



wwPDB EM Validation Summary Report ⓘ

Mar 18, 2024 – 05:37 pm GMT

PDB ID : 8QHD
EMDB ID : EMD-18408
Title : Hantaan virus polymerase in hexameric state
Authors : Durieux Trouilleton, Q.; Arragain, B.; Malet, H.
Deposited on : 2023-09-07
Resolution : 3.60 Å (reported)
Based on initial model : 8C4S

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

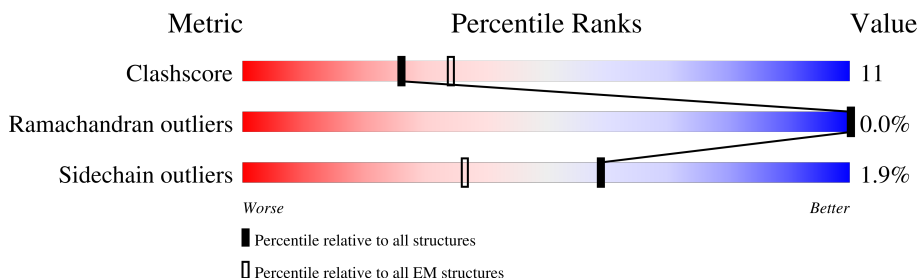
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2173	21% (red) 61% (green) 24% (yellow) • 14% (grey)
1	B	2173	19% (red) 61% (green) 24% (yellow) • 14% (grey)
1	C	2173	13% (red) 68% (green) 23% (yellow) • 8% (grey)
1	D	2173	62% (red) 74% (green) 20% (yellow) 7% (grey)
1	E	2173	15% (red) 68% (green) 23% (yellow) • 8% (grey)
1	F	2173	63% (red) 74% (green) 20% (yellow) 7% (grey)

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 95348 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 protein called RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	D	2030	16400	10555	2764	2994	87	0	0
1	B	1873	15128	9747	2547	2756	78	0	0
1	C	1999	16146	10400	2714	2945	87	0	0
1	F	2030	16400	10555	2764	2994	87	0	0
1	A	1873	15128	9747	2547	2756	78	0	0
1	E	1999	16146	10400	2714	2945	87	0	0

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-21	MET	-	initiating methionine	UNP P23456
D	-20	GLY	-	expression tag	UNP P23456
D	-19	HIS	-	expression tag	UNP P23456
D	-18	HIS	-	expression tag	UNP P23456
D	-17	HIS	-	expression tag	UNP P23456
D	-16	HIS	-	expression tag	UNP P23456
D	-15	HIS	-	expression tag	UNP P23456
D	-14	HIS	-	expression tag	UNP P23456
D	-13	ASP	-	expression tag	UNP P23456
D	-12	TYR	-	expression tag	UNP P23456
D	-11	ASP	-	expression tag	UNP P23456
D	-10	ILE	-	expression tag	UNP P23456
D	-9	PRO	-	expression tag	UNP P23456
D	-8	THR	-	expression tag	UNP P23456
D	-7	THR	-	expression tag	UNP P23456
D	-6	GLU	-	expression tag	UNP P23456
D	-5	ASN	-	expression tag	UNP P23456
D	-4	LEU	-	expression tag	UNP P23456

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	TYR	-	expression tag	UNP P23456
D	-2	PHE	-	expression tag	UNP P23456
D	-1	GLN	-	expression tag	UNP P23456
D	0	GLY	-	expression tag	UNP P23456
B	-21	MET	-	initiating methionine	UNP P23456
B	-20	GLY	-	expression tag	UNP P23456
B	-19	HIS	-	expression tag	UNP P23456
B	-18	HIS	-	expression tag	UNP P23456
B	-17	HIS	-	expression tag	UNP P23456
B	-16	HIS	-	expression tag	UNP P23456
B	-15	HIS	-	expression tag	UNP P23456
B	-14	HIS	-	expression tag	UNP P23456
B	-13	ASP	-	expression tag	UNP P23456
B	-12	TYR	-	expression tag	UNP P23456
B	-11	ASP	-	expression tag	UNP P23456
B	-10	ILE	-	expression tag	UNP P23456
B	-9	PRO	-	expression tag	UNP P23456
B	-8	THR	-	expression tag	UNP P23456
B	-7	THR	-	expression tag	UNP P23456
B	-6	GLU	-	expression tag	UNP P23456
B	-5	ASN	-	expression tag	UNP P23456
B	-4	LEU	-	expression tag	UNP P23456
B	-3	TYR	-	expression tag	UNP P23456
B	-2	PHE	-	expression tag	UNP P23456
B	-1	GLN	-	expression tag	UNP P23456
B	0	GLY	-	expression tag	UNP P23456
C	-21	MET	-	initiating methionine	UNP P23456
C	-20	GLY	-	expression tag	UNP P23456
C	-19	HIS	-	expression tag	UNP P23456
C	-18	HIS	-	expression tag	UNP P23456
C	-17	HIS	-	expression tag	UNP P23456
C	-16	HIS	-	expression tag	UNP P23456
C	-15	HIS	-	expression tag	UNP P23456
C	-14	HIS	-	expression tag	UNP P23456
C	-13	ASP	-	expression tag	UNP P23456
C	-12	TYR	-	expression tag	UNP P23456
C	-11	ASP	-	expression tag	UNP P23456
C	-10	ILE	-	expression tag	UNP P23456
C	-9	PRO	-	expression tag	UNP P23456
C	-8	THR	-	expression tag	UNP P23456
C	-7	THR	-	expression tag	UNP P23456
C	-6	GLU	-	expression tag	UNP P23456

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	ASN	-	expression tag	UNP P23456
C	-4	LEU	-	expression tag	UNP P23456
C	-3	TYR	-	expression tag	UNP P23456
C	-2	PHE	-	expression tag	UNP P23456
C	-1	GLN	-	expression tag	UNP P23456
C	0	GLY	-	expression tag	UNP P23456
F	-21	MET	-	initiating methionine	UNP P23456
F	-20	GLY	-	expression tag	UNP P23456
F	-19	HIS	-	expression tag	UNP P23456
F	-18	HIS	-	expression tag	UNP P23456
F	-17	HIS	-	expression tag	UNP P23456
F	-16	HIS	-	expression tag	UNP P23456
F	-15	HIS	-	expression tag	UNP P23456
F	-14	HIS	-	expression tag	UNP P23456
F	-13	ASP	-	expression tag	UNP P23456
F	-12	TYR	-	expression tag	UNP P23456
F	-11	ASP	-	expression tag	UNP P23456
F	-10	ILE	-	expression tag	UNP P23456
F	-9	PRO	-	expression tag	UNP P23456
F	-8	THR	-	expression tag	UNP P23456
F	-7	THR	-	expression tag	UNP P23456
F	-6	GLU	-	expression tag	UNP P23456
F	-5	ASN	-	expression tag	UNP P23456
F	-4	LEU	-	expression tag	UNP P23456
F	-3	TYR	-	expression tag	UNP P23456
F	-2	PHE	-	expression tag	UNP P23456
F	-1	GLN	-	expression tag	UNP P23456
F	0	GLY	-	expression tag	UNP P23456
A	-21	MET	-	initiating methionine	UNP P23456
A	-20	GLY	-	expression tag	UNP P23456
A	-19	HIS	-	expression tag	UNP P23456
A	-18	HIS	-	expression tag	UNP P23456
A	-17	HIS	-	expression tag	UNP P23456
A	-16	HIS	-	expression tag	UNP P23456
A	-15	HIS	-	expression tag	UNP P23456
A	-14	HIS	-	expression tag	UNP P23456
A	-13	ASP	-	expression tag	UNP P23456
A	-12	TYR	-	expression tag	UNP P23456
A	-11	ASP	-	expression tag	UNP P23456
A	-10	ILE	-	expression tag	UNP P23456
A	-9	PRO	-	expression tag	UNP P23456
A	-8	THR	-	expression tag	UNP P23456

Continued on next page...

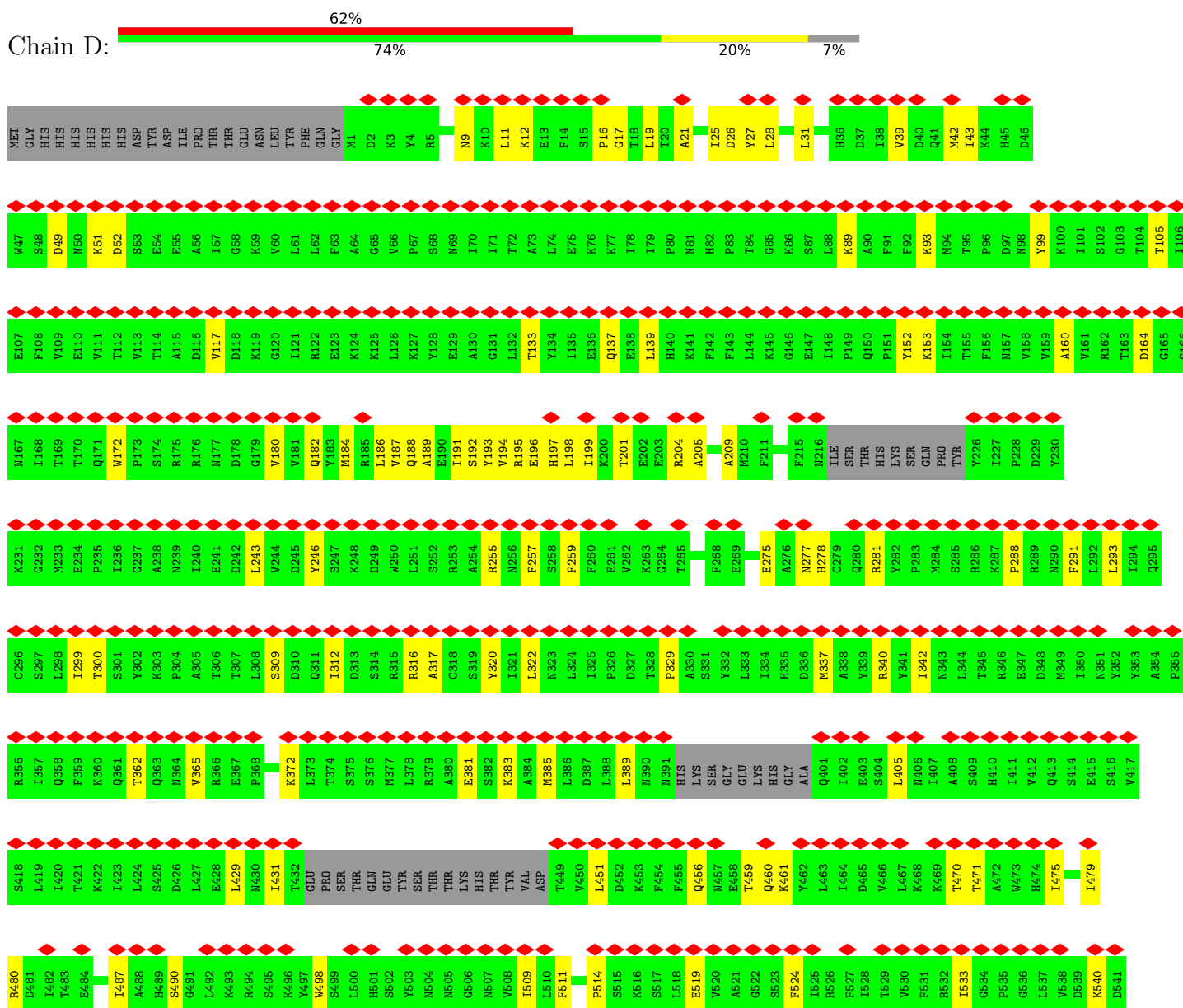
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	THR	-	expression tag	UNP P23456
A	-6	GLU	-	expression tag	UNP P23456
A	-5	ASN	-	expression tag	UNP P23456
A	-4	LEU	-	expression tag	UNP P23456
A	-3	TYR	-	expression tag	UNP P23456
A	-2	PHE	-	expression tag	UNP P23456
A	-1	GLN	-	expression tag	UNP P23456
A	0	GLY	-	expression tag	UNP P23456
E	-21	MET	-	initiating methionine	UNP P23456
E	-20	GLY	-	expression tag	UNP P23456
E	-19	HIS	-	expression tag	UNP P23456
E	-18	HIS	-	expression tag	UNP P23456
E	-17	HIS	-	expression tag	UNP P23456
E	-16	HIS	-	expression tag	UNP P23456
E	-15	HIS	-	expression tag	UNP P23456
E	-14	HIS	-	expression tag	UNP P23456
E	-13	ASP	-	expression tag	UNP P23456
E	-12	TYR	-	expression tag	UNP P23456
E	-11	ASP	-	expression tag	UNP P23456
E	-10	ILE	-	expression tag	UNP P23456
E	-9	PRO	-	expression tag	UNP P23456
E	-8	THR	-	expression tag	UNP P23456
E	-7	THR	-	expression tag	UNP P23456
E	-6	GLU	-	expression tag	UNP P23456
E	-5	ASN	-	expression tag	UNP P23456
E	-4	LEU	-	expression tag	UNP P23456
E	-3	TYR	-	expression tag	UNP P23456
E	-2	PHE	-	expression tag	UNP P23456
E	-1	GLN	-	expression tag	UNP P23456
E	0	GLY	-	expression tag	UNP P23456

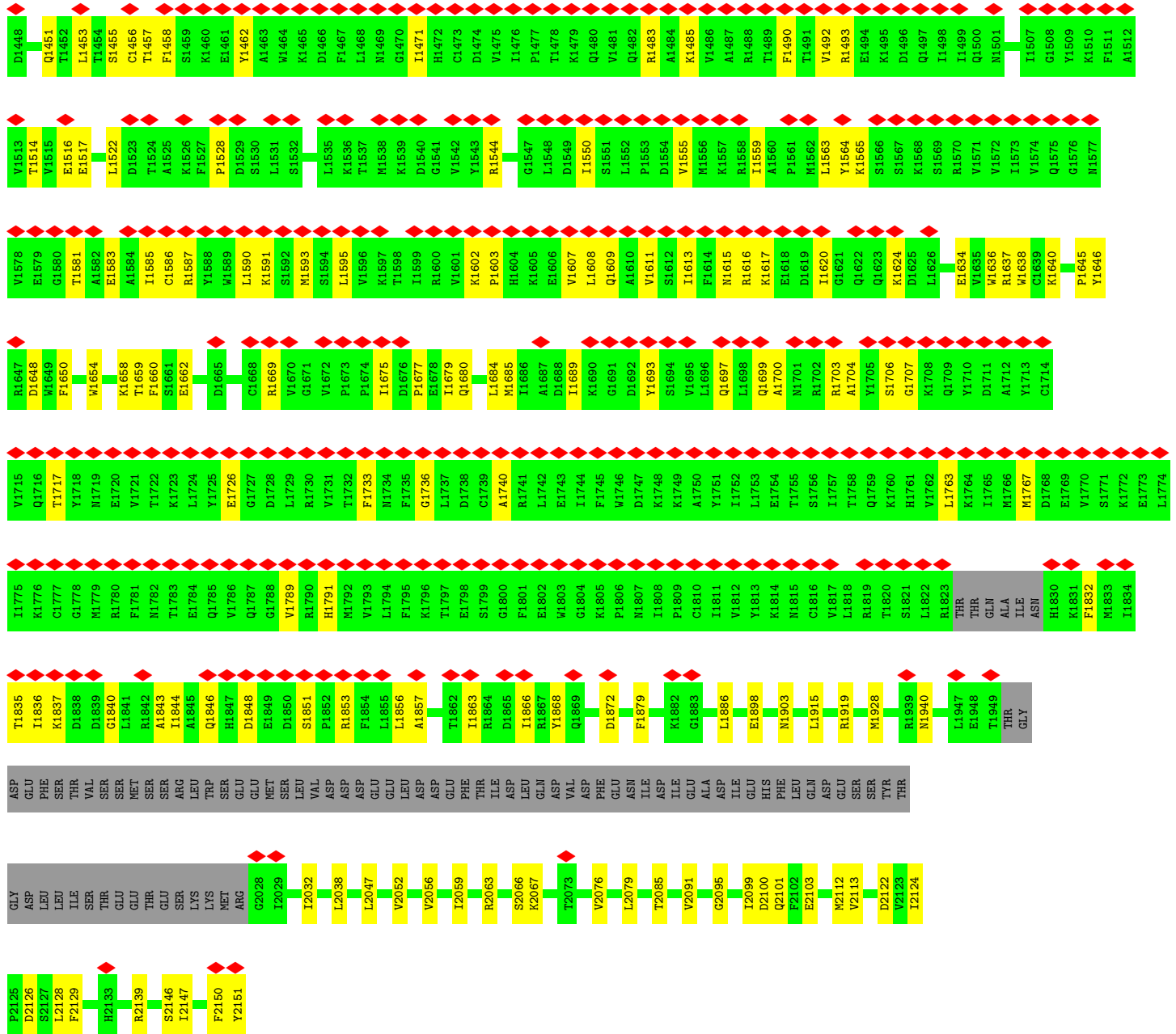
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

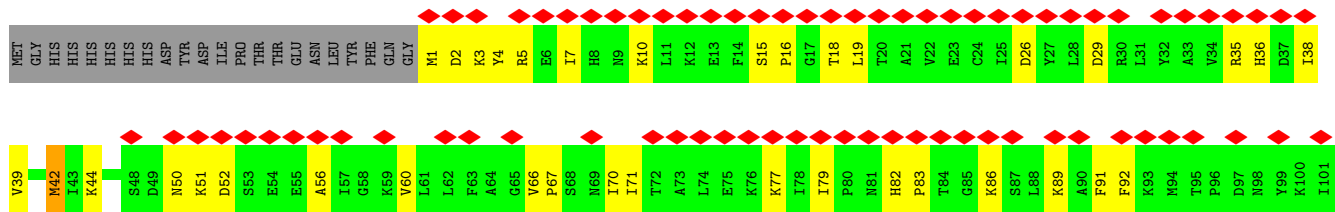
• Molecule 1: RNA-directed RNA polymerase L

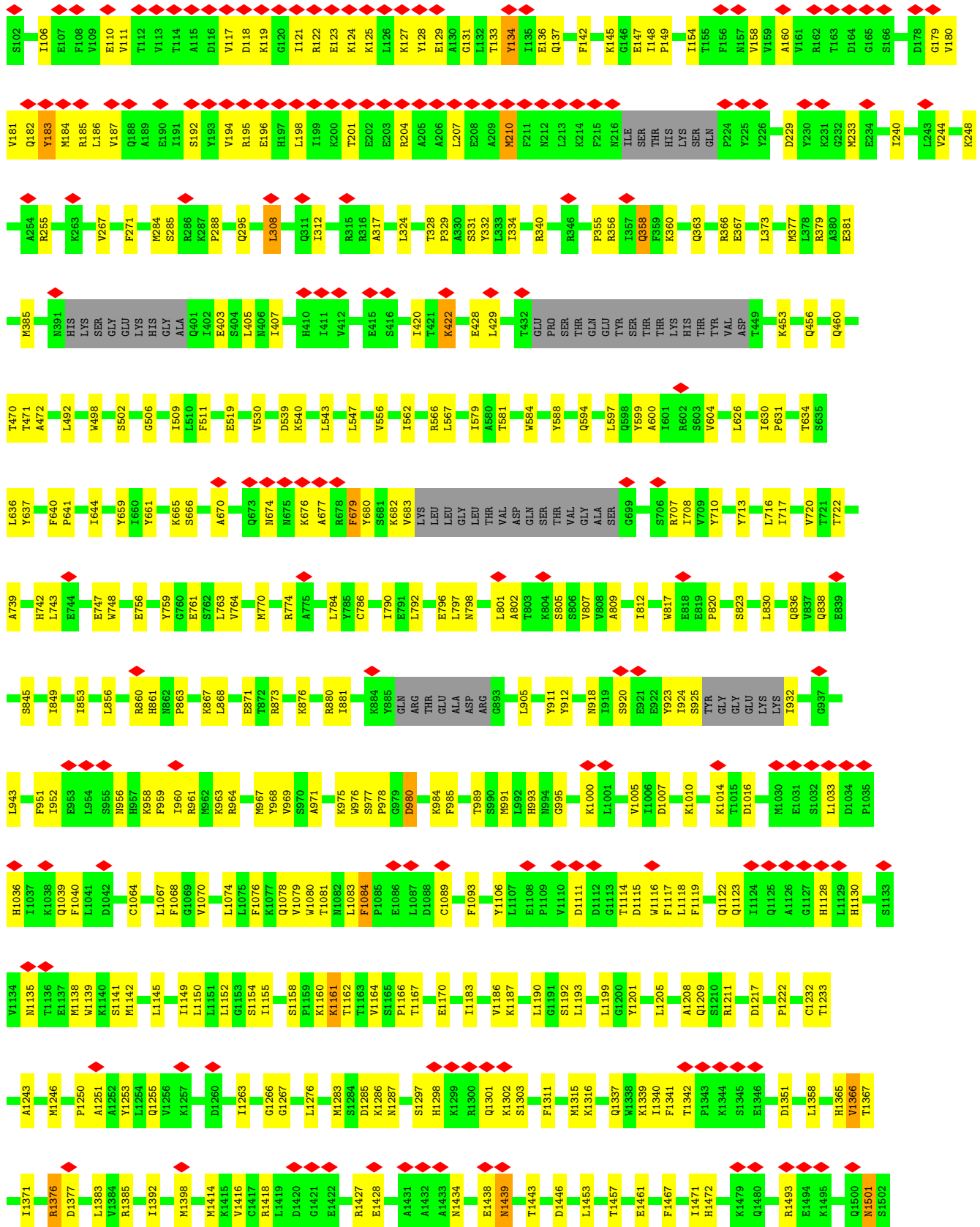


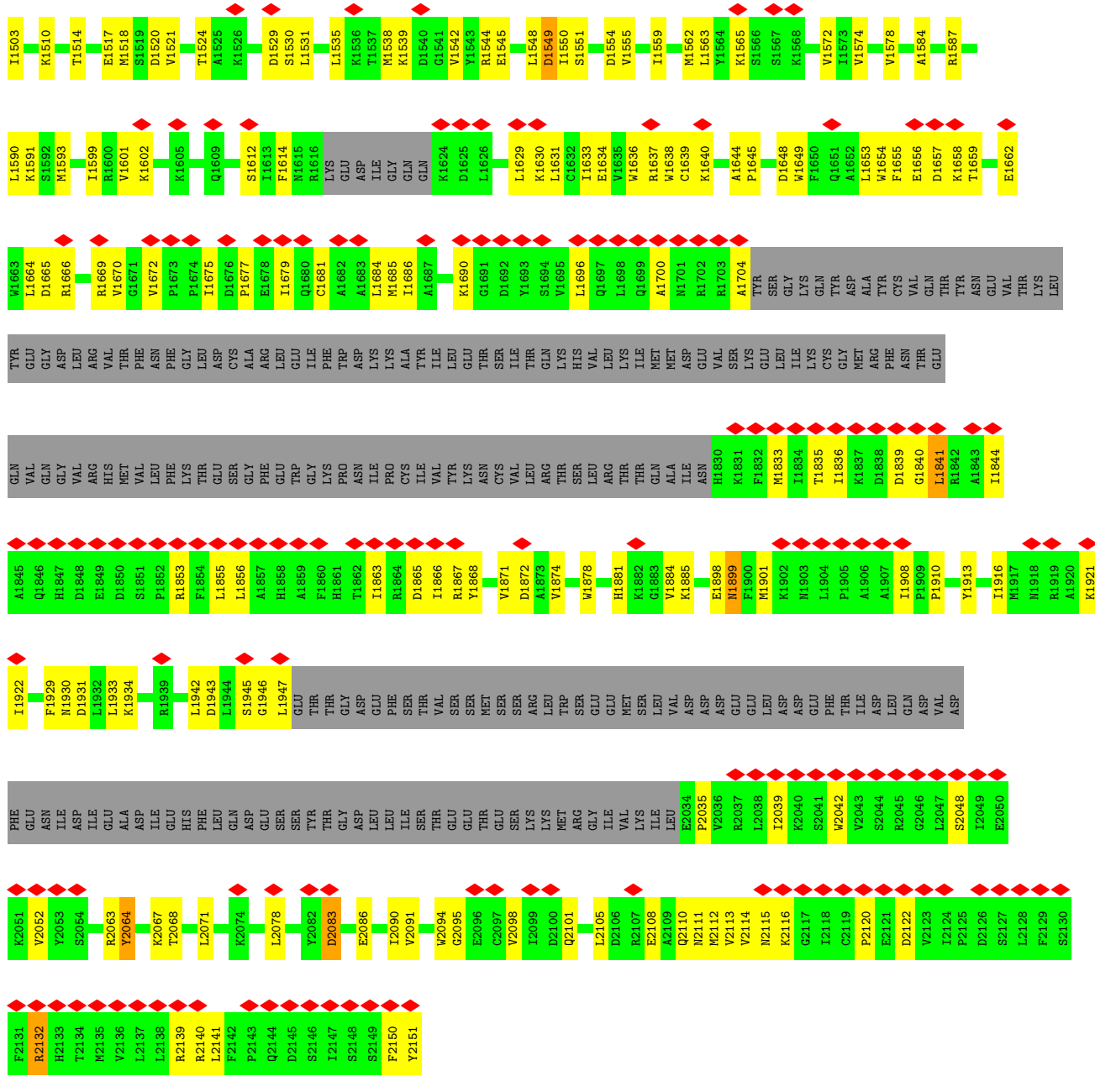
S1365	L1360	Q1364	Y1368	K1374	L1380	Y1384	L1387	N1388	P1389	D1390	S1391	I1392	V1393	T1394	A1395	M1396	T1397	M1398	Q1399	S1400	F1401	L1402	R1405	F1406	R1407	M1408	Q1409	M1414	K1415	R1418	L1419	D1420	G1421	W1422	W1423	V1424	E1428	V1429	A1433	M1434	Y1440	S1441	A1442	T1443	S1444	G1280	I1281	G1282	M1283	S1284	M1287	R1291	A1292	L1293	L1294	S1297	H1298	K1299	R1300	M1304	L1308	F1311	D1319	I1320	T1321	F1322	Q1323	H1324	E1325	R1326	L1327	L1328	Q1329	F1330	S1331	F1332	I1333	G1334	K1335	V1336	Q1337	W1338	K1339	L1340	F1341	T1342	P1343	K1344	S1345	E1346	F1347	E1348	F1349	A1350	D1351	Y1353	T1354	G1198	L1199	G1200	Y1201	F1202	R1211	K1214	A1215	L1216	D1217	L1218	G1219	A1220	S1221	P1222	Q1223	V1224	A1225	Q1226	L1227	A1228	L1231	R1238	L1239	Y1240	P1244	G1245	M1246	V1247	M1248	H1249	P1250	Y1253	L1254	H1258	T1259	D1260	L1265	G1266	G1267	N1268	G1269	A1270	M1271	S1272	I1273	M1274	E1275	L1276	A1277	T1278	A1279	G1172	S1173	L1174	F1175	F1176	E1177	G1178	C1179	A1180	V1181	S1182	I1183	P1184	F1185	V1186	K1187	I1188	L1189	L1190	G1191	S1192	L1193	S1194	D1195	L1196	W1197	M1072	S1073	L1074	L1075	F1076	K1077	Q1078	V1079	W1080	T1081	N1082	L1083	F1084	P1085	E1086	L1087	D1088	C1089	F1090	F1091	F1092	F1093	A1094	H1095	H1096	S1097	D1098	D1099	A1100	L1101	F1102	I1103	Y1104	L1107	E1108	P1109	V1110	D1111	D1112	G1113	T1114	D1115	W1116	F1117	L1118	F1119	V1120	S1121	Q1122	Q1123	S1124	Q1125	A1126	G1127	H1128	L1129	W1131	F1132	V1134	M1135	T1136	E1137	W1139	K1140	S1141	M1142	F1143	M1144	L1145	H1146	E1147	H1148	I1149	I1155	K1156	I1157	S1158	P1159	K1160	K1161	T1162	V1163	T1167	M1168	A1169	E1170	F1171	L1172	S1173	T1174	F1175	F1176	E1177	G1178	C1179	A1180	V1181	S1182	I1183	P1184	F1185	V1186	K1187	I1188	L1189	L1190	G1191	S1192	L1193	S1194	D1195	L1196	W1197	G1198	L1199	G1200	Y1201	F1202	R1211	K1214	A1215	L1216	D1217	L1218	G1219	A1220	S1221	P1222	Q1223	V1224	A1225	Q1226	L1227	A1228	L1231	R1238	L1239	Y1240	P1244	G1245	M1246	V1247	M1248	H1249	P1250	Y1253	L1254	H1258	T1259	D1260	L1265	G1266	G1267	N1268	G1269	A1270	M1271	S1272	I1273	M1274	E1275	L1276	A1277	T1278	A1279	G1133	L1134	F1135	V1136	E1137	W1139	K1140	S1141	M1142	F1143	M1144	L1145	H1146	E1147	H1148	I1149	I1155	K1156	I1157	S1158	P1159	K1160	K1161	T1162	V1163	T1167	M1168	A1169	E1170	F1171	L1172	S1173	T1174	F1175	F1176	E1177	G1178	C1179	A1180	V1181	S1182	I1183	P1184	F1185	V1186	K1187	I1188	L1189	L1190	G1191	S1192	L1193	S1194	D1195	L1196	W1197	G1198	L1199	G1200	Y1201	F1202	R1211	K1214	A1215	L1216	D1217	L1218	G1219	A1220	S1221	P1222	Q1223	V1224	A1225	Q1226	L1227	A1228	L1231	R1238	L1239	Y1240	P1244	G1245	M1246	V1247	M1248	H1249	P1250	Y1253	L1254	H1258	T1259	D1260	L1265	G1266	G1267	N1268	G1269	A1270	M1271	S1272	I1273	M1274	E1275	L1276	A1277	T1278	A1279	G1107	E1108	P1109	V1110	D1111	D1112	G1113	T1114	D1115	W1116	F1117	L1118	F1119	V1120	S1121	Q1122	Q1123	S1124	Q1125	A1126	G1127	H1128	L1129	W1131	F1132	V1134	M1135	T1136	E1137	W1139	K1140	S1141	M1142	F1143	M1144	L1145	H1146	E1147	H1148	I1149	I1155	K1156	I1157	S1158	P1159	K1160	K1161	T1162	V1163	T1167	M1168	A1169	E1170	F1171	L1172	S1173	T1174	F1175	F1176	E1177	G1178	C1179	A1180	V1181	S1182	I1183	P1184	F1185	V1186	K1187	I1188	L1189	L1190	G1191	S1192	L1193	S1194	D1195	L1196	W1197	G1198	L1199	G1200	Y1201	F1202	R1211	K1214	A1215	L1216	D1217	L1218	G1219	A1220	S1221	P1222	Q1223	V1224	A1225	Q1226	L1227	A1228	L1231	R1238	L1239	Y1240	P1244	G1245	M1246	V1247	M1248	H1249	P1250	Y1253	L1254	H1258	T1259	D1260	L1265	G1266	G1267	N1268	G1269	A1270	M1271	S1272	I1273	M1274	E1275	L1276	A1277	T1278	A1279	G1009	K1010	Q1011	Y1012	V1013	K1014	S1020	R1021	K1022	L1023	R1024	N1025	Y1026	I1027	D1028	S1029	M1030	E1031	S1032	L1033	D1034	P1035	H1036	I1037	K1038	Q1039	F1040	L1041	D1042	F1043	F1044	P1045	D1046	G1047	H1048	H1049	G1050	E1051	V1052	K1053	G1054	M1055	W1056	L1057	Q1058	G1059	N1060	L1061	M1062	G1063	C1064	S1065	S1066	L1067	F1068	G1069	V1070	A1071	L1006	R1007	Q1008	K1009	A1010	S1011	E1012	L1013	N1014	W1015	Y1016	I1017	D1018	S1019	M1020	E1021	S1022	L1023	R1024	N1025	Y1026	I1027	D1028	S1029	M1030	E1031	S1032	L1033	D1034	P1035	H1036	I1037	K1038	Q1039	F1040	L1041	D1042	F1043	F1044	P1045	D1046	G1047	H1048	H1049	G1050	E1051	V1052	K1053	G1054	M1055	W1056	L1057	Q1058	G1059	N1060	L1061	M1062	G1063	C1064	S1065	S1066	L1067	F1068	G1069	V1070	A1071	R1072	Q1073	K1074	A1075	M1076	S1077	L1078	N1079	Y1080	I1081	D1082	S1083	L1084	E1085	S1086	L1087	D1088	A1089	S1090	K1091	N1092	W1093	Y1094	I1095	D1096	S1097	M1098	E1099	L1100	N1101	G1102	H1103	Y1104	L1107	E1108	P1109	V1110	D1111	D1112	G1113	T1114	D1115	W1116	F1117	L1118	F1119	V1120	S1121	Q1122	Q1123	S1124	Q1125	A1126	G1127	H1128	L1129	W1131	F1132	V1134	M1135	T1136	E1137	W1139	K1140	S1141	M1142	F1143	M1144	L1145	H1146	E1147	H1148	I1149	I1155	K1156	I1157	S1158	P1159	K1160	K1161	T1162	V1163	T1167	M1168	A1169	E1170	F1171	L1172	S1173	T1174	F1175	F1176	E1177	G1178	C1179	A1180	V1181	S1182	I1183	P1184	F1185	V1186	K1187	I1188	L1189	L1190	G1191	S1192	L1193	S1194	D1195	L1196	W1197	G1198	L1199	G1200	Y1201	F1202	R1211	K1214	A1215	L1216	D1217	L1218	G1219	A1220	S1221	P1222	Q1223	V1224	A1225	Q1226	L1227	A1228	L1231	R1238	L1239	Y1240	P1244	G1245	M1246	V1247	M1248	H1249	P1250	Y1253	L1254	H1258	T1259	D1260	L1265	G1266	G1267	N1268	G1269	A1270	M1271	S1272	I1273	M1274	E1275	L1276	A1277	T1278	A1279	R1731	H1732	G1733	N1734	M1735	N1736	E1737	K1740	I1741	H1742	L1743	E1744	T1745	V1746	E1747	H1748	R1753	E1754	K1755	E1756	E1757	K1758	Y1759	G1760	E1761	S1762	L1763	P1764	E1765	N1766	G1767	Y1768	M1769	M1770	M1771	E1772	L1773	R1774	A1775	N1776	E1777	E1778	L1779	A1780	E1781	L1784	Y1785	C1786	Q1787	D1788	A1789	I1790	C1791	L1792	I1795	E1796	R1797	Q1798	K1799	A1800	S1801	E1802	T1803	K1804	S1805	S1806	V1807	N1808	A1809	N1810	S1811	I1812	L1813	S1814	K1815	N1816	W1817	E1818	E1819	F1820	Y1821	F1822	S1823	Q1824	T1825	R1826	N1827	I1828	S1829	L1830	K1831	A1832	Y1833	Q1836	Q1837	Q1838	E1839	D1840	G1841	H1842	S1845	S1846	V1847	R1854	Y1855	D1858	S1859	R1860	L1865	E1871	T1872	G1873	N1874	M1875	A1877	K1876	A1878	F1879	Y1880	S1881	A1882	L1883	K1884	Y1885	Q1886	R1887	T1888	E1889	A1890	D1891	R1892	G1893	F1894	F1895	I1896	T1897	T1898	L1899	P1900	T1901	L1905	E1903	Y1912	D1913	A1914	T1915	A1916	K1917	N1918	I1919	S1920	E1921	E1922	Y1923	I1924	S1925	Y1926	G1927	G1928	E1929	K1930	Y1931	I1932	L1933	A1934	I1935	Q1936	G1937	R1938	Q1939	K1940	S1941	E1942	A1943	R1944	W1945	A1946	S1947	G1948	E1949	S1950	F1951	I1952	E1953	L1954	S1955	N1956	H1957	K1958	F1959	I1960	R1961	M1962	K1963	R1964	K1965	L1966	M1967	Y1968	S1969	A1971	D1972	A1973	T1974	K1975	W1976	S1977	P1978	G1979	D1980	F1985	R1986	R1987	F1988	T1989	S1990	H1993	N1994	G1995	L1996	P1997	N1998	N1999	I1006	S1355	L1360	Q1364	Y1368	K1374	L1380	Y1384	L1387	N1388	P1389	D1390	S1391	I1392	V1393	T1394	A1395	M1396	T1397	M1398	Q1399	S1400	F1401	L1402	R1405	F1406	R1407	M1408	Q1409	M1414	K1415	R1418	L1419	D1420	G1421	W1422	W1423	V1424	E1428	V1429	A1433	M1434	Y1440	S1441	A1442	T1443	S1444	G1280	I1281	G1282	M1283	S1284	M1287	R1291	A1292	L1293	L1294	S1297	H1298	K1299	R1300	M1304	L1308	F1311	D1319	I1320	T1321	F1322	Q1323	H1324	E1325	R1326	L1327	L1328	Q1329	F1330	S1331	F1332	I1333	G1334	K1335	V1336	Q1337	W1338	K1339	L1340	F1341	T1342	P1343	K1344	S1345	E1346	F1347	E1348	F1349	A1350	D1351	Y1353	T1354	G1198	L1199	G1200	Y1201	F1202	R1211	K1214	A1215	L1216	D1217	L1218	G1219	A1220	S1221	P1222	Q1223	V1224	A1225	Q1226	L1227	A1228	L1231	R1238	L1239	Y1240	P1244	G1245	M1246	V1247	M1248	H1249	P1250	Y1253	L1254	H1258	T1259	D1260	L1265	G1266	G1267	N1268	G1269	A1270	M1271	S1272	I1273	M1274	E1275	L1276	A1277	T1278	A1279	G1107	E1108	P1109	V1110	D1111	D1112	G1113	T1114	D1115	W1116	F1117	L1118	F1119	V1120	S1121	Q1122	Q1123	S1124	Q1125	A1126	G1127	H1128	L1129	W1131	F1132	V1134	M1135	T1136	E1137	W1139	K1140	S1141	M1142	F1143	M1144	L1145	H1146	E1147	H1148	I1149	I1155	K1156	I1157	S1158	P1159	K1160	K1161	T1162	V1163	T1167	M1168	A1169	E1170	F1171	L1172	S1173	T1174	F1175	F1176	E1177	G1178	C1179	A1180	V1181	S1182	I1183	P1184	F1185	V1186	K1187	I1188	L1189	L1190	G1191	S1192	L1193	S1194	D1195	L1196	W1197	G1198	L1199	G1200	Y1201	F1202	R1211	K1214	A1215	L1216	D1217	L1218	G1219	A1220	S1221	P1222	Q1223	V1224	A1225	Q1226	L122
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	------



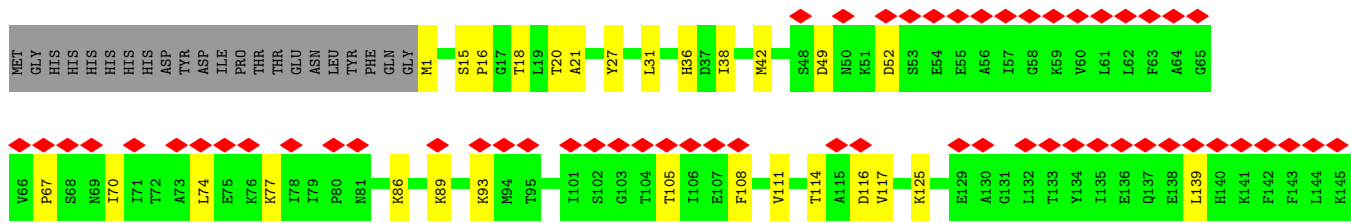
• Molecule 1: RNA-directed RNA polymerase L

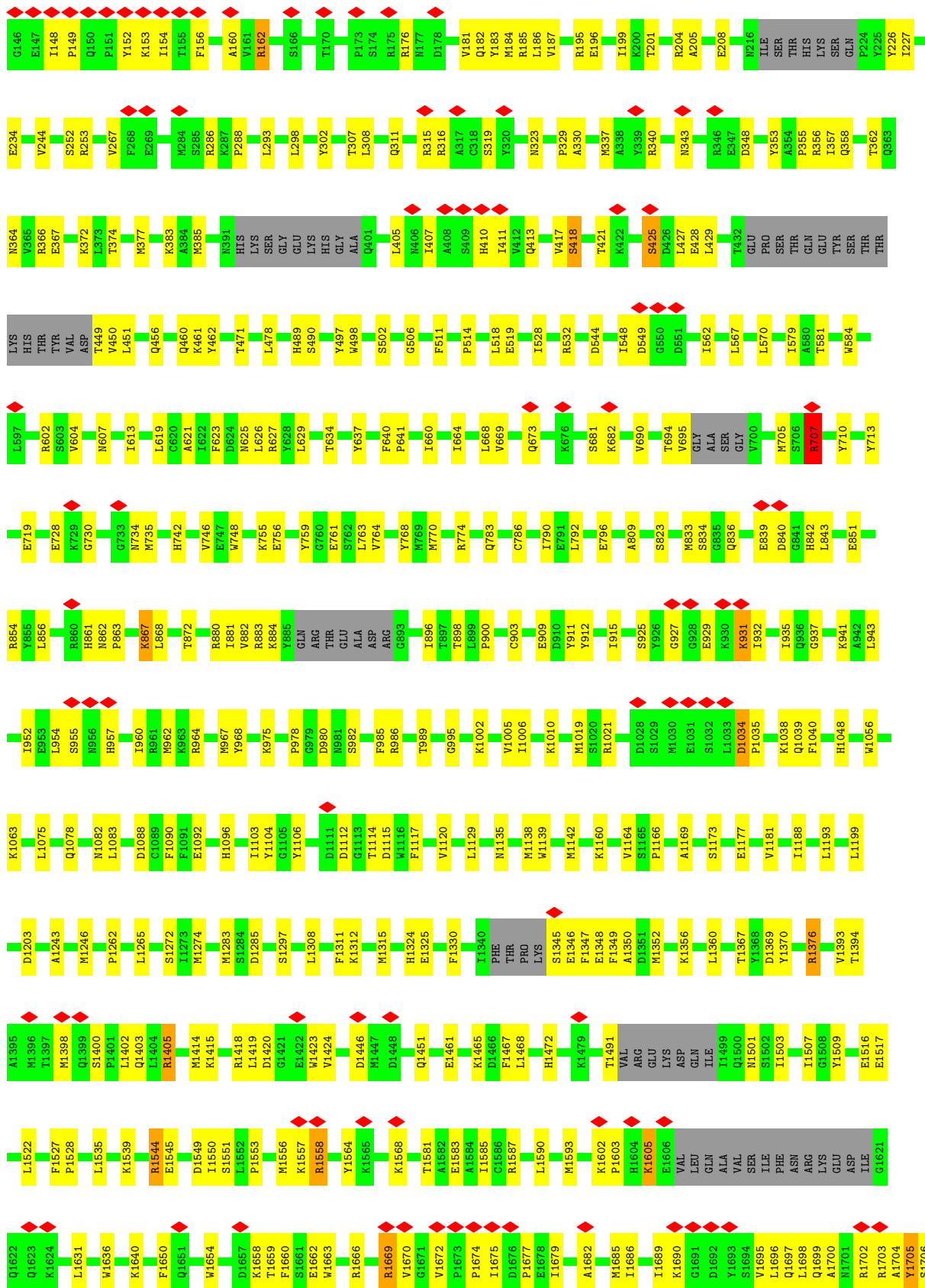


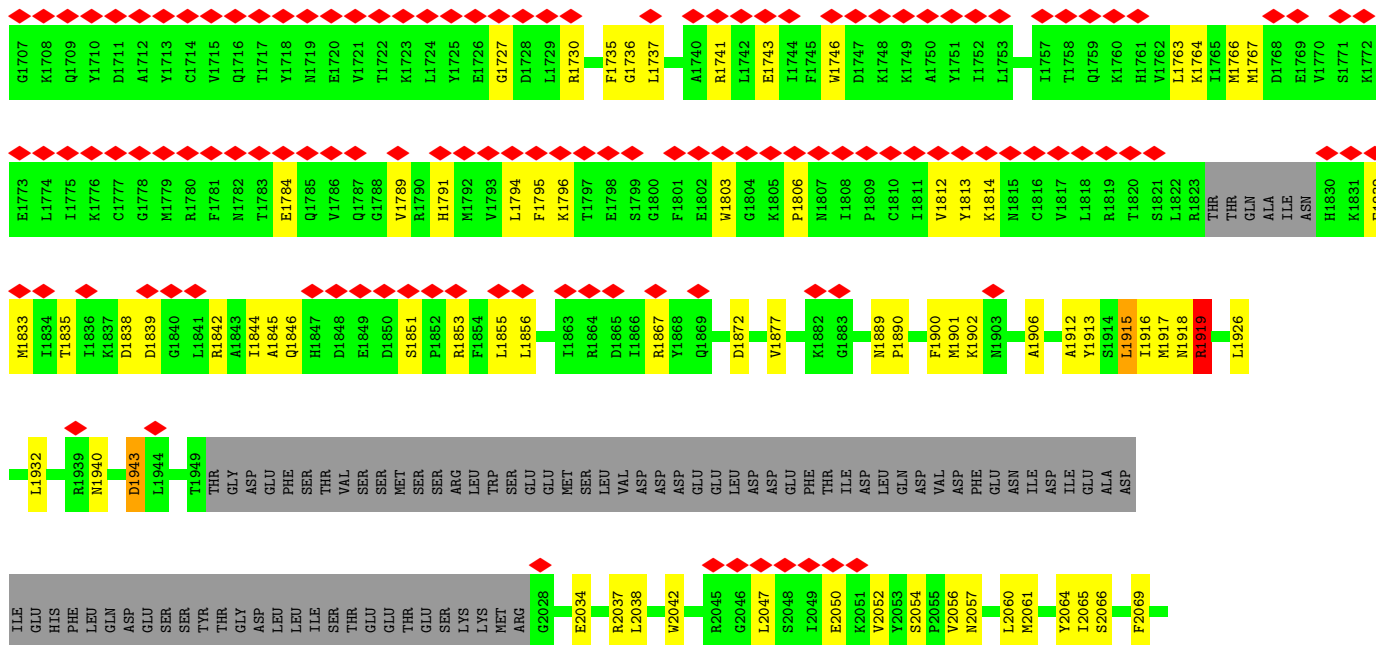




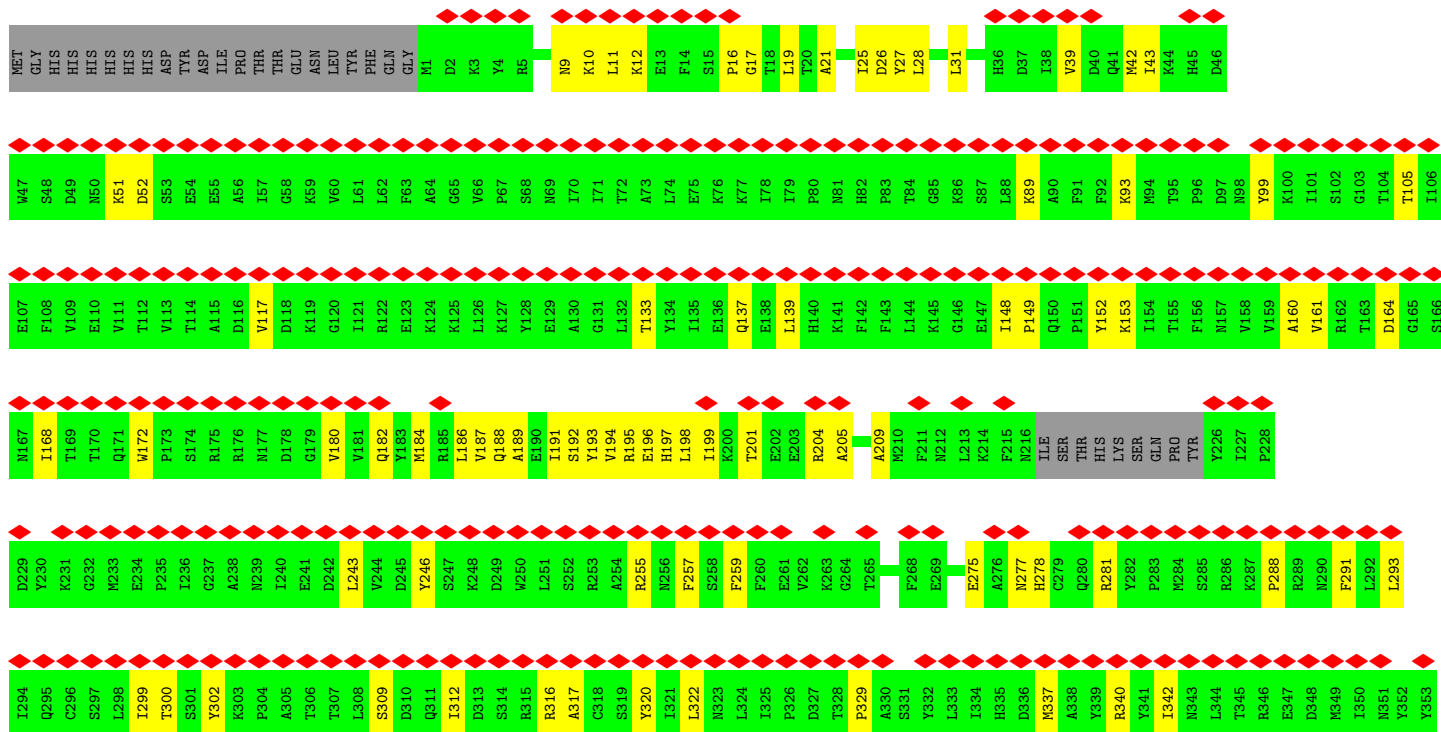
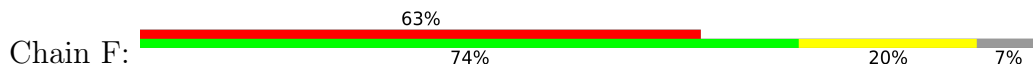
• Molecule 1: RNA-directed RNA polymerase L







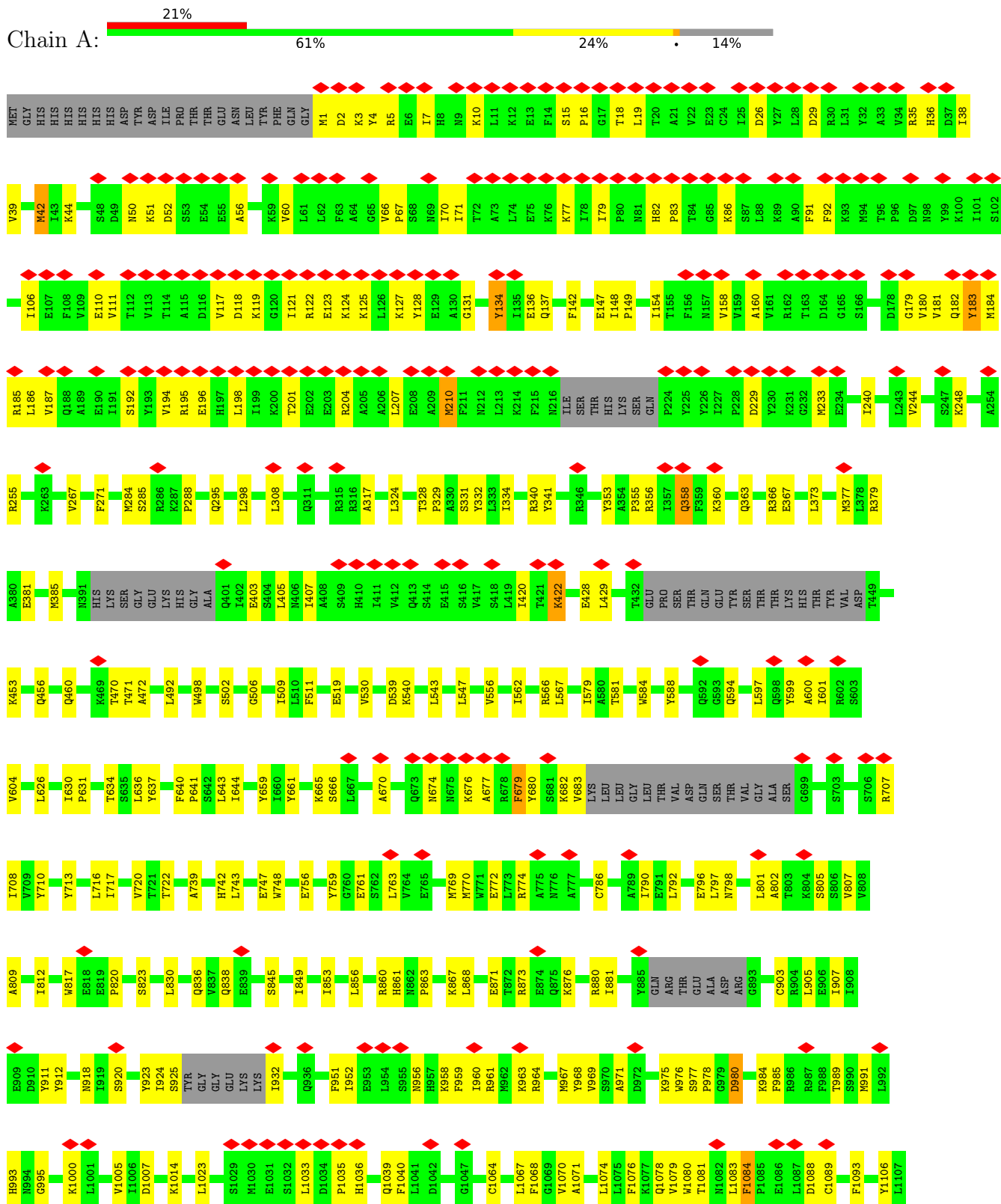
• Molecule 1: RNA-directed RNA polymerase L

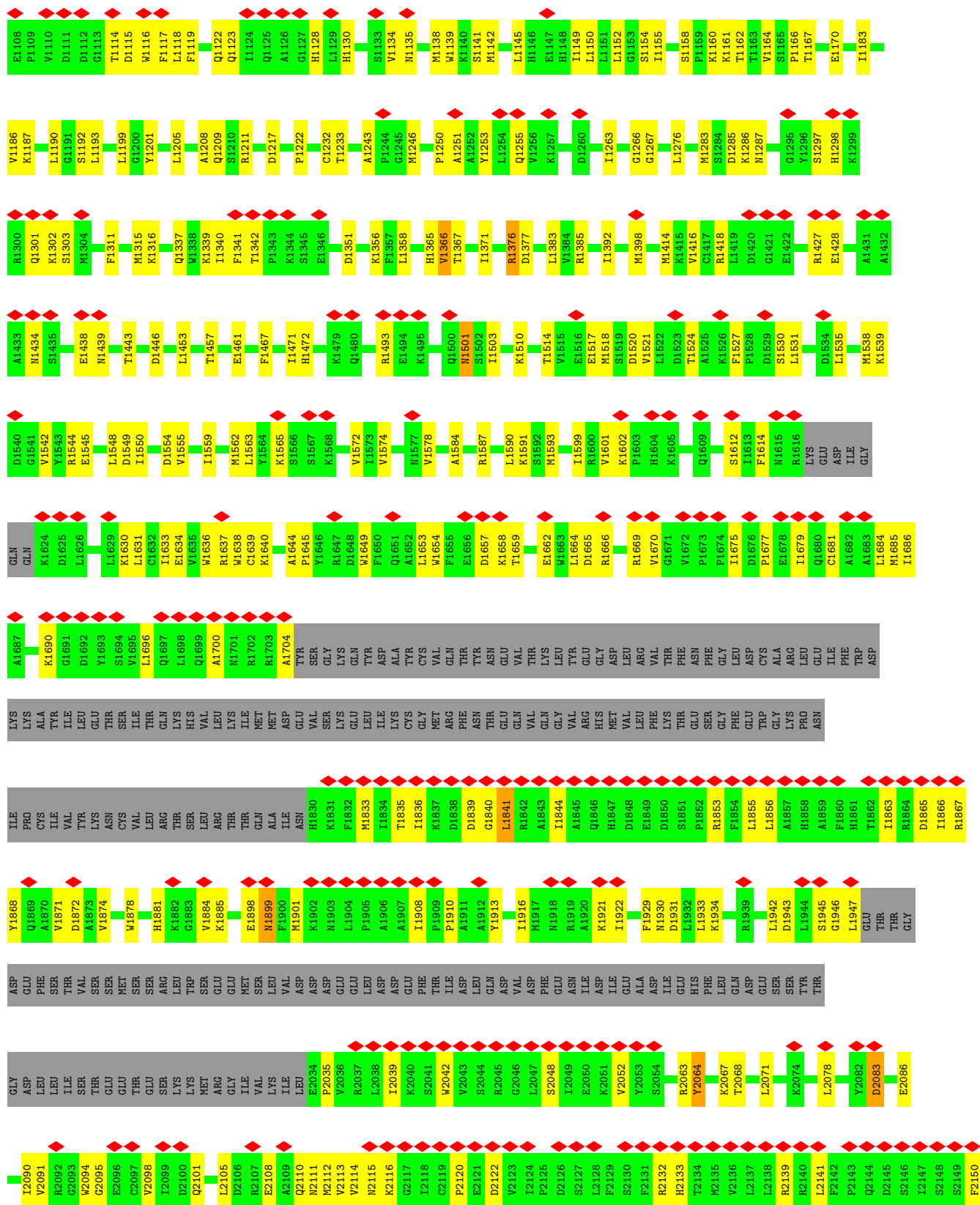


A354	P355	R356	I357	Q358	F359	K360	Q361	T362	N364	V365	R366	E367	P368	G369	K372	L373	T374	S375	S376	M377	L378	R379	A380	E381	S382	K383	A384	M385	L386	D387	L388	L389	N390	N391	HIS	LYS	SER	GLY	GLU	LYS	HIS	GLY	ALA	Q401	I402	E403	S404	L405	A408	S409	H410	I411	V412	Q413	S414	E415						
S416	V417	R480	S418	L419	I420	T421	K422	I423	L424	S425	D426	L427	E428	L429	M430	I431	T432	GLU	PRO	SER	THR	GLN	GLU	TYR	SER	THR	THR	LYS	HIS	THR	THR	VAL	ASP	T449	V450	L451	D452	K453	F454	F455	Q456	M457	E458	T459	Q460	K461	Y462	L463	I464	D465	V466	L467	K468	K469	T470	T471	A472	W473	H474	I475	D539	K540
I479	R480	D481	I482	T483	E484	I487	A488	H489	L492	K493	R494	S495	K496	Y497	W498	S499	L500	H501	S502	Y503	N504	N505	G506	N507	V508	I509	L510	F511	P514	S515	K516	S517	L518	E519	V520	A521	G522	S523	F524	I525	R526	F527	I528	T529	V530	F531	R532	I533	G534	P535	G536	L537	V538	D539	K540							
D541	N542	L543	T545	I546	L547	I548	D549	G550	D551	S552	Q553	W554	G555	V556	S557	K558	V559	M560	S561	S562	D563	L564	N565	R566	L567	L568	A569	L570	A573	F574	E575	K576	A577	L578	I579	A580	T581	A582	T583	W584	F585	Q586	I587	Y588	T589	D590	F591	Q592	G593	Q594	P595	L597	Q598	Y599	A600	I601						
R602	S603	V604	F605	A606	H608	F609	L610	L611	A612	I613	C614	Q615	K616	H617	K618	L619	C620	A621	I622	F623	D624	N625	L626	R627	Y628	L629	I630	P631	A632	V633	T634	Y637	F640	P641	S642	E645	K646	L647	F648	E649	R650	S654	S655	L656	E657	I660	Y661	Y662	M663	K665	S666	L667										
L668	V669	A670	Q673	N674	N675	K676	A677	R678	F679	Y680	S681	K682	V683	K684	L685	L686	G687	L688	T689	I690	D691	Q692	S693	T694	V695	GLY	ALA	SER	G699	V700	Y701	P702	S703	F704	W705	S706	R707	I708	W709	Y710	K711	H712	Y713	R714	S715	L716	I717	S718	E719	V720	T721	Y722	C723	F724	F725	L726	F727	E728				
K729	G730	L731	H732	G733	W734	W735	W736	E737	K740	L741	H742	L743	E744	T745	W746	E747	W748	R753	E754	I622	K755	E756	E757	K758	Y759	G760	E761	S762	L763	W764	E765	W766	G767	Y768	W769	W770	W771	W772	L773	R774	W775	W776	A777	E778	L779	E781	L784	Y785	C786	Q787	D788	A789	I790	E791	L792							
I795	E796	L797	W798	K799	W800	L801	A802	T803	R804	S805	S806	W807	W808	A809	N810	S811	L812	L813	S814	K815	N816	H817	E818	E819	F820	Y821	F822	S823	Q824	T825	R826	I827	T828	S829	L830	R831	G832	Q836	W837	R838	F839	D840	G841	H842	S845	S846	W847	R854	Y855	N858	S859	R860	L865									
E871	T872	R873	E874	Q875	A877	N878	A879	R880	I881	W882	R883	K884	Y885	Q886	R887	T888	E889	A890	D891	R892	G893	F894	F895	I896	T897	T901	L905	E909	Y912	D913	A914	I915	A916	K917	N918	I919	S920	E921	E922	Y923	I924	S925	Y926	G927	G928	E929	K930	K931	I932	L933	A934	I935	Q936	G937								
A938	L939	E940	K941	A942	L943	R944	W945	A946	S947	G948	E949	S950	F951	I952	E953	L954	S955	N956	H957	K958	F959	I960	R961	M962	K963	R964	K965	L966	M967	Y968	V969	S970	A971	D972	A973	T974	K975	W976	S977	P978	G979	D980	F985	R986	R987	F988	T989	S990	H993	N994	G995	L996	P997	N998	N999	T1006						
K1010	K1014	F1017	S1020	E1021	K1022	L1023	R1024	N1025	Y1026	I1027	D1028	S1029	M1030	E1031	S1032	L1033	D1034	P1035	H1036	I1037	K1038	Q1039	F1040	L1041	D1042	F1043	F1044	P1045	D1046	G1047	H1048	H1049	G1050	E1051	V1052	K1053	G1054	N1055	W1056	L1057	Q1058	G1059	N1060	L1061	N1062	K1063	C1064	S1065	L1067	F1068	G1069	A1071	M1072									
S1073	L1074	L1075	F1076	K1077	K1078	V1079	W1080	T1081	N1082	L1083	F1084	P1085	E1086	L1087	D1088	C1089	F1090	F1091	E1092	F1093	A1094	H1095	H1096	S1097	D1098	D1099	A1100	L1101	F1102	I1103	Y1104	L1107	E1108	P1109	V1110	D1111	D1112	G1113	T1114	D1115	W1116	F1117	L1118	F1119	Y1120	S1121	Q1122	Q1123	I1124	Q1125	A1126	G1127	H1128	S1129	L1130	W1131	F1132	S1133				
V1134	N1135	T1136	E1137	M1138	W1139	K1140	S1141	F1143	M1144	H1145	H1146	E1147	H1148	I1149	I1155	K1156	I1157	S1158	P1159	K1160	K1161	T1162	T1163	V1164	T1167	M1168	A1169	E1170	F1171	L1172	S1173	T1174	F1175	F1176	E1177	G1178	C1179	A1180	V1181	S1182	P1184	F1185	V1186	K1187	I1188	L1189	L1190	G1191	S1192	L1193	S1194	L1195	L1196	P1197	G1198							

V2091	L1199	L1430	I1498	S1569	L1763	H1823	M1918	ALA	G2028
G2095	G1200	A1433	I1499	R1570	K1764	THR	R1919	ASP	I2029
I2099	Y1201	M1434	Q1500	V1571	I1765	THR	A1920	ILE	L2032
D2100	F1202	M1434	Q1501	V1572	M1636	GLN	M1928	GLU	L2033
Q2101	F1203	R1353	M1501	V1573	R1637	ALA	M1939	PHE	L2038
F2102	D1203	I1354	G1508	I1574	C1638	ILE	R1940	LEU	L2047
R1211	R1211	S1355	G1509	V1575	C1639	ASN	R1949	ASP	V2052
K1214	K1214	L1360	K1510	I1577	K1640	H1830	M1949	ASP	V2056
A1215	A1215	Q1364	Y1509	Q1575	Y1645	F1645	L1947	ASP	I2069
L1216	L1216	Y1368	K1511	G1576	R1647	R1648	E1948	THR	R2063
D1217	D1217	Y1368	F1511	M1577	D1648	F1650	T1949	THR	S2066
L1218	L1218	K1374	A1512	E1579	V1649	F1650	T1949	THR	K2067
G1219	G1219	L1380	V1513	G1580	V1654	M1654	T1949	THR	T2073
A1220	A1220	L1380	W1515	T1581	W1654	F1655	M1949	GLY	V2076
S1221	S1221	L1380	E1516	A1582	F1655	F1655	N1940	ASP	S2077
P1222	P1222	V1384	E1517	E1583	K1658	K1658	M1949	GLU	L2078
Q1223	Q1223	M1385	L1522	E1583	I1658	I1658	L1947	THR	L2079
V1224	V1224	K1386	D1523	I1584	I1658	I1658	L1947	THR	T2085
A1225	A1225	K1386	T1524	I1585	T1659	T1659	L1947	THR	
A1226	A1226	L1387	T1524	C1586	F1660	F1660	L1947	THR	
Q1226	Q1226	L1387	K1526	R1587	S1661	S1661	L1947	THR	
L1227	L1227	D1389	F1527	Y1588	E1662	E1662	L1947	THR	
A1228	A1228	P1390	P1528	W1589	D1665	D1665	L1947	THR	
R1238	R1238	S1391	D1529	L1590	C1668	C1668	L1947	THR	
L1239	L1239	I1392	S1530	K1591	R1669	R1669	L1947	THR	
G1241	G1241	V1393	L1531	M1592	V1670	V1670	L1947	THR	
T1242	T1242	T1394	S1532	S1593	G1671	G1671	L1947	THR	
A1243	A1243	A1395	L1535	L1595	V1672	V1672	L1947	THR	
G1245	G1245	M1396	K1536	V1596	P1673	P1673	L1947	THR	
M1246	M1246	T1397	A1538	K1597	A1674	A1674	L1947	THR	
V1247	V1247	M1398	M1538	L1598	L1675	L1675	L1947	THR	
M1248	M1248	Q1399	K1539	I1599	D1676	D1676	L1947	THR	
H1249	H1249	S1400	G1540	R1600	E1677	E1677	L1947	THR	
P1250	P1250	P1401	G1541	V1601	Q1680	Q1680	L1947	THR	
Y1253	Y1253	L1402	Y1542	I1602	L1684	L1684	L1947	THR	
L1254	L1254	L1404	Y1543	P1603	M1685	M1685	L1947	THR	
Q1255	Q1255	R1405	R1544	K1604	I1686	I1686	L1947	THR	
H1258	H1258	F1406	G1547	H1605	D1688	D1688	L1947	THR	
T1259	T1259	R1407	I1548	E1606	E1688	E1688	L1947	THR	
D1260	D1260	M1408	D1549	V1607	I1689	I1689	L1947	THR	
L1265	L1265	Q1409	I1550	K1690	K1690	K1690	L1947	THR	
G1266	G1266	A1410	S1551	Q1609	G1691	G1691	L1947	THR	
G1267	G1267	M1414	L1552	A1610	A1611	A1611	L1947	THR	
G1267	G1267	K1415	P1553	V1611	V1612	V1612	L1947	THR	
G1269	G1269	R1418	D1554	S1612	S1612	S1612	L1947	THR	
A1270	A1270	L1419	V1555	F1613	F1613	F1613	L1947	THR	
M1271	M1271	D1420	M1556	I1614	I1614	I1614	L1947	THR	
S1272	S1272	G1421	K1557	M1615	M1615	M1615	L1947	THR	
I1273	I1273	L1420	A1483	R1616	R1616	R1616	L1947	THR	
I1274	I1274	D1421	K1485	K1617	K1617	K1617	L1947	THR	
E1275	E1275	G1421	V1486	E1618	E1618	E1618	L1947	THR	
L1276	L1276	W1422	A1487	I1618	I1618	I1618	L1947	THR	
A1277	A1277	V1423	R1488	M1701	M1701	M1701	L1947	THR	
T1278	T1278	V1424	T1489	R1702	R1702	R1702	L1947	THR	
		T1425	F1490	I1620	I1620	I1620	L1947	THR	
		F1426	T1491	E1621	E1621	E1621	L1947	THR	
		S1344	V1492	K1622	K1622	K1622	L1947	THR	
		S1345	F1427	Q1623	Q1623	Q1623	L1947	THR	
		E1346	E1427	L1624	L1624	L1624	L1947	THR	
		F1347	E1428	D1625	D1625	D1625	L1947	THR	
		E1348	V1429	L1626	L1626	L1626	L1947	THR	
		F1349		L1629	L1629	L1629	L1947	THR	

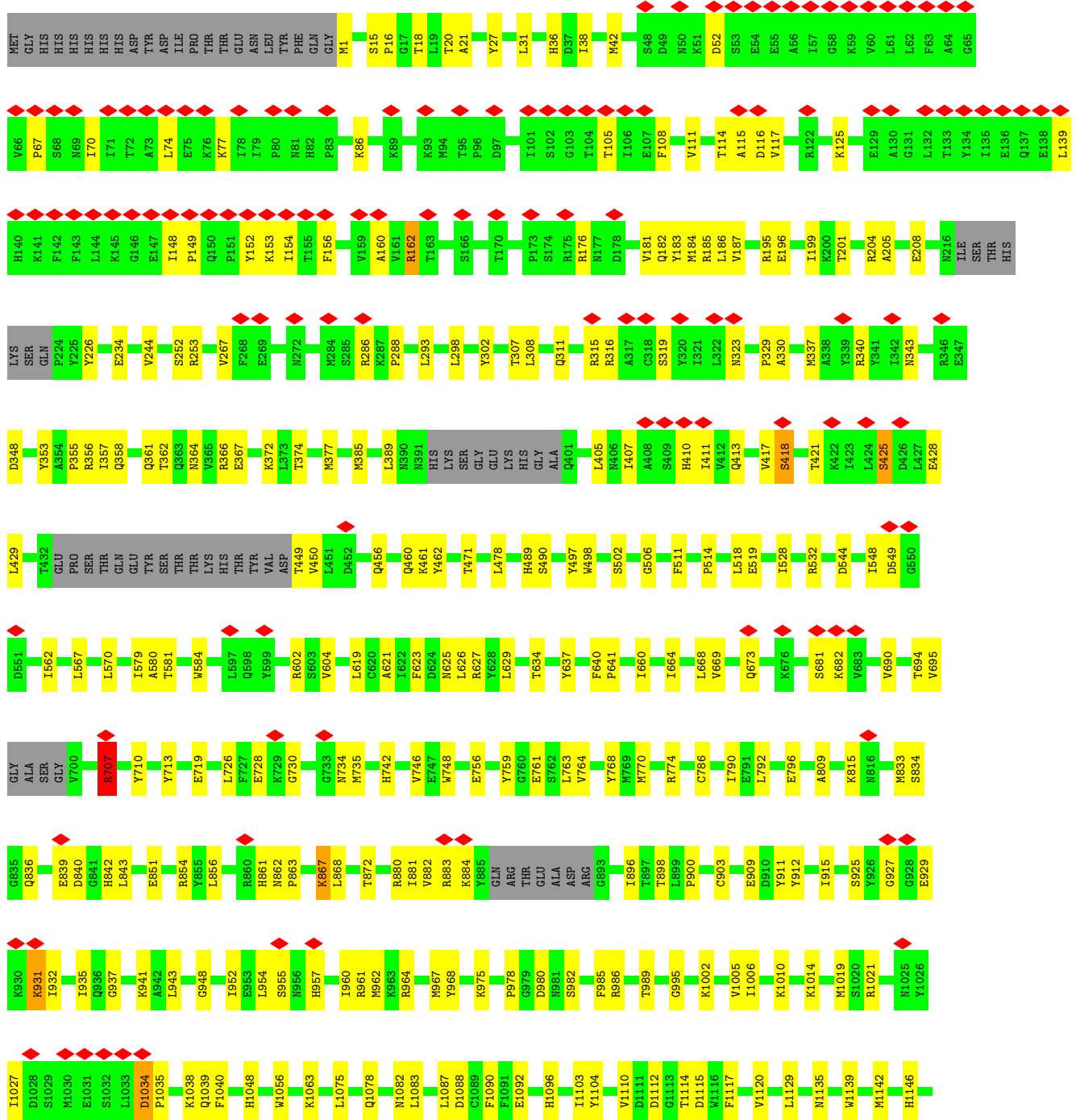
• Molecule 1: RNA-directed RNA polymerase L

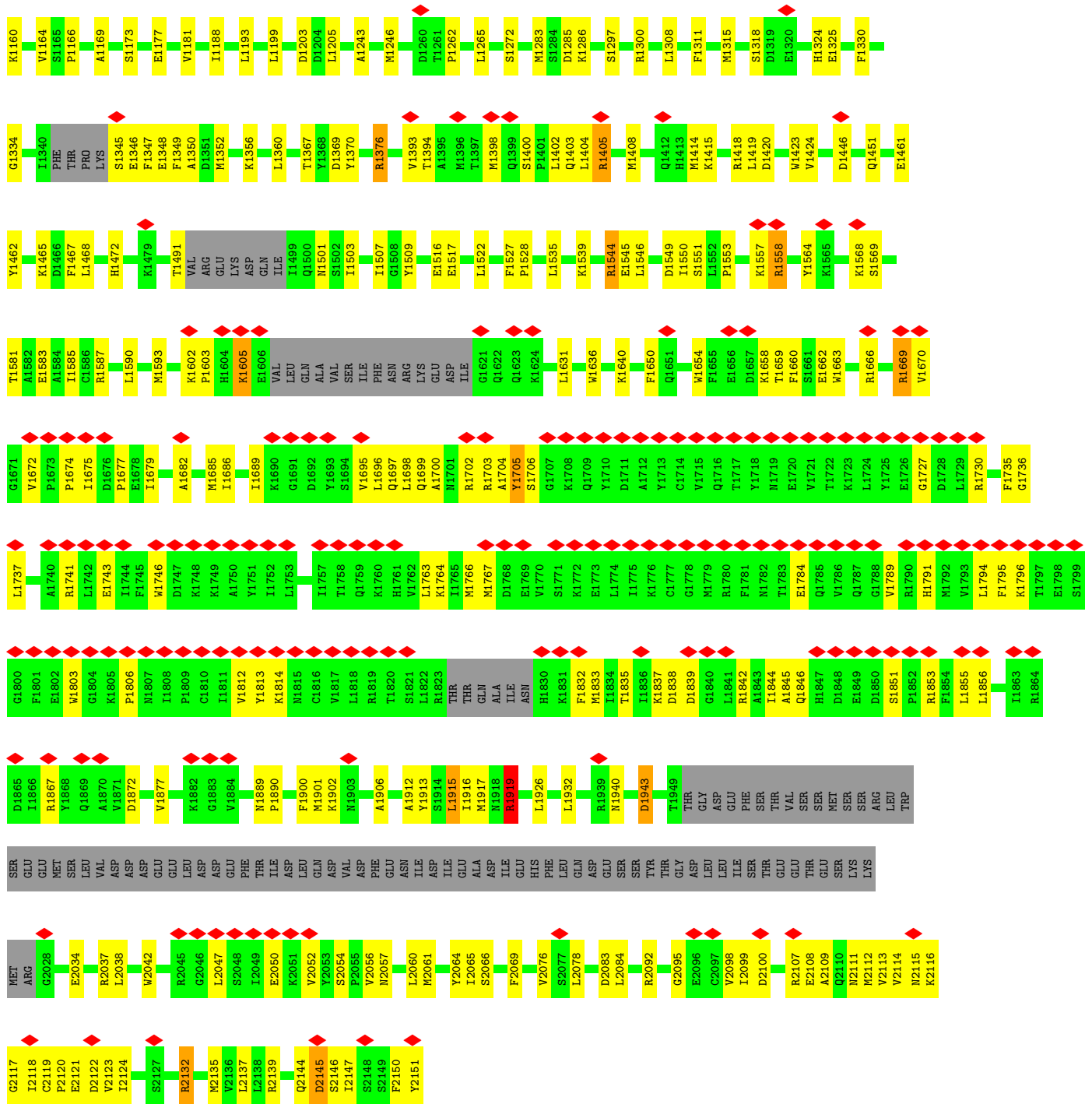




Y2151

• Molecule 1: RNA-directed RNA polymerase L





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	28695	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.980	Depositor
Minimum map value	-1.238	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.305	Depositor
Map size (Å)	587.3, 587.3, 587.3	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.839, 0.839, 0.839	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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 >5	RMSZ	# Z >5
1	A	0.29	0/15469	0.49	0/20911
1	B	0.29	0/15469	0.49	0/20911
1	C	0.31	0/16505	0.49	0/22303
1	D	0.27	0/16764	0.47	0/22656
1	E	0.31	0/16505	0.49	0/22303
1	F	0.27	0/16764	0.47	0/22656
All	All	0.29	0/97476	0.48	0/131740

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
1	A	0	1
1	B	0	2
1	C	0	4
1	E	0	4
All	All	0	11

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	2132	ARG	Sidechain
1	B	2139	ARG	Sidechain
1	C	162	ARG	Sidechain
1	C	185	ARG	Sidechain
1	C	707	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	15128	0	15210	413	0
1	B	15128	0	15210	418	0
1	C	16146	0	16240	441	0
1	D	16400	0	16506	381	0
1	E	16146	0	16240	445	0
1	F	16400	0	16506	382	0
All	All	95348	0	95912	2136	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 11.

The worst 5 of 2136 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)
1:D:196:GLU:HG3	1:C:2056:VAL:CG2	1.66	1.24
1:F:196:GLU:HG3	1:E:2056:VAL:CG2	1.66	1.23
1:D:196:GLU:HG3	1:C:2056:VAL:HG21	1.22	1.20
1:C:417:VAL:HG11	1:A:707:ARG:HB3	1.27	1.16
1:B:707:ARG:HH12	1:E:410:HIS:CE1	1.63	1.16

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
1	A	1853/2173 (85%)	1754 (95%)	98 (5%)	1 (0%)	51 83

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	1853/2173 (85%)	1754 (95%)	98 (5%)	1 (0%)	51	83
1	C	1977/2173 (91%)	1890 (96%)	87 (4%)	0	100	100
1	D	2016/2173 (93%)	1947 (97%)	69 (3%)	0	100	100
1	E	1977/2173 (91%)	1890 (96%)	87 (4%)	0	100	100
1	F	2016/2173 (93%)	1947 (97%)	69 (3%)	0	100	100
All	All	11692/13038 (90%)	11182 (96%)	508 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1366	VAL
1	A	1366	VAL

5.3.2 Protein sidechains [i](#)

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	
1	A	1668/1941 (86%)	1621 (97%)	47 (3%)	43	72
1	B	1668/1941 (86%)	1622 (97%)	46 (3%)	43	72
1	C	1781/1941 (92%)	1732 (97%)	49 (3%)	43	72
1	D	1809/1941 (93%)	1804 (100%)	5 (0%)	92	97
1	E	1781/1941 (92%)	1732 (97%)	49 (3%)	43	72
1	F	1809/1941 (93%)	1804 (100%)	5 (0%)	92	97
All	All	10516/11646 (90%)	10315 (98%)	201 (2%)	59	80

5 of 201 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	566	ARG
1	A	1841	LEU
1	E	2132	ARG
1	A	680	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1316	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	137	GLN
1	E	1403	GLN
1	F	1615	ASN
1	E	842	HIS
1	F	1298	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

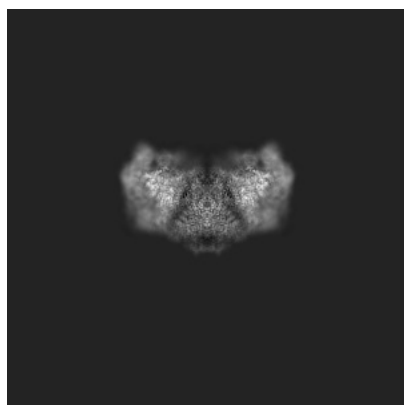
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18408. These allow visual inspection of the internal detail of the map and identification of artifacts.

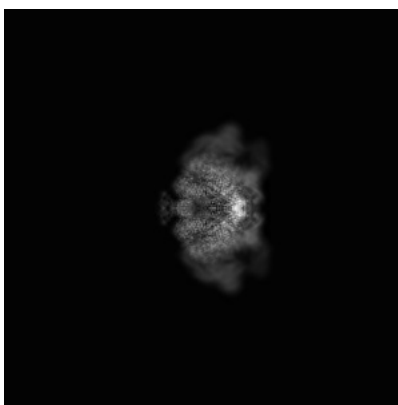
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

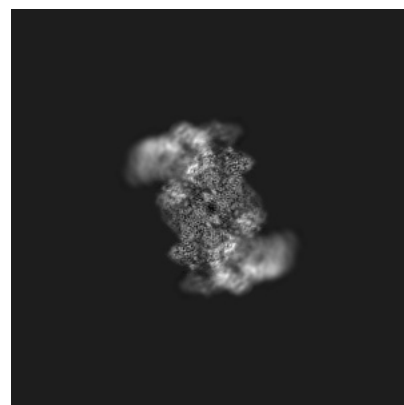
6.1.1 Primary map



X



Y



Z

The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

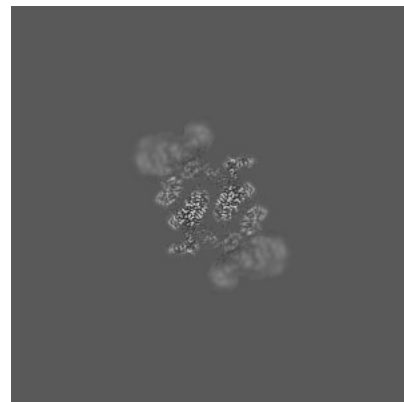
6.2.1 Primary map



X Index: 350



Y Index: 350

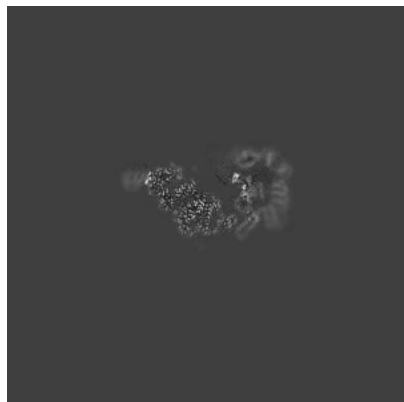


Z Index: 350

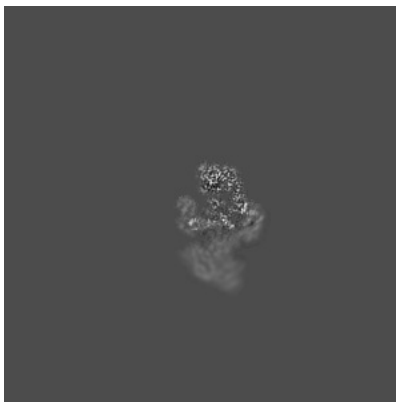
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

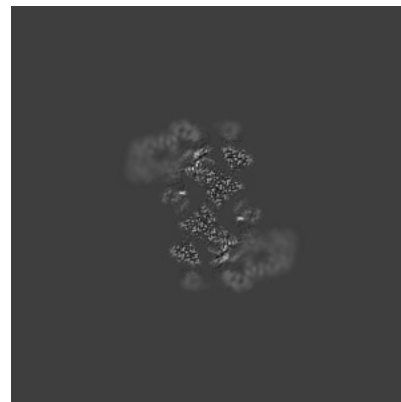
6.3.1 Primary map



X Index: 317



Y Index: 424

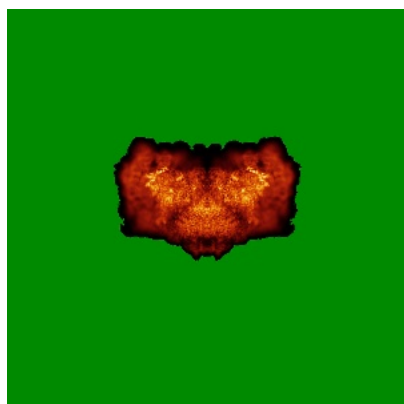


Z Index: 385

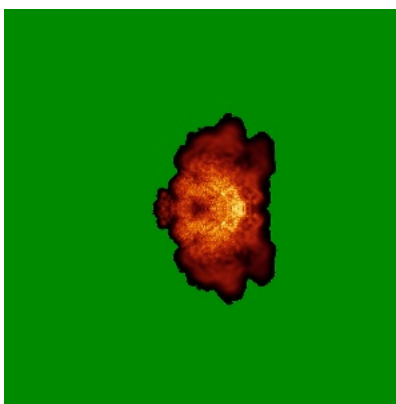
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

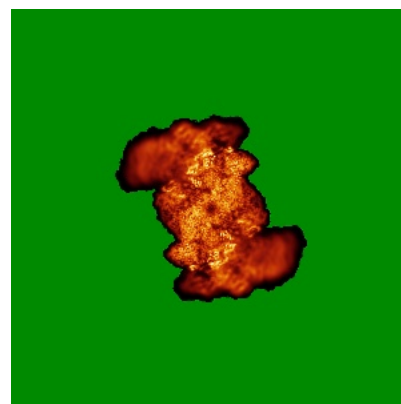
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.305. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

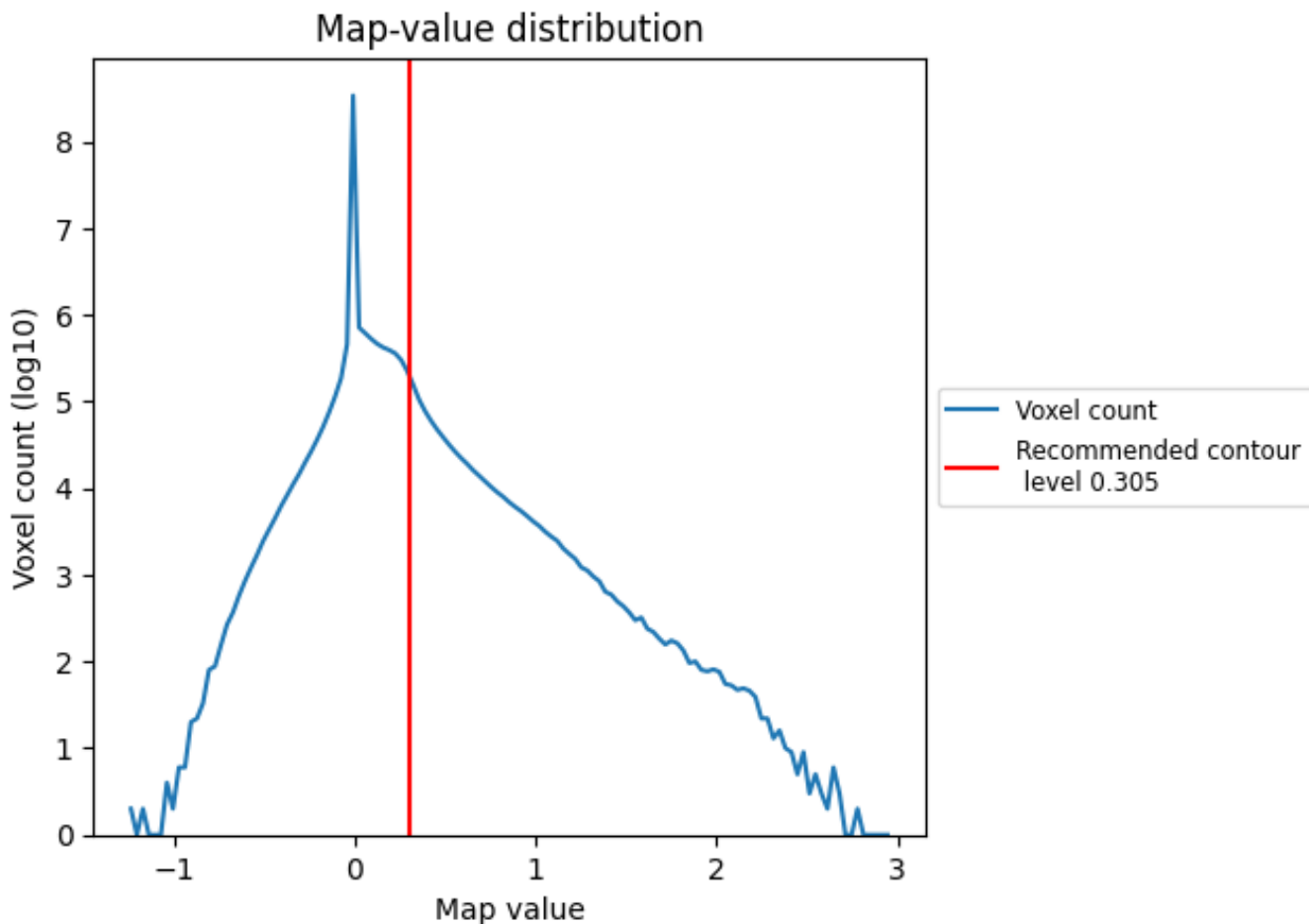
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

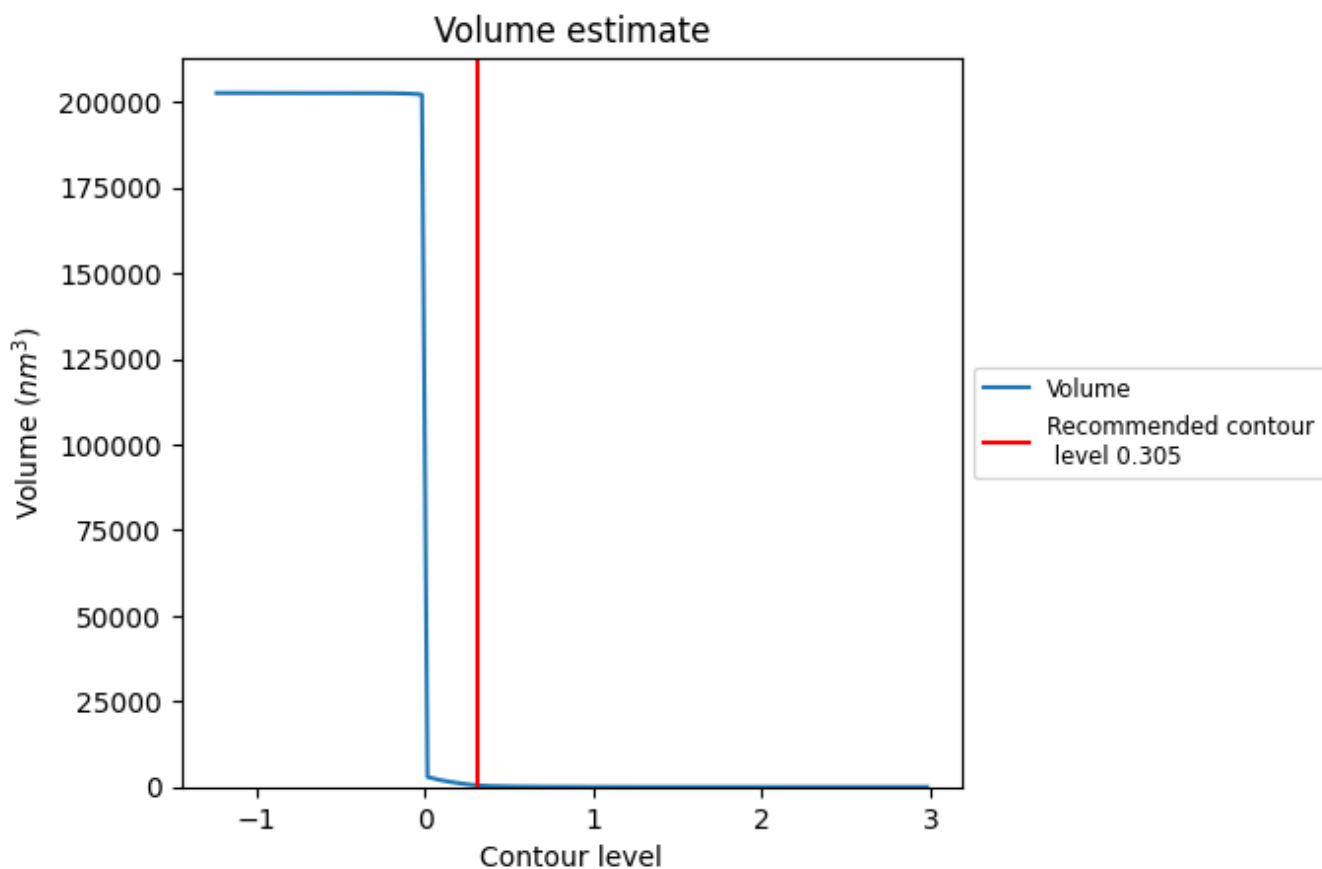
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

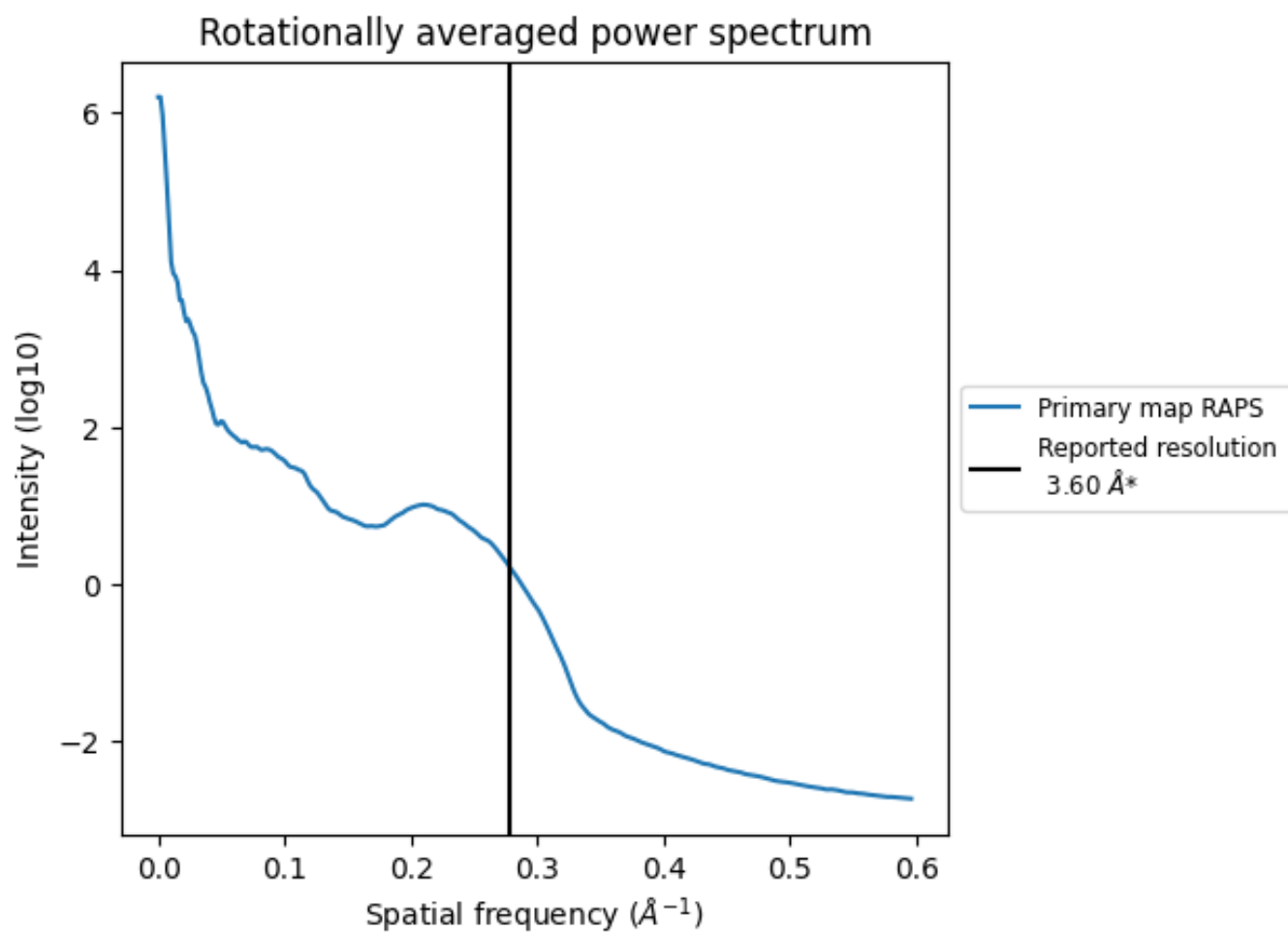
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 485 nm³; this corresponds to an approximate mass of 438 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.278\AA^{-1}

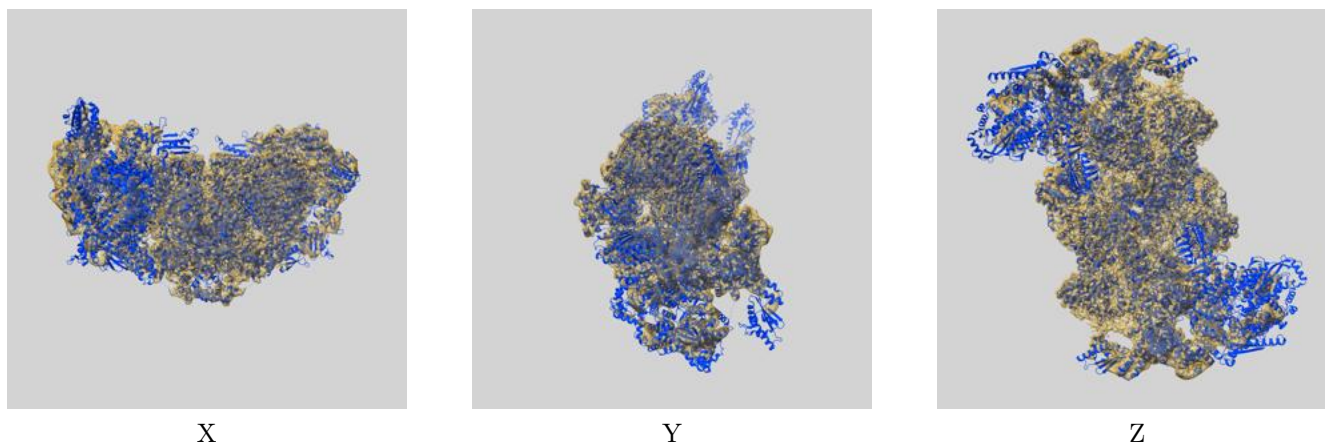
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

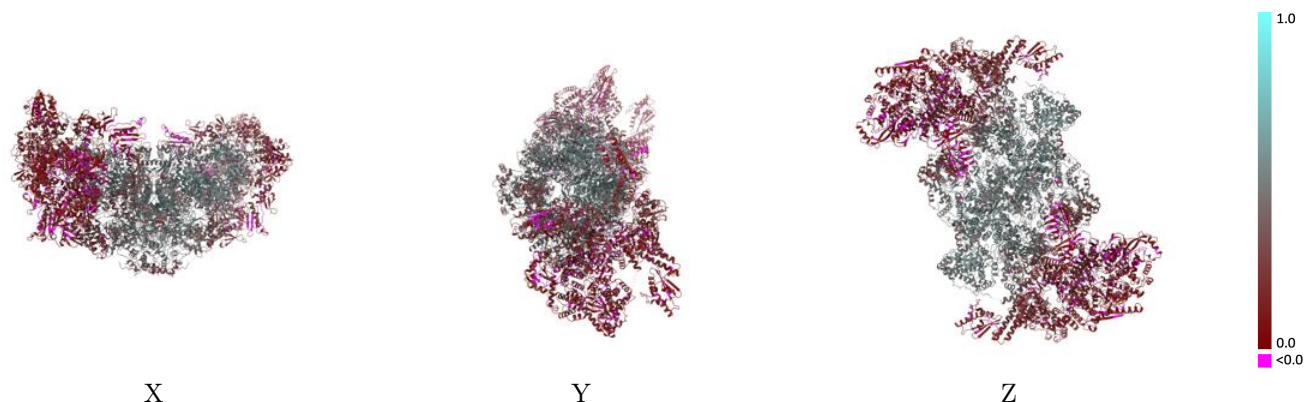
This section contains information regarding the fit between EMDB map EMD-18408 and PDB model 8QHD. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



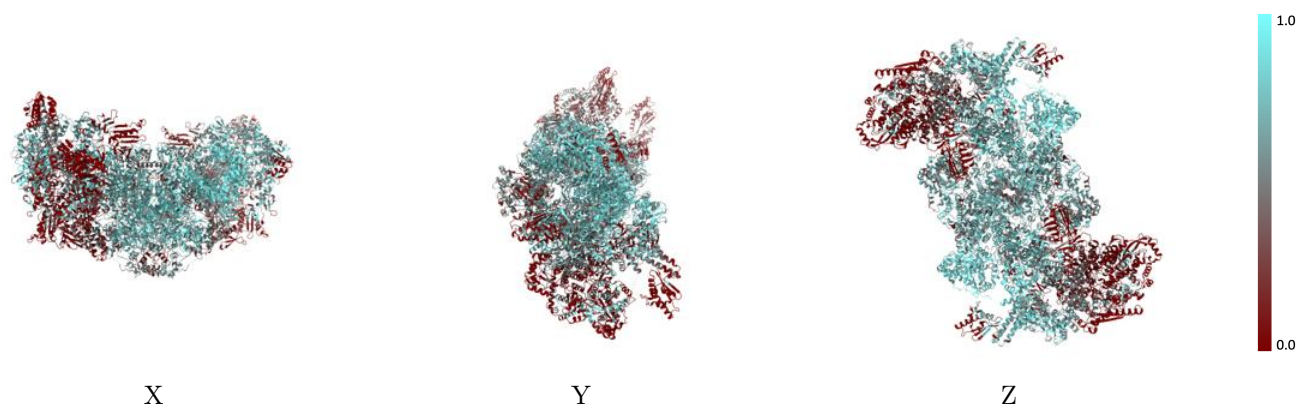
The images above show the 3D surface view of the map at the recommended contour level 0.305 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



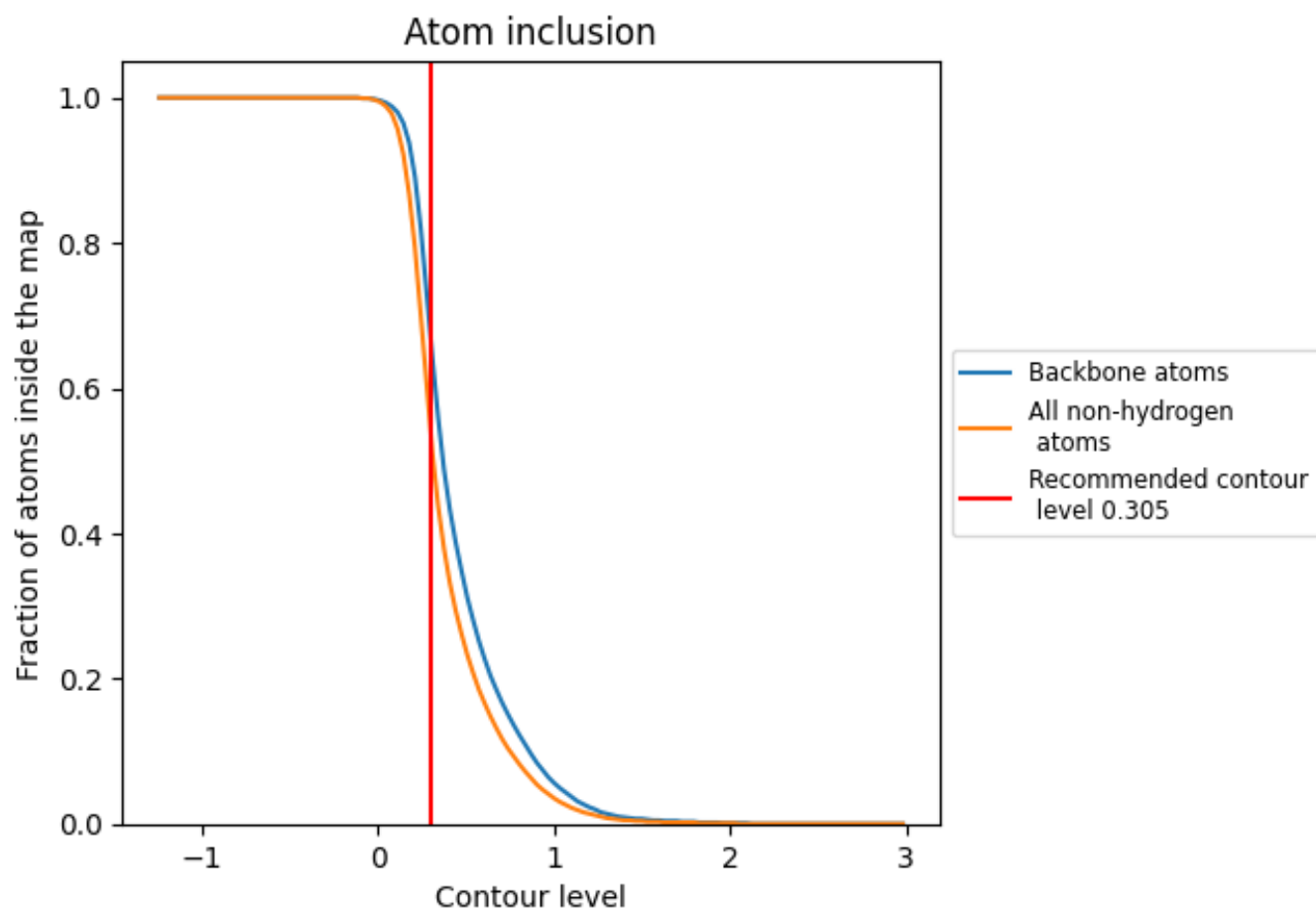
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.305).















9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 52% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.305) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5250	 0.3180
A	 0.5990	 0.4250
B	 0.6380	 0.4430
C	 0.7090	 0.4060
D	 0.2710	 0.1310
E	 0.6900	 0.3960
F	 0.2650	 0.1300

