



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:43 AM UTC

PDB ID : 7DVQ / pdb_00007dvq
EMDB ID : EMD-30875
Title : Cryo-EM Structure of the Activated Human Minor Spliceosome (minor Bact Complex)
Authors : Bai, R.; Wan, R.; Wang, L.; Xu, K.; Zhang, Q.; Lei, J.; Shi, Y.
Deposited on : 2021-01-14
Resolution : 2.89 Å(reported)

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:

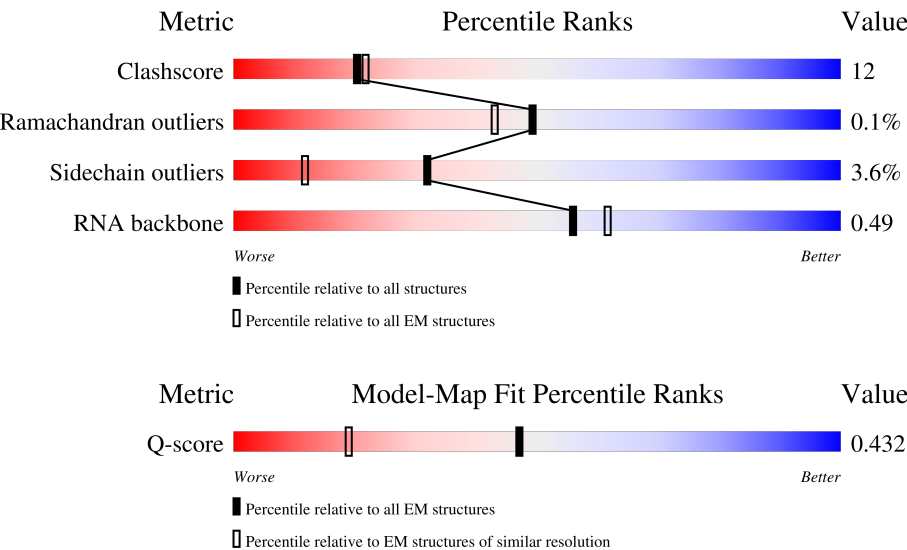
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 2.89 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12148 (2.39 - 3.39)

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	2335	
2	B	117	
3	C	972	

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Mol	Chain	Length	Quality of chain
4	D	2136	
5	E	357	
6	a	126	
6	h	126	
7	b	240	
7	i	240	
8	c	119	
8	j	119	
9	d	118	
9	k	118	
10	f	86	
10	m	86	
11	e	92	
11	l	92	
12	g	76	
12	n	76	
13	F	124	
14	G	142	
15	H	150	
16	v	230	
17	1	1304	
18	2	895	
19	3	1217	
20	4	424	
21	5	125	

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Mol	Chain	Length	Quality of chain
22	6	110	
23	7	86	
24	L	802	
25	J	848	
26	P	229	
27	R	536	
28	T	514	
29	X	396	
30	Y	322	
31	Z	619	
32	9	520	
33	z	472	
34	x	1041	
35	y	476	
36	M	343	
37	U	2752	
38	V	908	
39	8	904	
40	0	101	
41	I	367	
42	K	198	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 99906 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 Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2223	Total	C	N	O	S	0	0
			18354	11832	3206	3236	80		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	90	Total	C	N	O	P	0	0
			1898	850	320	638	90		

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	902	Total	C	N	O	S	0	0
			7125	4560	1185	1345	35		

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	1803	Total	C	N	O	S	0	0
			9215	5522	1841	1851	1		

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	299	Total	C	N	O	S	0	0
			2337	1470	409	445	13		

- Molecule 6 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	a	81	Total	C	N	O	0	0
			399	237	81	81		

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	h	80	Total	C	N	O	0	0
			392	233	79	80		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	b	82	Total	C	N	O	0	0
			405	241	82	82		
7	i	86	Total	C	N	O	0	0
			422	250	86	86		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	c	82	Total	C	N	O	0	0
			406	242	82	82		
8	j	82	Total	C	N	O	0	0
			406	242	82	82		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	d	97	Total	C	N	O	0	0
			480	286	97	97		
9	k	85	Total	C	N	O	0	0
			422	252	85	85		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	f	74	Total	C	N	O	0	0
			361	213	74	74		
10	m	74	Total	C	N	O	0	0
			361	213	74	74		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	e	79	Total	C	N	O	0	0
			391	233	79	79		
11	l	79	Total	C	N	O	0	0
			391	233	79	79		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	g	74	Total	C	N	O	0	0
			363	215	74	74		
12	n	68	Total	C	N	O	0	0
			334	198	68	68		

- Molecule 13 is a RNA chain called U6atac snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	60	Total	C	N	O	P	0	0
			1294	577	242	415	60		

- Molecule 14 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	63	Total	C	N	O	P	0	0
			1303	585	197	458	63		

- Molecule 15 is a RNA chain called U12 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	63	Total	C	N	O	P	0	0
			1350	604	247	436	63		

- Molecule 16 is a protein called Sodium channel modifier 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	v	119	Total	C	N	O	S	0	0
			963	601	179	178	5		

- Molecule 17 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	1	986	Total	C	N	O	P	S	0	0
			7879	5035	1361	1435	1	47		

- Molecule 18 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2	216	Total	C	N	O	S	0	0
			1674	1067	296	305	6		

- Molecule 19 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	3	1193	Total	C	N	O	P	S	
			9352	5932	1590	1784	1	45	
								0	0

- Molecule 20 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	4	78	Total	C	N	O		
			383	227	78	78	0	0

- Molecule 21 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	5	109	Total	C	N	O	S		
			906	582	157	163	4	0	0

- Molecule 22 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	6	105	Total	C	N	O	S		
			811	502	145	151	13	0	0

- Molecule 23 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	7	81	Total	C	N	O	S		
			669	422	117	124	6	0	0

- Molecule 24 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L	101	Total	C	N	O	S		
			843	540	152	147	4	0	0

- Molecule 25 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	J	522	Total	C	N	O	S		
			3457	2153	654	645	5	0	0

- Molecule 26 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P	44	Total	C	N	O	S	0	0
			384	243	71	68	2		

- Molecule 27 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	R	241	Total	C	N	O	S	0	0
			1923	1191	347	374	11		

- Molecule 28 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	320	Total	C	N	O	S	0	0
			2507	1582	456	462	7		

- Molecule 29 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	156	Total	C	N	O	S	0	0
			1271	815	227	227	2		

- Molecule 30 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	140	Total	C	N	O	S	0	0
			1095	692	192	206	5		

- Molecule 31 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	140	Total	C	N	O	S	0	0
			1129	703	214	207	5		

- Molecule 32 is a protein called RING-type E3 ubiquitin-protein ligase PPIL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	9	409	Total	C	N	O	S	0	0
			2691	1672	487	525	7		

- Molecule 33 is a protein called Peptidyl-prolyl cis-trans isomerase CWC27 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	z	177	Total	C	N	O	S	0	0
			1400	883	245	267	5		

- Molecule 34 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	x	599	Total	C	N	O	S	0	0
			3007	1794	607	605	1		

- Molecule 35 is a protein called G-patch domain and KOW motifs-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	y	13	Total	C	N	O	0	0
			105	66	22	17		

- Molecule 36 is a protein called RING finger protein 113A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	M	191	Total	C	N	O	S	0	0
			1572	983	282	295	12		

- Molecule 37 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	U	26	Total	C	N	O	S	0	0
			193	120	36	36	1		

- Molecule 38 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	V	468	Total	C	N	O	S	0	0
			3008	1873	548	574	13		

- Molecule 39 is a protein called Serine/arginine repetitive matrix protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	8	126	Total	C	N	O	S	0	0
			1011	652	168	185	6		

- Molecule 40 is a protein called Cysteine-rich PDZ-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	0	100	Total	C	N	O	S	0	0
			770	475	142	144	9		

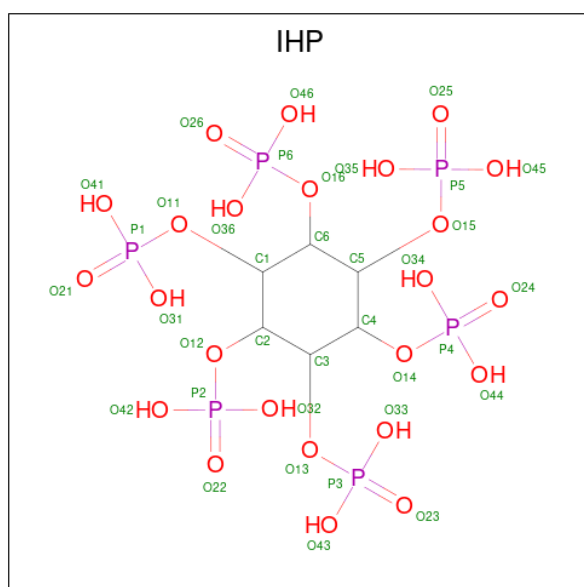
- Molecule 41 is a protein called RNA-binding protein 48.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	I	128	Total	C	N	O	S	0	0
			1062	683	184	190	5		

- Molecule 42 is a protein called Armadillo repeat-containing protein 7.

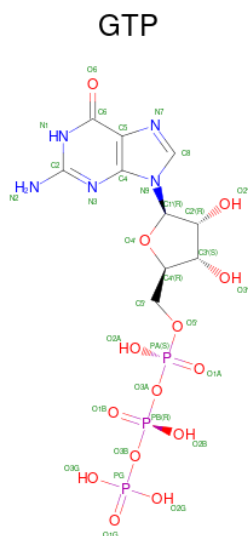
Mol	Chain	Residues	Atoms					AltConf	Trace
42	K	188	Total	C	N	O	S	0	0
			1314	824	229	256	5		

- Molecule 43 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
43	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 44 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
44	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

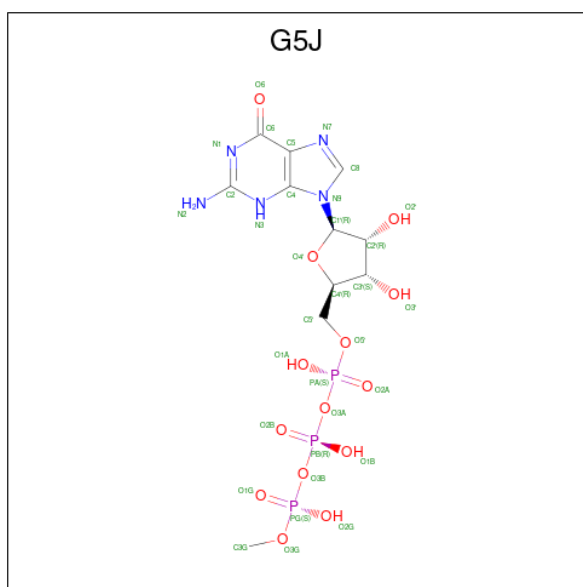
- Molecule 45 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
45	C	1	Total Mg 1 1	0
45	F	4	Total Mg 4 4	0

- Molecule 46 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
46	F	2	Total K 2 2	0

- Molecule 47 is 5'-O-[(S)-hydroxy{[(R)-hydroxy{[(S)-hydroxy(methoxy)phosphoryl]oxy}phosphoryl]oxy}phosphoryl]guanosine (CCD ID: G5J) (formula: C₁₁H₁₈N₅O₁₄P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
47	F	1	Total 33	C 11	N 5	O 14	P 3	0

- Molecule 48 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
48	v	1	Total 1	Zn 1	0
48	6	3	Total 3	Zn 3	0
48	M	1	Total 1	Zn 1	0
48	0	2	Total 2	Zn 2	0

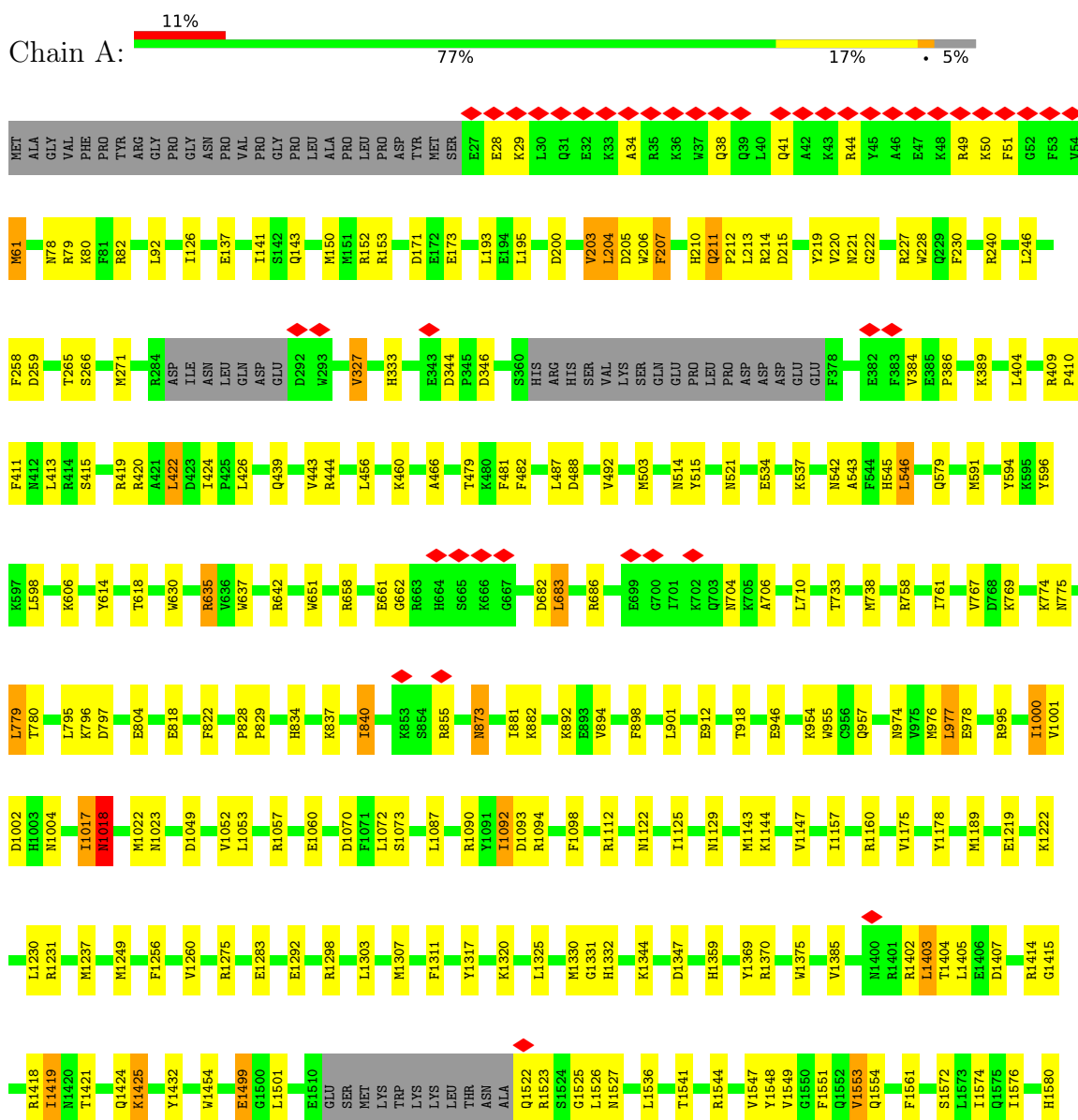
- Molecule 49 is water.

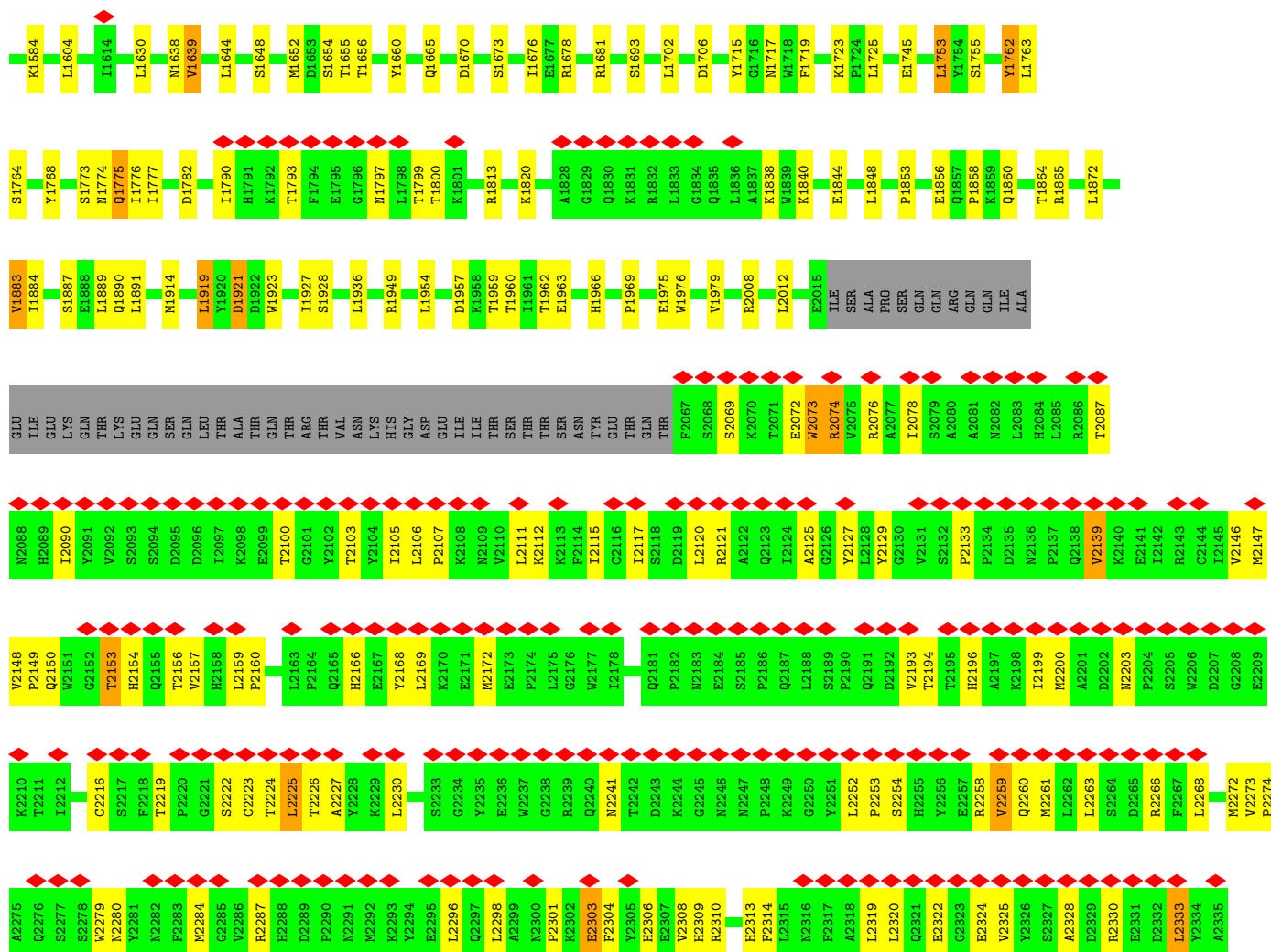
Mol	Chain	Residues	Atoms	AltConf
49	C	3	Total O 3 3	0

3 Residue-property plots

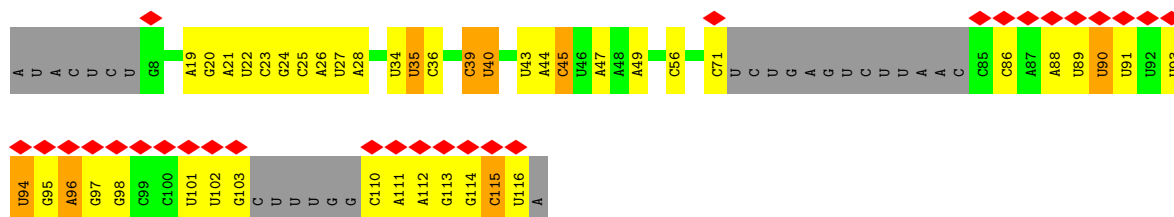
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Pre-mRNA-processing-splicing factor 8

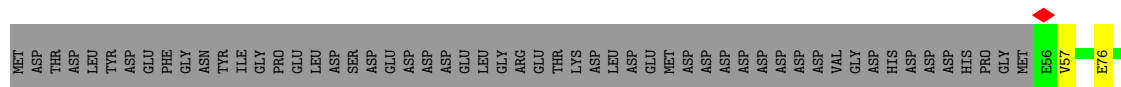
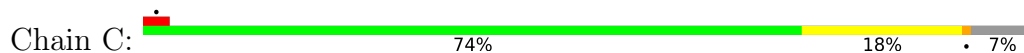




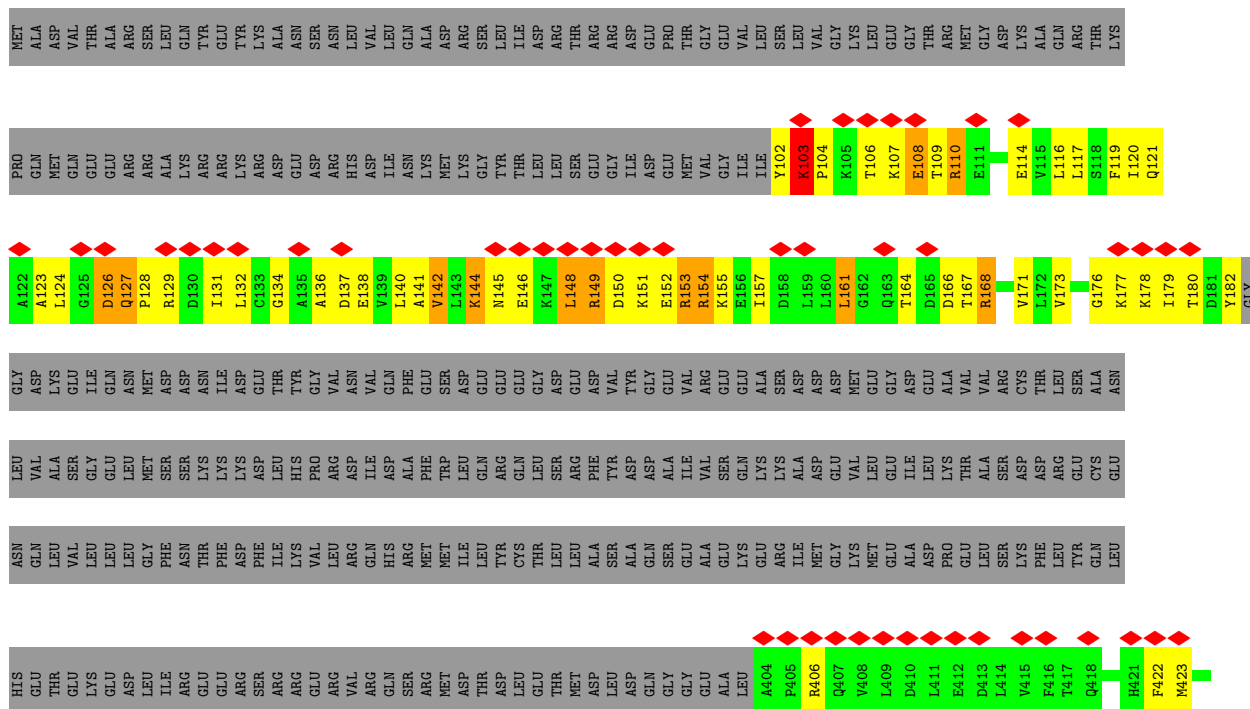
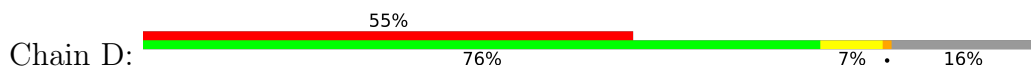
• Molecule 2: U5 snRNA



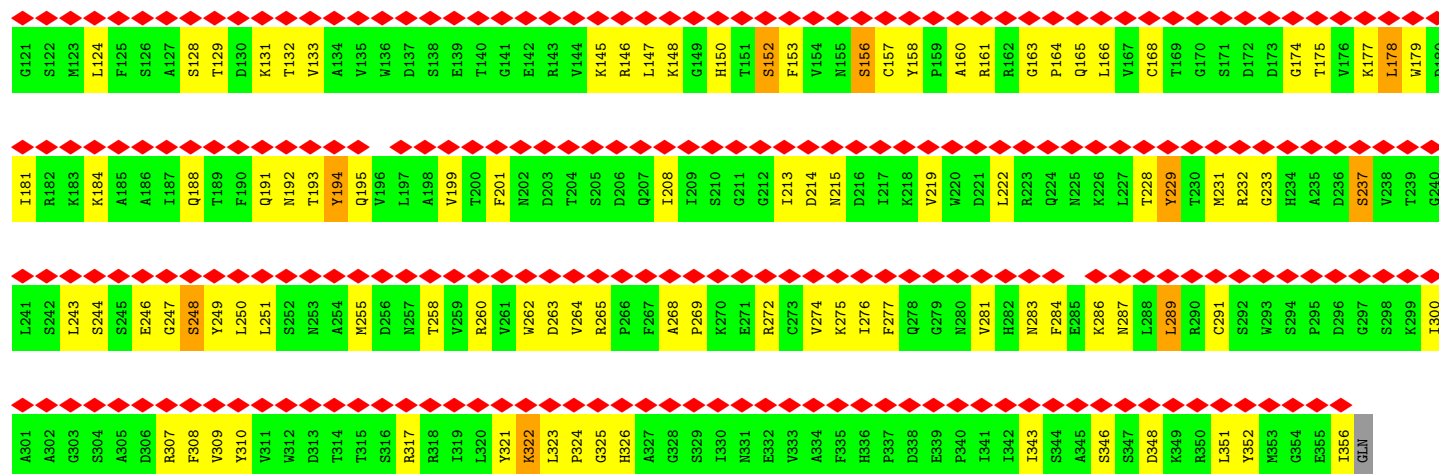
• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component



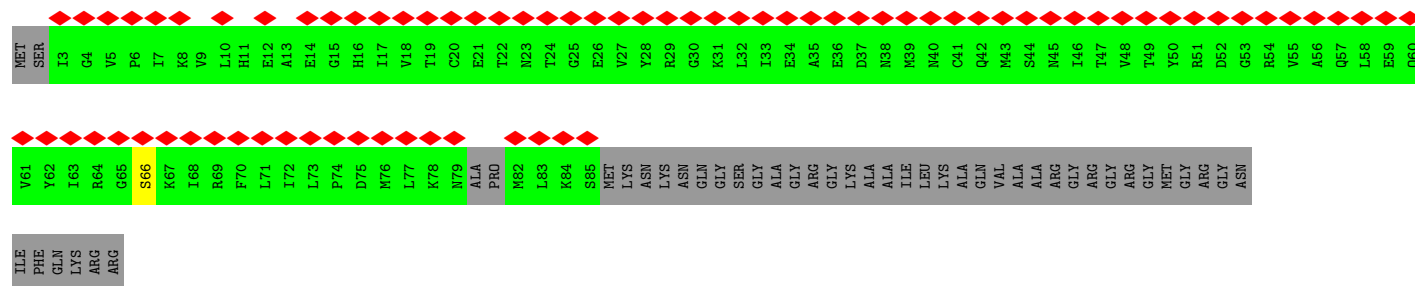
- Molecule 4: U5 small nuclear ribonucleoprotein 200 kDa helicase



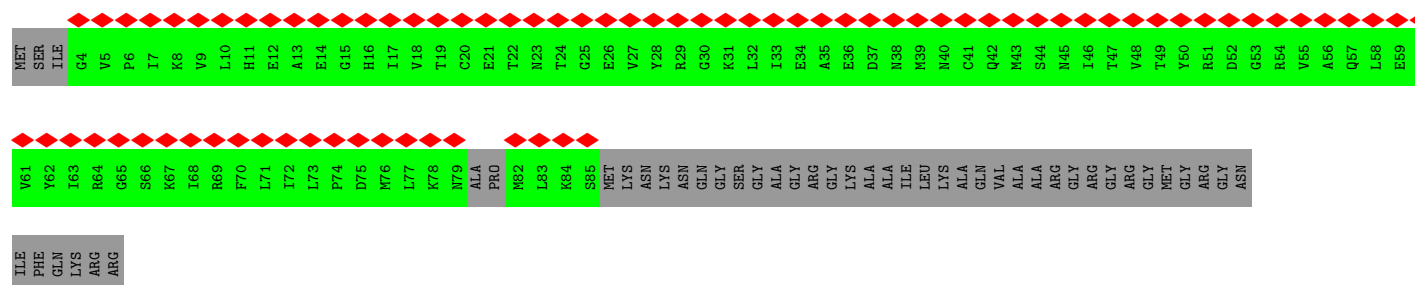
S1533	H1534	Q1536	T1537	R1538	L1539	L1540	S1541	I1481	E1482	A1543	K1544	P1545	V1546	Y1547	H1548	A1549	I1550	T1551	K1552	H1553	S1554	P1555	K1556	K1557	P1558	V1559	I1560	V1561	F1562	V1563	P1564	S1565	R1566	K1567	Q1568	T1569	R1570	L1571	T1572	A1573	I1574	D1575	I1576	L1577	T1578	T1579	C1580	A1581	A1582	D1583	I1584	Q1585	R1586	Q1587	R1588	F1589	L1590	H1591	C1592	
G1353	S1354	G1355	K1356	T1357	I1358	C1359	A1360	E1361	F1362	A1363	I1364	L1365	R1366	M1367	L1368	L1369	Q1370	S1371	S1372	E1373	G1374	R1375	C1376	V1377	Y1378	I1379	T1380	P1381	M1382	E1383	A1384	L1385	A1386	E1387	Q1388	V1389	I1390	M1391	D1392	L1393	Y1394	E1395	K1396	F1397	Q1398	D1399	R1400	L1401	N1402	K1403	K1404	V1405	V1406	L1407	L1408	T1409	G1410	T1412		
S1413	T1414	D1415	L1416	K1417	L1418	L1419	G1420	K1421	G1422	N1423	I1424	I1425	I1426	S1427	T1428	P1429	E1430	K1431	W1432	D1433	I1434	L1435	S1436	R1437	L1438	W1439	K1440	Q1441	R1442	K1443	N1444	V1445	Q1446	N1447	I1448	N1449	L1450	F1451	V1452	V1453	D1454	E1455	V1456	H1457	L1458	I1459	T1459	G1460	G1461	E1462	N1463	G1464	P1465	V1466	L1467	E1468	V1469	T1470	C1471	S1472
R1473	M1474	R1475	Y1476	I1477	S1478	S1479	I1480	T1481	E1482	R1483	P1484	I1485	R1486	I1487	V1488	A1489	L1490	S1491	S1492	S1493	L1494	S1495	N1496	A1497	K1498	D1499	V1500	A1501	H1502	W1503	L1504	G1505	C1506	S1507	A1508	T1509	L1510	T1511	F1512	V1513	F1514	H1515	P1516	V1517	V1518	R1519	P1520	V1521	P1522	L1523	E1524	L1525	H1526	Q1527	Q1528	F1529	F1530	M1531	T1532	
L1430	P431	D432	G433	S434	R439	K440	G441	Y442	E443	E444	V445	H446	V447	P448	A449	L450	K451	P452	G456	S457	E458	E459	Q460	L461	V464	E465	K466	L467	P468	K469	A473	G474	F475	E476	G477	F478	K479	T480	L488	L493	M498	L499	L500	A502	C502	A503	P504	T505	G506	A507	G508	K509								
L518	G522	I525	N526	M527	D528	G529	T530	I531	N532	V533	D534	D535	F536	K537	I538	M544	R545	G553	G556	T561	Y562	G563	I564	T565	V566	A567	E568	L569	T570	G571	D572	H573	Q574	L575	G576	K577	E578	E579	I580	S581	A582	T583	Q584	I585	G600	G601	E602	R603	T604	Q607										
L722	V725	H726	D740	L743	E744	K745	D746	T747	L748	G749	L750	F751	R752	R753	E754	G755	S756	A757	S758	T759	E760	E765	N771	D776	A783	A787	G788	M789	L800	K804	H805	I806	Q807	V808	L809	A816	V819	N820	H824	G830	T831	W841	T842	E843																
G854	P859	Q860	Y861	E866	T871	S872	H873	G874	E875	Y878	S881	L882	L883	N884	Q885	I889	E890	S891	D899	L907	G908	N909	Y910	K914	W919	A923	Y924	L925	G937	I938	S939	H940	D941	D942	L943	K944	G945	D946	P947	L948	L949	D950	Q951	D955	L956															
V957	H958	V970	D973	K974	T976	G977	N978	F979	Q980	V981	T982	E983	I987	Y991	Y992	N995	D996	T997	K1006	L1009	S1010	E1013	V1017	S1021	S1022	T1028	V1029	R1030	E1031	E1032	E1033	K1034	L1035	E1036	L1037	E1042	R1043	V1044	P1047	V1048	K1049	E1050	S1051	I1052	E1053															
L1070	K1071	L1072	E1073	G1074	F1075	R1090	A1094	W1123	C1127	K1134	L1135	P1136	E1137	E1144	K1145	F1148	P1149	F1150	D1155	L1156	E1160	I1165	R1166	M1167	P1168	K1169	K1183	L1184	E1185	L1186	S1187	V1188	H1189	L1190	Q1191	P1192	L1193	T1194	R1195	L1198	K1199	V1200	E1201	L1202	T1203	L1204														
T1205	P1206	D1207	F1208	Q1209	W1210	D1211	E1212	K1213	G1216	S1217	S1218	D1227	Y1228	D1229	S1230	E1231	L1234	H1235	K1244	Y1245	A1246	Q1247	D1248	E1249	I1252	T1253	F1254	F1255	V1256	P1257	V1258	F1259	E1260	P1261	L1262	P1263	P1264	Q1265	S1277	C1278	E1279	T1280	Q1281	V1284	S1285	F1286	L1287	H1288	L1289	I1290	L1291	P1292								
E1293	K1294	Y1295	P1296	T1297	P1298	T1299	E1300	L1301	L1302	D1303	L1304	Q1305	P1306	L1307	P1308	V1309	S1310	A1311	L1312	K1313	M1314	S1315	A1316	F1317	E1318	S1319	L1320	Y1321	Q1322	D1323	K1324	F1325	P1326	F1327	F1328	M1329	P1330	I1331	Q1332	T1333	Q1334	V1335	M1337	T1338	V1339	Y1340	M1341	S1342	D1343	D1344	M1345	V1346	F1347	V1348	G1349	A1350	P1351	T1352		



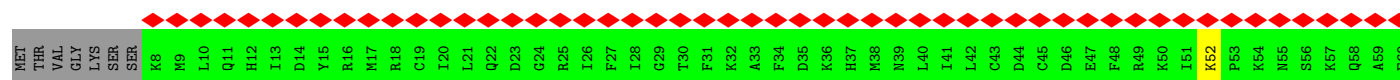
• Molecule 6: Small nuclear ribonucleoprotein Sm D3



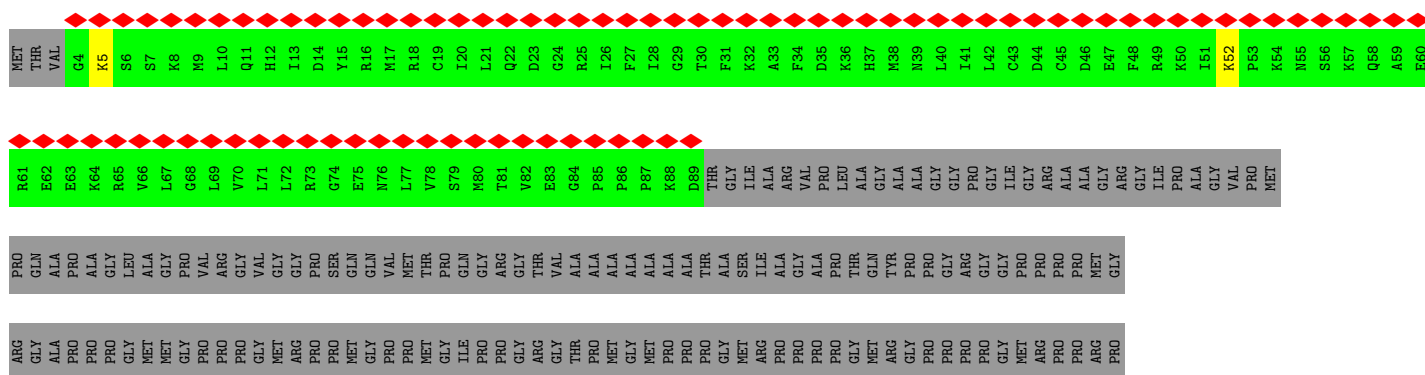
• Molecule 6: Small nuclear ribonucleoprotein Sm D3



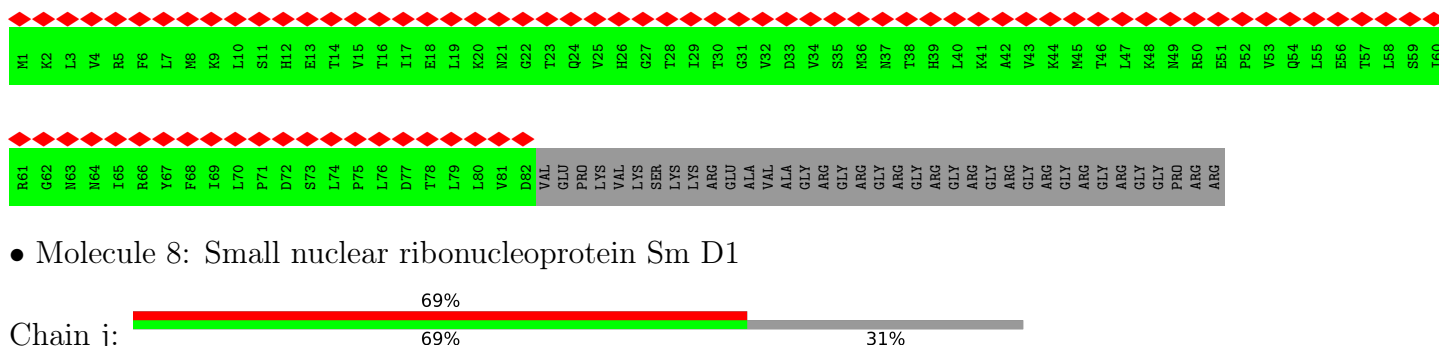
• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'



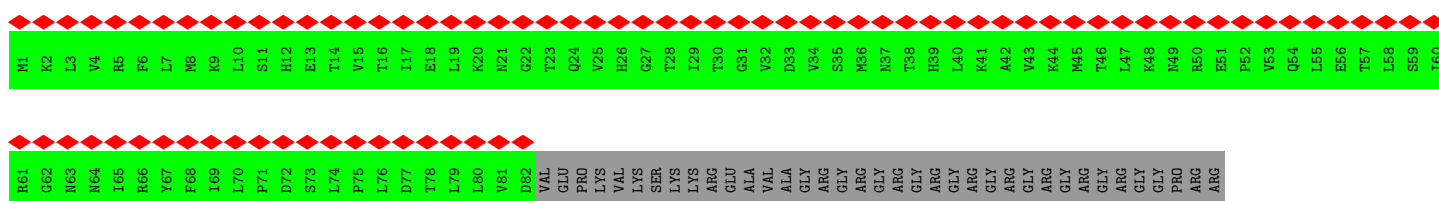
- Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'



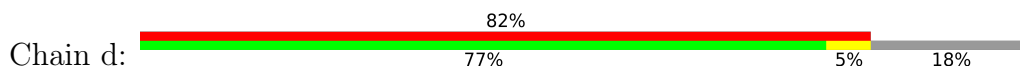
- Molecule 8: Small nuclear ribonucleoprotein Sm D1



- Molecule 8: Small nuclear ribonucleoprotein Sm D1

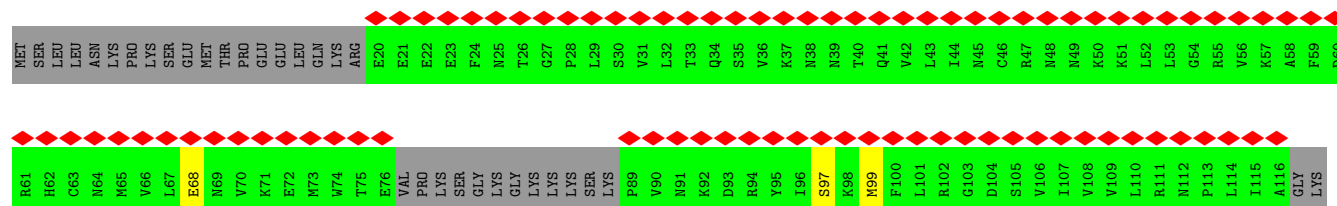


- Molecule 9: Small nuclear ribonucleoprotein Sm D2

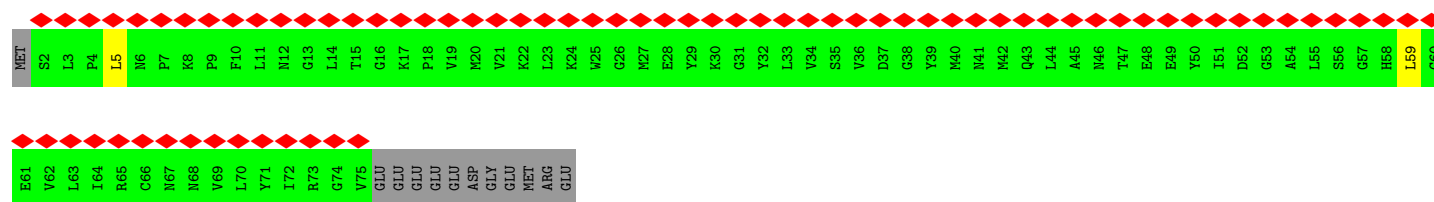
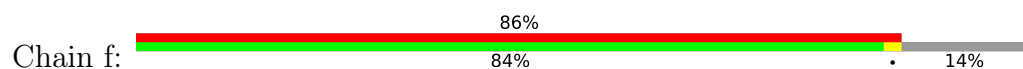




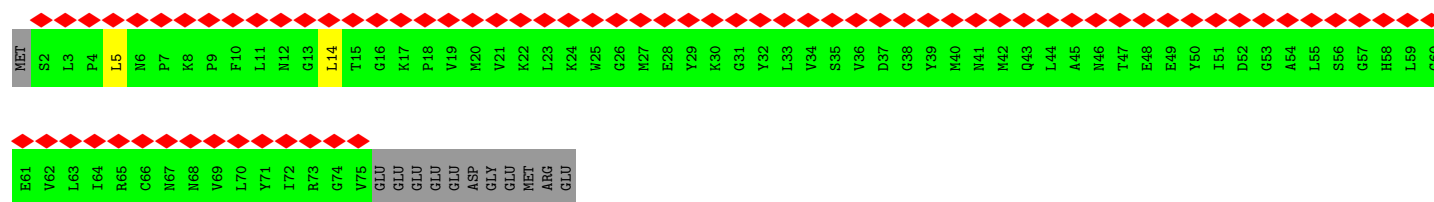
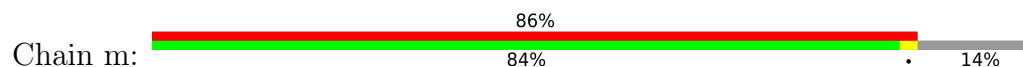
• Molecule 9: Small nuclear ribonucleoprotein Sm D2



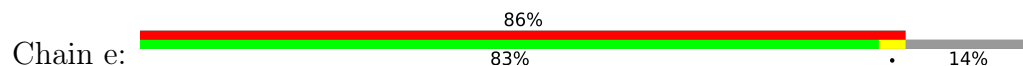
• Molecule 10: Small nuclear ribonucleoprotein F



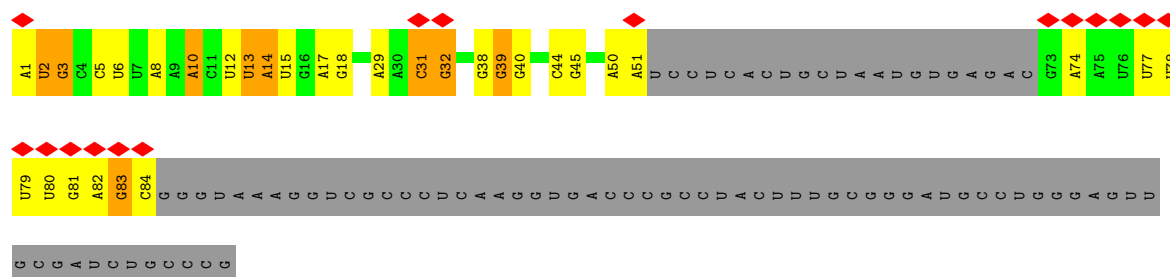
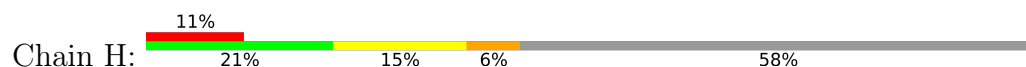
• Molecule 10: Small nuclear ribonucleoprotein F



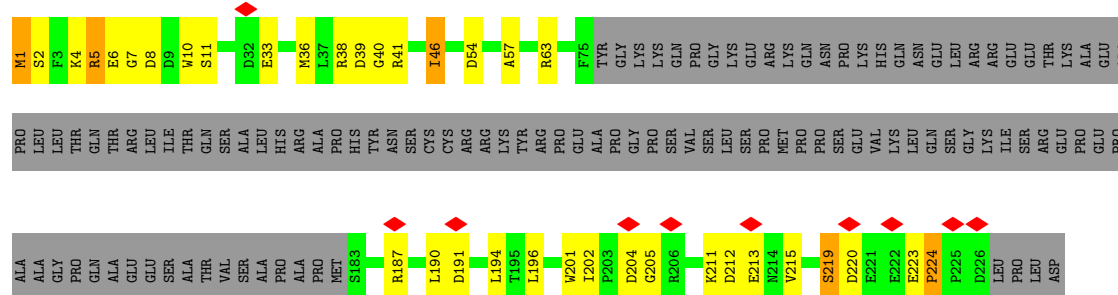
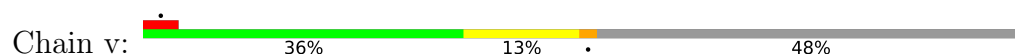
• Molecule 11: Small nuclear ribonucleoprotein E



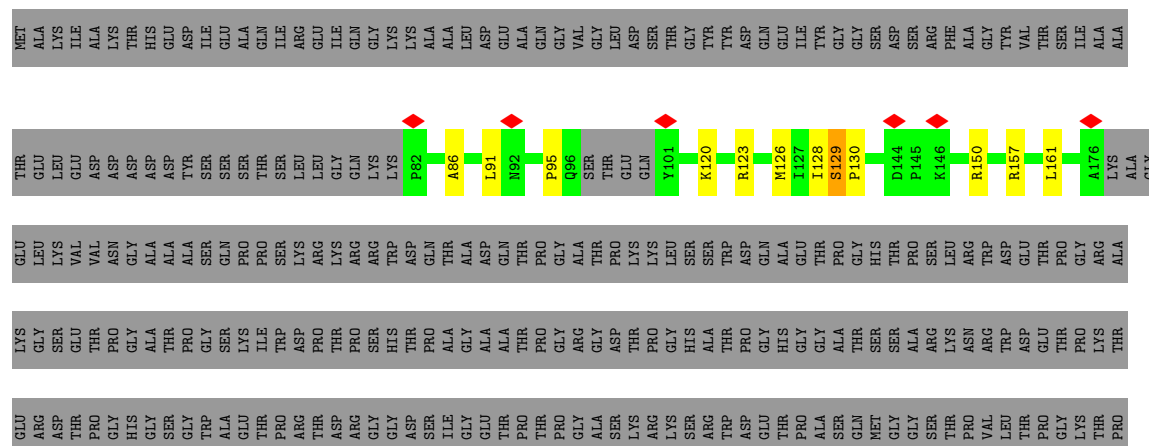
- Molecule 15: U12 snRNA

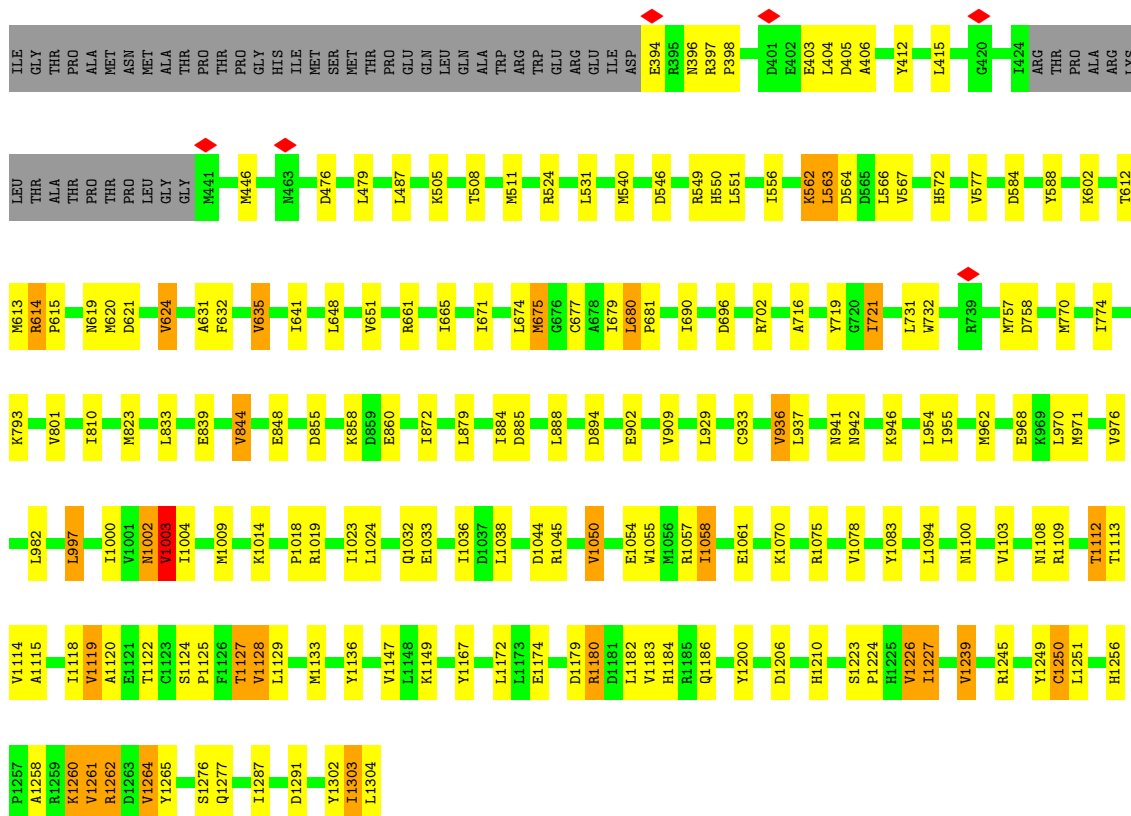


- Molecule 16: Sodium channel modifier 1

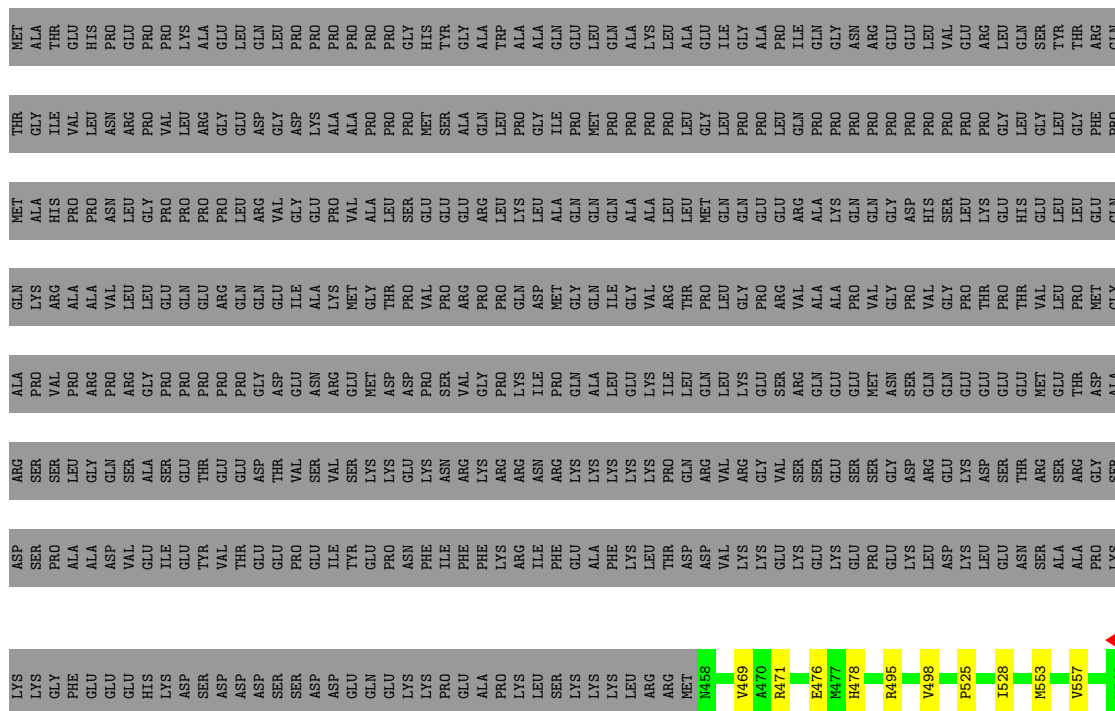


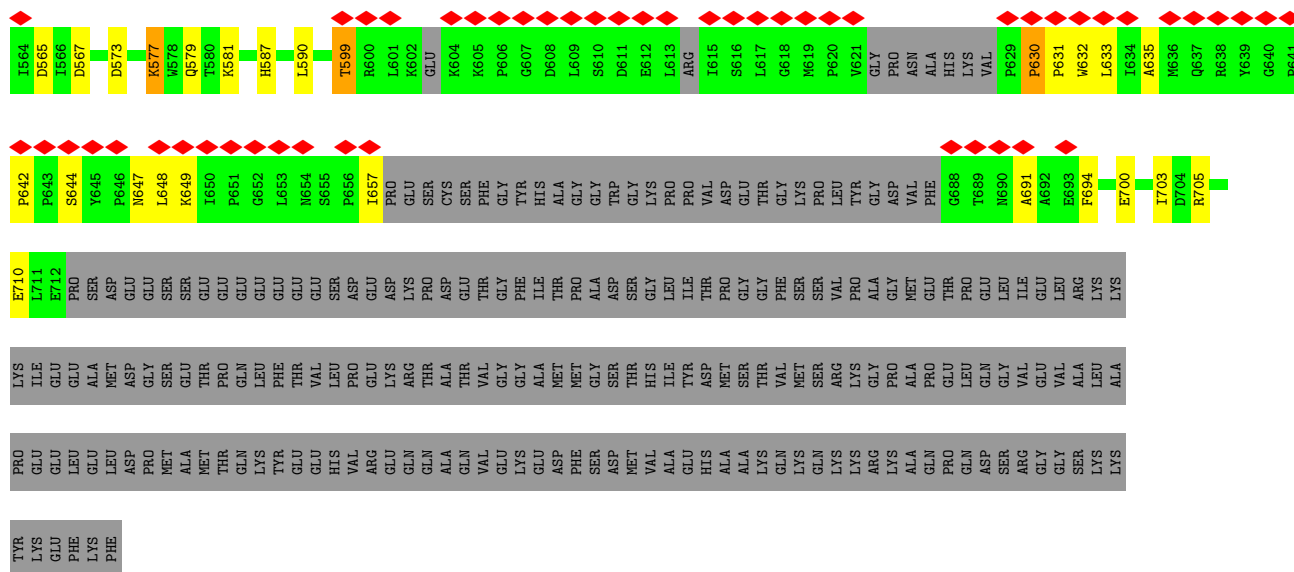
- Molecule 17: Splicing factor 3B subunit 1



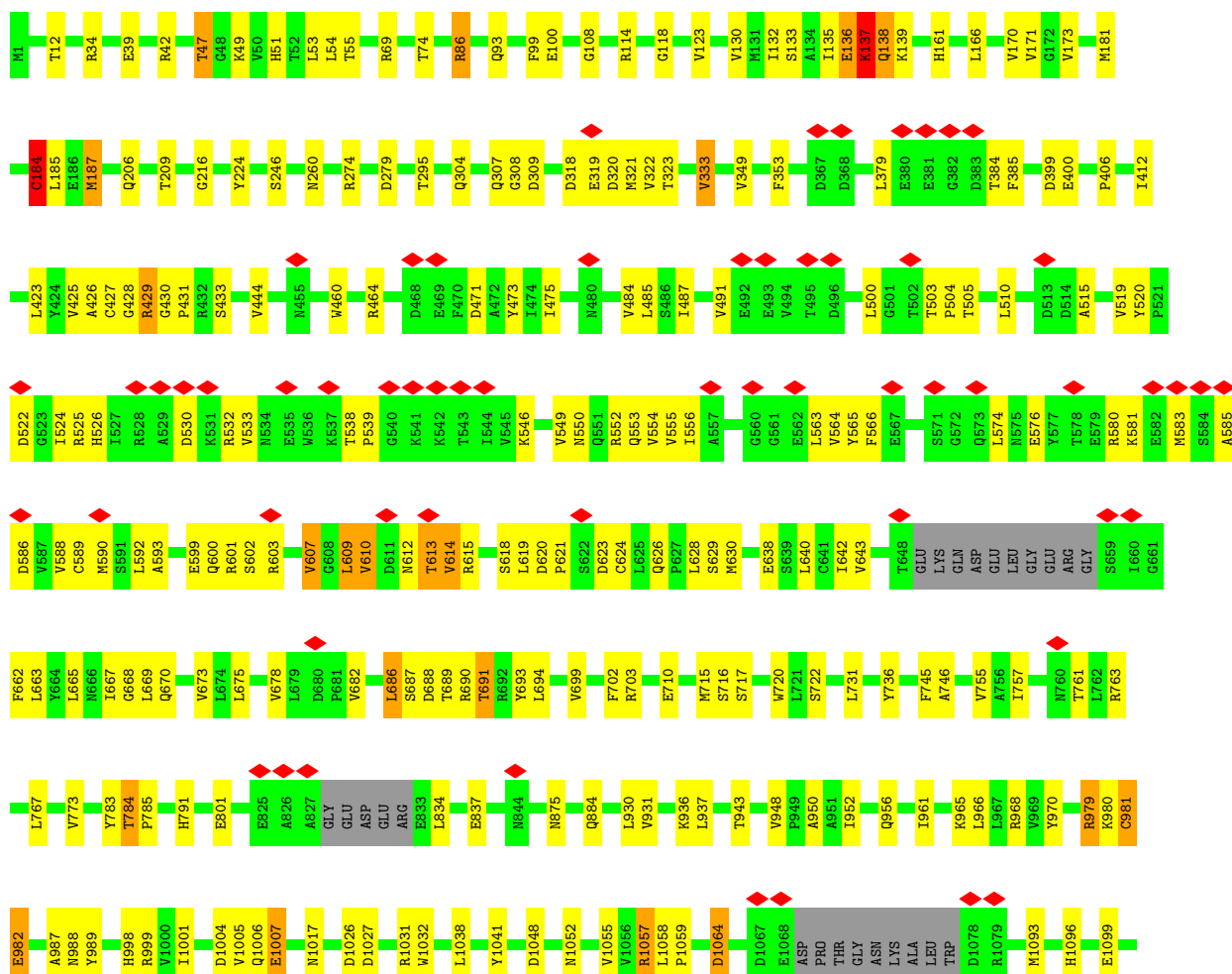
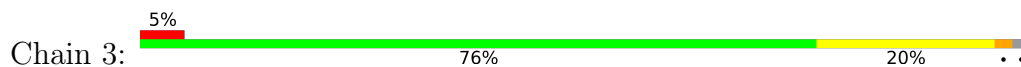


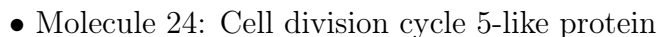
- Molecule 18: Splicing factor 3B subunit 2





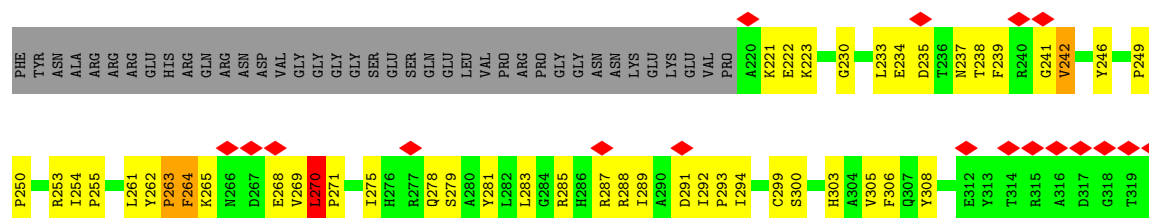
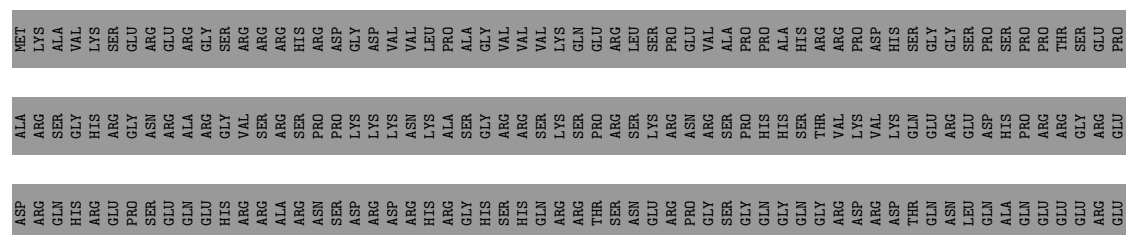
• Molecule 19: Splicing factor 3B subunit 3



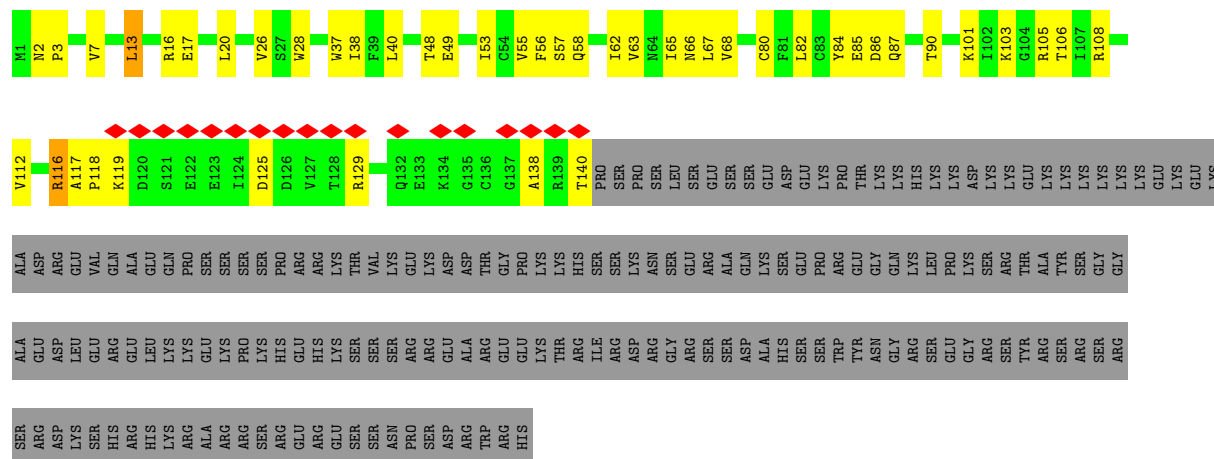
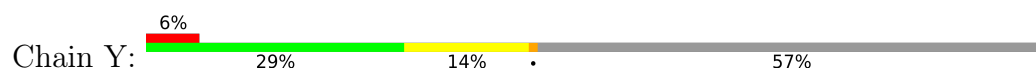


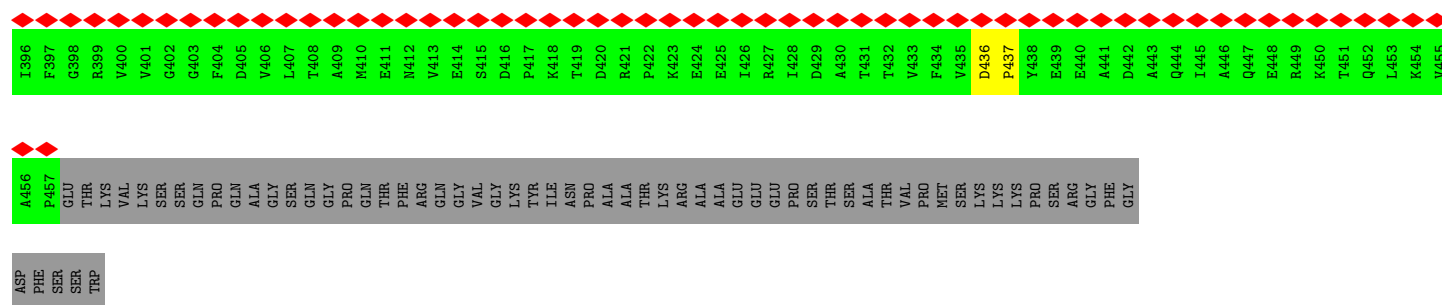


- Molecule 29: Smad nuclear-interacting protein 1

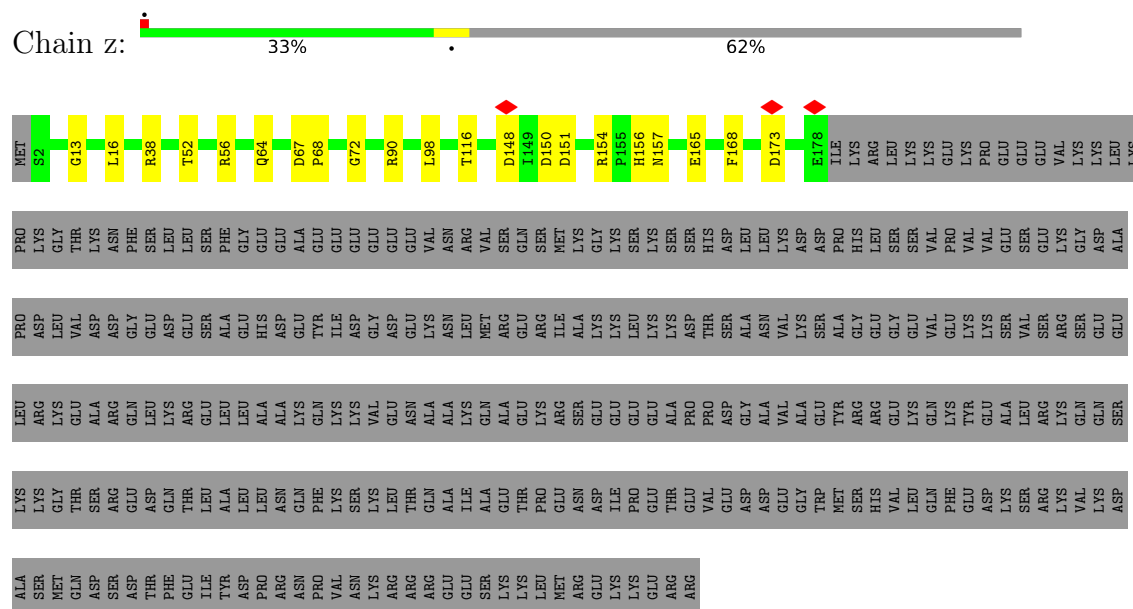


- Molecule 30: RNA-binding motif protein, X-linked 2

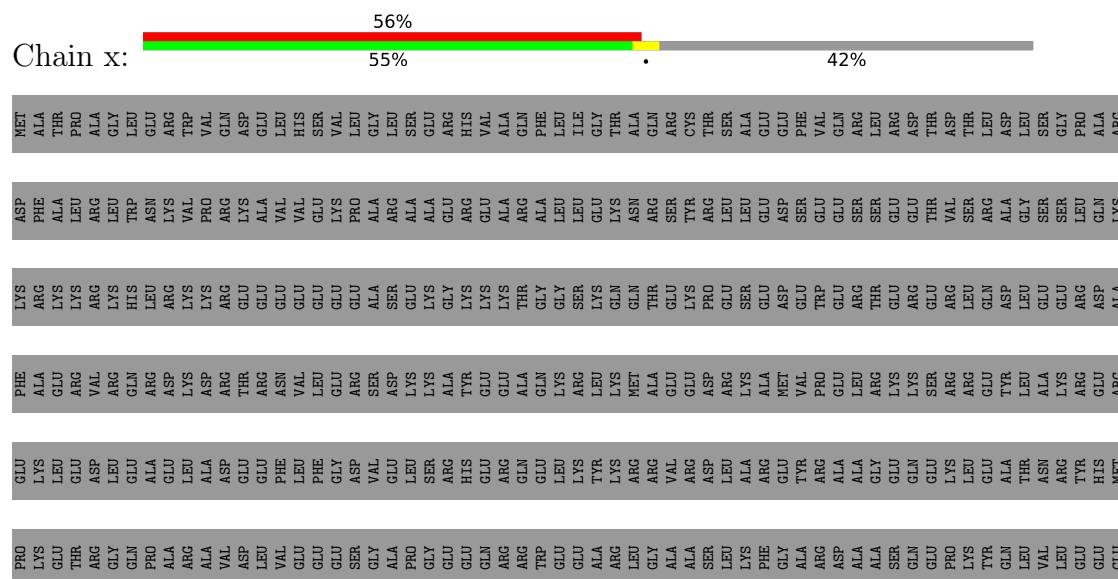


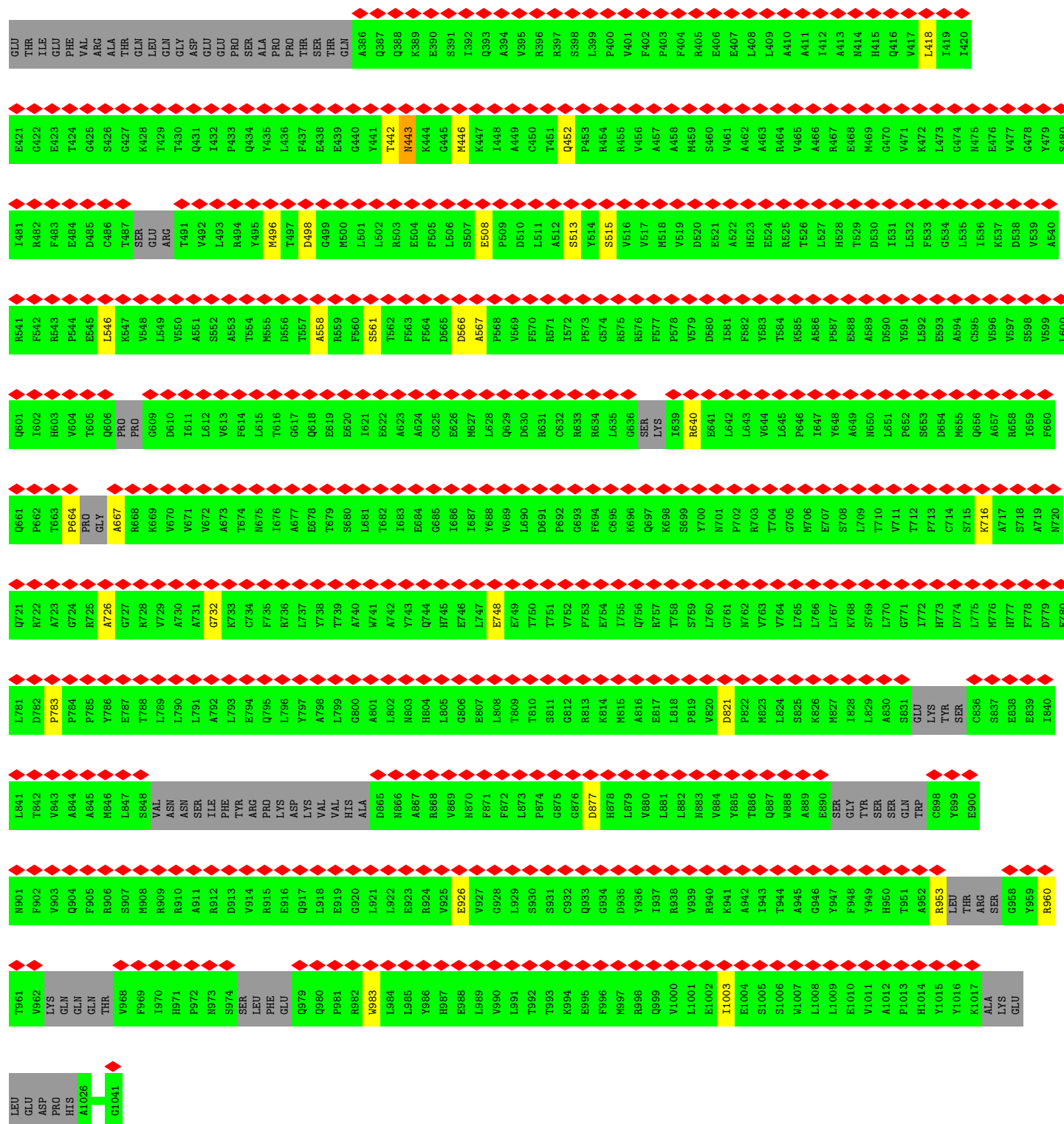


- Molecule 33: Peptidyl-prolyl cis-trans isomerase CWC27 homolog



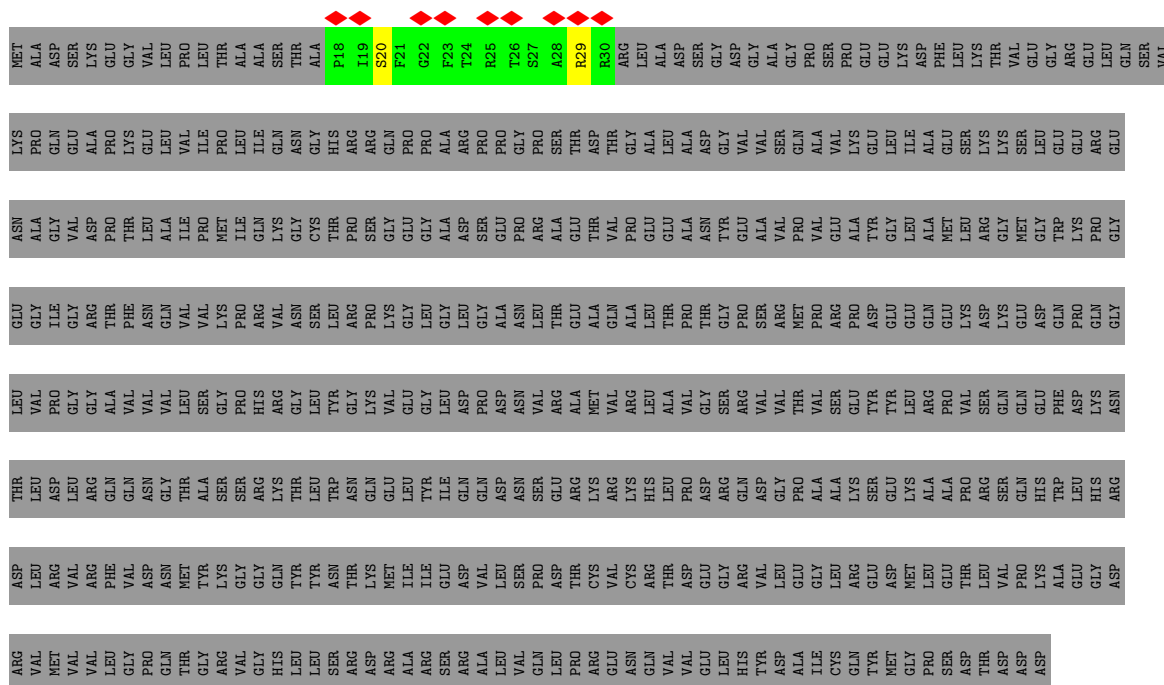
- Molecule 34: Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16



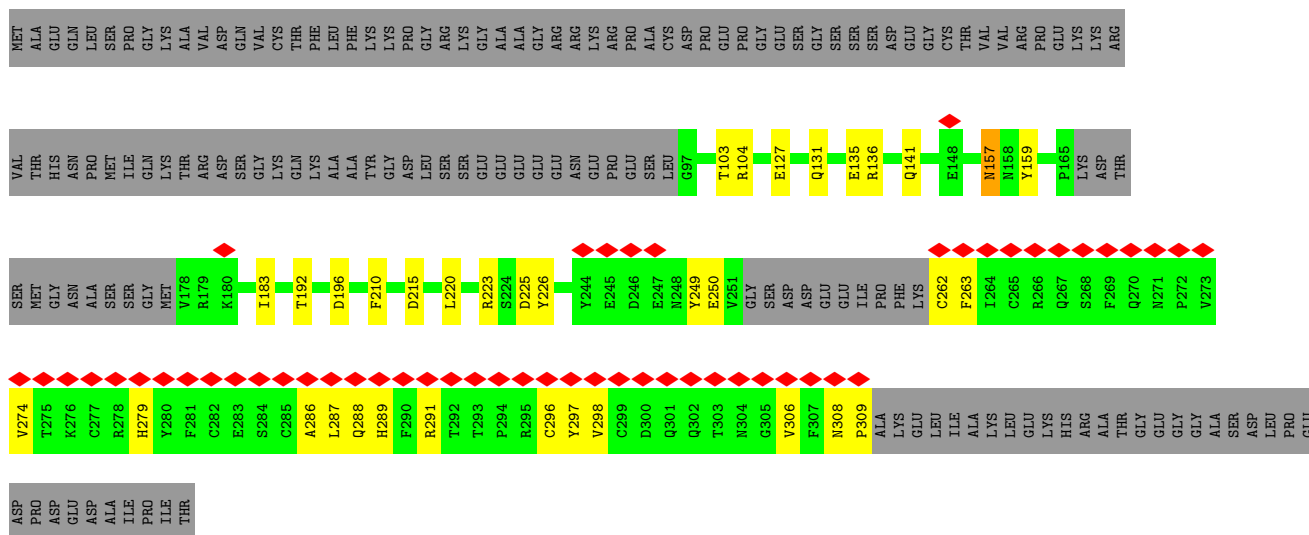


• Molecule 35: G-patch domain and KOW motifs-containing protein

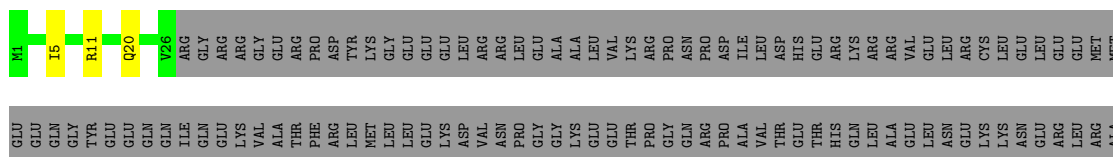
Chain y: 97%



- Molecule 36: RING finger protein 113A



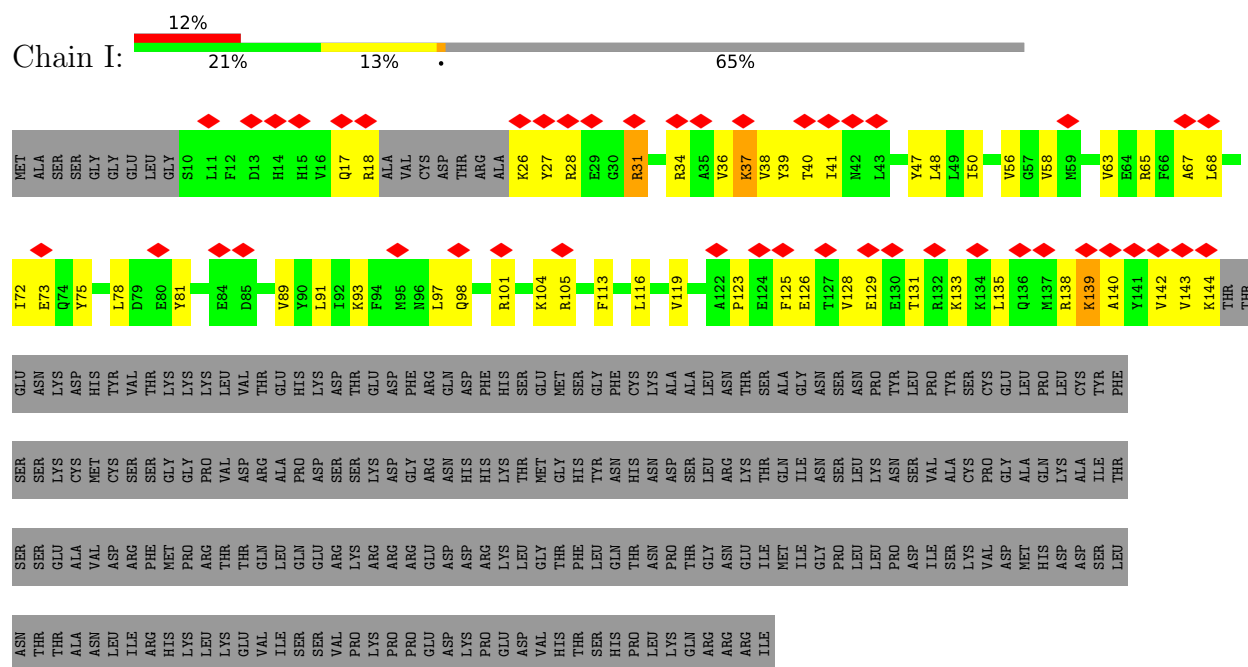
- Molecule 37: Serine/arginine repetitive matrix protein 2



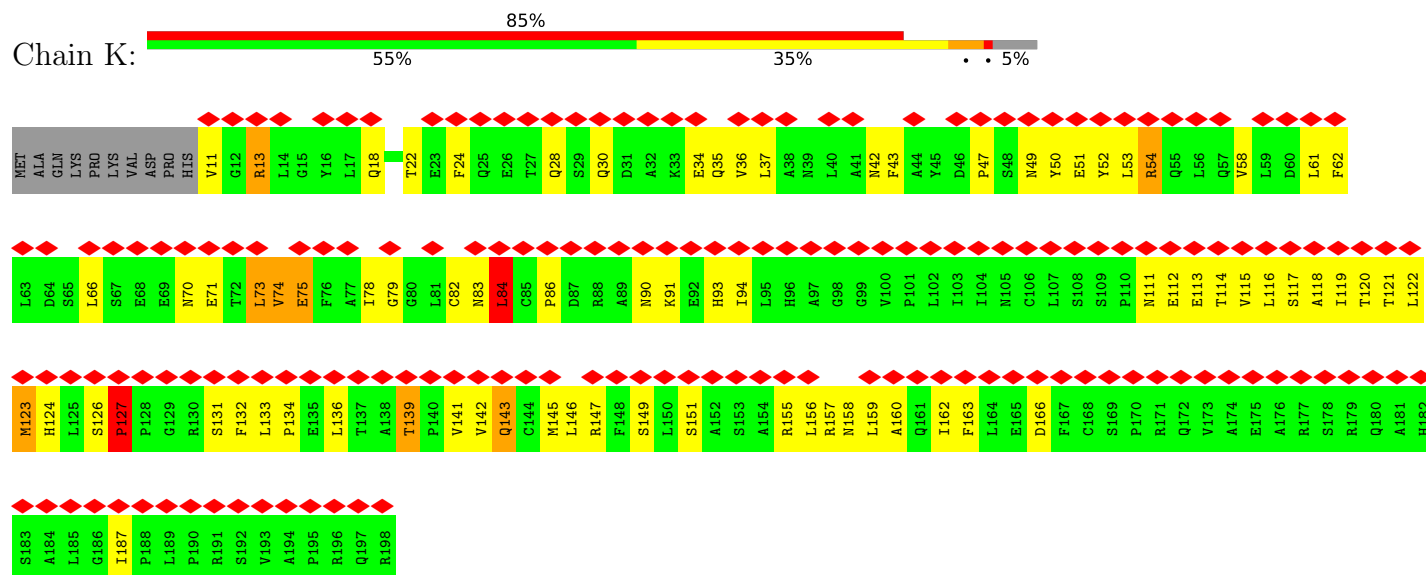








• Molecule 42: Armadillo repeat-containing protein 7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	101443	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.134	Depositor
Minimum map value	-0.056	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size ($\text{\AA}$)	644.52, 644.52, 644.52	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0742, 1.0742, 1.0742	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: IHP, K, GTP, SEP, TPO, MG, G5J, ZN

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	1.19	3/18863 (0.0%)	0.89	21/25599 (0.1%)
2	B	0.29	0/2115	0.37	0/3284
3	C	0.99	0/7287	0.86	8/9902 (0.1%)
4	D	0.53	0/9225	1.11	37/12826 (0.3%)
5	E	0.81	0/2390	1.00	8/3238 (0.2%)
6	a	0.71	0/397	0.93	0/549
6	h	0.78	0/390	0.99	0/539
7	b	0.84	0/404	1.12	2/561 (0.4%)
7	i	0.84	0/421	1.15	3/583 (0.5%)
8	c	0.88	0/405	1.12	0/563
8	j	0.87	0/405	1.11	0/563
9	d	1.09	0/479	1.22	1/666 (0.2%)
9	k	1.11	0/420	1.20	1/583 (0.2%)
10	f	1.20	0/360	1.25	0/497
10	m	1.21	1/360 (0.3%)	1.24	0/497
11	e	1.03	0/390	1.24	1/542 (0.2%)
11	l	1.02	0/390	1.24	0/542
12	g	0.86	0/362	1.08	1/501 (0.2%)
12	n	0.85	0/332	1.09	1/458 (0.2%)
13	F	0.26	0/1449	0.26	0/2257
14	G	0.26	0/1445	0.42	1/2238 (0.0%)
15	H	0.32	0/1511	0.36	0/2351
16	v	0.95	0/984	0.76	3/1326 (0.2%)
17	1	1.13	0/8025	0.87	10/10859 (0.1%)
18	2	0.98	0/1710	0.88	5/2306 (0.2%)
19	3	1.00	1/9531 (0.0%)	0.81	10/12931 (0.1%)
20	4	0.94	0/382	1.12	0/529
21	5	0.77	0/925	0.79	0/1247
22	6	1.09	0/825	1.01	4/1106 (0.4%)
23	7	1.27	0/688	0.92	2/930 (0.2%)
24	L	1.22	0/864	0.85	1/1165 (0.1%)
25	J	0.29	0/3494	0.64	4/4743 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	P	1.07	0/391	0.76	0/517
27	R	0.76	1/1954 (0.1%)	0.70	5/2622 (0.2%)
28	T	1.25	0/2574	0.95	2/3511 (0.1%)
29	X	0.25	0/1304	0.66	3/1760 (0.2%)
30	Y	1.05	0/1113	0.80	0/1501
31	Z	1.01	0/1153	0.80	0/1548
32	9	0.59	0/2732	0.80	4/3733 (0.1%)
33	z	1.05	0/1434	0.79	0/1941
34	x	0.57	1/2996 (0.0%)	0.80	10/4142 (0.2%)
35	y	0.21	0/107	0.45	0/141
36	M	0.97	0/1609	0.77	0/2164
37	U	0.92	0/196	0.80	0/265
38	V	0.92	1/3042 (0.0%)	0.95	0/4152
39	8	0.92	0/1028	0.85	0/1379
40	0	1.00	0/782	0.78	0/1043
41	I	0.33	0/1083	0.53	0/1454
42	K	0.34	0/1333	0.85	6/1826 (0.3%)
All	All	0.93	8/102059 (0.0%)	0.87	154/140180 (0.1%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	515	TYR	CA-C	-7.21	1.41	1.52
1	A	797	ASP	CA-C	-6.95	1.41	1.52
34	x	926	GLU	CA-CB	-5.71	1.45	1.53
38	V	562	TRP	CA-C	-5.43	1.45	1.52
1	A	333	HIS	C-N	-5.34	1.25	1.33

The worst 5 of 154 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	102	TYR	N-CA-C	9.87	122.12	111.36
22	6	60	ILE	N-CA-C	8.66	119.46	110.62
27	R	405	VAL	N-CA-C	8.64	120.62	109.30
27	R	412	PHE	N-CA-C	8.31	121.25	110.53
18	2	642	PRO	CA-C-N	8.25	128.21	119.05

There are no chirality outliers.

There are no planarity outliers.

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	A	18354	0	18179	405	0
2	B	1898	0	963	37	0
3	C	7125	0	7130	127	0
4	D	9215	0	4458	175	0
5	E	2337	0	2272	198	0
6	a	399	0	173	1	0
6	h	392	0	168	0	0
7	b	405	0	170	0	0
7	i	422	0	177	0	0
8	c	406	0	170	0	0
8	j	406	0	170	0	0
9	d	480	0	200	3	0
9	k	422	0	175	1	0
10	f	361	0	158	2	0
10	m	361	0	158	1	0
11	e	391	0	163	2	0
11	l	391	0	163	2	0
12	g	363	0	160	1	0
12	n	334	0	143	1	0
13	F	1294	0	650	44	0
14	G	1303	0	667	47	0
15	H	1350	0	679	31	0
16	v	963	0	945	56	0
17	1	7879	0	8044	173	0
18	2	1674	0	1580	43	0
19	3	9352	0	9273	230	0
20	4	383	0	173	24	0
21	5	906	0	913	32	0
22	6	811	0	788	21	0
23	7	669	0	631	7	0
24	L	843	0	852	17	0
25	J	3457	0	2537	161	0
26	P	384	0	382	11	0
27	R	1923	0	1889	124	0
28	T	2507	0	2451	40	0
29	X	1271	0	1252	93	0
30	Y	1095	0	1083	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	Z	1129	0	1077	23	0
32	9	2691	0	2121	93	0
33	z	1400	0	1344	13	0
34	x	3007	0	1453	18	0
35	y	105	0	107	2	0
36	M	1572	0	1483	40	0
37	U	193	0	196	3	0
38	V	3008	0	2291	18	0
39	8	1011	0	1035	20	0
40	0	770	0	778	28	0
41	I	1062	0	1067	67	0
42	K	1314	0	1177	99	0
43	A	36	0	6	0	0
44	C	32	0	12	3	0
45	C	1	0	0	0	0
45	F	4	0	0	0	0
46	F	2	0	0	0	0
47	F	33	0	0	3	0
48	0	2	0	0	0	0
48	6	3	0	0	0	0
48	M	1	0	0	0	0
48	v	1	0	0	0	0
49	C	3	0	0	0	0
All	All	99906	0	84286	2250	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 12.

The worst 5 of 2250 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1:641:ILE:HD11	17:1:675:MET:CE	1.58	1.34
20:4:14:THR:HA	20:4:59:VAL:O	1.32	1.30
5:E:62:LEU:HD12	5:E:351:LEU:CD1	1.66	1.26
25:J:337:MET:HE3	25:J:346:TRP:CH2	1.70	1.25
5:E:62:LEU:CD1	5:E:351:LEU:HD12	1.68	1.23

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	2213/2335 (95%)	2146 (97%)	66 (3%)	1 (0%)	100	100
3	C	900/972 (93%)	862 (96%)	38 (4%)	0	100	100
4	D	1799/2136 (84%)	1710 (95%)	84 (5%)	5 (0%)	36	65
5	E	297/357 (83%)	278 (94%)	19 (6%)	0	100	100
6	a	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
6	h	76/126 (60%)	74 (97%)	2 (3%)	0	100	100
7	b	80/240 (33%)	78 (98%)	2 (2%)	0	100	100
7	i	84/240 (35%)	82 (98%)	2 (2%)	0	100	100
8	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
8	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
9	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
9	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
10	f	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
10	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
11	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
11	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
12	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
12	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
16	v	115/230 (50%)	113 (98%)	2 (2%)	0	100	100
17	1	977/1304 (75%)	961 (98%)	16 (2%)	0	100	100
18	2	206/895 (23%)	198 (96%)	8 (4%)	0	100	100
19	3	1184/1217 (97%)	1136 (96%)	48 (4%)	0	100	100
20	4	76/424 (18%)	71 (93%)	5 (7%)	0	100	100
21	5	107/125 (86%)	104 (97%)	3 (3%)	0	100	100
22	6	103/110 (94%)	98 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	7	79/86 (92%)	78 (99%)	1 (1%)	0	100	100
24	L	99/802 (12%)	93 (94%)	6 (6%)	0	100	100
25	J	483/848 (57%)	447 (92%)	36 (8%)	0	100	100
26	P	42/229 (18%)	37 (88%)	5 (12%)	0	100	100
27	R	229/536 (43%)	219 (96%)	10 (4%)	0	100	100
28	T	318/514 (62%)	310 (98%)	8 (2%)	0	100	100
29	X	154/396 (39%)	137 (89%)	16 (10%)	1 (1%)	21	51
30	Y	138/322 (43%)	135 (98%)	3 (2%)	0	100	100
31	Z	138/619 (22%)	137 (99%)	1 (1%)	0	100	100
32	9	401/520 (77%)	382 (95%)	18 (4%)	1 (0%)	43	72
33	z	175/472 (37%)	169 (97%)	6 (3%)	0	100	100
34	x	575/1041 (55%)	554 (96%)	21 (4%)	0	100	100
35	y	11/476 (2%)	11 (100%)	0	0	100	100
36	M	185/343 (54%)	172 (93%)	13 (7%)	0	100	100
37	U	24/2752 (1%)	24 (100%)	0	0	100	100
38	V	464/908 (51%)	457 (98%)	7 (2%)	0	100	100
39	8	124/904 (14%)	124 (100%)	0	0	100	100
40	0	98/101 (97%)	98 (100%)	0	0	100	100
41	I	124/367 (34%)	120 (97%)	4 (3%)	0	100	100
42	K	186/198 (94%)	183 (98%)	2 (1%)	1 (0%)	24	54
All	All	13111/24253 (54%)	12617 (96%)	485 (4%)	9 (0%)	49	77

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	1584	ILE
4	D	1864	GLU
1	A	1092	ILE
29	X	263	PRO
42	K	127	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	
1	A	1979/2108 (94%)	1915 (97%)	64 (3%)	34	68
3	C	798/866 (92%)	781 (98%)	17 (2%)	47	77
4	D	76/1908 (4%)	56 (74%)	20 (26%)	0	2
5	E	255/300 (85%)	243 (95%)	12 (5%)	23	56
16	v	104/199 (52%)	100 (96%)	4 (4%)	29	64
17	1	854/1103 (77%)	809 (95%)	45 (5%)	20	52
18	2	163/776 (21%)	157 (96%)	6 (4%)	30	64
19	3	1031/1050 (98%)	997 (97%)	34 (3%)	33	67
21	5	97/109 (89%)	96 (99%)	1 (1%)	68	89
22	6	90/95 (95%)	88 (98%)	2 (2%)	45	77
23	7	72/77 (94%)	72 (100%)	0	100	100
24	L	87/709 (12%)	85 (98%)	2 (2%)	44	76
25	J	203/751 (27%)	194 (96%)	9 (4%)	25	59
26	P	42/203 (21%)	42 (100%)	0	100	100
27	R	206/459 (45%)	196 (95%)	10 (5%)	22	54
28	T	273/441 (62%)	268 (98%)	5 (2%)	51	80
29	X	134/349 (38%)	128 (96%)	6 (4%)	24	58
30	Y	117/291 (40%)	113 (97%)	4 (3%)	32	66
31	Z	110/545 (20%)	110 (100%)	0	100	100
32	9	195/456 (43%)	190 (97%)	5 (3%)	40	73
33	z	152/416 (36%)	152 (100%)	0	100	100
34	x	14/897 (2%)	14 (100%)	0	100	100
35	y	11/397 (3%)	11 (100%)	0	100	100
36	M	168/294 (57%)	165 (98%)	3 (2%)	51	80
37	U	21/2432 (1%)	20 (95%)	1 (5%)	23	55
38	V	193/838 (23%)	187 (97%)	6 (3%)	35	69
39	8	111/831 (13%)	111 (100%)	0	100	100
40	0	86/87 (99%)	82 (95%)	4 (5%)	23	56
41	I	112/326 (34%)	108 (96%)	4 (4%)	31	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
42	K	119/171 (70%)	102 (86%)	17 (14%)	3 11
All	All	7873/19484 (40%)	7592 (96%)	281 (4%)	32 65

5 of 281 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	X	239	PHE
30	Y	62	ILE
41	I	31	ARG
4	D	168	ARG
4	D	157	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
33	z	39	ASN
37	U	3	ASN
42	K	18	GLN
5	E	108	HIS
5	E	101	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	F	58/124 (46%)	14 (24%)	3 (5%)
14	G	62/142 (43%)	22 (35%)	5 (8%)
15	H	61/150 (40%)	14 (22%)	0
2	B	87/117 (74%)	21 (24%)	2 (2%)
All	All	268/533 (50%)	71 (26%)	10 (3%)

5 of 71 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	20	G
2	B	21	A
2	B	22	U
2	B	24	G
2	B	25	C

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	G	213	C
14	G	217	U
14	G	219	U
13	F	31	U
13	F	51	G

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	TPO	3	613	19	8,10,11	0.91	0	10,14,16	1.77	2 (20%)
17	SEP	1	129	17	8,9,10	1.11	1 (12%)	7,12,14	1.51	2 (28%)

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
19	TPO	3	613	19	-	1/9/11/13	-
17	SEP	1	129	17	-	5/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	1	129	SEP	P-O1P	2.22	1.57	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	3	613	TPO	P-OG1-CB	-4.97	109.83	123.33
19	3	613	TPO	O-C-CA	-2.26	118.95	124.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	1	129	SEP	O3P-P-OG	2.24	112.52	106.67
17	1	129	SEP	OG-CB-CA	2.09	110.18	108.14

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	1	129	SEP	N-CA-CB-OG
17	1	129	SEP	C-CA-CB-OG
17	1	129	SEP	CB-OG-P-O1P
17	1	129	SEP	CB-OG-P-O2P
17	1	129	SEP	CB-OG-P-O3P

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	3	613	TPO	1	0
17	1	129	SEP	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 14 are monoatomic - leaving 3 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$
43	IHP	A	3000	-	36,36,36	1.16	3 (8%)	60,60,60	1.14	4 (6%)
47	G5J	F	207	13	35,35,35	1.45	4 (11%)	44,55,55	0.94	2 (4%)
44	GTP	C	1500	45	33,34,34	2.08	12 (36%)	50,54,54	1.96	12 (24%)

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
43	IHP	A	3000	-	-	1/30/54/54	0/1/1/1
47	G5J	F	207	13	-	6/25/41/41	0/3/3/3
44	GTP	C	1500	45	-	4/22/38/38	0/3/3/3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	F	207	G5J	C5-C4	5.20	1.46	1.38
44	C	1500	GTP	PB-O3A	-4.17	1.55	1.59
47	F	207	G5J	C4-N9	-3.78	1.33	1.37
44	C	1500	GTP	C5-N7	-3.57	1.31	1.39
44	C	1500	GTP	PA-O3A	-3.55	1.55	1.59

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C	1500	GTP	C5-C4-N3	-5.45	119.71	128.39
44	C	1500	GTP	C2-N3-C4	4.78	120.53	112.30
44	C	1500	GTP	C2-N1-C6	-4.36	117.20	125.11
43	A	3000	IHP	C5-C6-C1	-3.74	102.23	110.43
44	C	1500	GTP	O2B-PB-O3B	3.54	116.83	107.27

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
44	C	1500	GTP	O4'-C4'-C5'-O5'
47	F	207	G5J	C5'-O5'-PA-O3A
47	F	207	G5J	O4'-C4'-C5'-O5'
44	C	1500	GTP	C3'-C4'-C5'-O5'
47	F	207	G5J	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 6 short contacts:

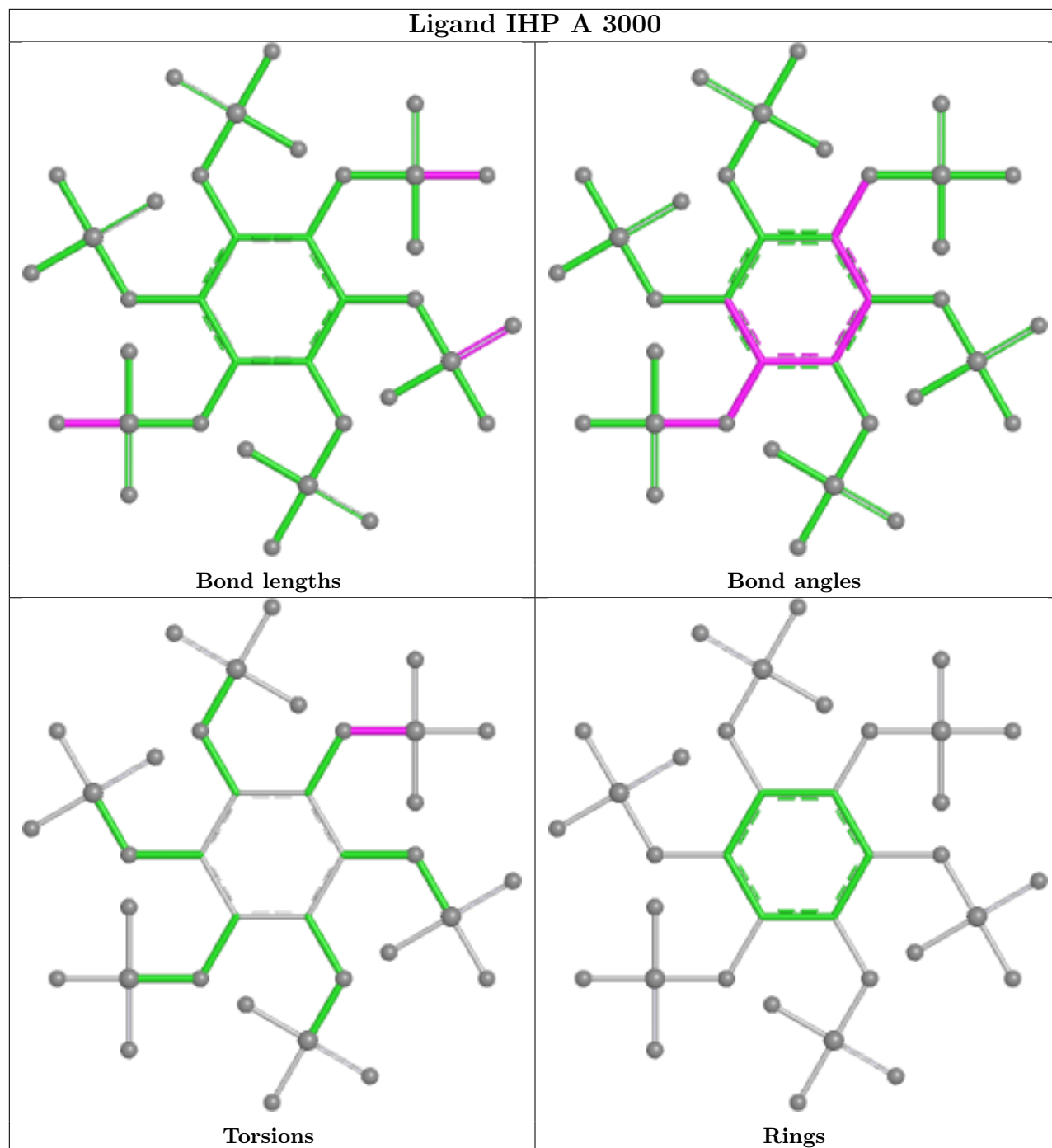
Mol	Chain	Res	Type	Clashes	Symm-Clashes
47	F	207	G5J	3	0

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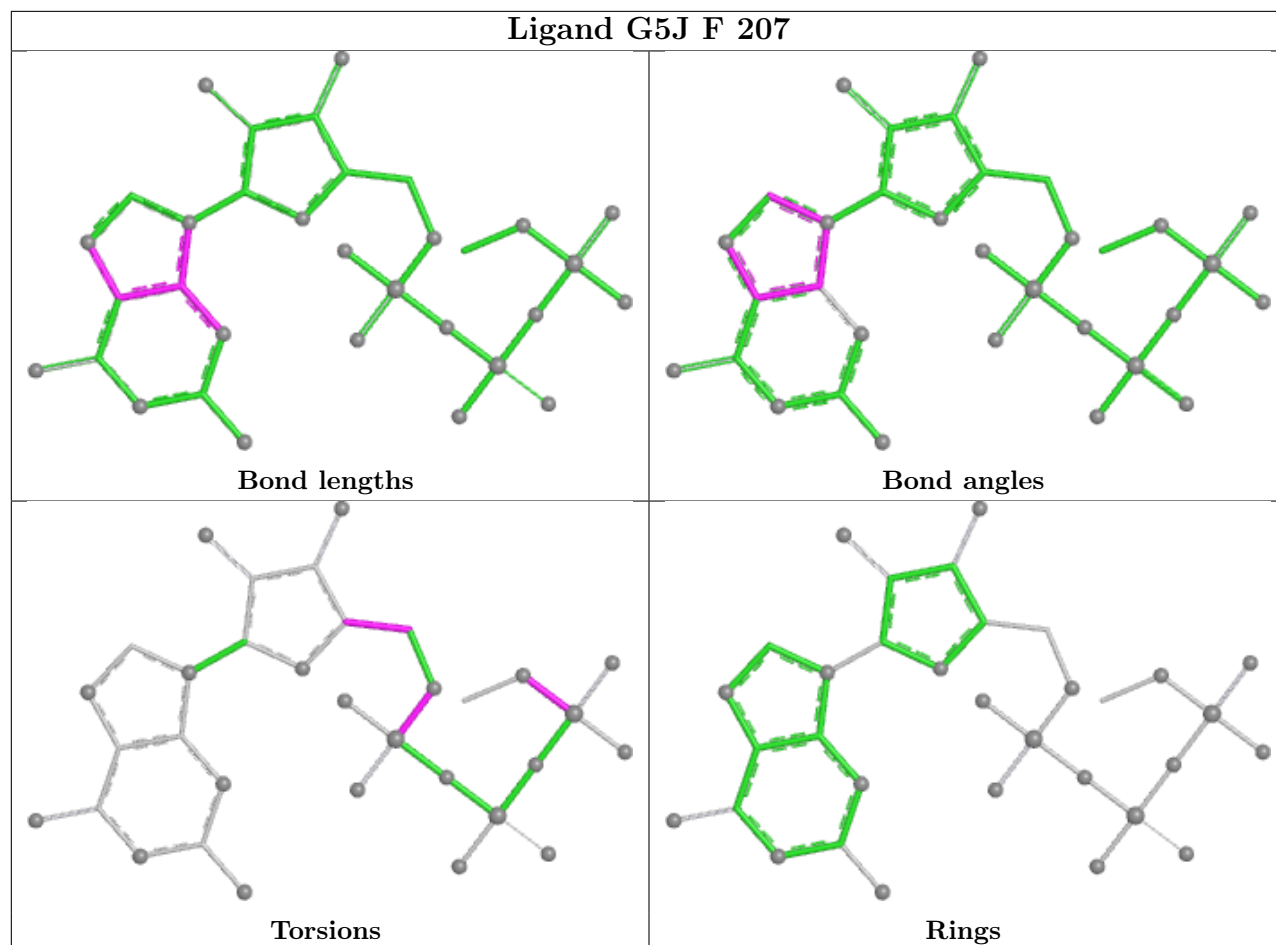
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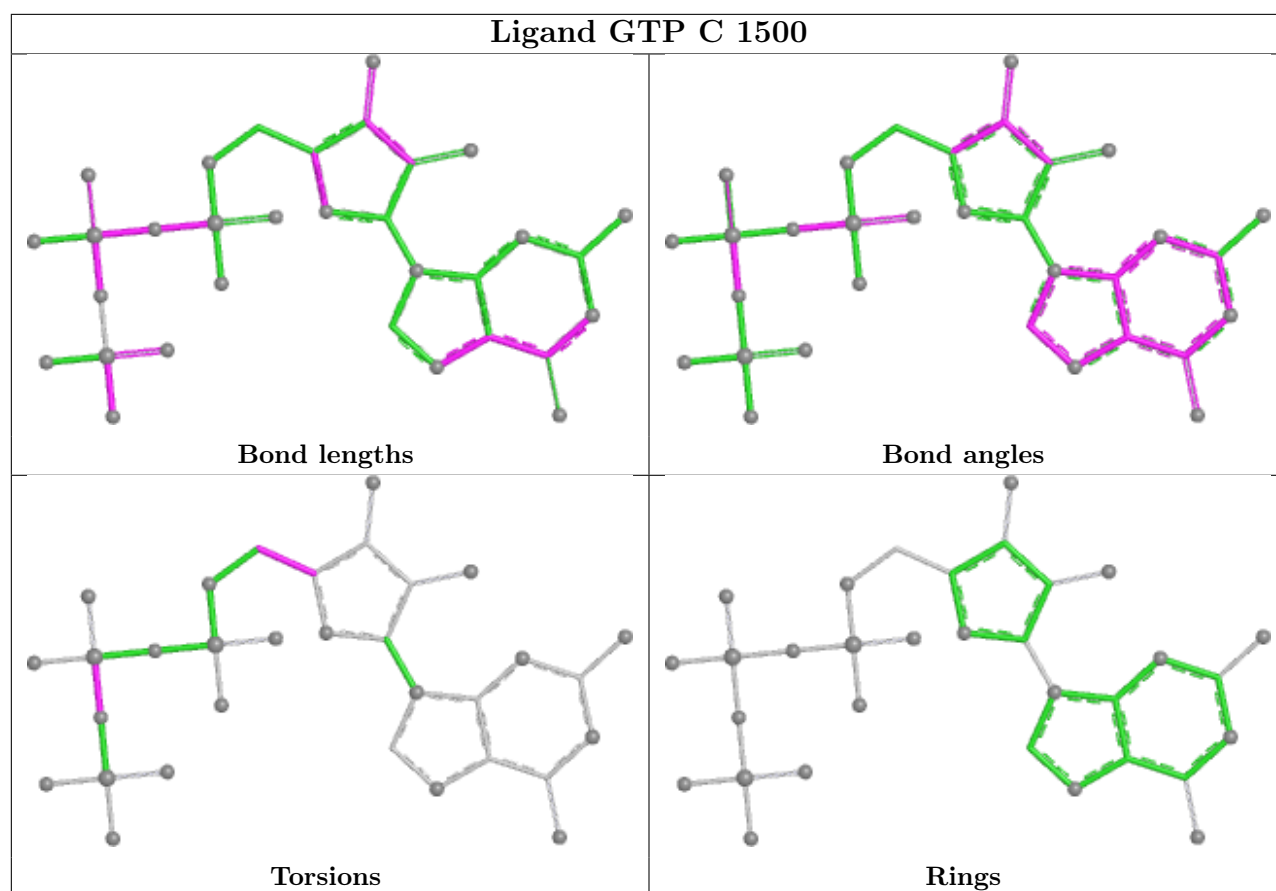
Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	C	1500	GTP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



Ligand G5J F 207





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.

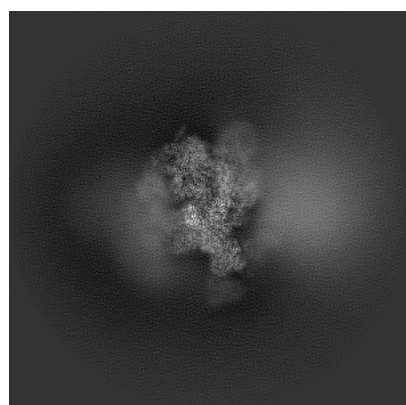
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30875. These allow visual inspection of the internal detail of the map and identification of artifacts.

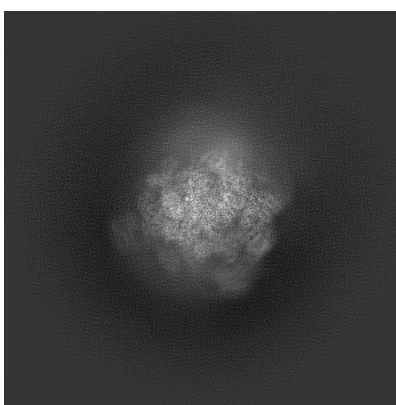
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

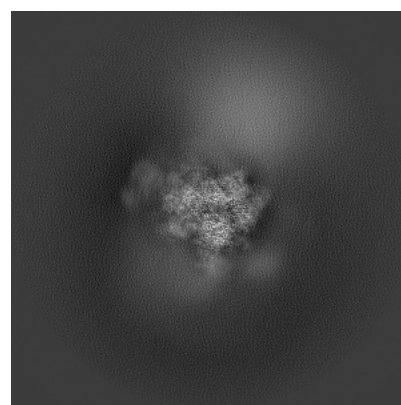
6.1.1 Primary map



X



Y

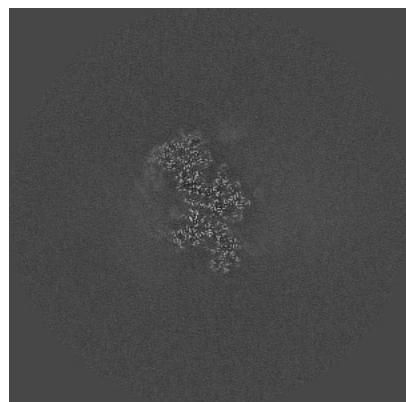


Z

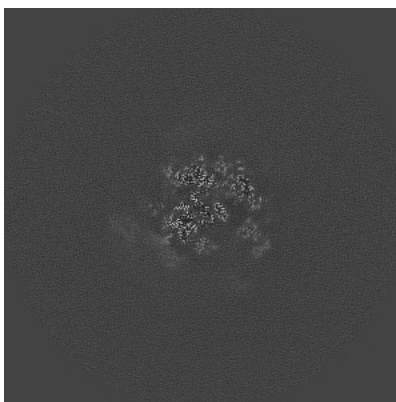
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

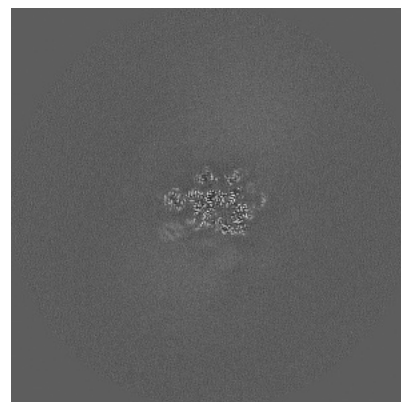
6.2.1 Primary map



X Index: 300



Y Index: 300

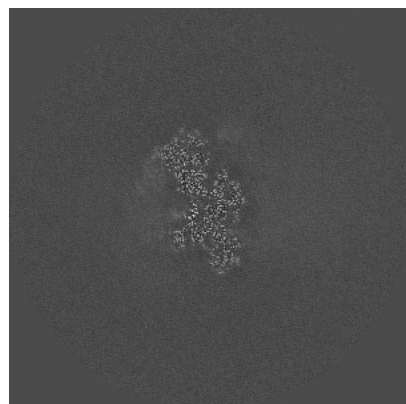


Z Index: 300

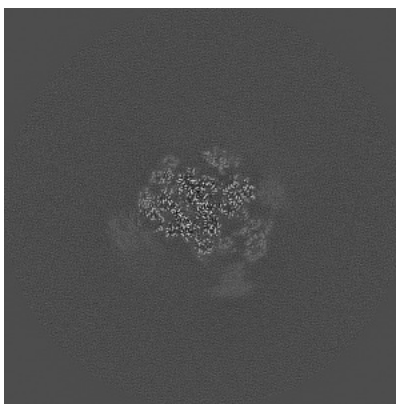
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 304



Y Index: 316

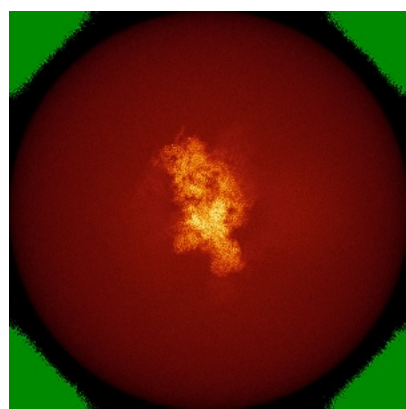


Z Index: 284

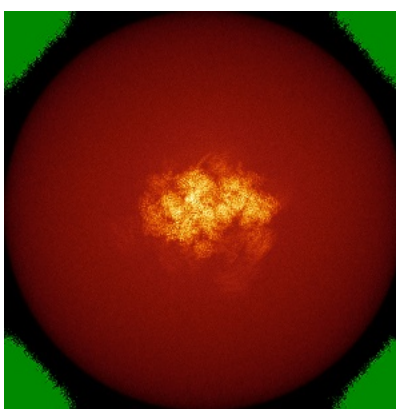
The images above show the largest variance slices of the map in three orthogonal directions.

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

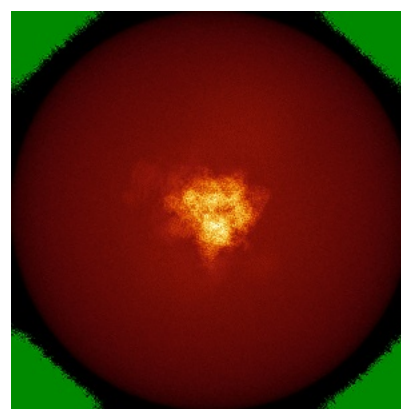
6.4.1 Primary map



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

This section was not generated.

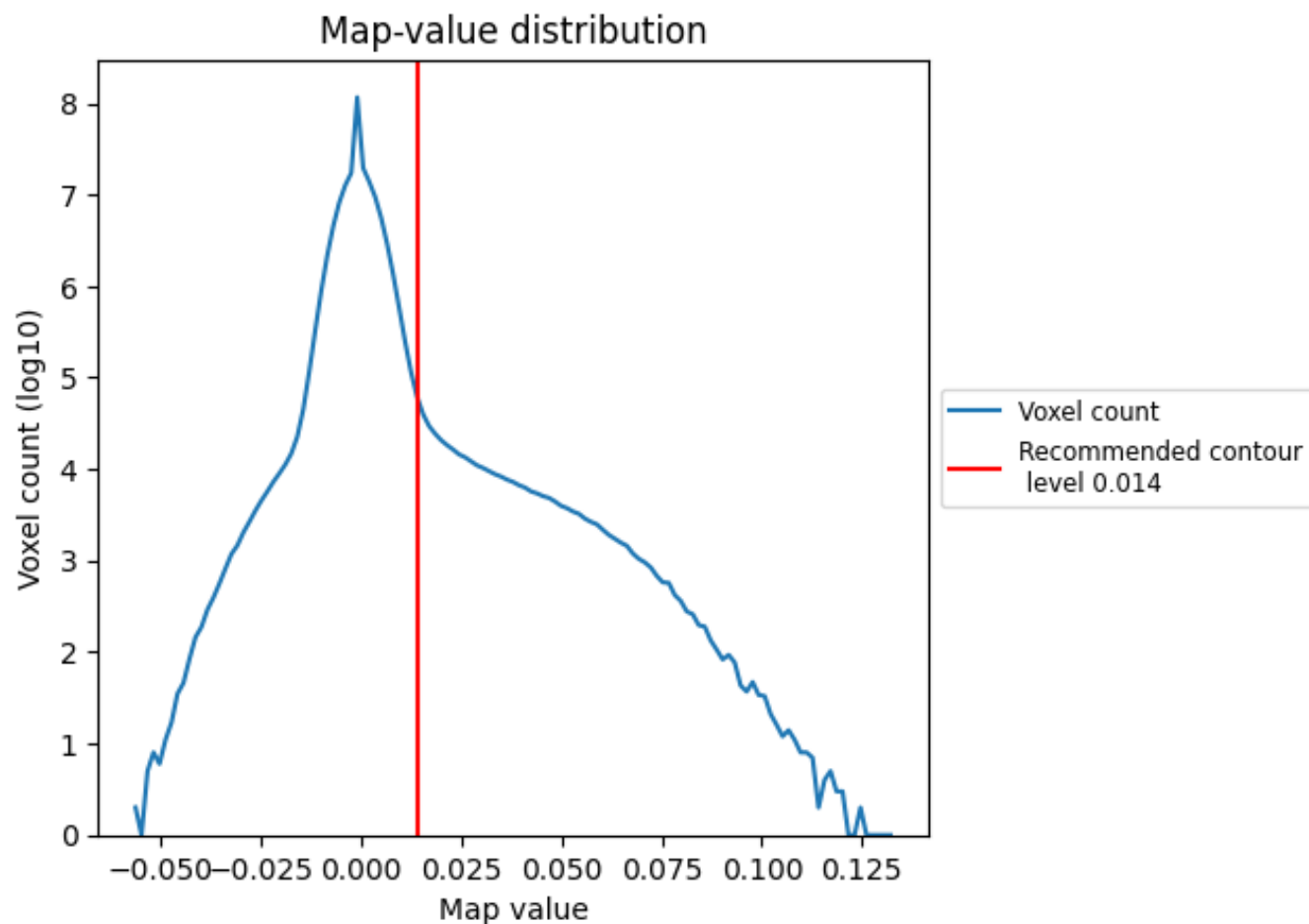
6.6 Mask visualisation

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

7 Map analysis [i](#)

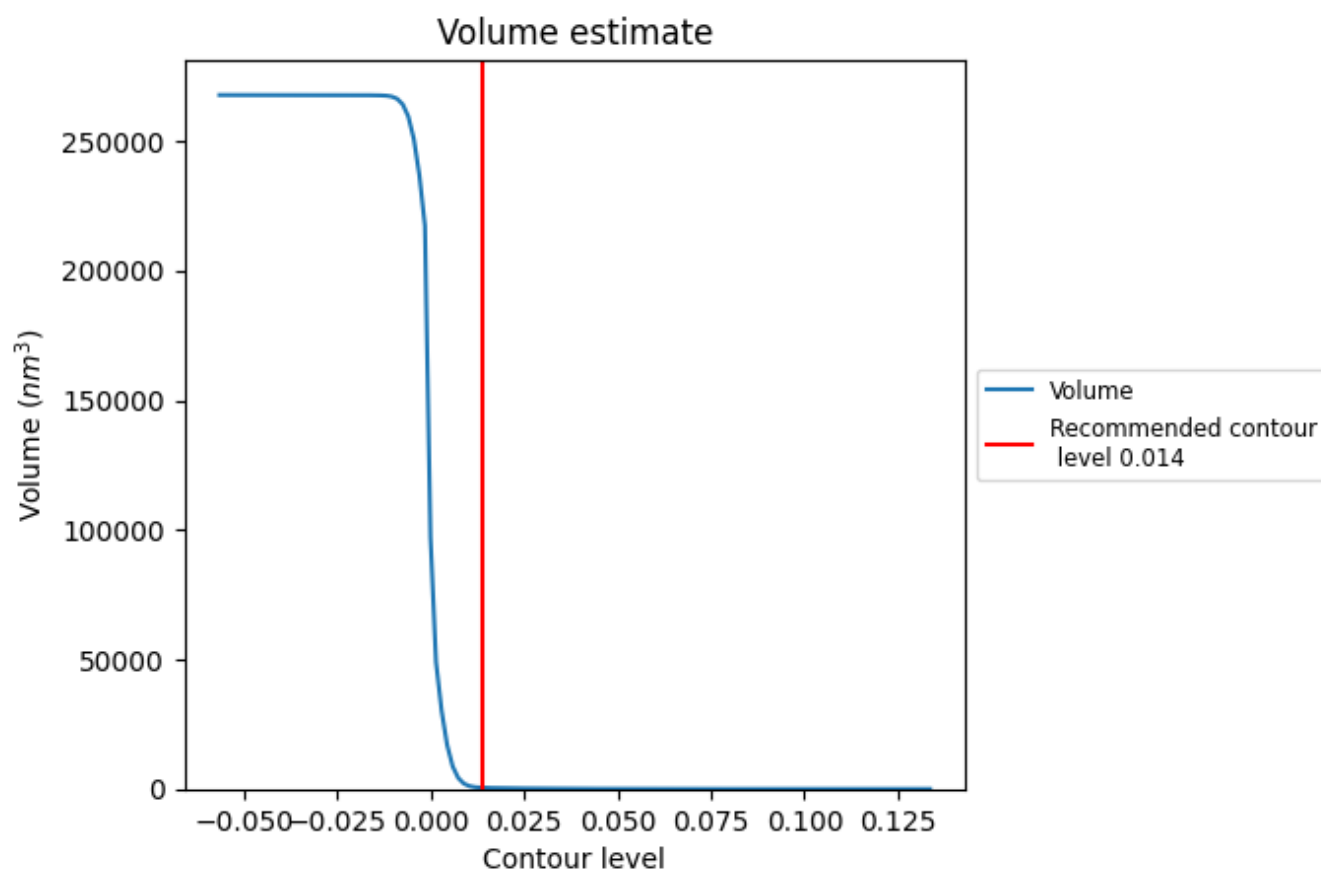
This section contains the results of statistical analysis of the map.

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.

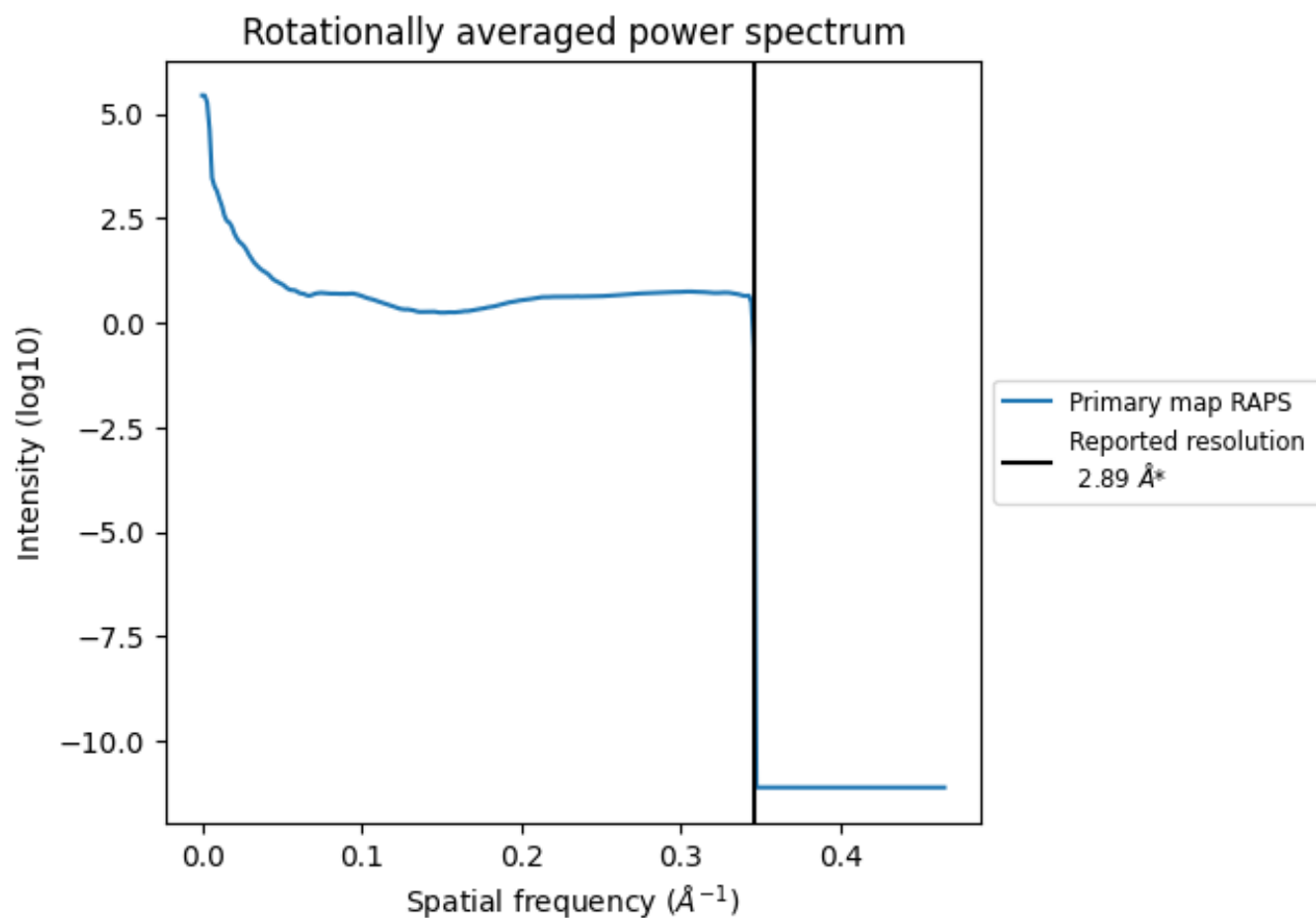
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 486 nm^3 ; this corresponds to an approximate mass of 439 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

8 Fourier-Shell correlation

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

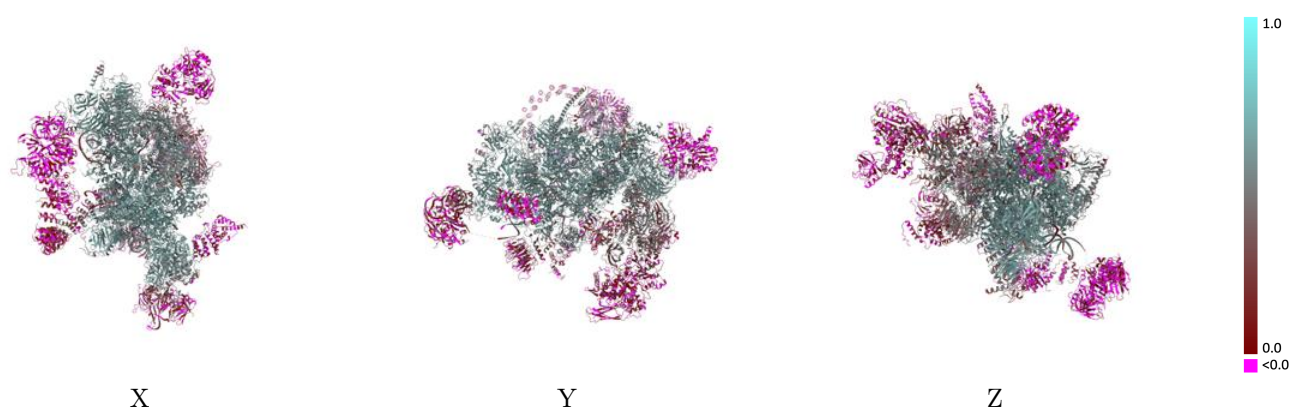
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30875 and PDB model 7DVQ. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)

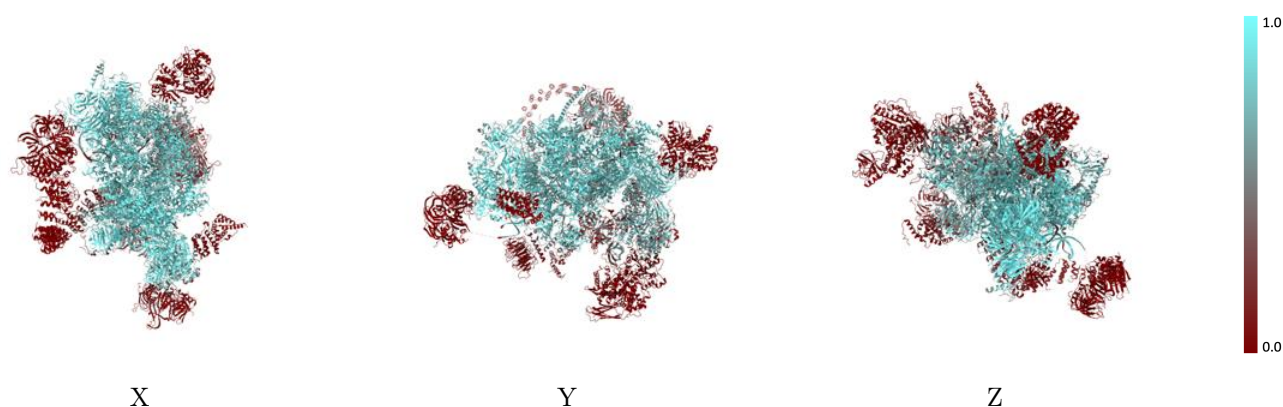
This section was not generated.

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



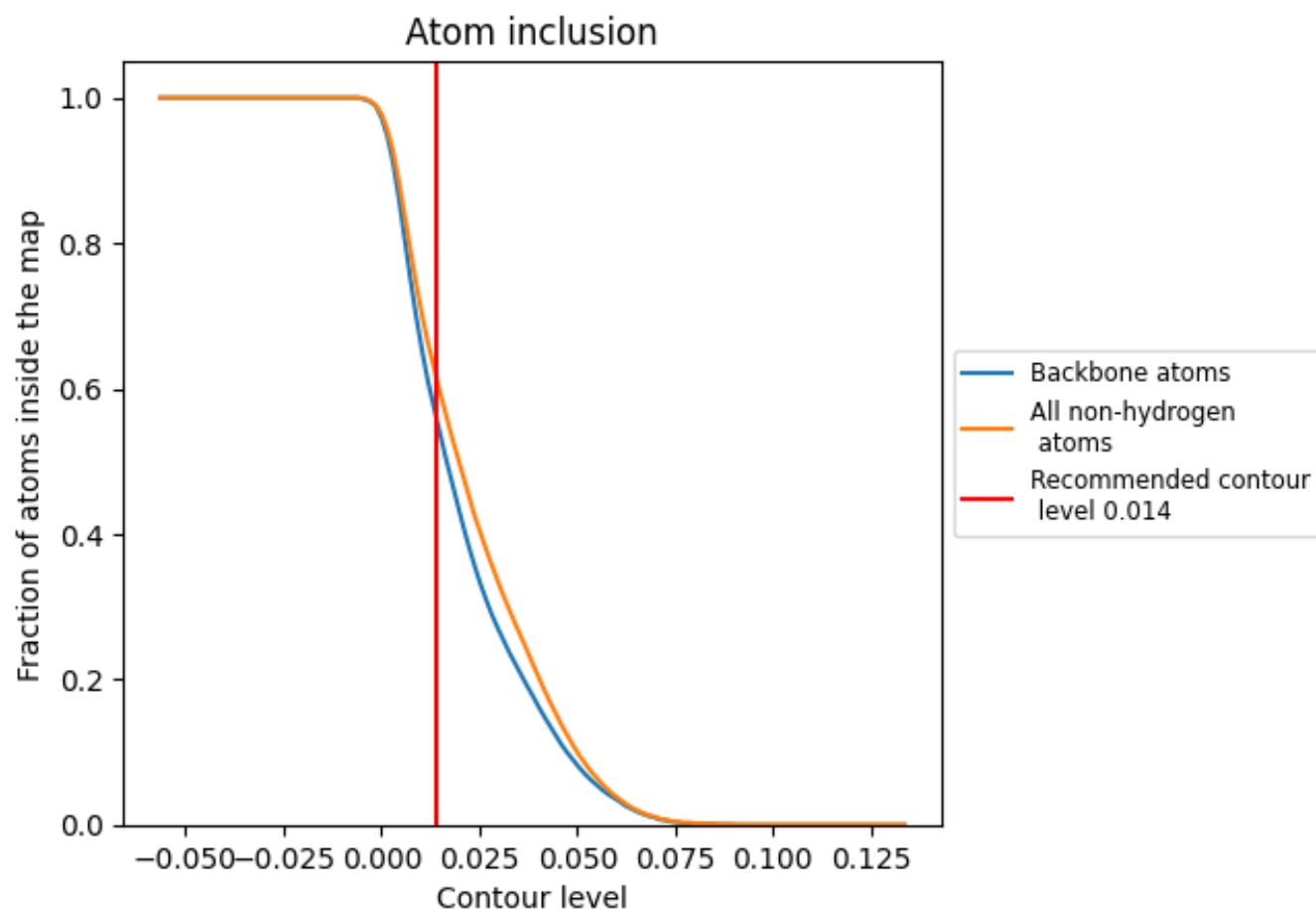
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6160	 0.4320
0	 0.8640	 0.6050
1	 0.8840	 0.5900
2	 0.7180	 0.5030
3	 0.8240	 0.5400
4	 0.0500	 0.0180
5	 0.7480	 0.5010
6	 0.9240	 0.6120
7	 0.8850	 0.5890
8	 0.8130	 0.5490
9	 0.5000	 0.3510
A	 0.8240	 0.5630
B	 0.6310	 0.4010
C	 0.8440	 0.5630
D	 0.3160	 0.2360
E	 0.0330	 0.1220
F	 0.7790	 0.4750
G	 0.7180	 0.4570
H	 0.6700	 0.4050
I	 0.4980	 0.3360
J	 0.0750	 0.2170
K	 0.1660	 0.1400
L	 0.8980	 0.5950
M	 0.6270	 0.4630
P	 0.7410	 0.5350
R	 0.6330	 0.5000
T	 0.9430	 0.6110
U	 0.9250	 0.6080
V	 0.4990	 0.3300
X	 0.6770	 0.4420
Y	 0.8180	 0.5610
Z	 0.7390	 0.5420
a	 0.0880	 0.2650
b	 0.0320	 0.1610
c	 0.0200	 0.0820



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Chain	Atom inclusion	Q-score
d	 0.0150	 0.0700
e	 0.0080	 0.0930
f	 0.0050	 0.0620
g	 0.0140	 0.1750
h	 0.0000	 -0.0340
i	 0.0020	 -0.0230
j	 0.0000	 0.0510
k	 0.0020	 0.0090
l	 0.0030	 -0.0030
m	 0.0030	 0.0080
n	 0.0030	 -0.0330
v	 0.8140	 0.5130
x	 0.0320	 0.0370
y	 0.3030	 0.2890
z	 0.8920	 0.5800