molecule 20: uS9

Chain Q:  66% 29% . .



- Molecule 21: eS17

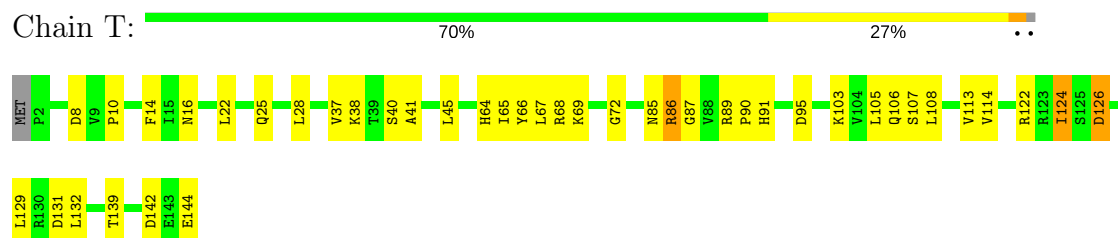
Chain R:  65% 18% 2% 1% 14%



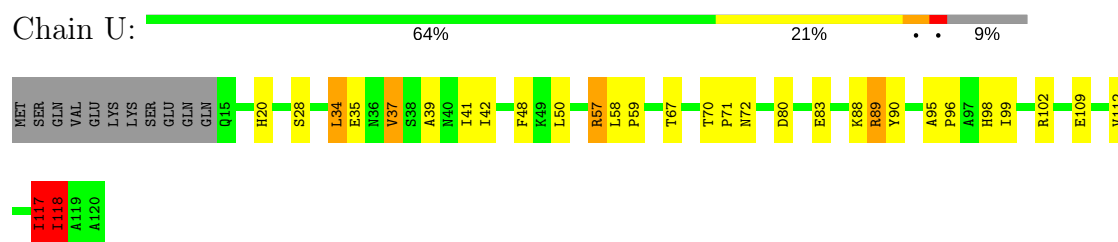
- Molecule 22: uS13



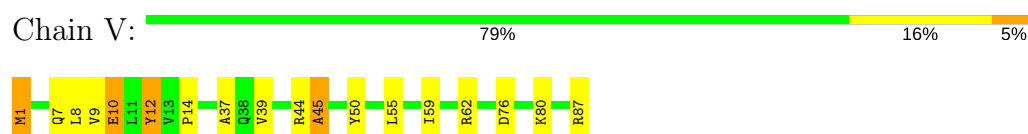
• Molecule 23: eS19



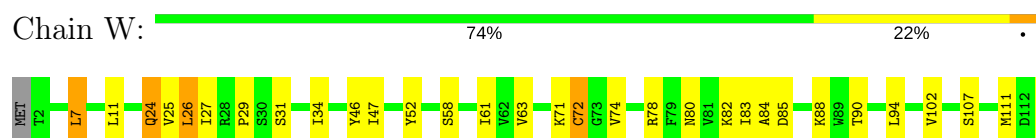
• Molecule 24: uS10



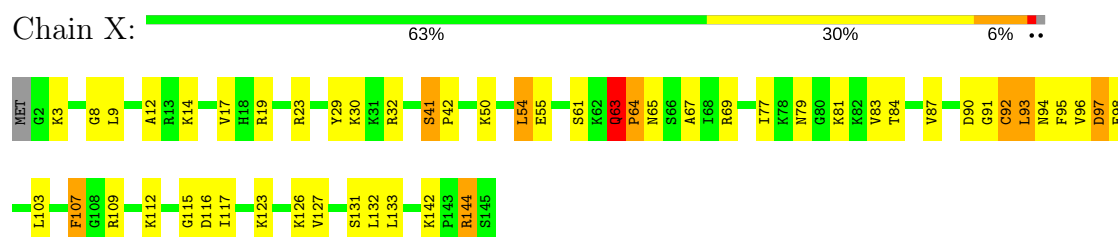
• Molecule 25: eS21



• Molecule 26: uS8

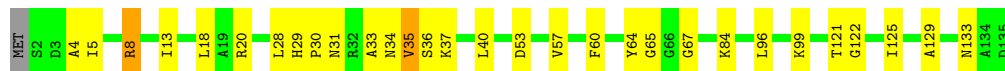


• Molecule 27: uS12



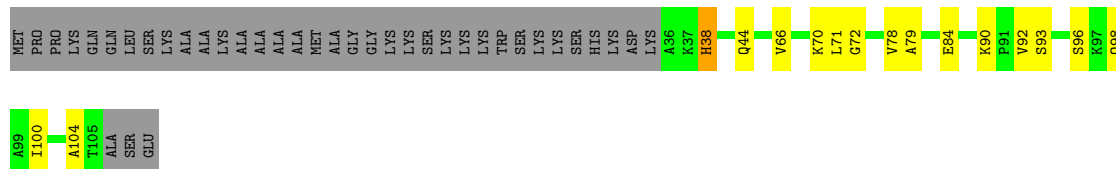
- Molecule 28: eS24

Chain Y:  77% 21% ..



- Molecule 29: eS25

Chain Z:  50% 14% • 35%



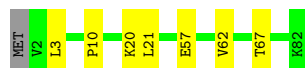
- Molecule 30: eS26

Chain a:  70% 12% • 18%




- Molecule 31: eS27

Chain b:  90% 9% •



- Molecule 32: eS28

Chain c:  81% 10% • 7%



- Molecule 33: uS14

Chain d:  79% 14% • 5%

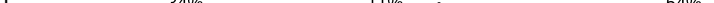


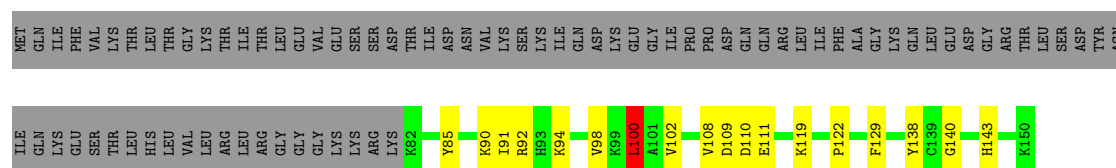
- Molecule 34: eS30

Chain e:  71% 14% 14%

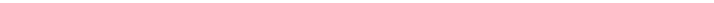


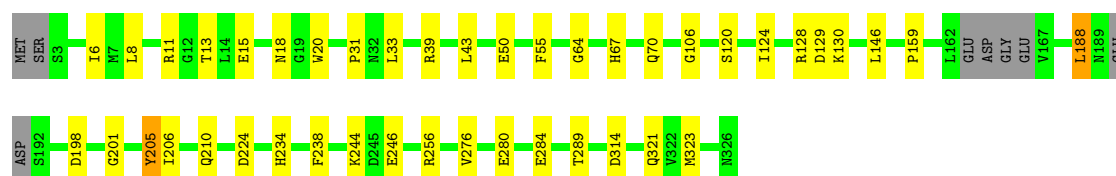
- Molecule 35: eS31

Chain f:  34% 11% 54%



- Molecule 36: RACK1

Chain g:  84% 13%



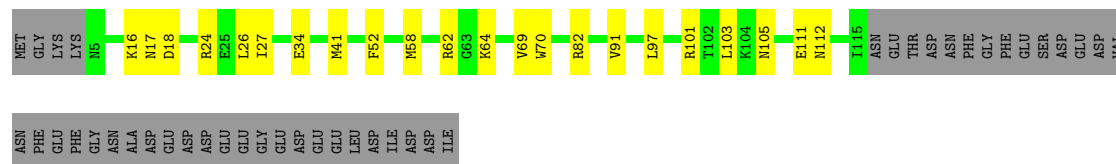
- Molecule 37: eL41

Chain h:  88% 12%



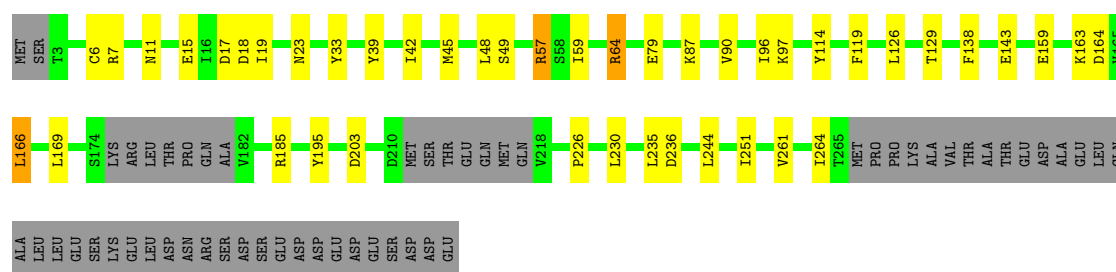
- Molecule 38: eIF1A

Chain i:  58% 14% 27%



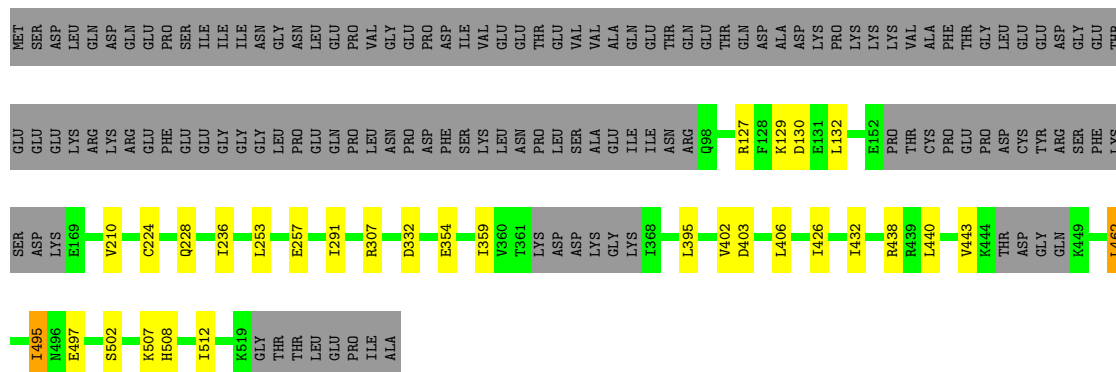
- Molecule 39: eIF2 alpha

Chain j:  67% 13% . 18%



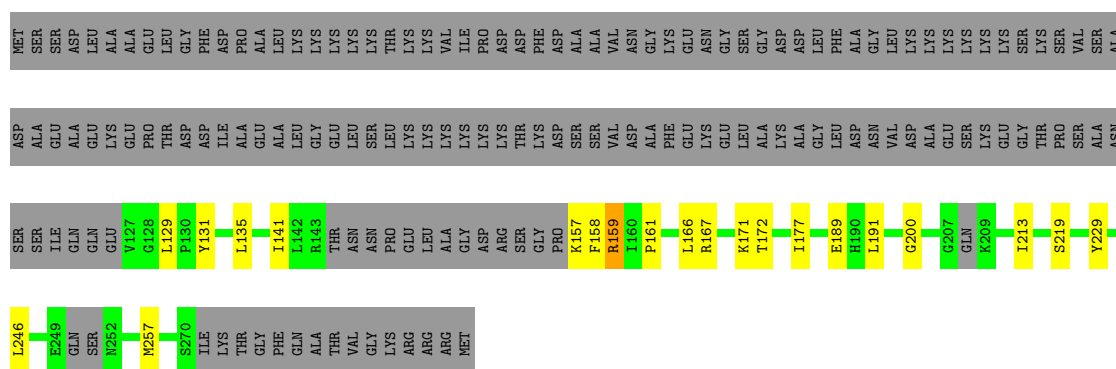
- Molecule 40: eIF2 gamma

Chain k:  69% 6% 25%



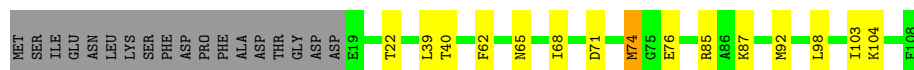
• Molecule 41: eIF2 beta

Chain l: 38% 7% 55%



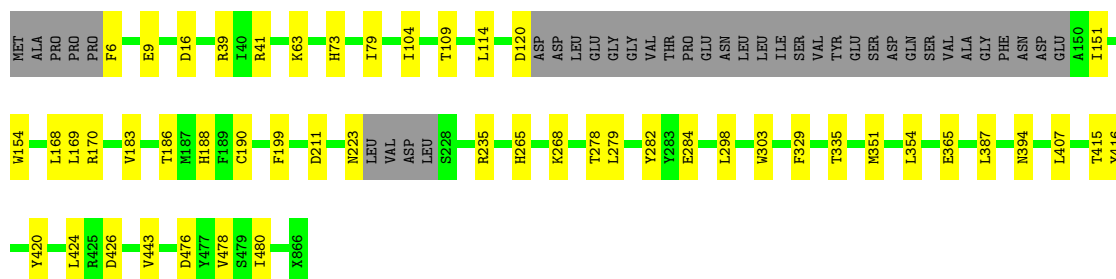
• Molecule 42: eIF1

Chain m: 69% 13% 17%



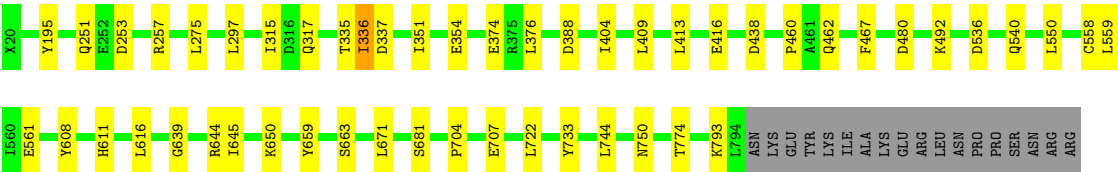
• Molecule 43: eIF3a

Chain o: 85% 9% 6%



• Molecule 44: eIF3c

Chain p: 89% 8% 3%



• Molecule 45: eIF3i



• Molecule 46: eIF3b



• Molecule 47: eIF3g





## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	21401	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	27	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	104478	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: GCP, ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	1	0.38	1/1797 (0.1%)	0.69	0/2799
10	G	0.41	0/1835	0.72	1/2451 (0.0%)
11	H	0.42	0/1507	0.71	0/2028
12	I	0.41	0/1515	0.73	2/2029 (0.1%)
13	J	0.40	0/1495	0.75	1/2001 (0.0%)
14	K	0.48	0/831	0.77	1/1123 (0.1%)
15	L	0.41	0/1276	0.63	0/1718
16	M	0.46	0/891	0.80	1/1201 (0.1%)
17	N	0.41	0/1210	0.77	0/1628
18	O	0.38	0/953	0.68	0/1279
19	P	0.42	0/946	0.71	1/1273 (0.1%)
2	2	0.27	0/42269	0.69	7/65862 (0.0%)
20	Q	0.43	0/1125	0.71	0/1510
21	R	0.43	0/969	0.77	1/1299 (0.1%)
22	S	0.43	0/1212	0.78	0/1629
23	T	0.40	0/1129	0.72	0/1520
24	U	0.40	0/857	0.73	0/1158
25	V	0.36	0/696	0.66	0/938
26	W	0.39	0/1039	0.74	1/1399 (0.1%)
27	X	0.40	0/1137	0.75	2/1516 (0.1%)
28	Y	0.40	0/1075	0.69	0/1433
29	Z	0.44	0/567	0.69	0/762
3	3	0.30	0/317	0.69	0/489
30	a	0.36	0/791	0.67	0/1059
31	b	0.38	0/619	0.65	0/837
32	c	0.38	0/489	0.71	0/655
33	d	0.41	0/457	0.62	0/607
34	e	0.40	0/440	0.73	0/586
35	f	0.49	0/559	0.73	1/747 (0.1%)
36	g	0.41	0/2521	0.64	1/3431 (0.0%)
37	h	0.36	0/234	0.75	0/300
38	i	0.39	0/894	0.70	0/1188

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	j	0.47	0/2034	0.77	2/2737 (0.1%)
4	A	0.42	0/1666	0.78	2/2279 (0.1%)
40	k	0.47	0/3079	0.70	1/4157 (0.0%)
41	l	0.47	0/1051	0.76	1/1402 (0.1%)
42	m	0.41	0/724	0.75	1/968 (0.1%)
43	o	0.49	0/3796	0.80	0/5128
44	p	0.49	0/4602	0.76	2/6226 (0.0%)
45	q	0.50	0/2757	0.67	0/3733
46	r	0.49	0/282	0.74	0/373
47	s	0.47	0/426	0.64	0/571
5	B	0.40	0/1793	0.72	2/2414 (0.1%)
6	C	0.39	0/1659	0.69	0/2252
7	D	0.42	0/1769	0.72	1/2378 (0.0%)
8	E	0.38	0/2122	0.67	0/2861
9	F	0.41	0/1628	0.75	0/2198
All	All	0.38	1/103040 (0.0%)	0.71	32/148132 (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
27	X	0	1
28	Y	0	1
41	l	0	1
9	F	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1	A	OP3-P	-9.88	1.49	1.61

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	685	A	C2'-C3'-O3'	8.09	127.30	109.50
12	I	29	LEU	CA-CB-CG	7.26	132.00	115.30
39	j	166	LEU	CA-CB-CG	6.66	130.62	115.30
41	l	191	LEU	CA-CB-CG	6.50	130.25	115.30
26	W	26	LEU	CA-CB-CG	6.10	129.33	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	F	191	THR	Peptide
27	X	63	GLN	Peptide
28	Y	29	HIS	Peptide
41	l	158	PHE	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	1	1607	0	815	48	0
2	2	37797	0	19016	882	0
3	3	287	0	149	2	0
4	A	1626	0	1633	20	0
5	B	1769	0	1829	13	0
6	C	1629	0	1710	26	0
7	D	1744	0	1826	24	0
8	E	2078	0	2157	24	0
9	F	1609	0	1679	30	0
10	G	1812	0	1911	23	0
11	H	1483	0	1579	18	0
12	I	1489	0	1504	19	0
13	J	1471	0	1554	16	0
14	K	809	0	810	17	0
15	L	1248	0	1311	10	0
16	M	885	0	917	17	0
17	N	1187	0	1251	18	0
18	O	942	0	979	18	0
19	P	927	0	971	17	0
20	Q	1105	0	1170	19	0
21	R	959	0	1006	17	0
22	S	1193	0	1217	22	0
23	T	1110	0	1124	18	0
24	U	845	0	913	13	0
25	V	687	0	682	7	0
26	W	1021	0	1056	14	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	X	1119	0	1198	20	0
28	Y	1061	0	1111	11	0
29	Z	558	0	585	7	0
30	a	779	0	831	0	0
31	b	609	0	630	0	0
32	c	487	0	528	0	0
33	d	446	0	436	0	0
34	e	433	0	470	0	0
35	f	546	0	557	0	0
36	g	2466	0	2406	0	0
37	h	233	0	284	0	0
38	i	884	0	891	0	0
39	j	2006	0	2066	0	0
40	k	3034	0	3195	0	0
41	l	1036	0	1079	0	0
42	m	716	0	742	0	0
43	o	4189	0	3874	0	0
44	p	4899	0	4599	0	0
45	q	2693	0	2609	0	0
46	r	277	0	273	0	0
47	s	418	0	411	0	0
48	2	80	0	0	0	0
48	k	1	0	0	0	0
49	a	1	0	0	0	0
49	b	1	0	0	0	0
49	f	1	0	0	0	0
49	l	1	0	0	0	0
50	k	8	0	8	0	0
51	k	32	0	14	0	0
All	All	98333	0	79566	1306	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 9.

The worst 5 of 1306 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)
2:2:567:G:H22	2:2:573:G:N2	1.34	1.24
2:2:567:G:N2	2:2:573:G:H22	1.36	1.23
2:2:480:A:N1	2:2:506:U:O4	1.89	1.05
2:2:1292:U:O4	2:2:1321:A:N1	1.89	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:18:G:H1'	1:1:58:A:N1	1.71	1.04

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	206/254 (81%)	170 (82%)	27 (13%)	9 (4%)	3	30
5	B	218/255 (86%)	185 (85%)	25 (12%)	8 (4%)	4	34
6	C	215/259 (83%)	186 (86%)	22 (10%)	7 (3%)	4	37
7	D	221/237 (93%)	196 (89%)	16 (7%)	9 (4%)	3	31
8	E	258/261 (99%)	225 (87%)	28 (11%)	5 (2%)	9	48
9	F	204/227 (90%)	169 (83%)	28 (14%)	7 (3%)	4	36
10	G	224/236 (95%)	197 (88%)	23 (10%)	4 (2%)	10	49
11	H	182/190 (96%)	157 (86%)	15 (8%)	10 (6%)	2	25
12	I	184/201 (92%)	160 (87%)	15 (8%)	9 (5%)	2	28
13	J	180/188 (96%)	154 (86%)	19 (11%)	7 (4%)	3	32
14	K	94/106 (89%)	81 (86%)	7 (7%)	6 (6%)	1	22
15	L	153/156 (98%)	133 (87%)	13 (8%)	7 (5%)	3	29
16	M	113/134 (84%)	85 (75%)	21 (19%)	7 (6%)	2	23
17	N	148/151 (98%)	134 (90%)	13 (9%)	1 (1%)	25	68
18	O	125/137 (91%)	102 (82%)	16 (13%)	7 (6%)	2	25
19	P	115/142 (81%)	96 (84%)	13 (11%)	6 (5%)	2	26
20	Q	139/143 (97%)	108 (78%)	20 (14%)	11 (8%)	1	17
21	R	116/136 (85%)	101 (87%)	13 (11%)	2 (2%)	11	51
22	S	143/146 (98%)	111 (78%)	21 (15%)	11 (8%)	1	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	T	141/144 (98%)	126 (89%)	15 (11%)	0	100	100
24	U	104/117 (89%)	84 (81%)	16 (15%)	4 (4%)	4	33
25	V	85/87 (98%)	74 (87%)	7 (8%)	4 (5%)	3	29
26	W	127/130 (98%)	112 (88%)	10 (8%)	5 (4%)	3	32
27	X	142/145 (98%)	117 (82%)	14 (10%)	11 (8%)	1	18
28	Y	132/135 (98%)	118 (89%)	7 (5%)	7 (5%)	2	26
29	Z	68/108 (63%)	50 (74%)	17 (25%)	1 (2%)	12	53
30	a	96/119 (81%)	81 (84%)	11 (12%)	4 (4%)	3	31
31	b	79/82 (96%)	61 (77%)	15 (19%)	3 (4%)	4	33
32	c	60/67 (90%)	51 (85%)	6 (10%)	3 (5%)	2	27
33	d	51/56 (91%)	33 (65%)	15 (29%)	3 (6%)	2	23
34	e	52/63 (82%)	45 (86%)	6 (12%)	1 (2%)	9	48
35	f	67/150 (45%)	48 (72%)	9 (13%)	10 (15%)	0	5
36	g	312/326 (96%)	257 (82%)	45 (14%)	10 (3%)	5	37
37	h	23/25 (92%)	23 (100%)	0	0	100	100
38	i	109/153 (71%)	92 (84%)	14 (13%)	3 (3%)	6	40
39	j	243/304 (80%)	205 (84%)	32 (13%)	6 (2%)	6	42
40	k	388/527 (74%)	339 (87%)	43 (11%)	6 (2%)	12	53
41	l	120/285 (42%)	100 (83%)	16 (13%)	4 (3%)	4	37
42	m	88/108 (82%)	76 (86%)	10 (11%)	2 (2%)	7	44
43	o	451/588 (77%)	417 (92%)	31 (7%)	3 (1%)	25	68
44	p	554/652 (85%)	497 (90%)	45 (8%)	12 (2%)	8	45
45	q	340/347 (98%)	302 (89%)	33 (10%)	5 (2%)	12	53
46	r	29/31 (94%)	27 (93%)	2 (7%)	0	100	100
47	s	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
All	All	7149/8360 (86%)	6131 (86%)	778 (11%)	240 (3%)	7	36

5 of 240 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	95	ALA
4	A	166	GLY
6	C	141	VAL

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Mol	Chain	Res	Type
6	C	235	TRP
7	D	216	PRO

### 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	174/211 (82%)	147 (84%)	27 (16%)	3	19
5	B	198/228 (87%)	174 (88%)	24 (12%)	6	28
6	C	176/203 (87%)	153 (87%)	23 (13%)	5	25
7	D	185/196 (94%)	152 (82%)	33 (18%)	2	14
8	E	223/224 (100%)	186 (83%)	37 (17%)	2	17
9	F	174/194 (90%)	140 (80%)	34 (20%)	1	11
10	G	192/200 (96%)	174 (91%)	18 (9%)	10	38
11	H	164/170 (96%)	138 (84%)	26 (16%)	3	19
12	I	147/159 (92%)	133 (90%)	14 (10%)	10	37
13	J	153/158 (97%)	135 (88%)	18 (12%)	6	28
14	K	88/96 (92%)	70 (80%)	18 (20%)	1	9
15	L	136/137 (99%)	128 (94%)	8 (6%)	23	56
16	M	93/109 (85%)	82 (88%)	11 (12%)	6	28
17	N	127/128 (99%)	108 (85%)	19 (15%)	3	21
18	O	96/104 (92%)	88 (92%)	8 (8%)	13	45
19	P	100/119 (84%)	83 (83%)	17 (17%)	2	16
20	Q	117/119 (98%)	99 (85%)	18 (15%)	3	19
21	R	109/124 (88%)	91 (84%)	18 (16%)	2	17
22	S	128/129 (99%)	105 (82%)	23 (18%)	2	13
23	T	117/118 (99%)	97 (83%)	20 (17%)	2	16
24	U	96/107 (90%)	83 (86%)	13 (14%)	4	25
25	V	73/73 (100%)	66 (90%)	7 (10%)	10	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	W	110/111 (99%)	102 (93%)	8 (7%)	16	50
27	X	119/120 (99%)	102 (86%)	17 (14%)	4	23
28	Y	108/109 (99%)	102 (94%)	6 (6%)	25	58
29	Z	60/88 (68%)	55 (92%)	5 (8%)	13	45
30	a	83/100 (83%)	71 (86%)	12 (14%)	4	22
31	b	71/72 (99%)	67 (94%)	4 (6%)	25	58
32	c	54/59 (92%)	48 (89%)	6 (11%)	7	30
33	d	46/48 (96%)	39 (85%)	7 (15%)	3	20
34	e	47/55 (86%)	39 (83%)	8 (17%)	2	16
35	f	57/133 (43%)	48 (84%)	9 (16%)	3	19
36	g	265/272 (97%)	231 (87%)	34 (13%)	5	26
37	h	23/23 (100%)	20 (87%)	3 (13%)	5	26
38	i	93/130 (72%)	74 (80%)	19 (20%)	1	9
39	j	224/274 (82%)	185 (83%)	39 (17%)	2	15
40	k	332/449 (74%)	306 (92%)	26 (8%)	15	47
41	l	119/246 (48%)	103 (87%)	16 (13%)	4	25
42	m	77/96 (80%)	64 (83%)	13 (17%)	2	17
43	o	411/444 (93%)	364 (89%)	47 (11%)	7	29
44	p	507/536 (95%)	469 (92%)	38 (8%)	16	49
45	q	297/301 (99%)	280 (94%)	17 (6%)	24	57
46	r	30/30 (100%)	27 (90%)	3 (10%)	9	35
47	s	43/43 (100%)	37 (86%)	6 (14%)	4	24
All	All	6242/7045 (89%)	5465 (88%)	777 (12%)	9	27

5 of 777 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	Q	139	GLN
26	W	7	LEU
44	p	297	LEU
21	R	45	ARG
23	T	8	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
17	N	105	ASN
24	U	72	ASN
43	o	299	HIS
20	Q	83	GLN
22	S	21	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	74/75 (98%)	32 (43%)	0
2	2	1778/1781 (99%)	879 (49%)	0
3	3	13/25 (52%)	11 (84%)	0
All	All	1865/1881 (99%)	922 (49%)	0

5 of 922 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	8	U
1	1	9	G
1	1	10	G
1	1	14	A
1	1	15	G

There are no RNA pucker outliers to report.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 87 ligands modelled in this entry, 85 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length

(or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
50	MET	k	601	-	7,7,8	0.94	1 (14%)	5,7,9	0.80	0
51	GCP	k	603	48	25,34,34	2.67	8 (32%)	28,54,54	1.08	1 (3%)

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
50	MET	k	601	-	-	0/4/6/8	0/0/0/0
51	GCP	k	603	48	-	0/18/38/38	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	k	603	GCP	C4-N9	-9.64	1.34	1.47
51	k	603	GCP	C8-N9	-3.82	1.35	1.46
51	k	603	GCP	PG-O3G	-2.68	1.48	1.54
51	k	603	GCP	C2-N1	-2.03	1.35	1.44
51	k	603	GCP	PB-O2B	2.05	1.61	1.56

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	k	603	GCP	PA-O3A-PB	-3.34	121.61	132.39

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 ⓘ

There are no chain breaks in this entry.