



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:38 PM BST

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 EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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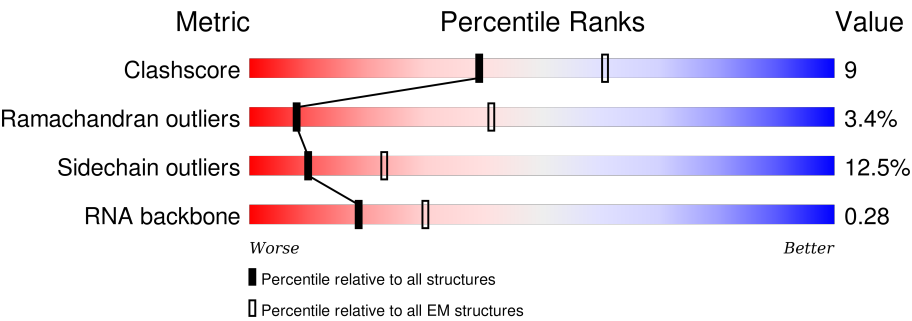
MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 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	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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

Mol	Chain	Length	Quality of chain
1	1	75	<div><div>28%</div><div>45%</div><div>27%</div></div>
2	2	1781	<div><div>26%</div><div>51%</div><div>23%</div></div>
3	3	25	<div><div>•</div><div>52%</div><div>44%</div></div>
4	A	254	<div><div>59%</div><div>19%</div><div>•</div><div>18%</div></div>
5	B	255	<div><div>66%</div><div>20%</div><div>•</div><div>13%</div></div>
6	C	259	<div><div>59%</div><div>23%</div><div>•</div><div>16%</div></div>
7	D	237	<div><div>65%</div><div>24%</div><div>•</div><div>6%</div></div>
8	E	261	<div><div>70%</div><div>27%</div><div>•</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		

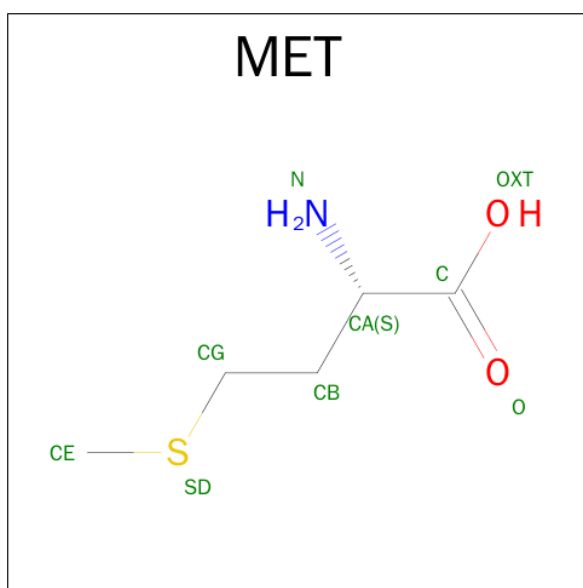
- Molecule 48 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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).

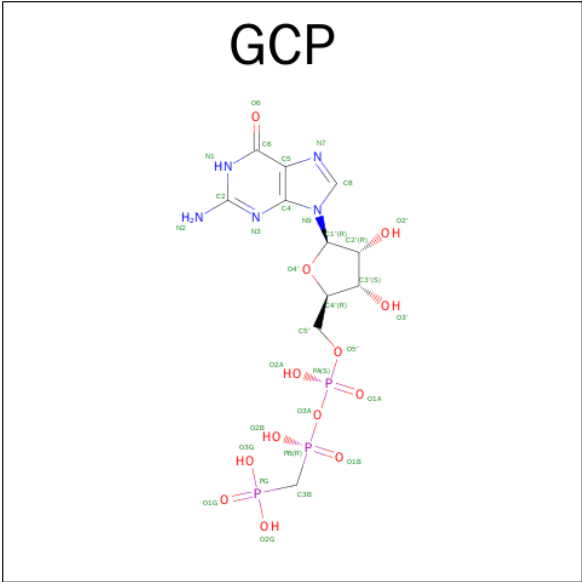
Mol	Chain	Residues	Atoms		AltConf
49	b	1	Total	Zn	0
			1	1	
49	a	1	Total	Zn	0
			1	1	
49	l	1	Total	Zn	0
			1	1	
49	f	1	Total	Zn	0
			1	1	

- 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	

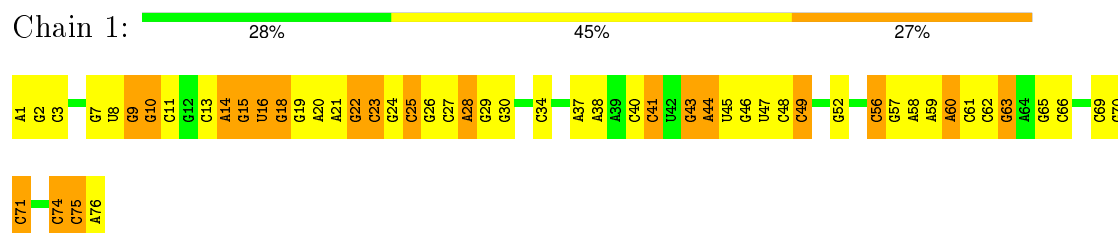
- Molecule 51 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula:  $C_{11}H_{18}N_5O_{13}P_3$ ).



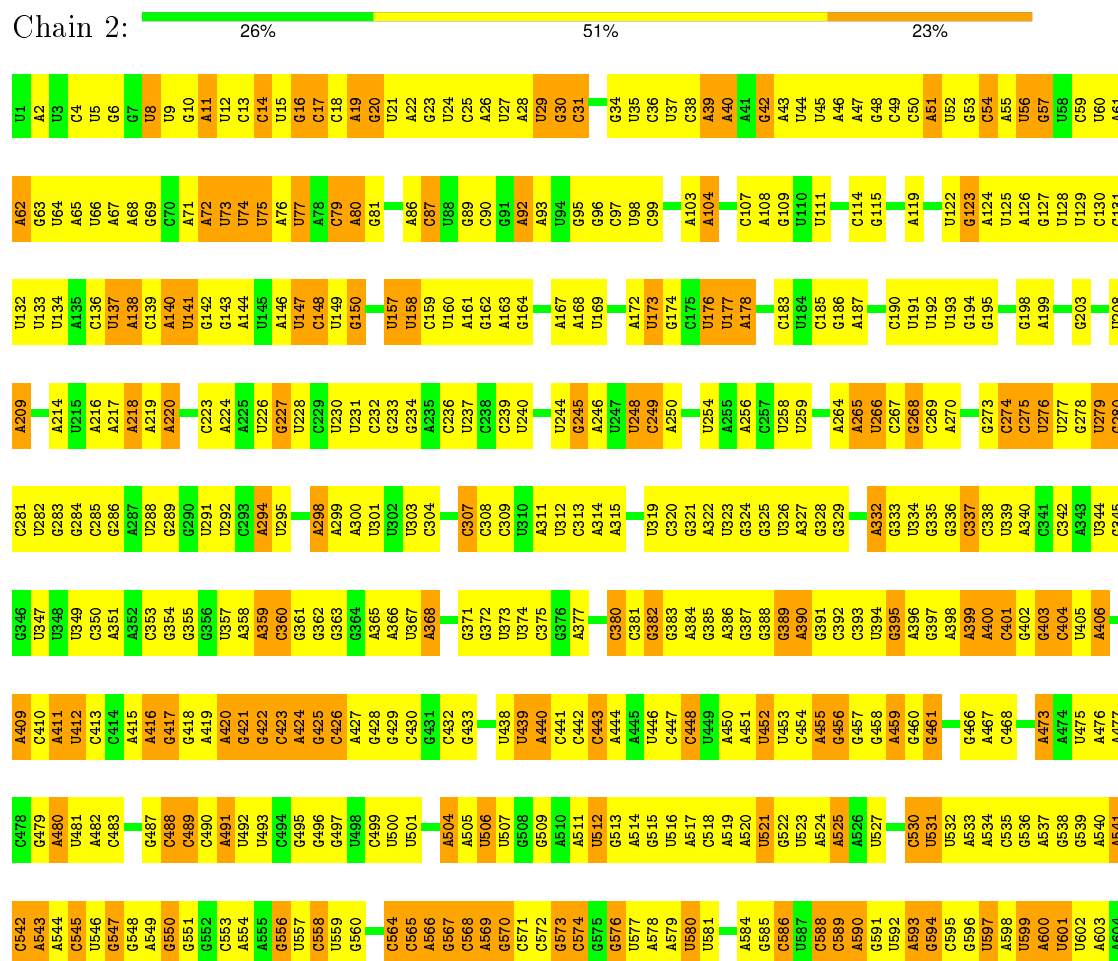
### 3 Residue-property plots

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

#### • Molecule 1: Met-tRNAi (U31:A39 variant)



#### • Molecule 2: 18S rRNA

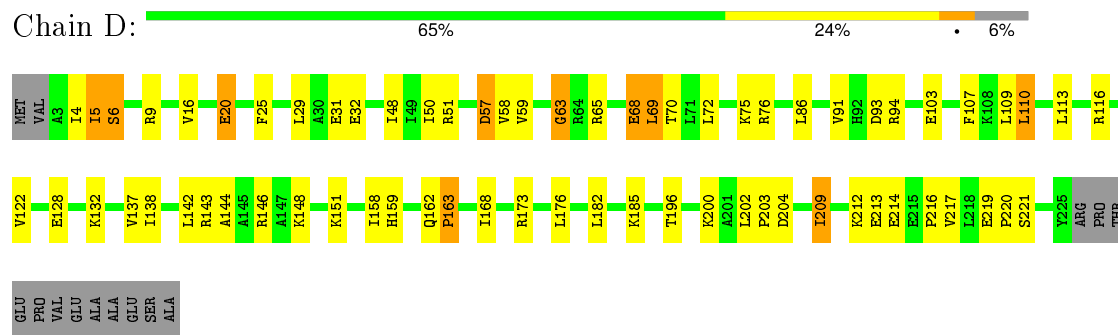


U1619	A1557	C1480	A1420	G1357	U1288	C1221	A1159	U1084	C1032	A966	A897	U827	G761	G688	A605
G1620	U1558	A1451	U1421	C1358	U1289	A1222	C1160	C1095	C1033	U967	G898	A828	A762	G688	G606
C1621	U1559	A1452	A1422	A1359	G1290	A1223	C1161	U1096	G1034	C968	A904	U829	G763	C692	U607
C1622	G1560	C1483	A1423	C1360	G1291	U1224	A1162	U1097		A969	A905	U830	U764	U693	U608
C1623	C1561	G1494	C1424	U1361	U1292	A1225	G1163	U1098	A1038	A970	A906	U831	U765	U694	G609
U1624	A1495	A1425	U1362	U1362	G1293	A1226	G1164	G1099	A1039	G971	U907	U832	U766	U695	U610
U1625	C1486	G1426	G1363	G1363	G1294	G1227	A1165	G1100	G1040	C974	U908	U833	U767	C696	U611
U1626	U1487	G1427	C1364	C1364	A1295	G1228	C1166	G1101	G1041	G975	U909	U834	C768	C697	G612
G1627	U1565	G1428	C1365	C1365	G1296	A1229	U1167	U1102	A1042	G976	C909	U835		U698	G613
U1628	C1489	C1429	G1366	G1366	U1297	U1230	G1168	U1103	U1043	A977	U910	G836	G772	C700	G615
C1629	A1490	U1430	G1367	G1367	G1298	U1231	G1169	G1104	C1044	A978	U911	G837	G773	G700	U616
G1630	A1491	G1431	U1368	U1368	A1299	G1232	A1170	G1106	G1045		U912	U838	C774	U701	U617
A1631	C1492	U1432	U1300	G1370	U1301	G1236	C1172	G1107	G1046		U913	U839	C774	G702	U618
C1632	G1493	G1433	U1302	G1371	U1302	A1237	C1173	G1108	G1047	U981	U914	U840	G775	G703	A618
A1633	U1494	A1434	U1303		U1303	G1237	U1174	G1109	U1048	A982	U915	C841	G776	C704	A619
C1634	U1495	U1435	G1303		G1303	G1240	G1175	G1110	G1049	G983	U916	U842	C777	C705	A620
G1635	G1496	G1436	U1304	C1374	U1304	G1243	G1176	G1111	G1050	G984		U843	C778	A706	A621
G1636	G1497	G1437	U1305	U1375	U1305	A1244	C1177	G1112	G1051	G985	U919	G844	A779	A622	A622
C1637	A1575	C1498	C1438	U1376	U1306	G1245	G1178	G1113	G1052	G986	U920	G845	A780	G623	G623
C1638	U1576	C1499	U1439	C1377	G1307	G1247	G1179	G1114	U1053	A987	G921	A846	A781	C709	G624
G1640	U1577	G1500	U1440	U1378	U1308			U1115	U1054		A922	C847	G782	G711	G630
G1643	U1580	A1503	G1443	G1381	A1311	G1254	A1182	G1116	U1055	A991	A923	C848	G783	U712	U631
C1644	A1581	G1504	A1444	A1382	A1312	U1250	U1184	G1117	U1056	A992	G924	C851	U784	A713	U632
U1648	G1582	G1505	C1445	G1383	U1313	C1251	U1185	U1118	U1057	A993	C925	G852	G785	C714	U633
G1651	U1583	U1506	G1446	G1384	U1314		U1186	G1119	U1058	A994	U926	U853	G786	U715	U634
G1652	A1584	C1507	U1447	G1385	U1315	G1254	G1187	G1120	U1059	G996	U927	U854	A788	C716	U635
C1653	A1585		U1448	G1386	A1316	A1255	A1188	A1061	C1060	A997	C930	A855	U789	C717	A638
U1654	G1586	G1511	U1449	C1387	G1317	U1256	G1189	G1125	U1062	U998	U931	U856	A790	U718	U639
U1655	C1587	U1512	U1450	U1388	A1318	U1257	U1190	G1126	A1064	A1000	A932	G857	A791	G720	U640
G1656	U1588	A1513	G1451	U1389	U1319	U1258	C1191	G1127	C1065		U934	U859	U793	U721	U641
U1659	C1589	A1514	G1452	U1390	A1320	U1259	A1192	U1128	C1066	U1003	G935	A861	A795	G722	G642
G1660	U1590	U1515	G1453	C1391	C1321	U1260	C1193	G1129	C1067	A1004	C936	U862	C797	G723	U643
G1661	U1593	U1516	G1454	G1392	C1322	U1261	C1194		A1068	C1005	G937	U863	A798	G724	G644
C1662	U1594	U1517	G1455	G1393	G1323	G1262	C1196	A1132	C1069	C1006	A938	U864		G725	U645
U1667	C1597	U1518	G1456	U1396	A1324	G1263	C1197	G1133	U1070	C1007	A939	G865	A803	G726	U646
G1670	A1598	U1520	A1458	C1397	A1328	G1266	G1198	U1135	G1072	U1008	A940	G866	U804	G727	U647
C1671	U1599	G1521	C1459	A1398	G1267	G1267	G1199	A1136	G1073	C1009	G941	U867	A805	G728	U648
U1672	C1600	A1522	A1460	A1399	C1332	U1268	G1200	A1137	C1074	U1011	A943		A806	C731	G650
C1673	U1601	A1523	G1461	U1333	U1333	G1269	A1201	A1138	A1075	A1012	U944	U872	G809	G732	U651
U1674	U1602	G1528	G1462	C1401	U1334	U1270	A1202	G1139	C1076	G1013	U945	G873	A733	G733	C652
G1675	C1603	U1529	C1463	C1402	A1335	U1271	A1203	G1140	C1077	U1014	U946	G874	A734	C653	G654
U1676	U1604		G1464	A1404	A1336	G1272	C1204	C1078	U1078	C1015	G947	G875	A811	C735	G655
G1677	G1605	U1533	U1465	U1405	C1337	C1273	U1205	A1142	U1079	U1016	C948	G876	U812	G736	U656
A1678	C1534	G1534	A1466	U1406	U1338	A1274	C1206	U1143	A1080	U1017	C949	G877	A813	A737	C657
U1679	U1536	U1536	A1467	U1407	U1339	U1275	U1144	U1145	C1081	U1018	A950	G878	G814	G738	C
C1680	G1537	U1537	A1468	A1408	A1340	G1276	C1208	G1145	G1082	A1019	A951	C879	G815	C741	G676
U1681	U1538	C1538	G1470	G1440	A1340	G1277	C1209	A1146	A1083	C1020	G952		A816	G742	G677
G1682	A1539	U1539	U1471	U1411	A1343	C1278	A1210	G1149	G1084	C1021	G953	A883	G817	U743	U678
U1683	U1540	G1540	U1472	U1412	A1344	G1279	G1211	A1095	A1085	A1022		G884	G818	U744	U679
C1684	G1541	U1541	U1473	U1413	A1345	G1280	G1212	A1086	U1086	U1023	G956	U885	U819	U745	U680
U1685	C1542	G1542	G1474	U1414	A1346	U1281	U1213	A1087	A1024	U957	U886	U886	U820		U681
G1686	G1543	U1543	G1475	G1415	A1347	U1282	C1214	U1088	U1088	A1025	U958	U887	U821	A753	
U1687	U1544	G1544	G1476	G1416	G1348	C1283	C1215	U1089	A1026	U959	U888	U888	G822		
C1688	A1545	U1545	G1477	G1417	U1352	U1284	A1216	G1154	A1090	C1027		G894	U824	A754	A684
	U1546	U1546	G1478	C1418	U1353	U1285	A1156	C1155	A1091	U1030	A962	U895	U825	A755	A685
	U1556	U1556	C1479	A1419	G1353	A1287	G1218	C1157	A1092	U1031	A965	C896	C826		C687

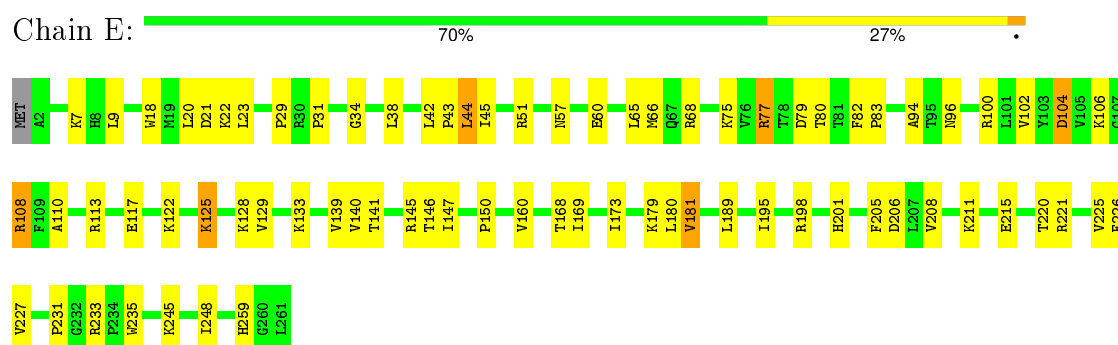




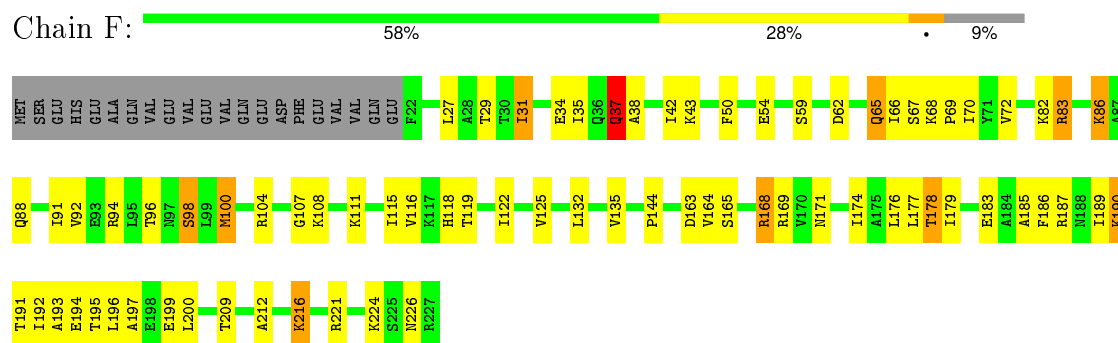
- Molecule 7: uS3



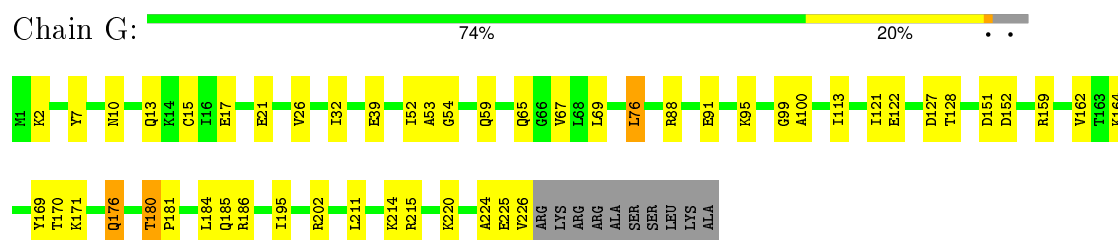
- Molecule 8: eS4



- Molecule 9: uS7

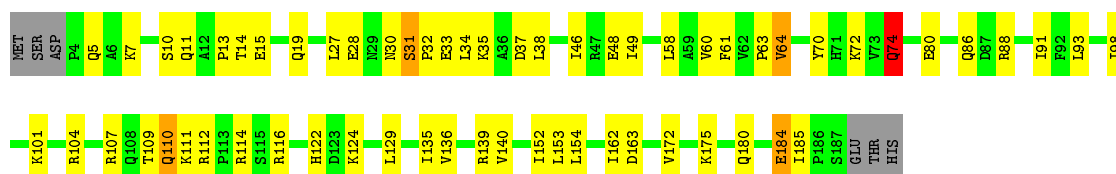


- Molecule 10: eS6



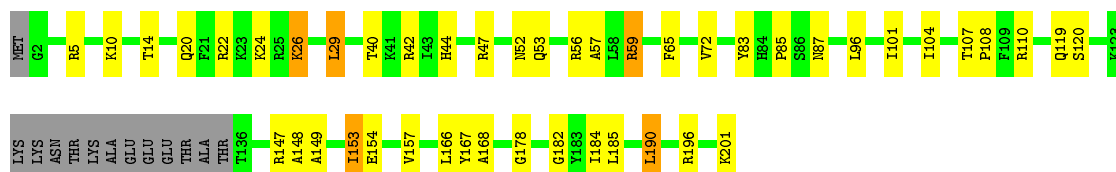
- Molecule 11: eS7





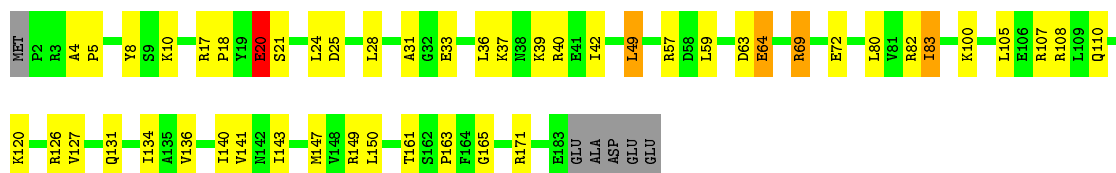
• Molecule 12: eS8

Chain I: 71% 20% 6%



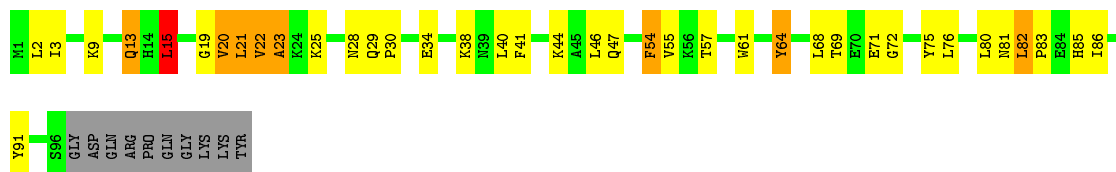
• Molecule 13: uS4

Chain J: 71% 23% 6%



• Molecule 14: eS10

Chain K: 54% 28% 8% 9%



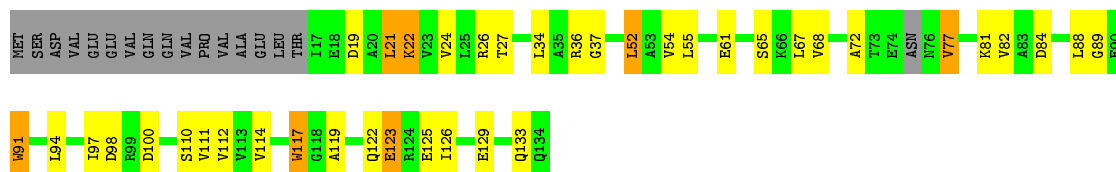
• Molecule 15: uS17

Chain L: 83% 14% 3%



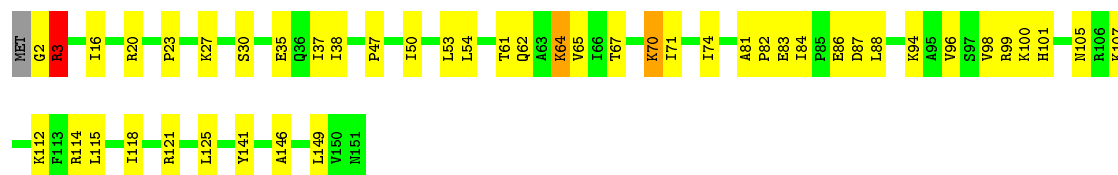
• Molecule 16: eS12

Chain M: 57% 25% 5% 13%



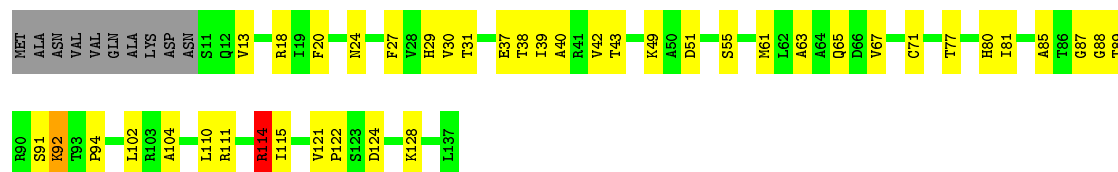
- Molecule 17: uS15

Chain N:  69% 28% ...



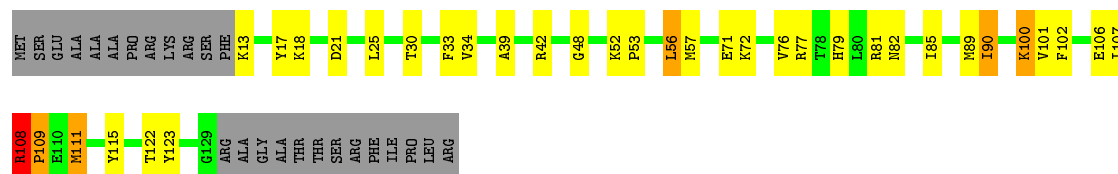
- Molecule 18: uS11

Chain 0:  62% 29% 7%



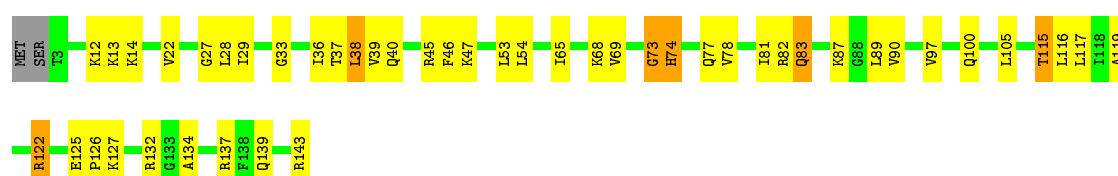
- Molecule 19: uS19

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



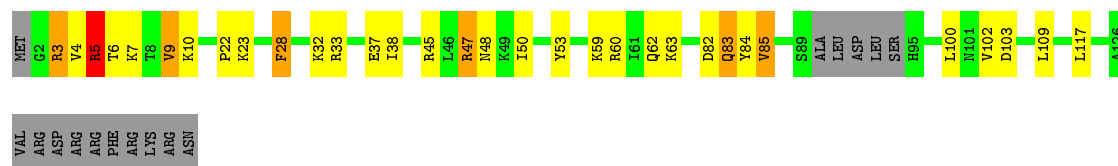
- Molecule 20: uS9

Chain Q:  66% 29% ..



- Molecule 21: eS17

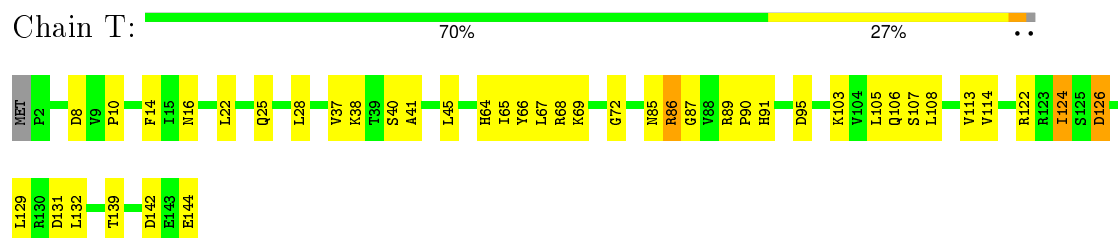
Chain R:  65% 18% . . 12%



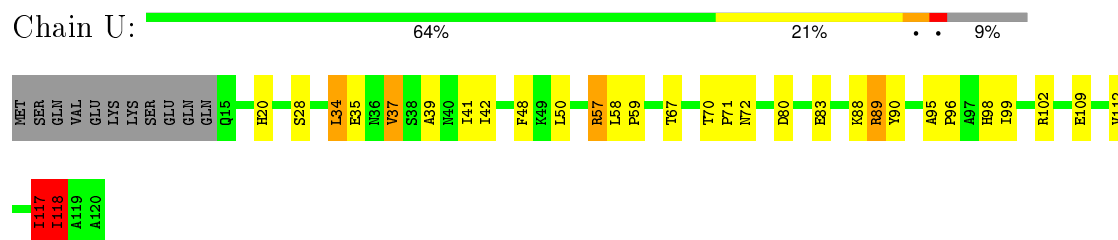
- Molecule 22: uS13



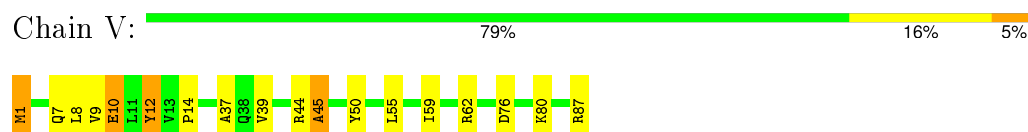
- Molecule 23: eS19



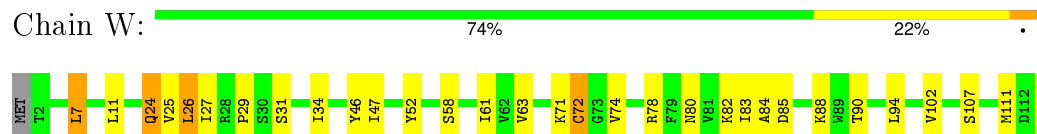
- Molecule 24: uS10



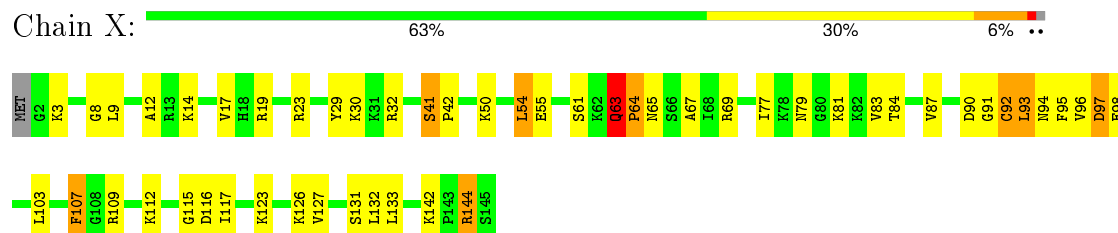
- Molecule 25: eS21




- Molecule 26: uS8



- Molecule 27: uS12



- Molecule 28: eS24

Chain Y: 



- Molecule 29: eS25

Chain Z: 



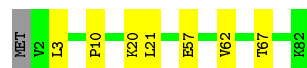
- Molecule 30: eS26

Chain a: 




- Molecule 31: eS27

Chain b: 




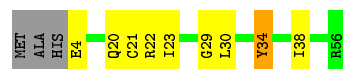
- Molecule 32: eS28

Chain c: 



- Molecule 33: uS14

Chain d: 

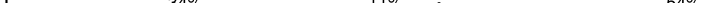


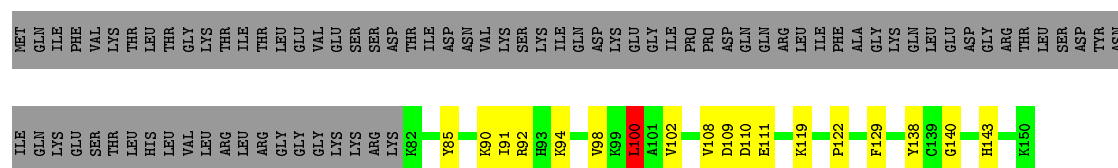
- Molecule 34: eS30

Chain e: 

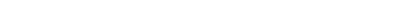


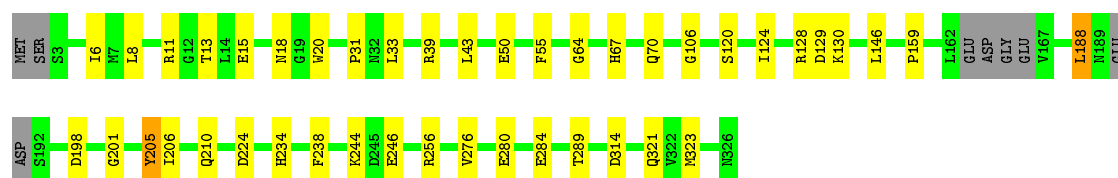
- Molecule 35: eS31

Chain f:  34% 11% 54%

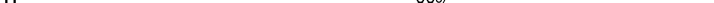


- Molecule 36: RACK1

Chain g:  84% 13% •



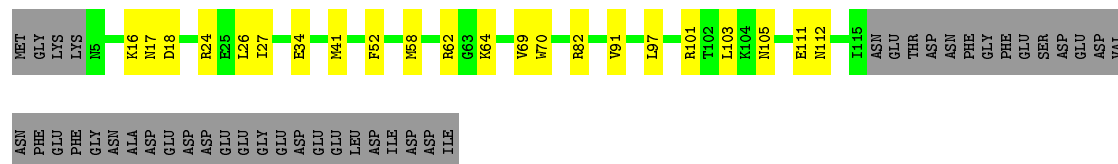
- Molecule 37: eL41

Chain h:  88% 12%



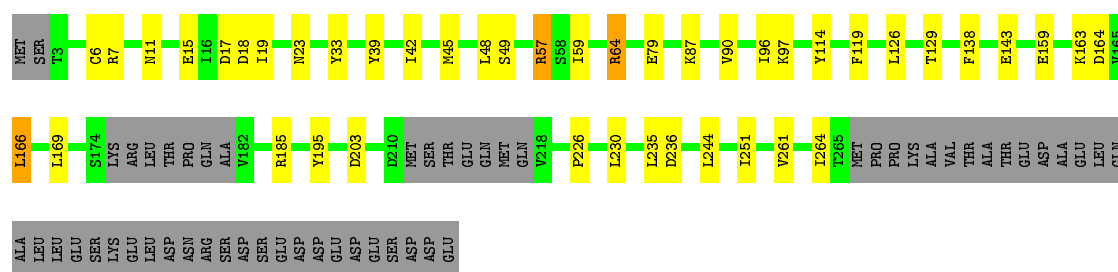
- Molecule 38: eIF1A

Chain i:  58% 14% 27%



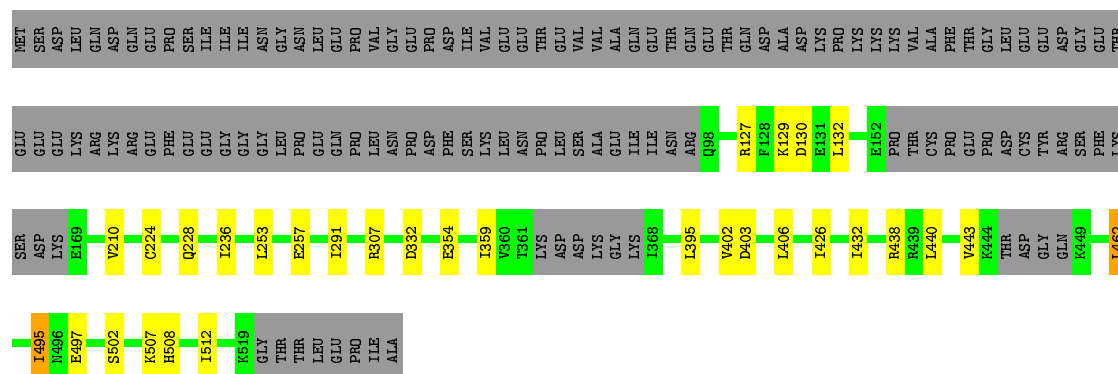
- Molecule 39: eIF2 alpha

Chain j:  67% 13% • 18%

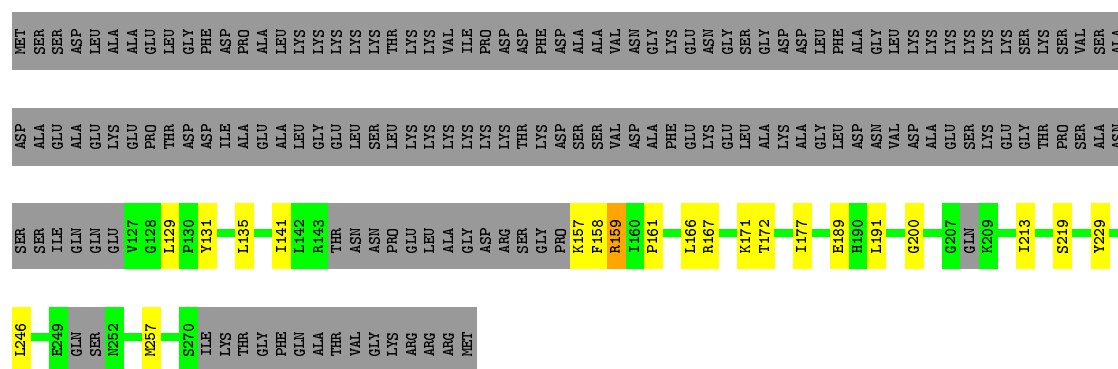
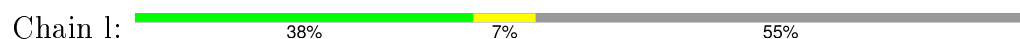


- Molecule 40: eIF2 gamma

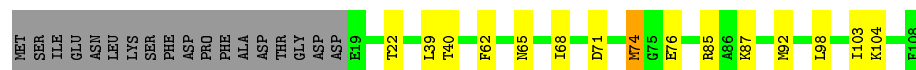
Chain k:  69% 6% 25%



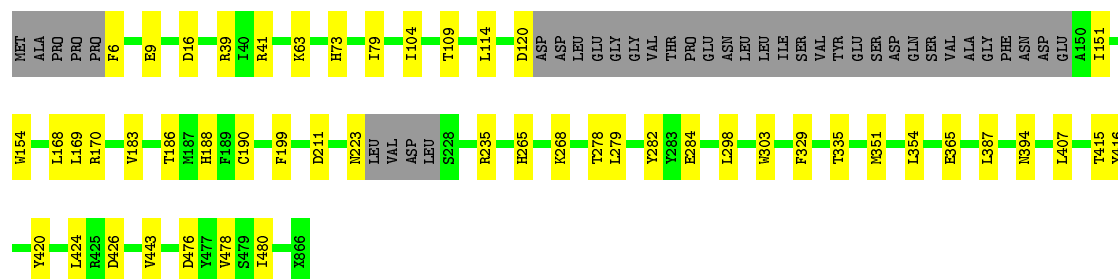
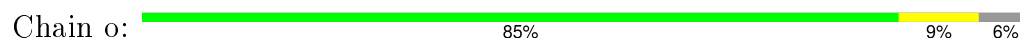
• Molecule 41: eIF2 beta



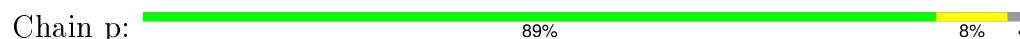
• Molecule 42: eIF1

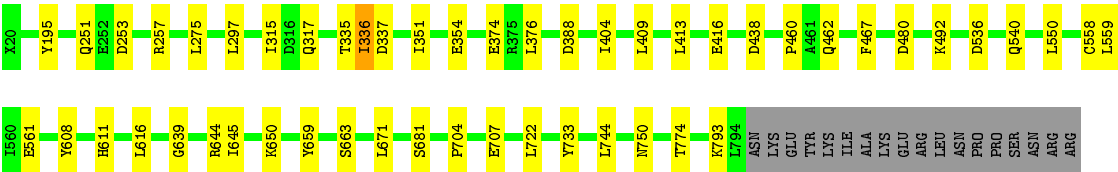


• Molecule 43: eIF3a

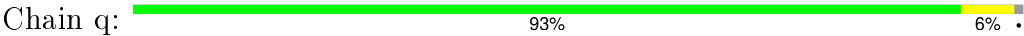


• Molecule 44: eIF3c

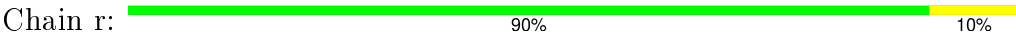




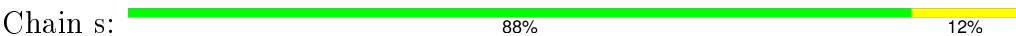
• Molecule 45: eIF3i



• 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 images	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	59000	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

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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	34
5	B	218/255 (86%)	185 (85%)	25 (12%)	8 (4%)	4	39
6	C	215/259 (83%)	186 (86%)	22 (10%)	7 (3%)	5	42
7	D	221/237 (93%)	196 (89%)	16 (7%)	9 (4%)	3	35
8	E	258/261 (99%)	225 (87%)	28 (11%)	5 (2%)	10	53
9	F	204/227 (90%)	169 (83%)	28 (14%)	7 (3%)	5	41
10	G	224/236 (95%)	197 (88%)	23 (10%)	4 (2%)	11	54
11	H	182/190 (96%)	157 (86%)	15 (8%)	10 (6%)	2	29
12	I	184/201 (92%)	160 (87%)	15 (8%)	9 (5%)	3	31
13	J	180/188 (96%)	154 (86%)	19 (11%)	7 (4%)	4	37
14	K	94/106 (89%)	81 (86%)	7 (7%)	6 (6%)	2	25
15	L	153/156 (98%)	133 (87%)	13 (8%)	7 (5%)	3	33
16	M	113/134 (84%)	85 (75%)	21 (19%)	7 (6%)	2	26
17	N	148/151 (98%)	134 (90%)	13 (9%)	1 (1%)	26	71
18	O	125/137 (91%)	102 (82%)	16 (13%)	7 (6%)	2	28
19	P	115/142 (81%)	96 (84%)	13 (11%)	6 (5%)	2	30
20	Q	139/143 (97%)	108 (78%)	20 (14%)	11 (8%)	1	19
21	R	116/136 (85%)	101 (87%)	13 (11%)	2 (2%)	11	56
22	S	143/146 (98%)	111 (78%)	21 (15%)	11 (8%)	1	19

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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	38
25	V	85/87 (98%)	74 (87%)	7 (8%)	4 (5%)	3	32
26	W	127/130 (98%)	112 (88%)	10 (8%)	5 (4%)	4	37
27	X	142/145 (98%)	117 (82%)	14 (10%)	11 (8%)	1	19
28	Y	132/135 (98%)	118 (89%)	7 (5%)	7 (5%)	2	30
29	Z	68/108 (63%)	50 (74%)	17 (25%)	1 (2%)	13	58
30	a	96/119 (81%)	81 (84%)	11 (12%)	4 (4%)	3	35
31	b	79/82 (96%)	61 (77%)	15 (19%)	3 (4%)	4	38
32	c	60/67 (90%)	51 (85%)	6 (10%)	3 (5%)	3	31
33	d	51/56 (91%)	33 (65%)	15 (29%)	3 (6%)	2	27
34	e	52/63 (82%)	45 (86%)	6 (12%)	1 (2%)	10	53
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	42
37	h	23/25 (92%)	23 (100%)	0	0	100	100
38	i	109/153 (71%)	92 (84%)	14 (13%)	3 (3%)	6	45
39	j	243/304 (80%)	205 (84%)	32 (13%)	6 (2%)	7	47
40	k	388/527 (74%)	339 (87%)	43 (11%)	6 (2%)	13	58
41	l	120/285 (42%)	100 (83%)	16 (13%)	4 (3%)	5	42
42	m	88/108 (82%)	76 (86%)	10 (11%)	2 (2%)	8	49
43	o	451/588 (77%)	417 (92%)	31 (7%)	3 (1%)	26	71
44	p	554/652 (85%)	497 (90%)	45 (8%)	12 (2%)	8	50
45	q	340/347 (98%)	302 (89%)	33 (10%)	5 (2%)	13	58
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%)	8	41

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	23
5	B	198/228 (87%)	174 (88%)	24 (12%)	6	32
6	C	176/203 (87%)	153 (87%)	23 (13%)	5	29
7	D	185/196 (94%)	152 (82%)	33 (18%)	2	17
8	E	223/224 (100%)	186 (83%)	37 (17%)	3	20
9	F	174/194 (90%)	140 (80%)	34 (20%)	2	13
10	G	192/200 (96%)	174 (91%)	18 (9%)	11	44
11	H	164/170 (96%)	138 (84%)	26 (16%)	3	22
12	I	147/159 (92%)	133 (90%)	14 (10%)	11	43
13	J	153/158 (97%)	135 (88%)	18 (12%)	6	34
14	K	88/96 (92%)	70 (80%)	18 (20%)	1	12
15	L	136/137 (99%)	128 (94%)	8 (6%)	24	63
16	M	93/109 (85%)	82 (88%)	11 (12%)	6	34
17	N	127/128 (99%)	108 (85%)	19 (15%)	3	24
18	O	96/104 (92%)	88 (92%)	8 (8%)	14	51
19	P	100/119 (84%)	83 (83%)	17 (17%)	2	19
20	Q	117/119 (98%)	99 (85%)	18 (15%)	3	23
21	R	109/124 (88%)	91 (84%)	18 (16%)	3	20
22	S	128/129 (99%)	105 (82%)	23 (18%)	2	16
23	T	117/118 (99%)	97 (83%)	20 (17%)	2	18
24	U	96/107 (90%)	83 (86%)	13 (14%)	5	28
25	V	73/73 (100%)	66 (90%)	7 (10%)	10	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	W	110/111 (99%)	102 (93%)	8 (7%)	17	56
27	X	119/120 (99%)	102 (86%)	17 (14%)	4	27
28	Y	108/109 (99%)	102 (94%)	6 (6%)	26	65
29	Z	60/88 (68%)	55 (92%)	5 (8%)	14	51
30	a	83/100 (83%)	71 (86%)	12 (14%)	4	26
31	b	71/72 (99%)	67 (94%)	4 (6%)	26	65
32	c	54/59 (92%)	48 (89%)	6 (11%)	8	36
33	d	46/48 (96%)	39 (85%)	7 (15%)	3	24
34	e	47/55 (86%)	39 (83%)	8 (17%)	2	19
35	f	57/133 (43%)	48 (84%)	9 (16%)	3	22
36	g	265/272 (97%)	231 (87%)	34 (13%)	5	30
37	h	23/23 (100%)	20 (87%)	3 (13%)	5	30
38	i	93/130 (72%)	74 (80%)	19 (20%)	1	12
39	j	224/274 (82%)	185 (83%)	39 (17%)	2	18
40	k	332/449 (74%)	306 (92%)	26 (8%)	16	53
41	l	119/246 (48%)	103 (87%)	16 (13%)	5	29
42	m	77/96 (80%)	64 (83%)	13 (17%)	2	19
43	o	411/444 (93%)	364 (89%)	47 (11%)	7	35
44	p	507/536 (95%)	469 (92%)	38 (8%)	17	55
45	q	297/301 (99%)	280 (94%)	17 (6%)	25	64
46	r	30/30 (100%)	27 (90%)	3 (10%)	9	41
47	s	43/43 (100%)	37 (86%)	6 (14%)	4	28
All	All	6242/7045 (89%)	5465 (88%)	777 (12%)	10	31

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%)	7 (9%)
2	2	1778/1781 (99%)	879 (49%)	146 (8%)
3	3	13/25 (52%)	11 (84%)	1 (7%)
All	All	1865/1881 (99%)	922 (49%)	154 (8%)

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

5 of 154 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	721	U
2	2	995	U
2	2	1571	A
2	2	781	A
2	2	855	A

## 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	-	5,7,8	0.39	0	4,7,9	0.93	0
51	GCP	k	603	48	29,34,34	1.85	7 (24%)	32,54,54	1.75	5 (15%)

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	-	0/15/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	k	603	GCP	PG-O3G	-2.58	1.48	1.54
51	k	603	GCP	PB-O2B	2.06	1.61	1.56
51	k	603	GCP	PG-O2G	2.67	1.61	1.54
51	k	603	GCP	PB-O3A	3.06	1.61	1.58
51	k	603	GCP	C5-C4	3.50	1.48	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	k	603	GCP	C5-C6-N1	-4.11	118.16	123.52
51	k	603	GCP	N3-C2-N1	-3.80	122.38	127.56
51	k	603	GCP	C6-C5-C4	-3.20	117.20	120.86
51	k	603	GCP	O4'-C1'-N9	2.39	112.62	108.11
51	k	603	GCP	C6-N1-C2	5.62	122.46	115.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.