



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:06 AM UTC

PDB ID : 8I0P / pdb_00008i0p
EMDB ID : EMD-35105
Title : The cryo-EM structure of human pre-Bact complex
Authors : Zhan, X.; Lu, Y.; Shi, Y.
Deposited on : 2023-01-11
Resolution : 3.40 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

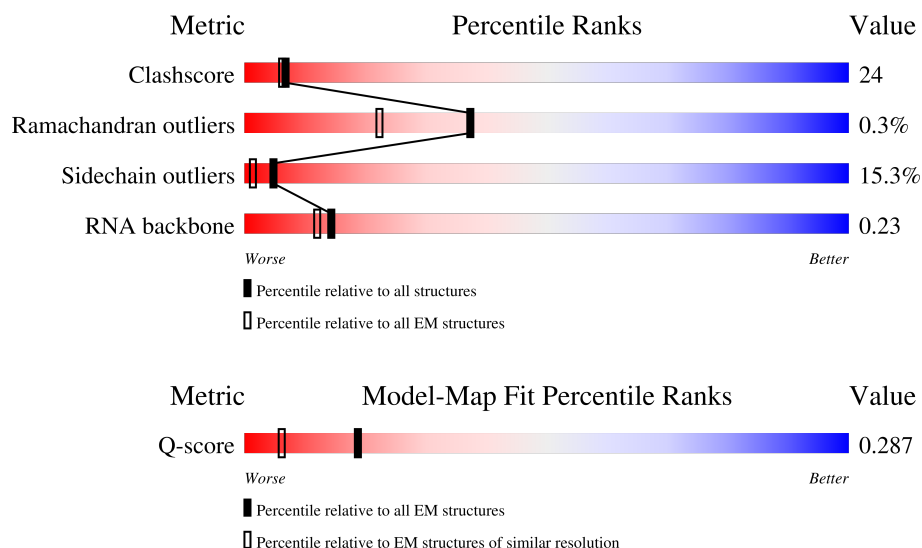
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	F	107	
7	G	220	
8	H	188	
9	I	855	
10	J	848	
11	K	393	
12	L	802	
13	N	144	
14	O	420	
15	P	229	
16	Q	1485	
17	R	536	
18	T	514	
19	X	396	
20	Y	322	
21	Z	619	
22	1	1304	
23	3	1217	
24	o	255	
25	p	225	
26	c	118	
26	h	118	
27	d	86	

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Mol	Chain	Length	Quality of chain
27	i	86	
28	a	240	
28	m	240	
29	g	126	
29	l	126	
30	f	76	
30	k	76	
31	e	92	
31	j	92	
32	b	119	
32	n	119	
33	w	501	
34	u	793	
35	2	895	
36	4	424	
37	6	125	
38	7	110	
39	5	86	
40	9	520	
41	8	904	
42	y	301	
43	v	464	
44	z	25	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	SEP	1	129	-	-	X	-

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 103887 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	2149	Total	C	N	O	S	0	0
			16165	10296	2906	2900	63		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	98	Total	C	N	O	P	0	0
			2066	925	347	696	98		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	896	Total	C	N	O	S	0	0
			7077	4528	1176	1338	35		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	1722	Total	C	N	O	0	0
			8528	5084	1722	1722		

- 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
			2338	1470	410	445	13		

- Molecule 6 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	95	Total	C	N	O	P	0	0
			2035	910	377	653	95		

- Molecule 7 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	63	Total	C	N	O	P	0	0
			1321	592	217	449	63		

- Molecule 8 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	165	Total	C	N	O	P	0	0
			3497	1562	600	1170	165		

- Molecule 9 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	593	Total	C	N	O	0	0
			2991	1805	593	593		

- Molecule 10 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	249	Total	C	N	O	S	0	0
			2116	1355	380	375	6		

- Molecule 11 is a protein called DNA/RNA-binding protein KIN17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	312	Total	C	N	O	S	0	0
			2173	1338	413	412	10		

- Molecule 12 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	99	Total	C	N	O	S	0	0
			829	532	149	144	4		

- Molecule 13 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	N	134	Total	C	N	O	0	0
			662	394	134	134		

- Molecule 14 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	O	271	Total	C	N	O	0	0
			1340	798	271	271		

- Molecule 15 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	42	Total	C	N	O	S	0	0
			362	231	63	66	2		

- Molecule 16 is a protein called RNA helicase aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	Q	1329	Total	C	N	O	0	0
			6730	4072	1329	1329		

- Molecule 17 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	192	Total	C	N	O	S	0	0
			1520	937	278	297	8		

- Molecule 18 is a protein called Pleiotropic regulator 1.

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

- Molecule 19 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	154	Total	C	N	O	S	0	0
			1279	819	231	227	2		

- Molecule 20 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	118	Total	C	N	O	S	0	0
			948	605	163	176	4		

- Molecule 21 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Z	55	Total	C	N	O	0	0
			439	282	85	72		

- Molecule 22 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	1	993	Total	C	N	O	P	S	0	0
			7845	5003	1360	1435	1	46		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3	1180	Total	C	N	O	S	0	0
			9240	5868	1569	1758	45		

- Molecule 24 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	o	162	Total	C	N	O	0	0
			816	492	162	162		

- Molecule 25 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	p	169	Total	C	N	O	0	0
			851	513	169	169		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	h	95	Total	C	N	O	0	0
			482	292	95	95		
26	c	97	Total	C	N	O	0	0
			388	194	97	97		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	i	72	Total	C	N	O	0	0
			359	215	72	72		
27	d	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	m	82	Total	C	N	O	0	0
			413	249	82	82		
28	a	84	Total	C	N	O	0	0
			336	168	84	84		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	l	83	Total	C	N	O	0	0
			415	249	83	83		
29	g	81	Total	C	N	O	0	0
			324	162	81	81		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	k	73	Total	C	N	O	0	0
			364	218	73	73		
30	f	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 31 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	j	81	Total	C	N	O	0	0
			403	241	81	81		
31	e	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 32 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	n	80	Total	C	N	O	0	0
			402	242	80	80		
32	b	82	Total	C	N	O	0	0
			328	164	82	82		

- Molecule 33 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	w	434	Total	C	N	O	S	0	0
			2275	1287	491	493	4		

- Molecule 34 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	u	187	Total	C	N	O		0	0
			834	460	187	187			

- Molecule 35 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2	231	Total	C	N	O	S	0	0
			1651	1037	309	301	4		

- Molecule 36 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	4	161	Total	C	N	O		0	0
			792	470	161	161			

- Molecule 37 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	6	109	Total	C	N	O	S	0	0
			906	582	157	163	4		

- Molecule 38 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	7	105	Total	C	N	O	S	0	0
			811	502	145	151	13		

- Molecule 39 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5	81	Total	C	N	O	S	0	0
			669	422	117	124	6		

- Molecule 40 is a protein called RING-type E3 ubiquitin-protein ligase PPIL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	9	384	Total	C	N	O	S	0	0
			2681	1665	484	524	8		

- Molecule 41 is a protein called Serine/arginine repetitive matrix protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	8	115	Total	C	N	O	S	0	0
			931	602	154	170	5		

- Molecule 42 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	y	79	Total	C	N	O	0	0
			390	232	79	79		

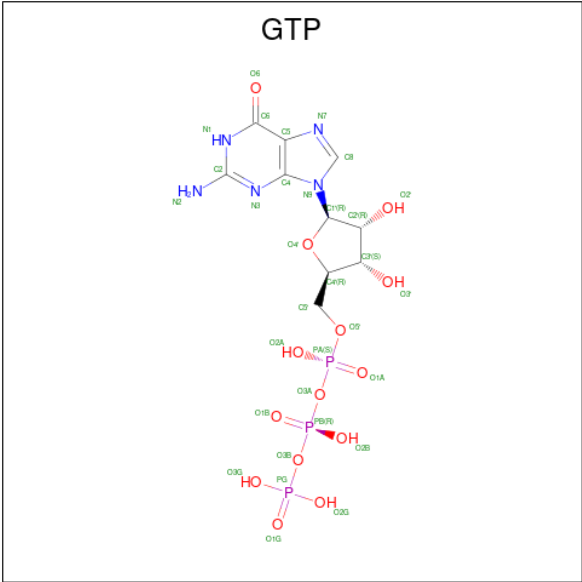
- Molecule 43 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	166	Total	C	N	O	S	0	0
			997	576	211	207	3		

- Molecule 44 is a protein called Unknown polymer.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	z	25	Total	C	N	O	0	0
			124	74	25	25		

- Molecule 45 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

- Molecule 46 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	C	1	Total	Mg	0
			1	1	

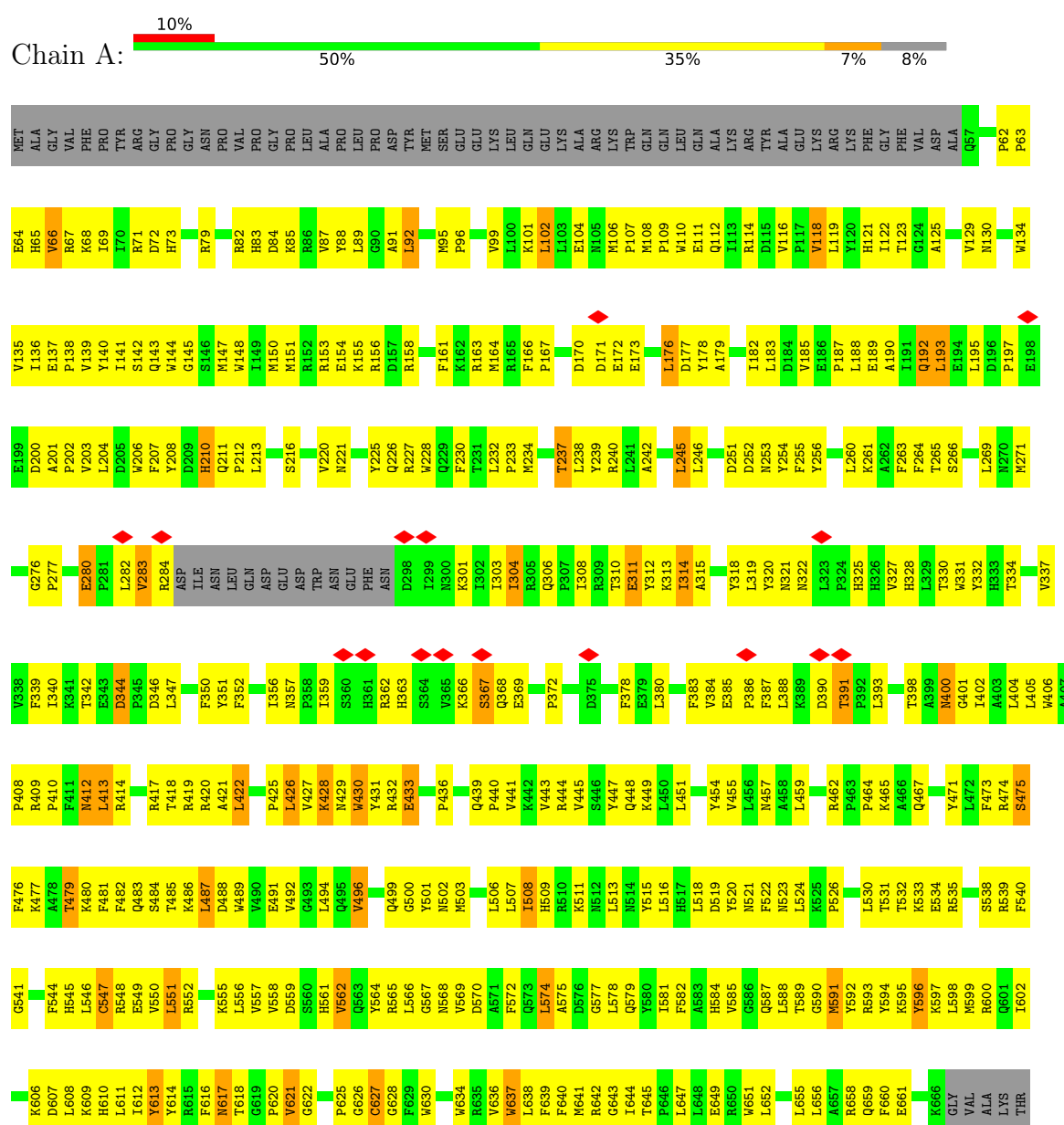
- Molecule 47 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	K	1	Total	Zn	0
			1	1	
47	7	3	Total	Zn	0
			3	3	

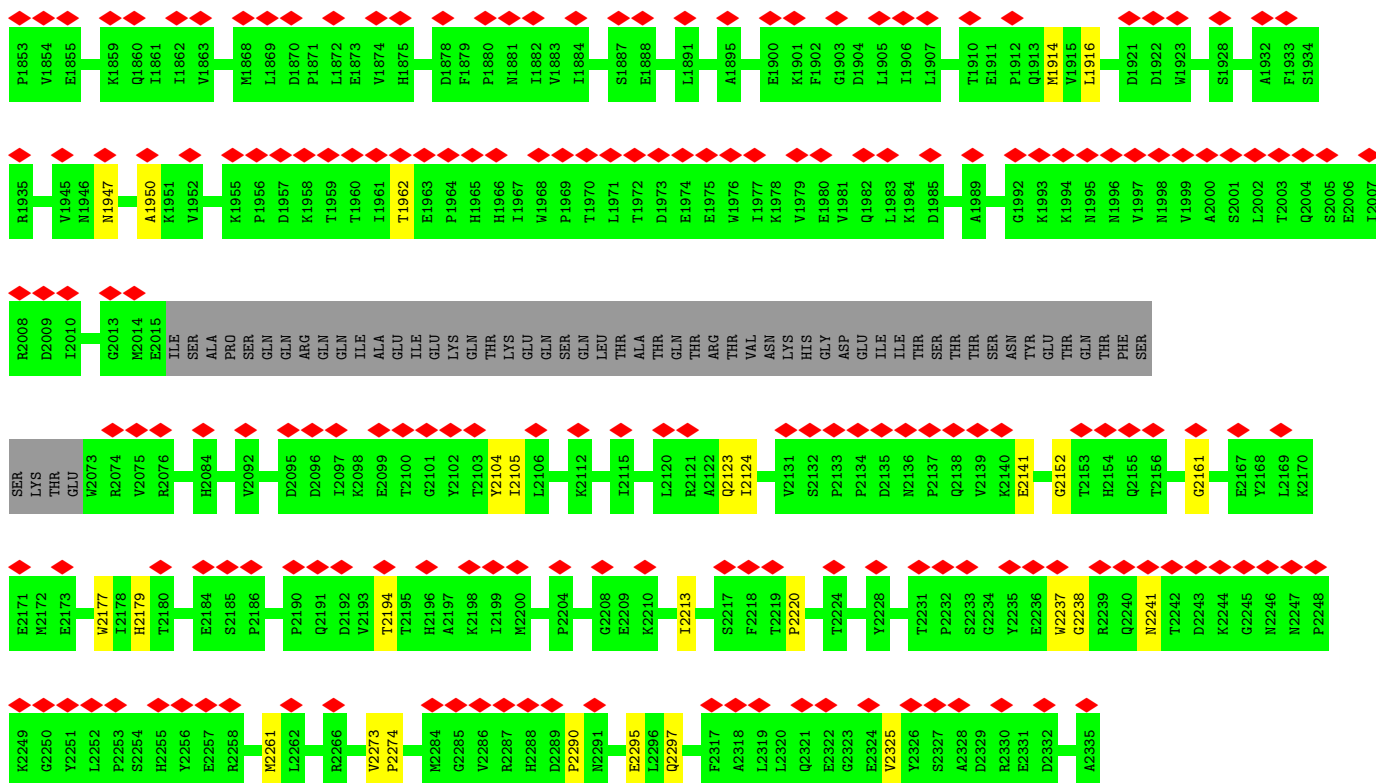
3 Residue-property plots

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.

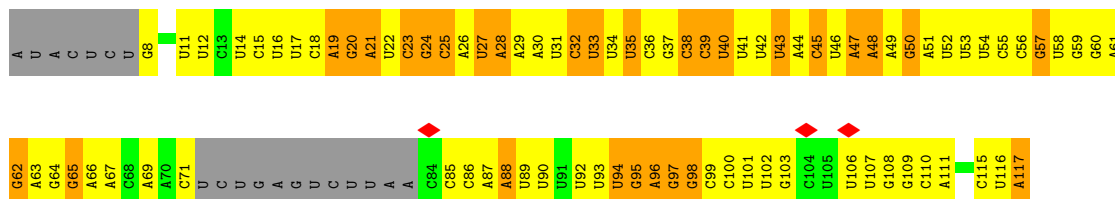
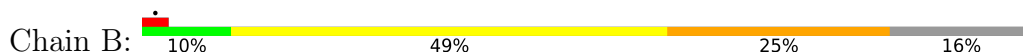
• Molecule 1: Pre-mRNA-processing-splicing factor 8



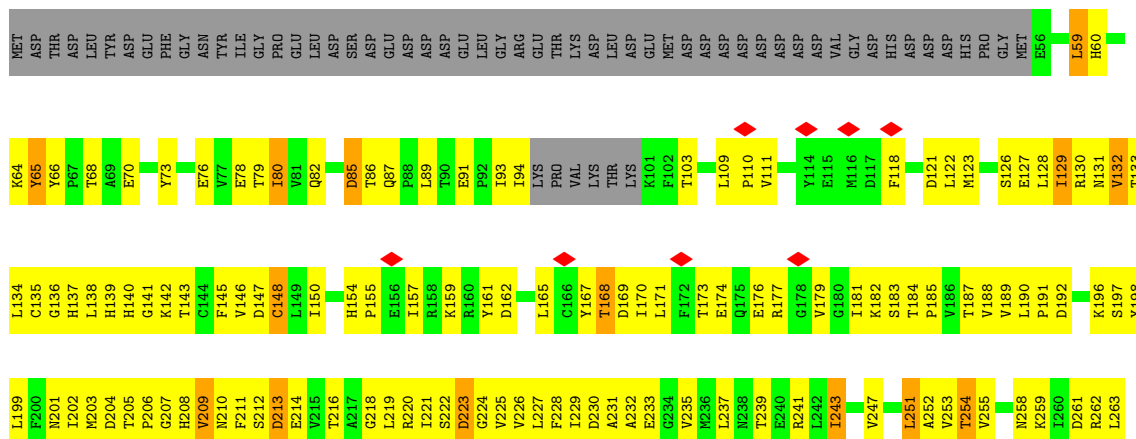
R1744	E1745	R1746	R1747	R1748	P1758	T1759	GLU	PR0	TYR	LEU	SR	GLN	ASN	TYR	GLY	GLU	LEU	PHE	SR	ASN	Q1775	I1776	I1777	I1778	I1779	V1780	V1785	T1789	L1798	A1806	I1809	L1817	K1820	S1825	Q1830	K1831	R1832	L1833	K1838	A1846	I1849	R1850	S1851	L1852																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
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P1313	V1314	V1315	F1316	Y1317	T1318	F1319	K1320	M1327	L1328	S1329	M1330	G1331	H1332	V1333	L1334	ILE	PRO	GLN	SR	ASP	LEU	ARG	TRP	SR	LYS	GLN	THR	THR	VAL	GLY	ILE	THR	PHE	R1354	S1355	G1356	M1357	S1358	H1359	E1360	E1361	D1362	Q1363	L1364	I1365	P1366	L1368	Y1369	R1370	Y1371	I1372	Q1373	F1374	E1376	S1377																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
E1235	S1236	M1237	R1243	L1248	M1249	T1255	F1256	T1257	K1258	M1261	N1264	L1267	I1268	M1271	T1272	Y1273	F1274	R1275	E1276	V1278	T1281	Q1282	E1283	L1284	L1285	D1286	L1287	L1288	V1289	M1293	K1294	L1295	H1296	T1297	R1298	I1299	K1300	I1301	G1302	L1303	N1304	K1306	M1307	F1308	S1309	R1310	F1311	P1312																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
T1167	V1168	E1171	S1172	S1173	F1174	S1175	V1176	Y1177	F1178	S1179	K1180	D1181	M1182	P1183	L1184	L1185	L1186	M1189	E1193	C1194	R1195	H1196	L1197	P1198	L1199	G1200	T1201	T1202	S1203	L1204	H1205	E1206	H1209	K1210	D1211	V1213	W1214	N1215	L1216	Q1217	N1218	E1219	V1220	T1221	K1222	E1223	N1224	T1225	F1229	L1230	R1231	V1232	D1234																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
I1077	A1078	T1079	E1080	H1083	P1084	I1085	L1086	L1087	F1088	G1089	K1090	Y1091	I1092	I1095	D1102	A1103	D1104	E1105	A1106	R1107	D1108	L1109	I1110	L1114	D1119	P1120	N1124	N1130	K1131	K1132	G1133	W1134	D1137	A1138	R1139	K1144	V1147	F1154	I1157	K1158	N1159	R1163	T1166																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
R820	R821	F822	S823	R824	K746	P827	D748																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											</



• Molecule 2: U5 snRNA

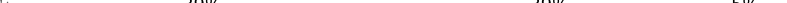


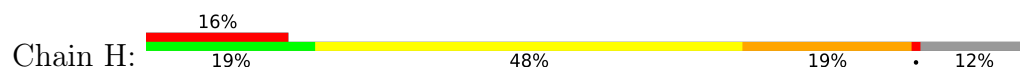
• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component

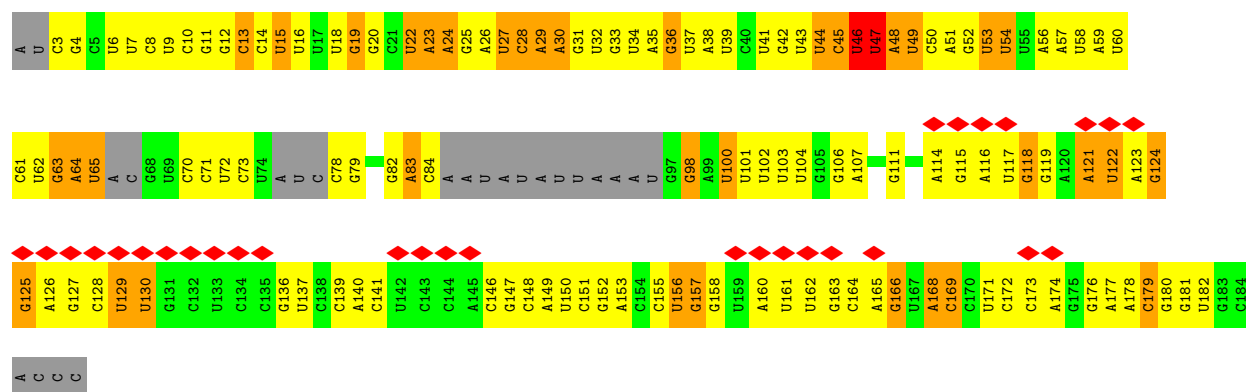




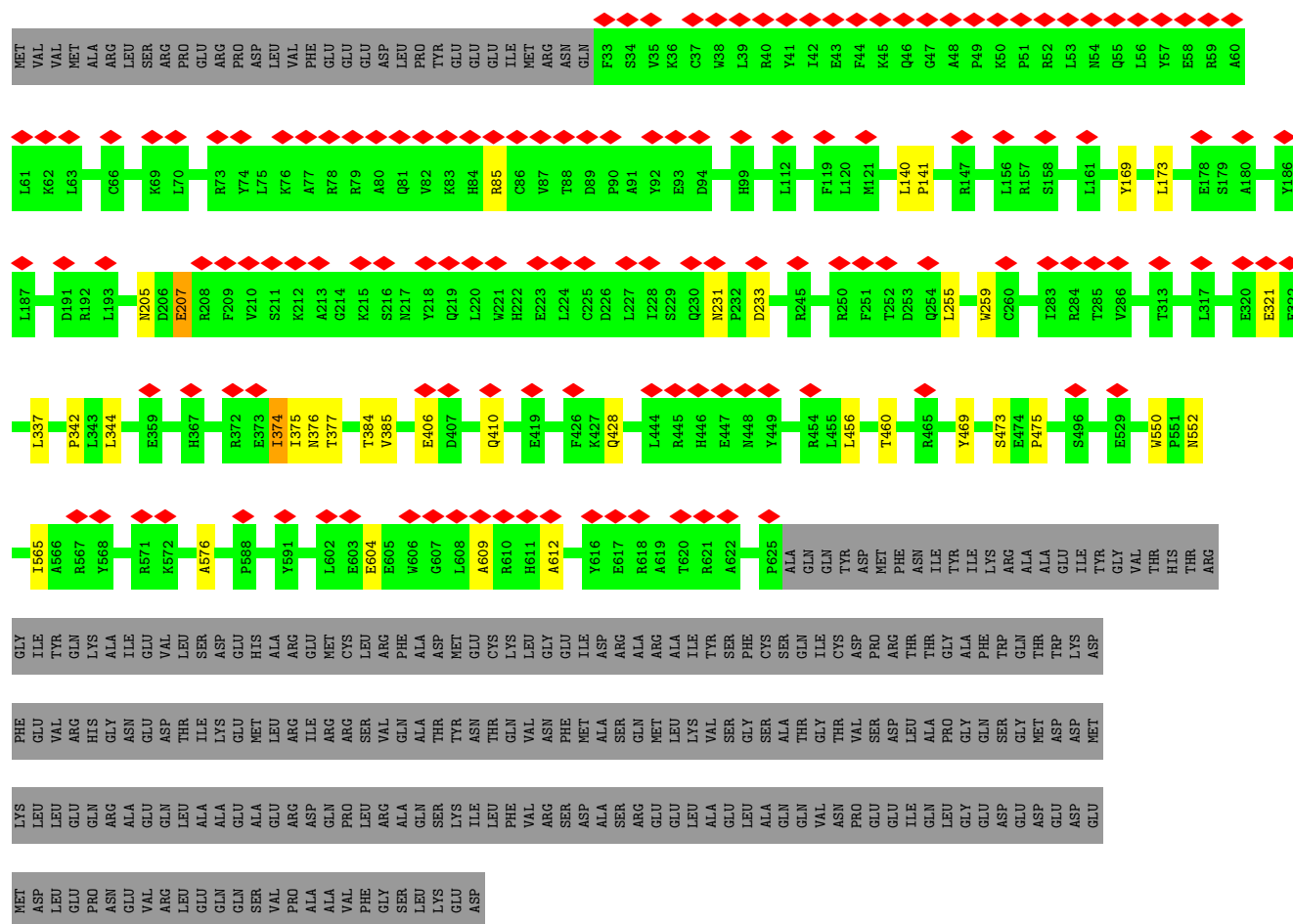
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V2120	P1308	L1368	T1428	P1429	Y1679	W1756	G1816	H1877	L1940	T2000	R2060	V2120
K2121	V1309	L1369	E1430	E1439	Y1679	T1756	M1817	K1878	A1941	D2001	E2061	K2121
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S2123	A1311	Q1371	W1432	S1493	Y1682	T1758	A1820	N1880	M1943	Q2003	G2063	S2123
V2124	L1312	S1372	D1433	L1494	D1683	L1760	Y1821	N1881	E1944	L2004	W2064	V2124
D2125	R1313	E1373	I1434	S1495	L1684	Y1761	Y1822	P1882	L1945	A2005	W2065	D2125
VAL	N1314	G1374	L1435	M1496	L1685	R1762	Y1823	F1884	A1946	D2006	V2066	VAL
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GLU	A1316	C1376	R1437	K1498	L1601	M1764	I1825	V1887	M1948	A2008	I2068	GLU
ALA	F1317	Y1377	R1438	D1499	E1602	T1765	Y1826	P1887	V1949	R2009	G2069	ALA
GLU	E1318	Y1378	W1439	V1500	K1603	Q1766	T1827	H1888	T1950	F2010	D2070	GLU
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SER	D1323	E1383	K1443	L1504	L1609	P1694	L1831	N1892	W1954	Y2014	N2074	SER
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	N1345	V1406	E1468	A1549	A1640	L1735	D1734	L1793	S1794	W2036	V2095	
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	E1361	K1421	R1483	Q1587	L1660			M1808	R1869	V2051	D2111	
	F1362	L1422						D1809	Q1870	T2052	A2112	
								V1810	L1871	A2053	Y2113	
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- Chain E: 





• Molecule 9: Pre-mRNA-splicing factor SYF1



• Molecule 10: Crooked neck-like protein 1

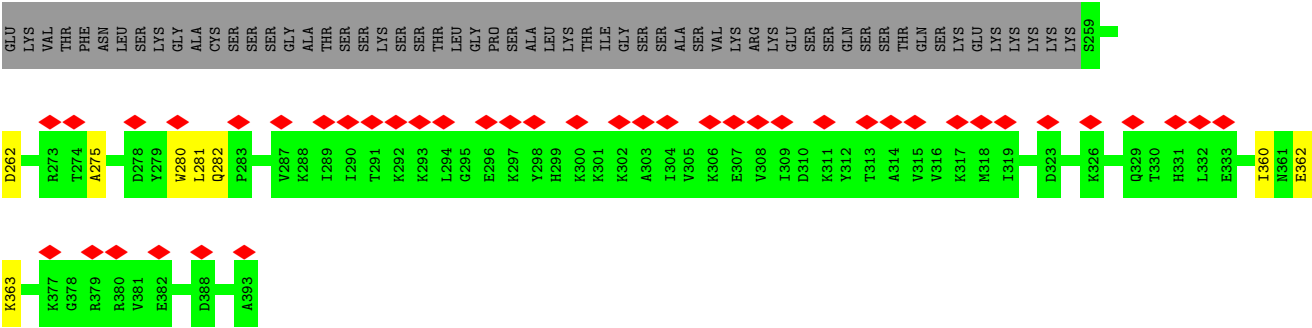


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● Molecule 11: DNA/RNA-binding protein KIN17

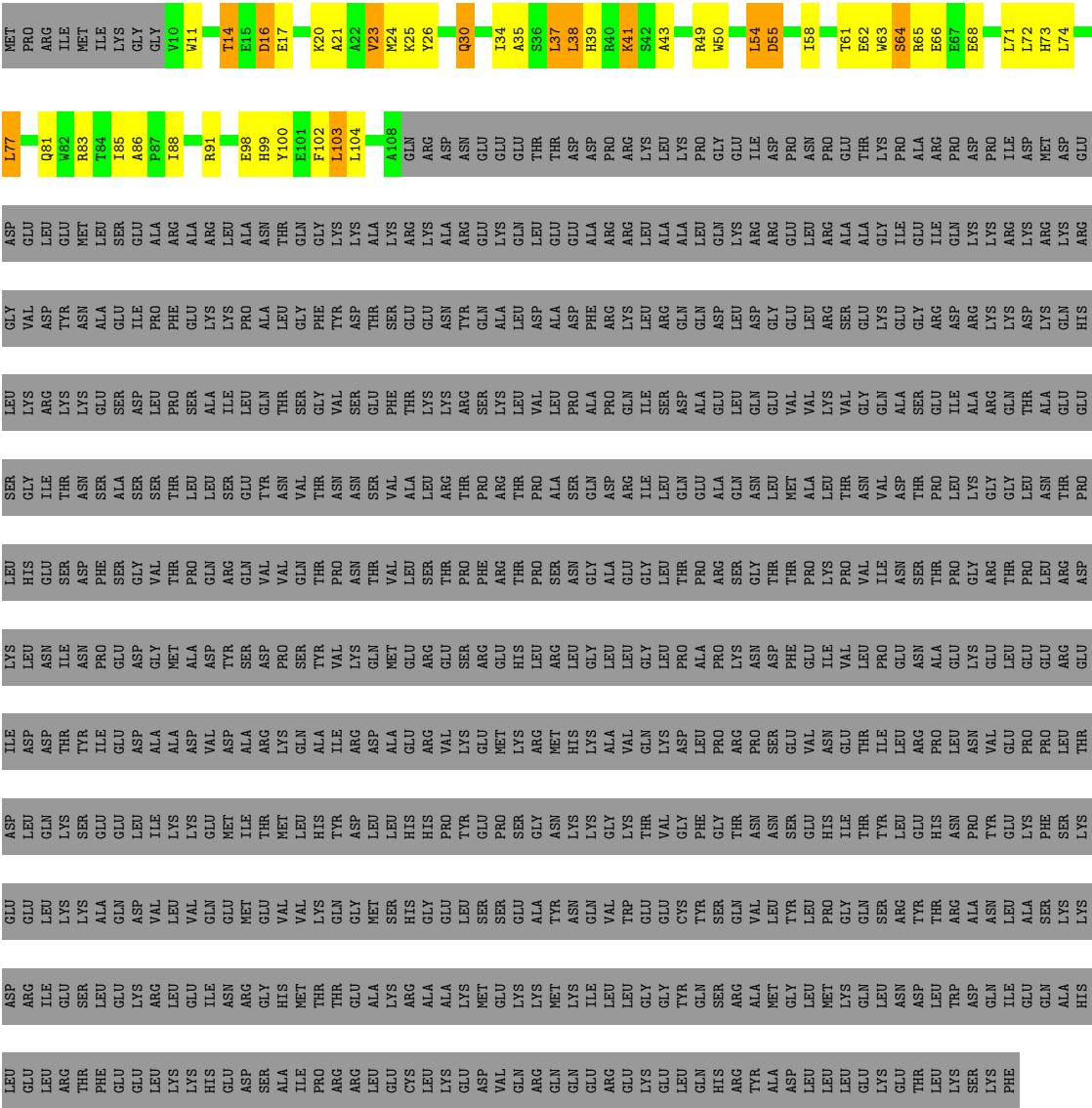


MET	GLY	LYS	SER	ASP	PHE	L7	T8	I12	A13	R14	R15	R81	R82	R83	F84	G85	T86	K87	R88	I93	Y94	Y95	N96	E97	Y98	R99	G100	H101	R102	I105	C106	R107	D108	E109	W112	L115	T116	D117	F118	T119	E120	S121	W122	G123	R124	E125	K129	V130	D131	E132	T133	Y138	I139																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							

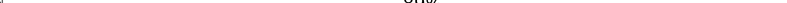


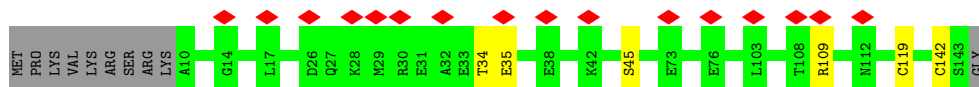
● Molecule 12: Cell division cycle 5-like protein

Chain L: 6% . . 88%

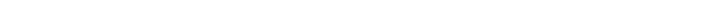


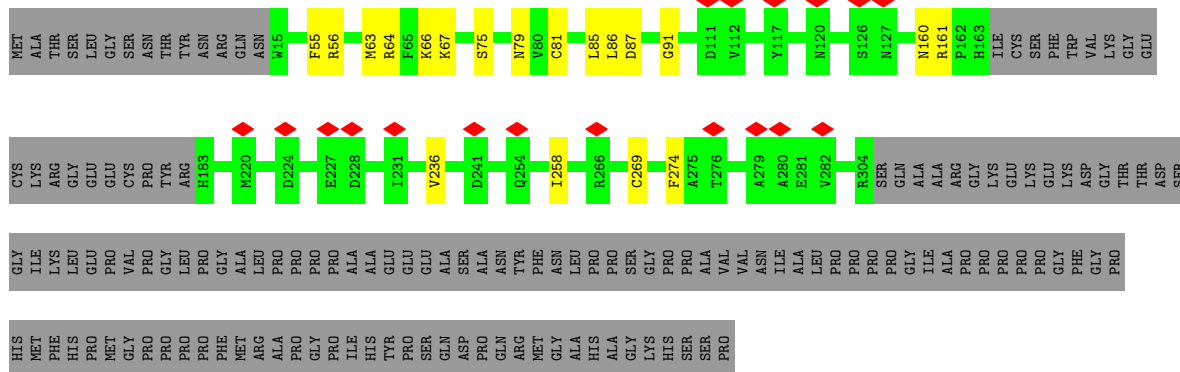
● Molecule 13: Protein BUD31 homolog

Chain N:  11% 89% 7%

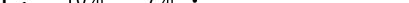


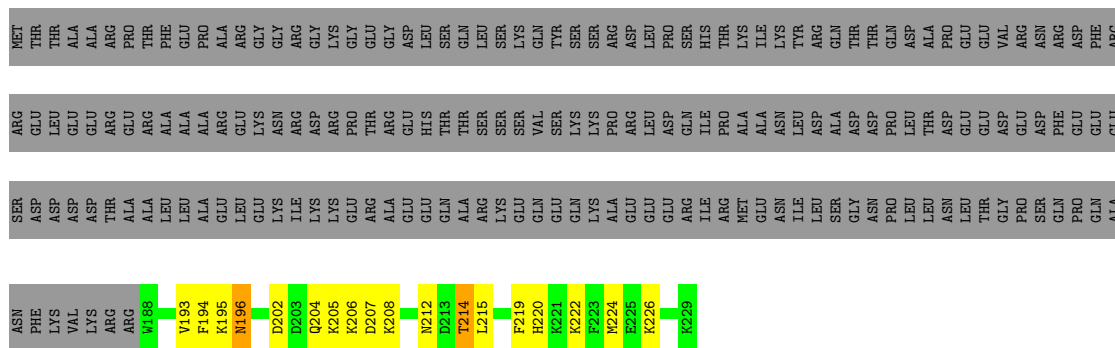
- Molecule 14: Pre-mRNA-splicing factor RBM22

Chain 0:  60% 5% 35%



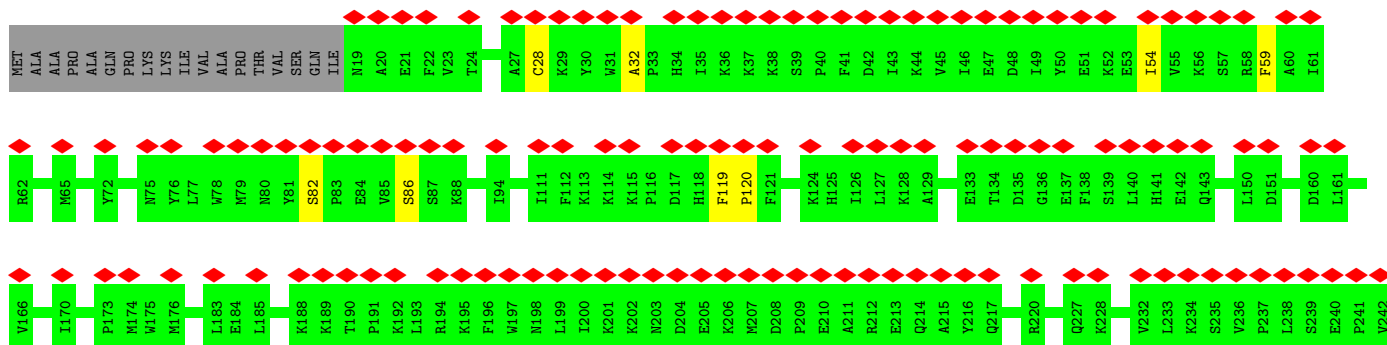
- Molecule 15: Spliceosome-associated protein CWC15 homolog

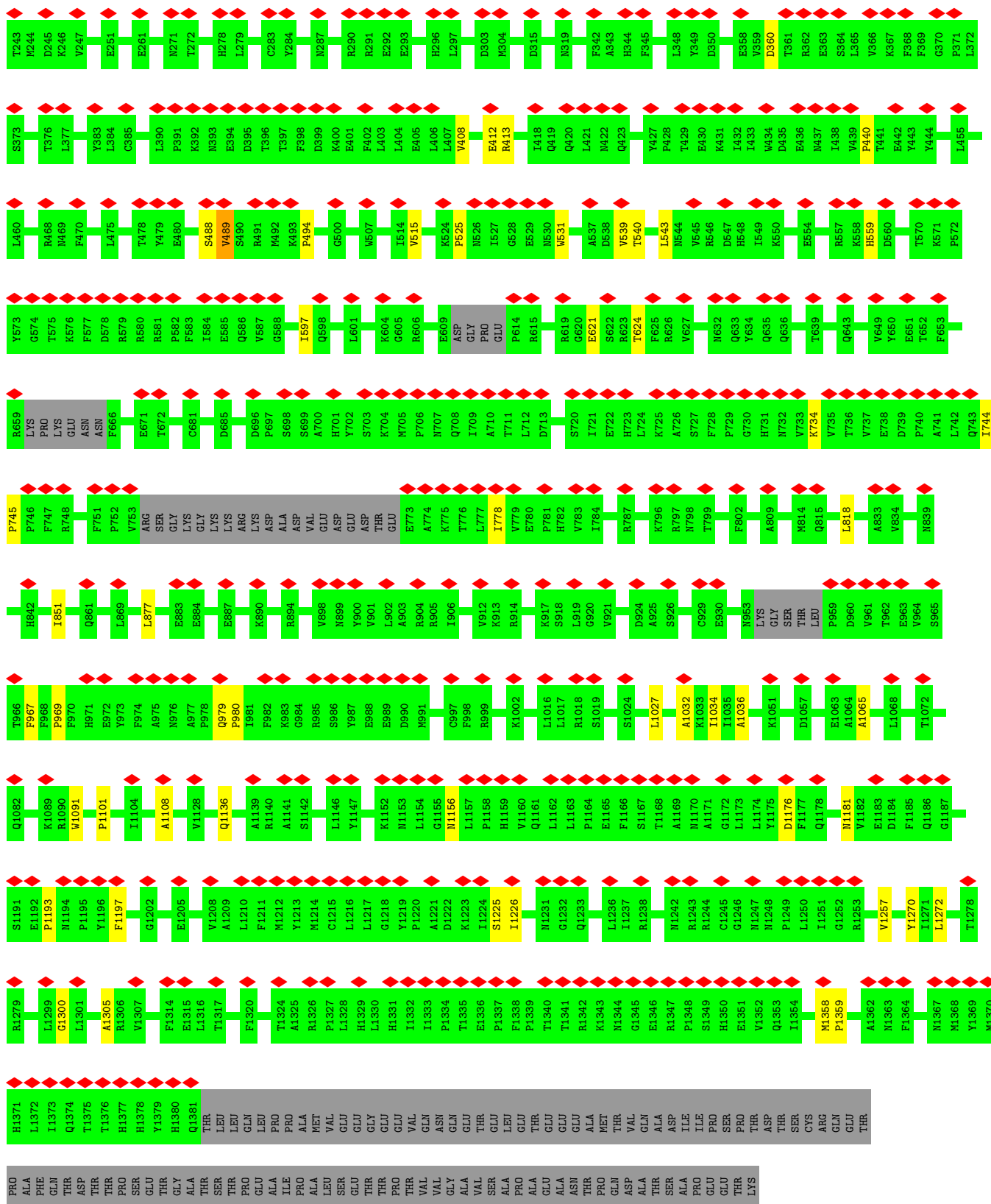
Chain P:  10% 7% 82%



- Molecule 16: RNA helicase aquarius

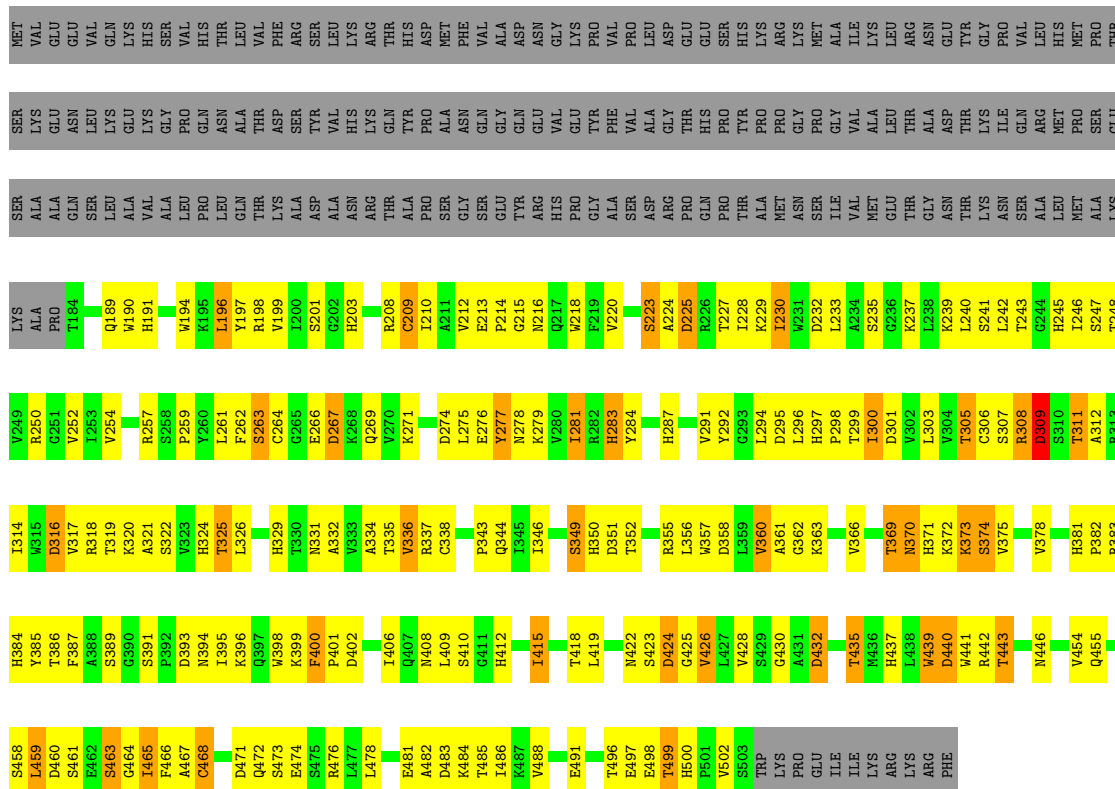
Chain Q:  36% 85% 11%



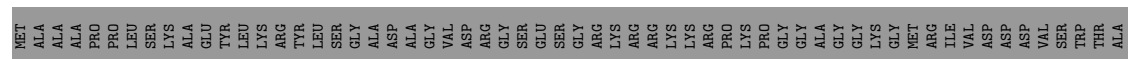


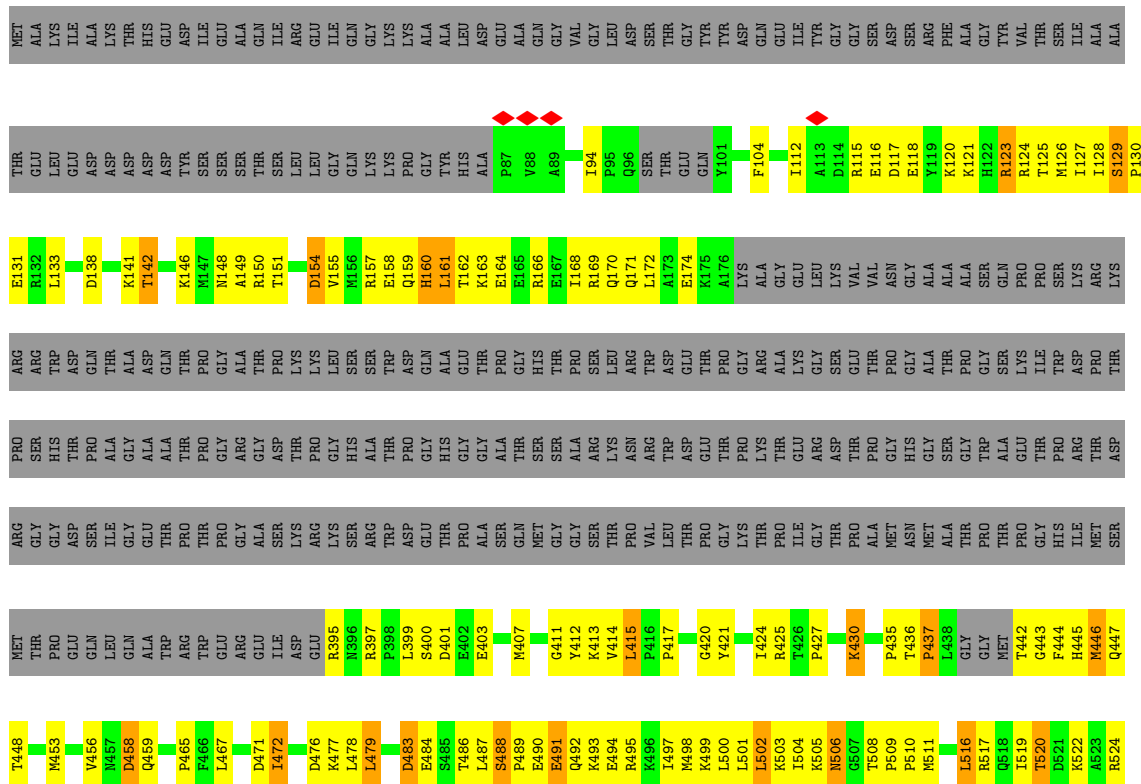
• Molecule 17: SNW domain-containing protein 1

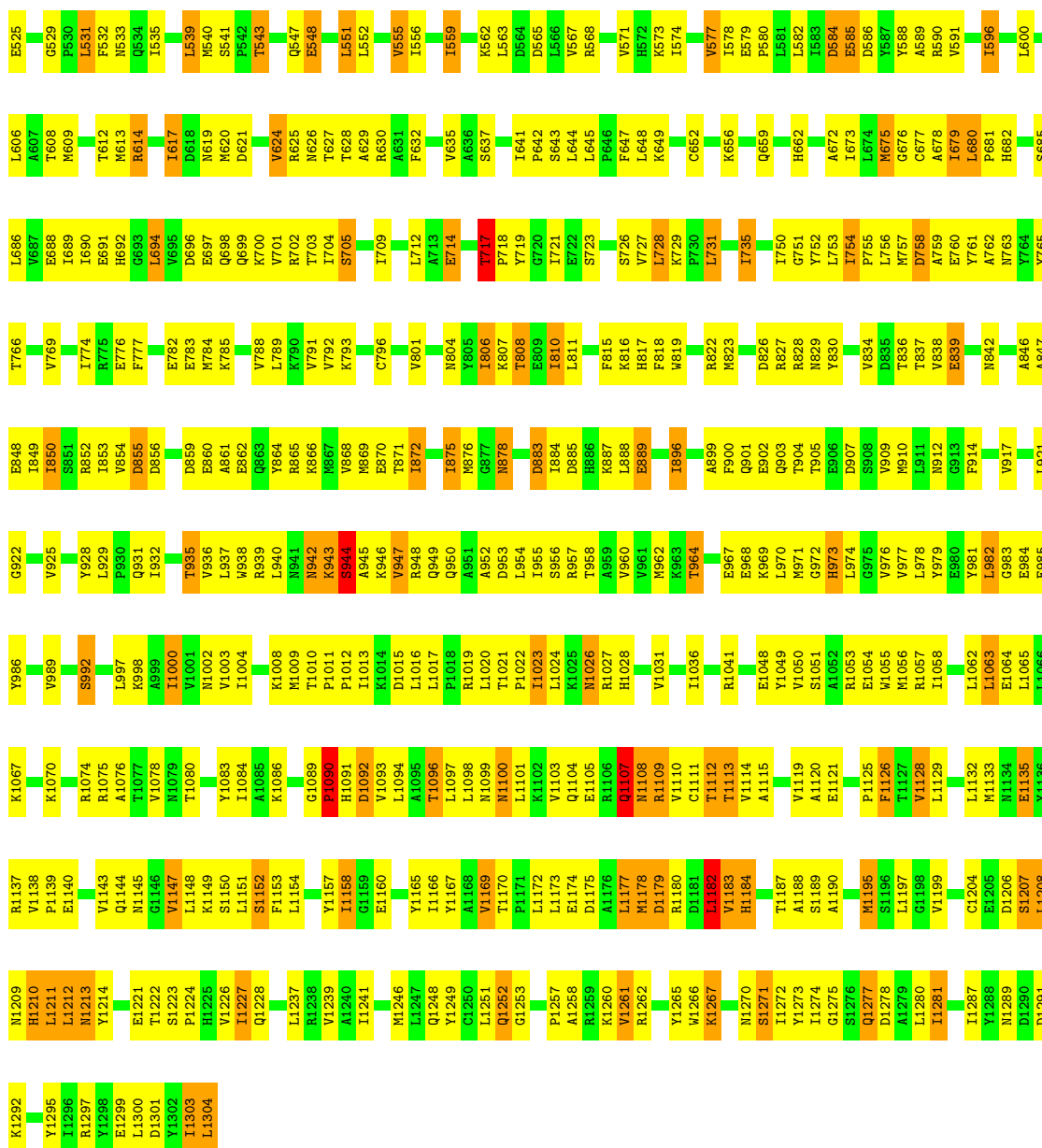
Chain R: 20% 12% 64%



Chain X:

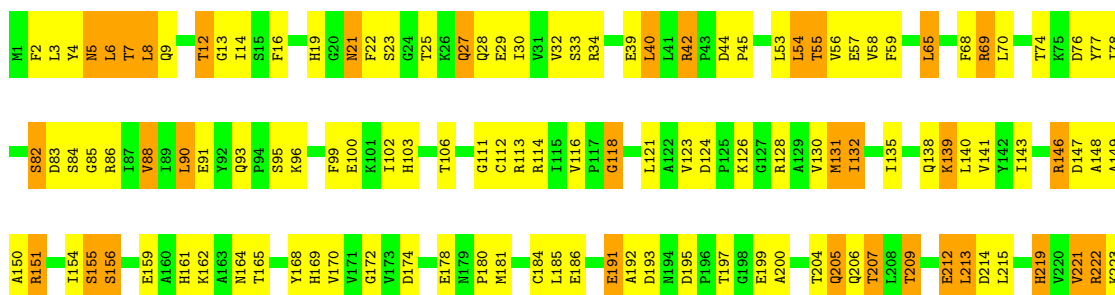


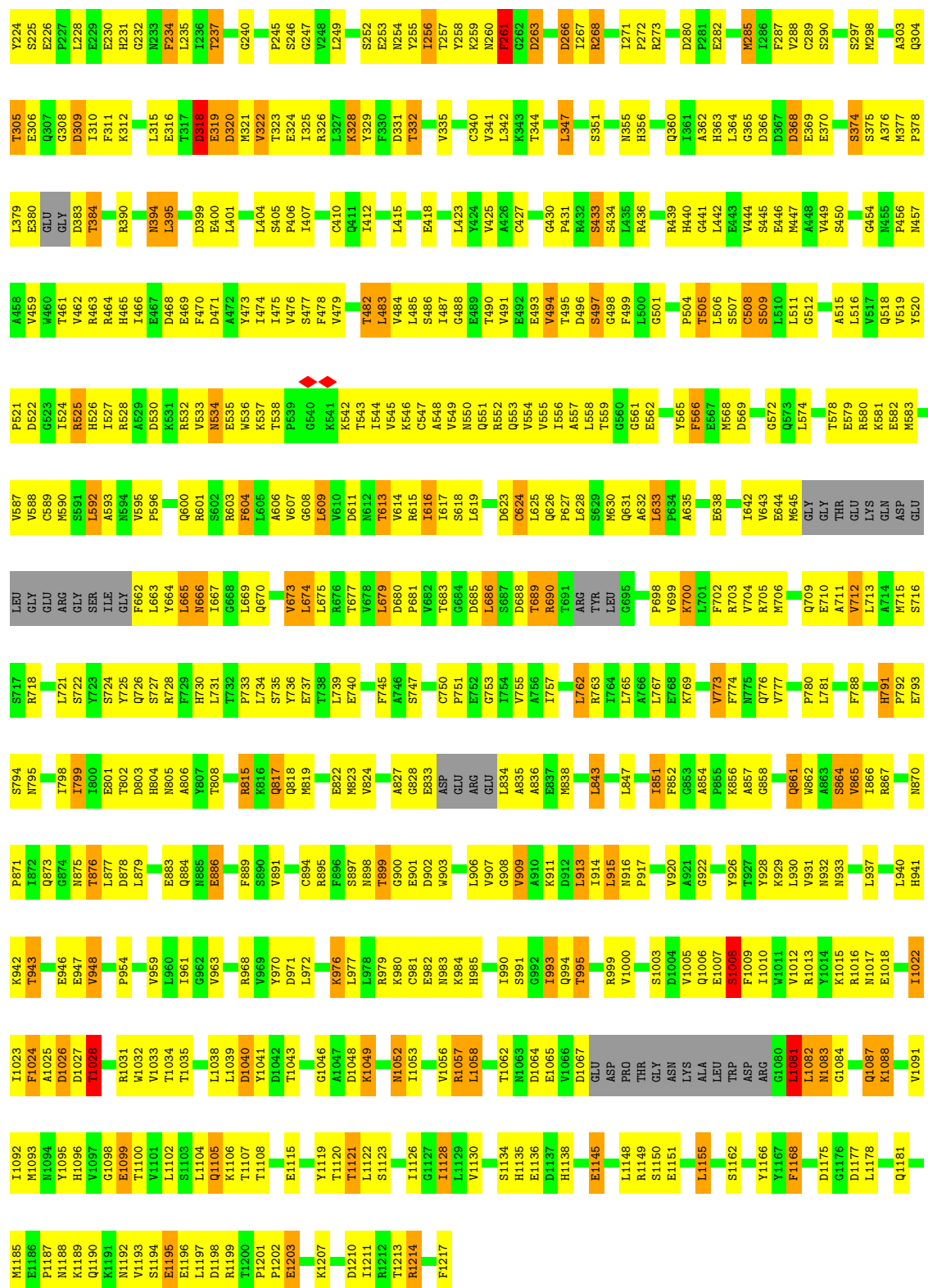




• Molecule 23: Splicing factor 3B subunit 3

Chain 3: 41% 46% 10%

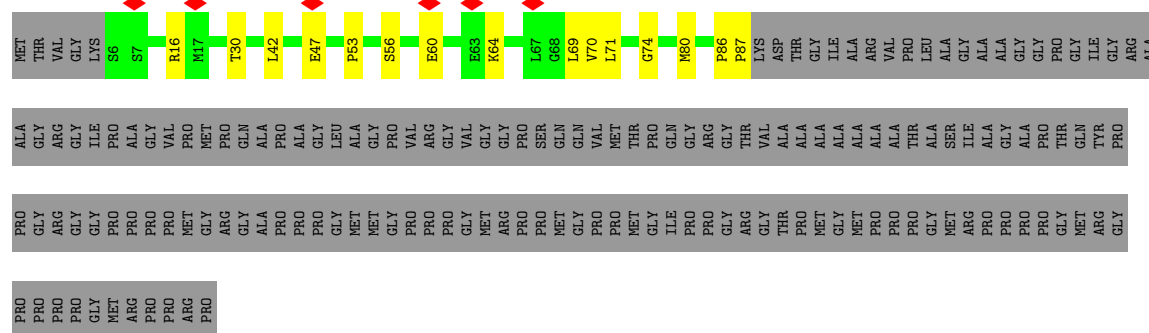




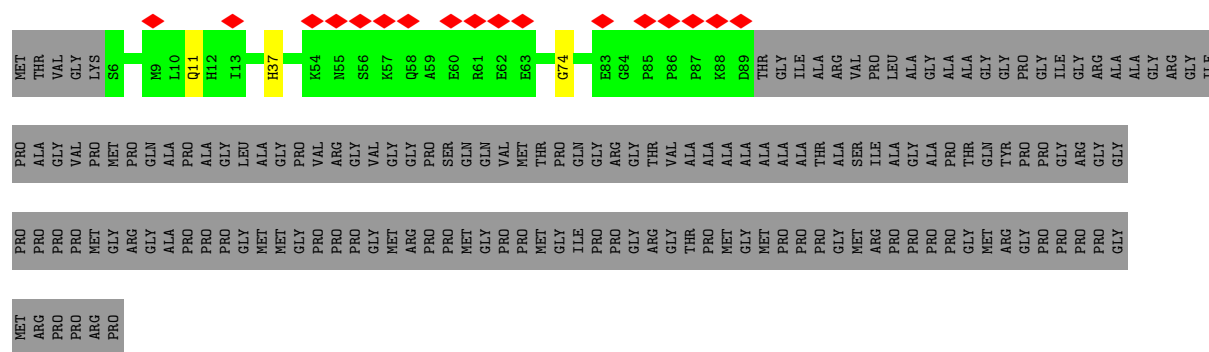
● Molecule 24: U2 small nuclear ribonucleoprotein A'



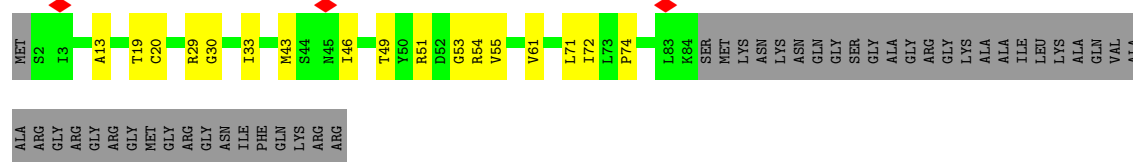
- Molecule 28: Small nuclear ribonucleoprotein-associated proteins B and B'



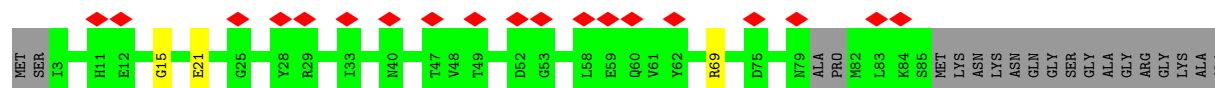
- Molecule 28: Small nuclear ribonucleoprotein-associated proteins B and B'



- Molecule 29: Small nuclear ribonucleoprotein Sm D3



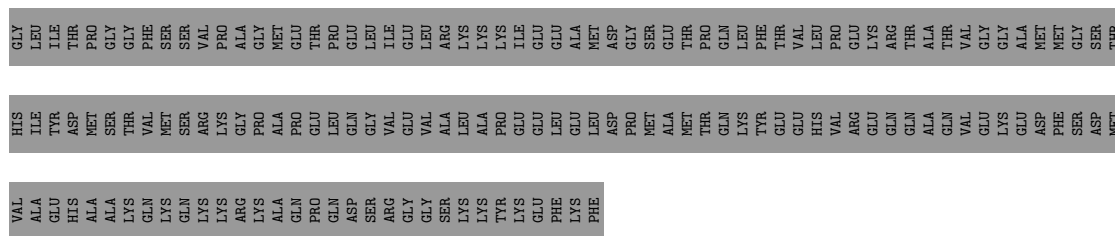
- Molecule 29: Small nuclear ribonucleoprotein Sm D3



[illegible]

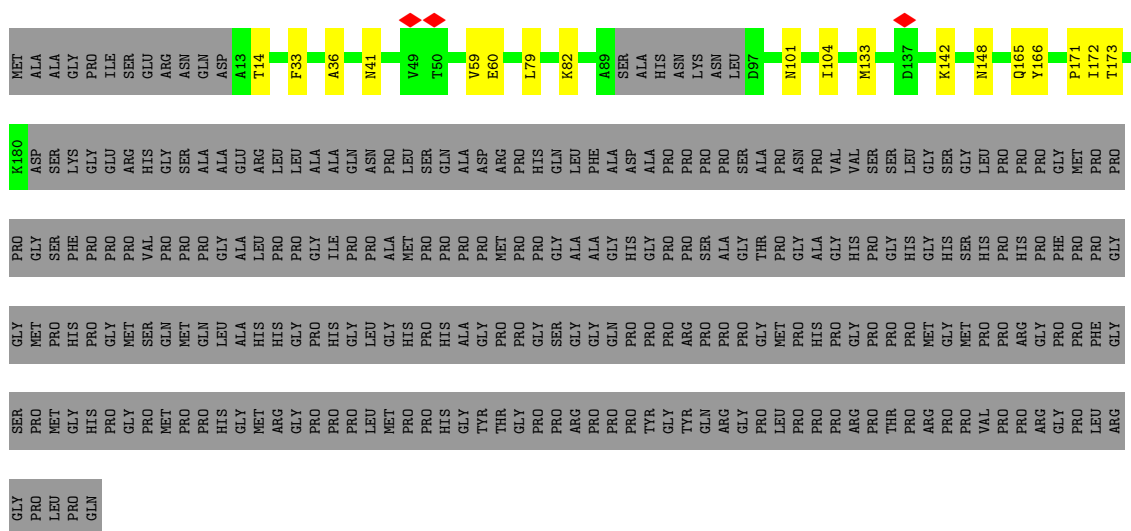
- Molecule 35: Splicing factor 3B subunit 2

[illegible]

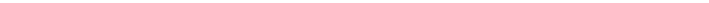


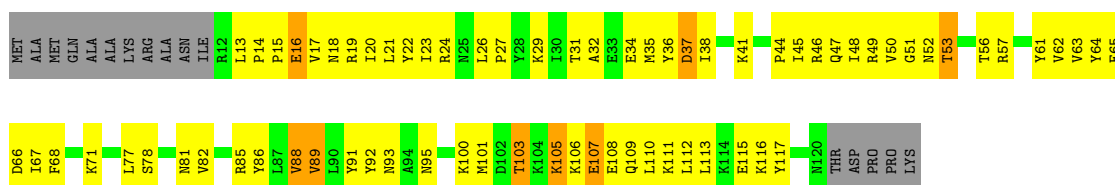
- Molecule 36: Splicing factor 3B subunit 4

Chain 4: 34% 62%

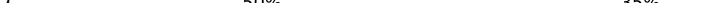


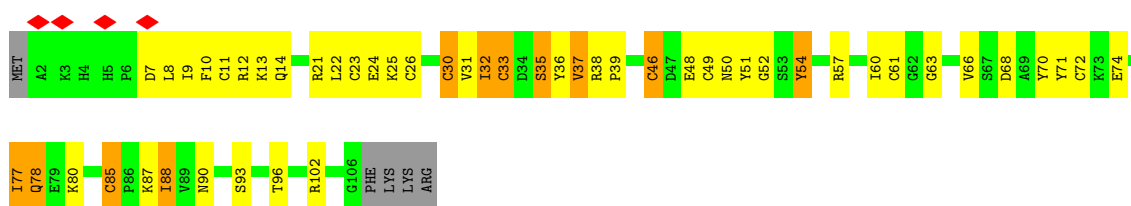
- Molecule 37: Splicing factor 3B subunit 6

Chain 6:  30% 50% 6% 13%



- Molecule 38: PHD finger-like domain-containing protein 5A

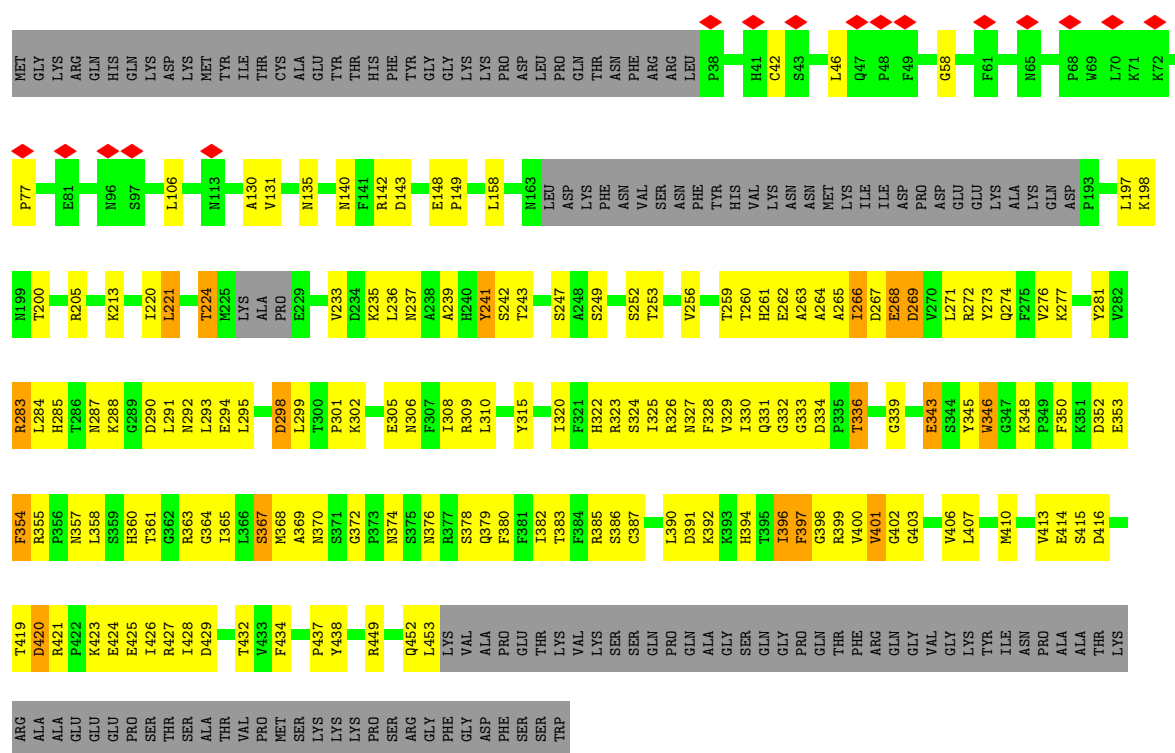
Chain 7: 



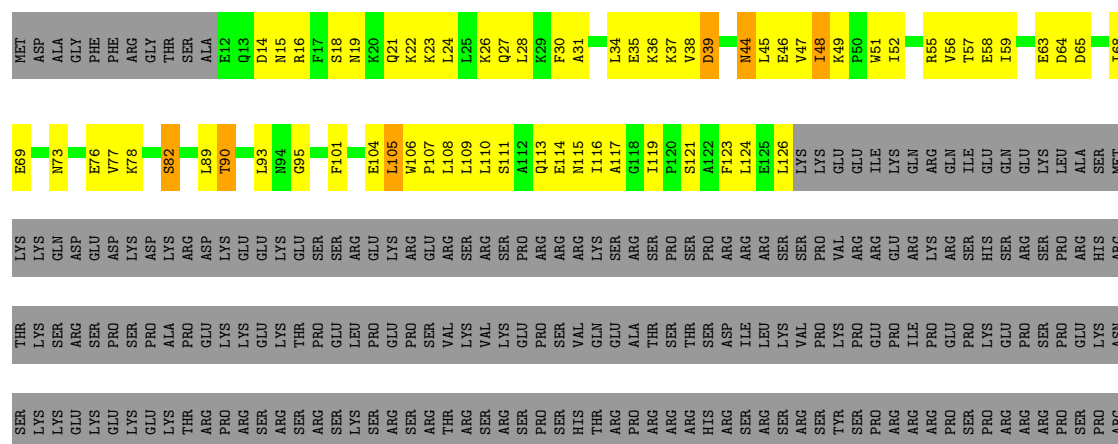
- Molecule 39: Splicing factor 3B subunit 5



Chain 9: 44% 27% 26%



Chain 8: 5% 7% . 87%







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46696	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.456	Depositor
Minimum map value	-1.255	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.19	Depositor
Map size ($\text{\AA}$)	516.96, 516.96, 516.96	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.077, 1.077, 1.077	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.68	6/16545 (0.0%)	0.76	27/22533 (0.1%)
2	B	0.26	0/2303	0.46	0/3579
3	C	0.26	0/7237	0.55	0/9834
4	D	0.18	0/8527	0.47	0/11887
5	E	0.24	0/2392	0.54	0/3242
6	F	0.30	0/2279	0.56	0/3551
7	G	0.43	0/1470	0.65	0/2281
8	H	0.34	0/3900	0.52	6/6065 (0.1%)
9	I	0.22	0/3013	0.62	0/4223
10	J	0.26	0/2171	0.56	0/2929
11	K	0.47	0/2203	0.81	0/2983
12	L	0.69	0/850	0.73	0/1146
13	N	0.19	0/661	0.42	0/919
14	O	0.20	0/1338	0.45	0/1861
15	P	0.65	0/369	0.83	0/489
16	Q	0.18	0/6796	0.43	0/9527
17	R	0.56	0/1544	0.84	3/2074 (0.1%)
18	T	0.64	0/2574	0.74	1/3511 (0.0%)
19	X	0.31	0/1312	0.57	0/1769
20	Y	0.54	0/966	0.58	0/1303
21	Z	0.40	0/455	0.59	0/617
22	1	0.83	11/7983 (0.1%)	0.88	19/10805 (0.2%)
23	3	0.94	1/9428 (0.0%)	0.87	13/12794 (0.1%)
24	o	0.19	0/821	0.47	0/1149
25	p	0.26	0/857	0.48	0/1196
26	c	0.19	0/387	0.53	0/482
26	h	0.21	0/485	0.48	0/677
27	d	0.18	0/295	0.49	0/367
27	i	0.19	0/362	0.48	0/502
28	a	0.19	0/335	0.54	0/417
28	m	0.22	0/416	0.53	0/581
29	g	0.18	0/322	0.48	0/399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
29	l	0.21	0/417	0.44	0/581
30	f	0.17	0/295	0.45	0/367
30	k	0.20	0/366	0.49	0/509
31	e	0.17	0/307	0.50	0/382
31	j	0.20	0/403	0.45	0/561
32	b	0.18	0/327	0.47	0/407
32	n	0.20	0/404	0.56	0/564
33	w	0.71	2/2311 (0.1%)	1.17	19/3008 (0.6%)
34	u	0.18	0/842	0.38	0/1110
35	2	1.28	21/1679 (1.3%)	1.71	31/2267 (1.4%)
36	4	0.22	0/790	0.51	0/1095
37	6	0.40	0/925	0.57	0/1247
38	7	0.70	1/825 (0.1%)	0.73	0/1106
39	5	1.07	0/688	0.86	0/930
40	9	0.29	0/2723	0.57	0/3697
41	8	0.46	0/946	0.59	0/1270
42	y	0.18	0/389	0.45	0/540
43	v	1.10	9/1010 (0.9%)	1.59	23/1326 (1.7%)
All	All	0.57	51/106243 (0.0%)	0.71	142/146659 (0.1%)

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	11
4	D	0	1
5	E	0	1
9	I	0	4
11	K	0	2
16	Q	0	1
22	1	0	8
23	3	0	3
33	w	0	1
35	2	0	1
40	9	0	1
43	v	0	1
All	All	0	35

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	1	1090	PRO	N-CA	15.73	1.67	1.47
1	A	827	PHE	C-N	14.23	1.50	1.33
35	2	485	PRO	N-CA	13.35	1.65	1.47
33	w	496	LYS	C-O	12.57	1.38	1.24
35	2	510	TYR	C-O	12.53	1.39	1.24

The worst 5 of 142 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	2	484	ASP	CA-C-N	18.14	138.10	119.24
35	2	484	ASP	C-N-CA	18.14	138.10	119.24
22	1	1089	GLY	CA-C-N	16.27	140.18	119.84
22	1	1089	GLY	C-N-CA	16.27	140.18	119.84
1	A	827	PHE	CA-C-N	14.15	134.95	120.38

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	109	PRO	Peptide
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	698	PRO	Peptide
1	A	699	GLU	Peptide

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	16165	0	14621	996	0
2	B	2066	0	1047	128	0
3	C	7077	0	7067	520	0
4	D	8528	0	3745	31	0
5	E	2338	0	2275	129	0
6	F	2035	0	1028	165	0
7	G	1321	0	673	146	0
8	H	3497	0	1770	143	0
9	I	2991	0	1473	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	2116	0	1977	96	0
11	K	2173	0	1770	128	0
12	L	829	0	837	61	0
13	N	662	0	284	5	0
14	O	1340	0	581	11	0
15	P	362	0	356	18	0
16	Q	6730	0	3268	30	0
17	R	1520	0	1482	101	0
18	T	2507	0	2451	196	0
19	X	1279	0	1284	81	0
20	Y	948	0	954	64	0
21	Z	439	0	410	16	0
22	1	7845	0	7915	525	0
23	3	9240	0	9164	554	0
24	o	816	0	386	16	0
25	p	851	0	423	23	0
26	c	388	0	102	1	0
26	h	482	0	220	5	0
27	d	296	0	87	5	0
27	i	359	0	179	7	0
28	a	336	0	89	2	0
28	m	413	0	194	11	0
29	g	324	0	89	3	0
29	l	415	0	198	14	0
30	f	296	0	84	2	0
30	k	364	0	176	10	0
31	e	308	0	83	3	0
31	j	403	0	173	12	0
32	b	328	0	89	4	0
32	n	402	0	184	7	0
33	w	2275	0	1347	106	0
34	u	834	0	325	0	0
35	2	1651	0	1438	163	0
36	4	792	0	367	9	0
37	6	906	0	913	69	0
38	7	811	0	789	42	0
39	5	669	0	631	31	0
40	9	2681	0	2270	141	0
41	8	931	0	960	66	0
42	y	390	0	190	2	0
43	v	997	0	745	60	0
44	z	124	0	26	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	C	32	0	12	8	0
46	C	1	0	0	0	0
47	7	3	0	0	0	0
47	K	1	0	0	0	0
All	All	103887	0	79201	4466	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 24.

The worst 5 of 4466 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:A:1308:PRO:HB3	1:A:1548:TYR:CE2	1.15	1.65
35:2:530:ARG:HG2	35:2:578:TRP:CH2	1.15	1.64
35:2:530:ARG:CG	35:2:578:TRP:HH2	1.19	1.53
35:2:530:ARG:CG	35:2:578:TRP:CH2	1.89	1.53
35:2:530:ARG:HG2	35:2:578:TRP:CZ3	1.46	1.50

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	2135/2335 (91%)	1880 (88%)	240 (11%)	15 (1%)	18	47
3	C	892/972 (92%)	827 (93%)	65 (7%)	0	100	100
4	D	1720/2136 (80%)	1602 (93%)	114 (7%)	4 (0%)	43	71
5	E	297/357 (83%)	274 (92%)	23 (8%)	0	100	100
9	I	591/855 (69%)	494 (84%)	93 (16%)	4 (1%)	18	47
10	J	245/848 (29%)	226 (92%)	17 (7%)	2 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	K	308/393 (78%)	292 (95%)	14 (4%)	2 (1%)	21	50
12	L	97/802 (12%)	94 (97%)	3 (3%)	0	100	100
13	N	132/144 (92%)	123 (93%)	9 (7%)	0	100	100
14	O	267/420 (64%)	255 (96%)	12 (4%)	0	100	100
15	P	40/229 (18%)	31 (78%)	9 (22%)	0	100	100
16	Q	1319/1485 (89%)	1256 (95%)	62 (5%)	1 (0%)	48	78
17	R	184/536 (34%)	172 (94%)	12 (6%)	0	100	100
18	T	318/514 (62%)	281 (88%)	36 (11%)	1 (0%)	36	65
19	X	152/396 (38%)	142 (93%)	10 (7%)	0	100	100
20	Y	116/322 (36%)	106 (91%)	10 (9%)	0	100	100
21	Z	53/619 (9%)	48 (91%)	5 (9%)	0	100	100
22	1	984/1304 (76%)	872 (89%)	102 (10%)	10 (1%)	12	40
23	3	1168/1217 (96%)	1023 (88%)	141 (12%)	4 (0%)	36	65
24	o	160/255 (63%)	148 (92%)	12 (8%)	0	100	100
25	p	165/225 (73%)	152 (92%)	13 (8%)	0	100	100
26	c	95/118 (80%)	84 (88%)	11 (12%)	0	100	100
26	h	91/118 (77%)	86 (94%)	4 (4%)	1 (1%)	11	38
27	d	72/86 (84%)	66 (92%)	6 (8%)	0	100	100
27	i	70/86 (81%)	65 (93%)	5 (7%)	0	100	100
28	a	82/240 (34%)	77 (94%)	5 (6%)	0	100	100
28	m	80/240 (33%)	75 (94%)	5 (6%)	0	100	100
29	g	77/126 (61%)	70 (91%)	7 (9%)	0	100	100
29	l	81/126 (64%)	74 (91%)	7 (9%)	0	100	100
30	f	72/76 (95%)	67 (93%)	5 (7%)	0	100	100
30	k	71/76 (93%)	67 (94%)	4 (6%)	0	100	100
31	e	75/92 (82%)	68 (91%)	7 (9%)	0	100	100
31	j	79/92 (86%)	70 (89%)	9 (11%)	0	100	100
32	b	80/119 (67%)	75 (94%)	5 (6%)	0	100	100
32	n	78/119 (66%)	72 (92%)	6 (8%)	0	100	100
33	w	428/501 (85%)	403 (94%)	23 (5%)	2 (0%)	24	54
34	u	183/793 (23%)	175 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	2	225/895 (25%)	205 (91%)	17 (8%)	3 (1%)	9	33
36	4	157/424 (37%)	145 (92%)	12 (8%)	0	100	100
37	6	107/125 (86%)	98 (92%)	9 (8%)	0	100	100
38	7	103/110 (94%)	89 (86%)	14 (14%)	0	100	100
39	5	79/86 (92%)	70 (89%)	9 (11%)	0	100	100
40	9	378/520 (73%)	343 (91%)	34 (9%)	1 (0%)	36	65
41	8	113/904 (12%)	104 (92%)	9 (8%)	0	100	100
42	y	77/301 (26%)	73 (95%)	4 (5%)	0	100	100
43	v	158/464 (34%)	143 (90%)	15 (10%)	0	100	100
All	All	14454/23201 (62%)	13162 (91%)	1242 (9%)	50 (0%)	37	65

5 of 50 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	802	THR
1	A	1553	VAL
22	1	430	LYS
22	1	435	PRO
22	1	437	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	1476/2108 (70%)	1236 (84%)	240 (16%)	2	10
3	C	792/866 (92%)	719 (91%)	73 (9%)	8	29
5	E	256/300 (85%)	232 (91%)	24 (9%)	8	29
9	I	23/749 (3%)	23 (100%)	0	100	100
10	J	205/751 (27%)	190 (93%)	15 (7%)	13	39
11	K	164/354 (46%)	139 (85%)	25 (15%)	3	10
12	L	86/709 (12%)	72 (84%)	14 (16%)	2	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	P	40/203 (20%)	36 (90%)	4 (10%)	7	26
16	Q	71/1336 (5%)	71 (100%)	0	100	100
17	R	160/459 (35%)	133 (83%)	27 (17%)	2	9
18	T	273/441 (62%)	227 (83%)	46 (17%)	2	9
19	X	139/349 (40%)	125 (90%)	14 (10%)	7	25
20	Y	105/291 (36%)	81 (77%)	24 (23%)	1	2
21	Z	40/545 (7%)	37 (92%)	3 (8%)	12	38
22	1	834/1103 (76%)	687 (82%)	147 (18%)	2	8
23	3	1020/1051 (97%)	808 (79%)	212 (21%)	1	4
24	o	6/218 (3%)	6 (100%)	0	100	100
25	p	8/195 (4%)	8 (100%)	0	100	100
26	h	5/110 (4%)	5 (100%)	0	100	100
27	i	4/74 (5%)	4 (100%)	0	100	100
28	m	4/177 (2%)	4 (100%)	0	100	100
29	l	3/101 (3%)	3 (100%)	0	100	100
30	k	3/66 (4%)	3 (100%)	0	100	100
31	j	1/84 (1%)	1 (100%)	0	100	100
32	n	3/101 (3%)	3 (100%)	0	100	100
33	w	112/446 (25%)	93 (83%)	19 (17%)	2	9
34	u	10/709 (1%)	10 (100%)	0	100	100
35	2	134/776 (17%)	96 (72%)	38 (28%)	0	1
37	6	97/109 (89%)	85 (88%)	12 (12%)	4	18
38	7	90/95 (95%)	75 (83%)	15 (17%)	2	9
39	5	72/77 (94%)	63 (88%)	9 (12%)	4	18
40	9	223/456 (49%)	197 (88%)	26 (12%)	5	20
41	8	104/831 (12%)	96 (92%)	8 (8%)	12	37
43	v	73/382 (19%)	55 (75%)	18 (25%)	1	2
All	All	6636/16622 (40%)	5623 (85%)	1013 (15%)	5	10

5 of 1013 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	T	463	SER

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Mol	Chain	Res	Type
33	w	500	LEU
22	1	735	ILE
33	w	472	GLN
38	7	60	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 147 such sidechains are listed below:

Mol	Chain	Res	Type
23	3	791	HIS
41	8	97	ASN
23	3	870	ASN
35	2	478	HIS
3	C	798	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	96/117 (82%)	37 (38%)	3 (3%)
6	F	94/107 (87%)	51 (54%)	8 (8%)
7	G	62/220 (28%)	40 (64%)	10 (16%)
8	H	161/188 (85%)	59 (36%)	4 (2%)
All	All	413/632 (65%)	187 (45%)	25 (6%)

5 of 187 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	19	A
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	G	84	U
7	G	101	U
8	H	47	U
7	G	89	U
7	G	104	C

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
22	SEP	1	129	22	8,9,10	1.17	0	7,12,14	1.54	1 (14%)

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
22	SEP	1	129	22	-	1/6/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	1	129	SEP	OG-CB-CA	-3.43	104.81	108.14

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	1	129	SEP	CB-OG-P-O2P

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	1	129	SEP	5	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 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	$\# Z > 2$
45	GTP	C	1500	46	33,34,34	0.98	2 (6%)	50,54,54	1.56	10 (20%)

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
45	GTP	C	1500	46	-	10/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	C	1500	GTP	C2-N3	2.24	1.38	1.33
45	C	1500	GTP	PA-O3A	2.12	1.61	1.59

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	C	1500	GTP	C5-C4-N3	-4.55	121.14	128.39
45	C	1500	GTP	C2-N3-C4	4.38	119.85	112.30
45	C	1500	GTP	N9-C4-N3	3.12	132.19	125.95
45	C	1500	GTP	N9-C8-N7	-2.90	108.03	113.40
45	C	1500	GTP	C2-N1-C6	-2.69	120.24	125.11

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

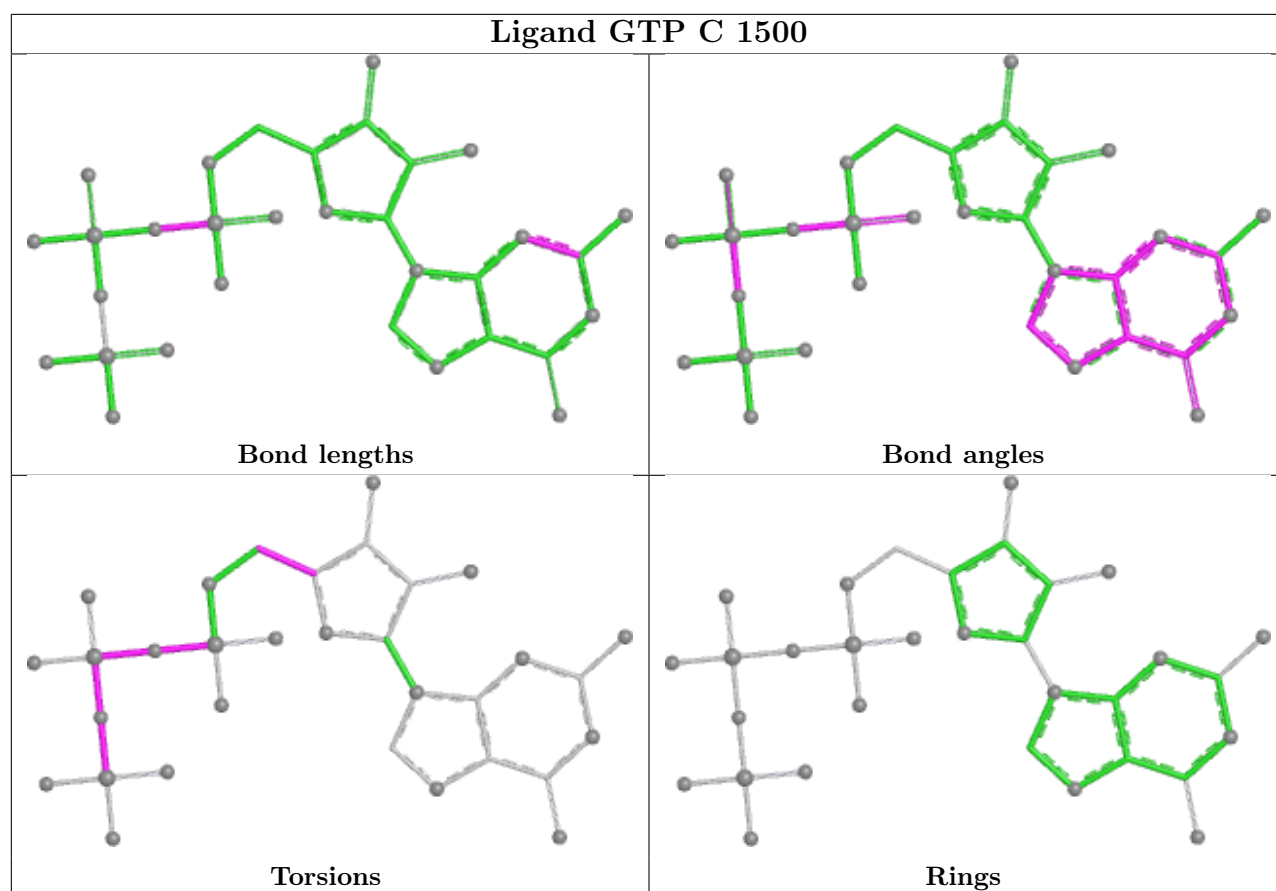
Mol	Chain	Res	Type	Atoms
45	C	1500	GTP	O4'-C4'-C5'-O5'
45	C	1500	GTP	C3'-C4'-C5'-O5'
45	C	1500	GTP	PB-O3B-PG-O1G
45	C	1500	GTP	PG-O3B-PB-O2B
45	C	1500	GTP	PA-O3A-PB-O2B

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	C	1500	GTP	8	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.



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.

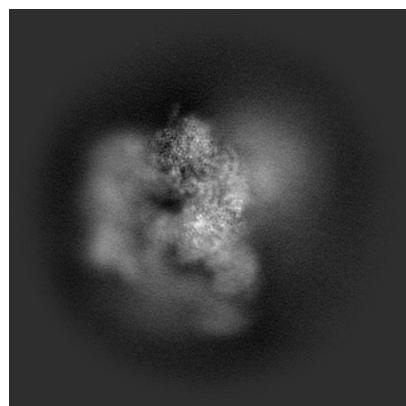
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35105. These allow visual inspection of the internal detail of the map and identification of artifacts.

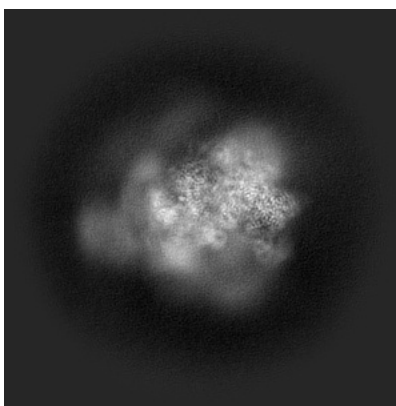
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

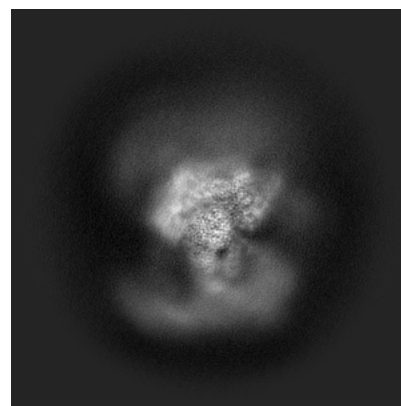
6.1.1 Primary map



X

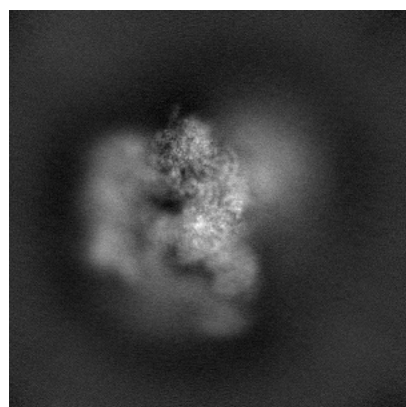


Y

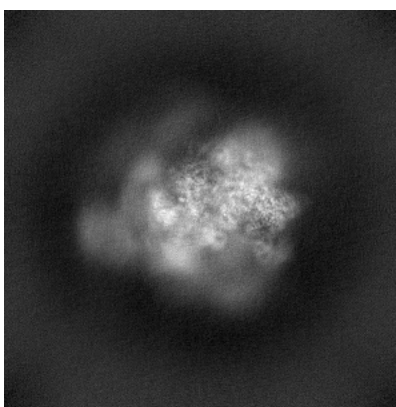


Z

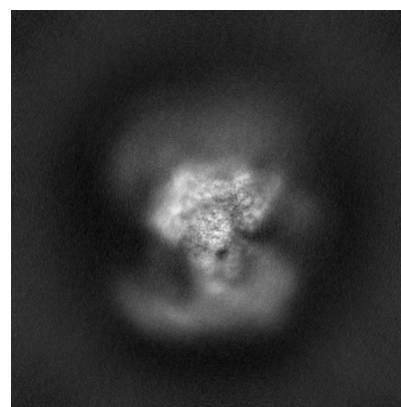
6.1.2 Raw map



X



Y

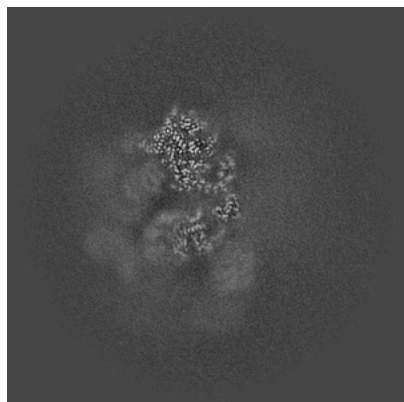


Z

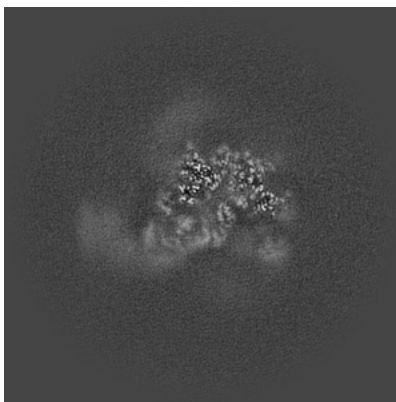
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

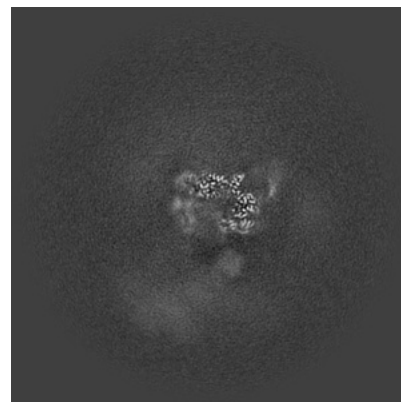
6.2.1 Primary map



X Index: 240

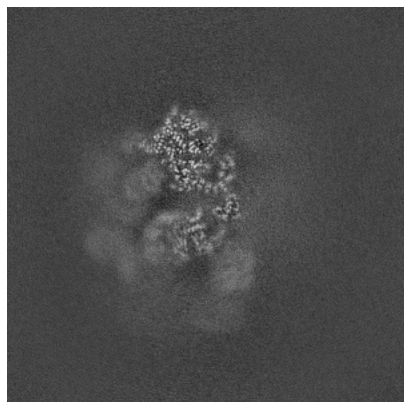


Y Index: 240

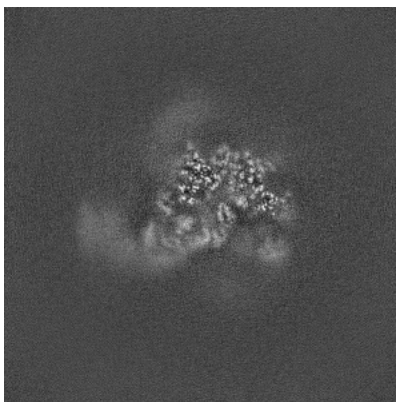


Z Index: 240

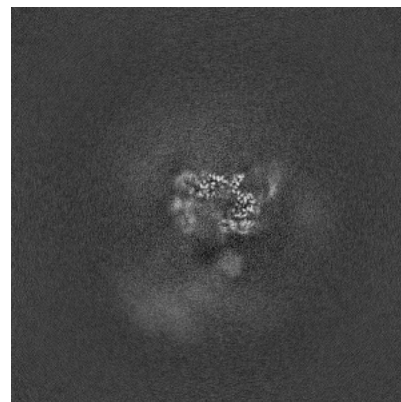
6.2.2 Raw map



X Index: 240



Y Index: 240

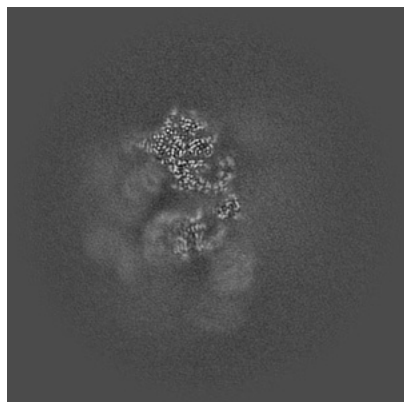


Z Index: 240

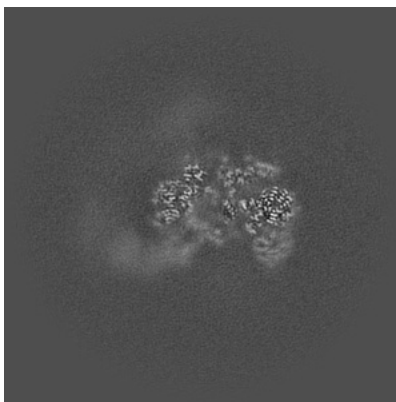
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

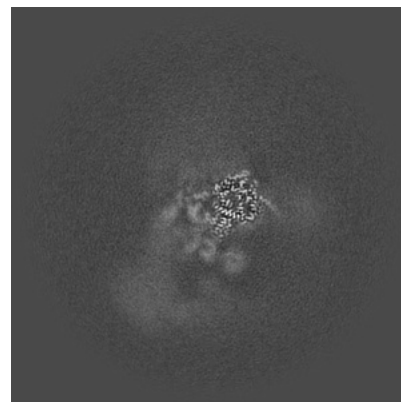
6.3.1 Primary map



X Index: 239

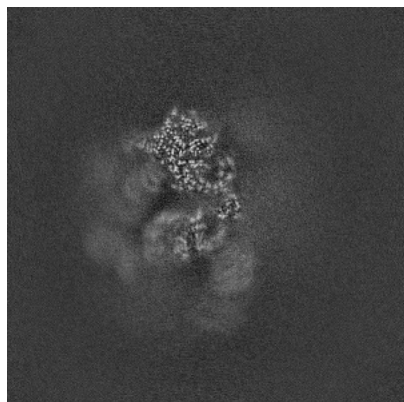


Y Index: 225

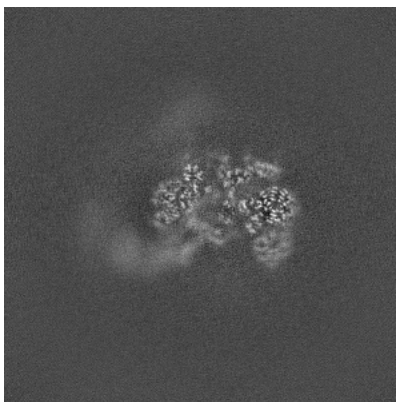


Z Index: 222

6.3.2 Raw map



X Index: 239



Y Index: 226

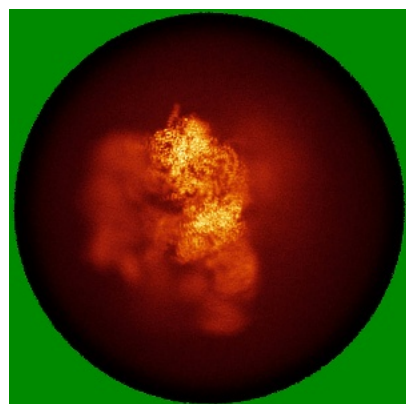


Z Index: 222

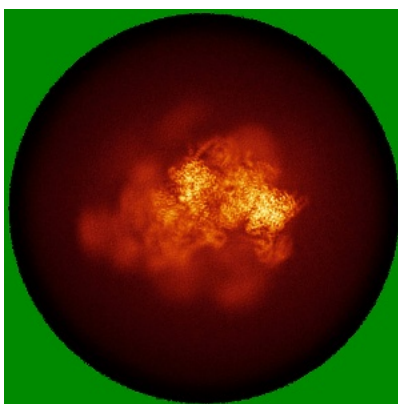
The images above show the largest variance slices of the map in three orthogonal directions.

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

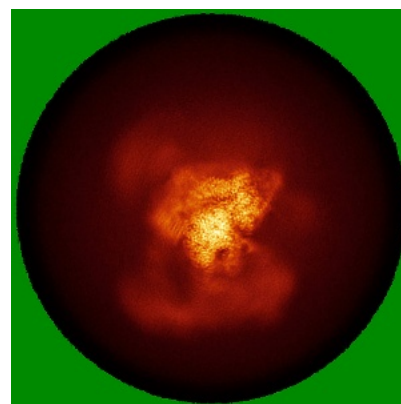
6.4.1 Primary map



X

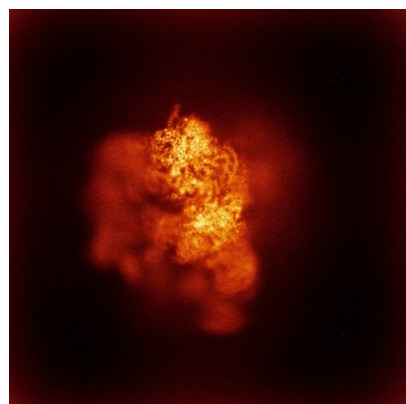


Y

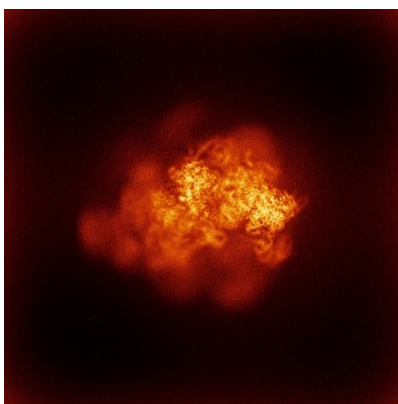


Z

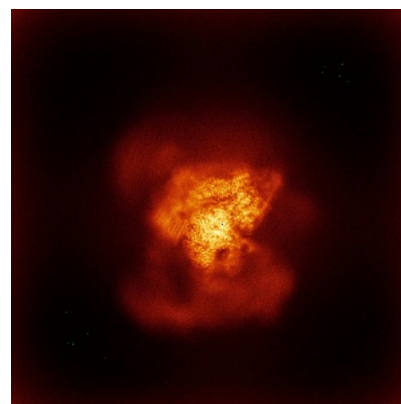
6.4.2 Raw map



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



X



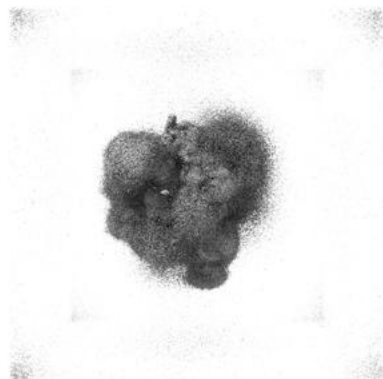
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.19. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

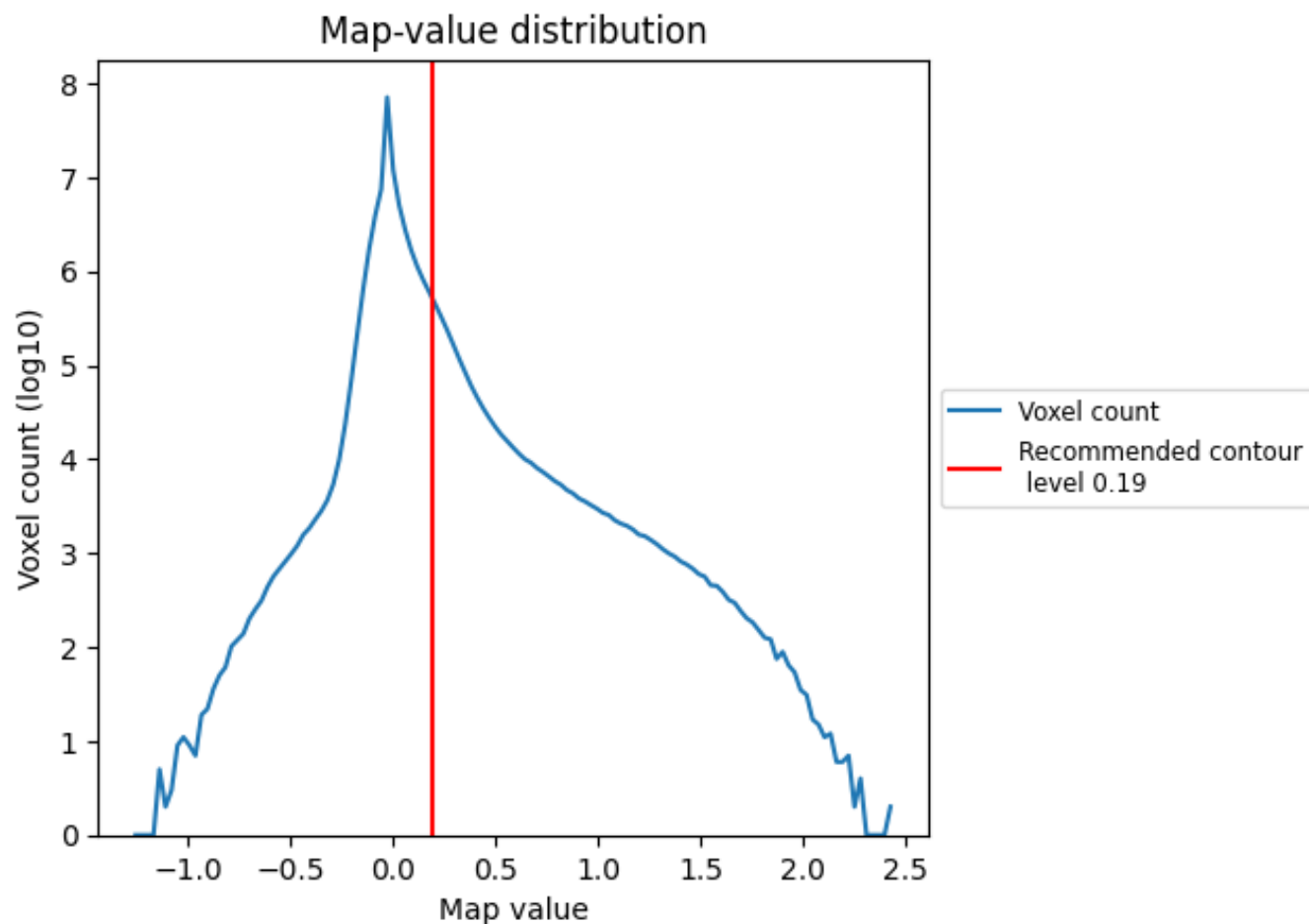
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

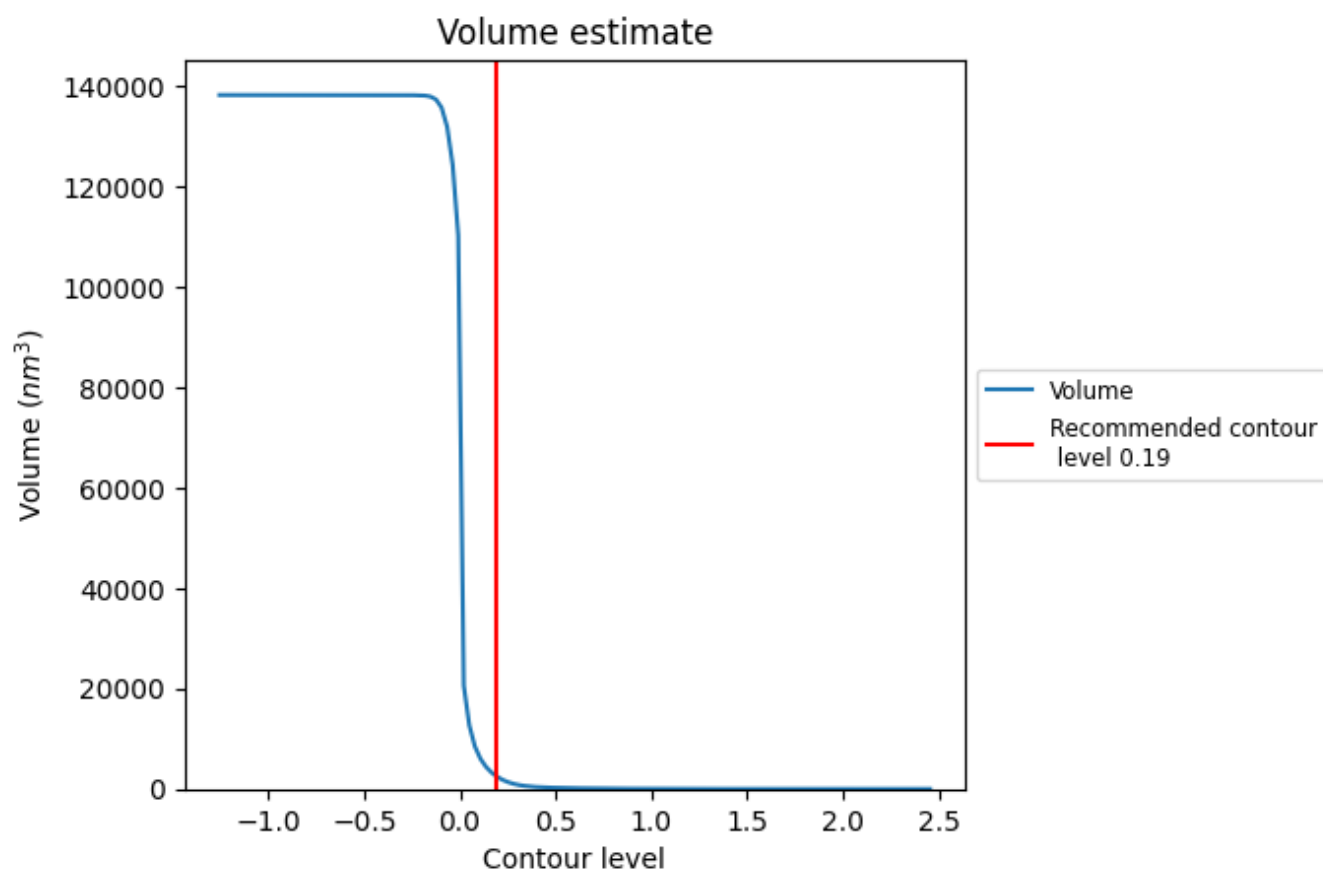
This section contains the results of statistical analysis of the map.

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.

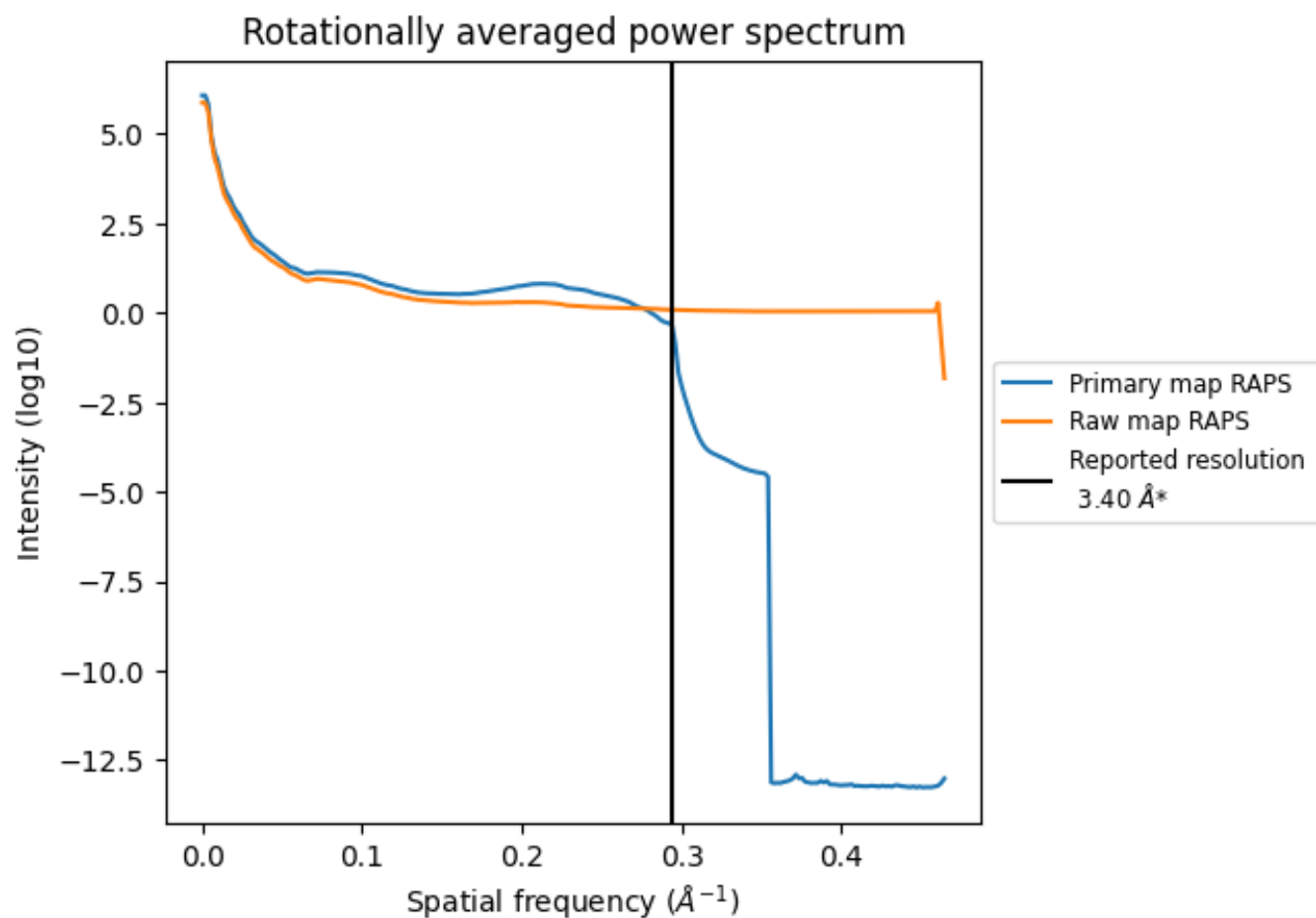
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2577 nm^3 ; this corresponds to an approximate mass of 2328 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 ⓘ

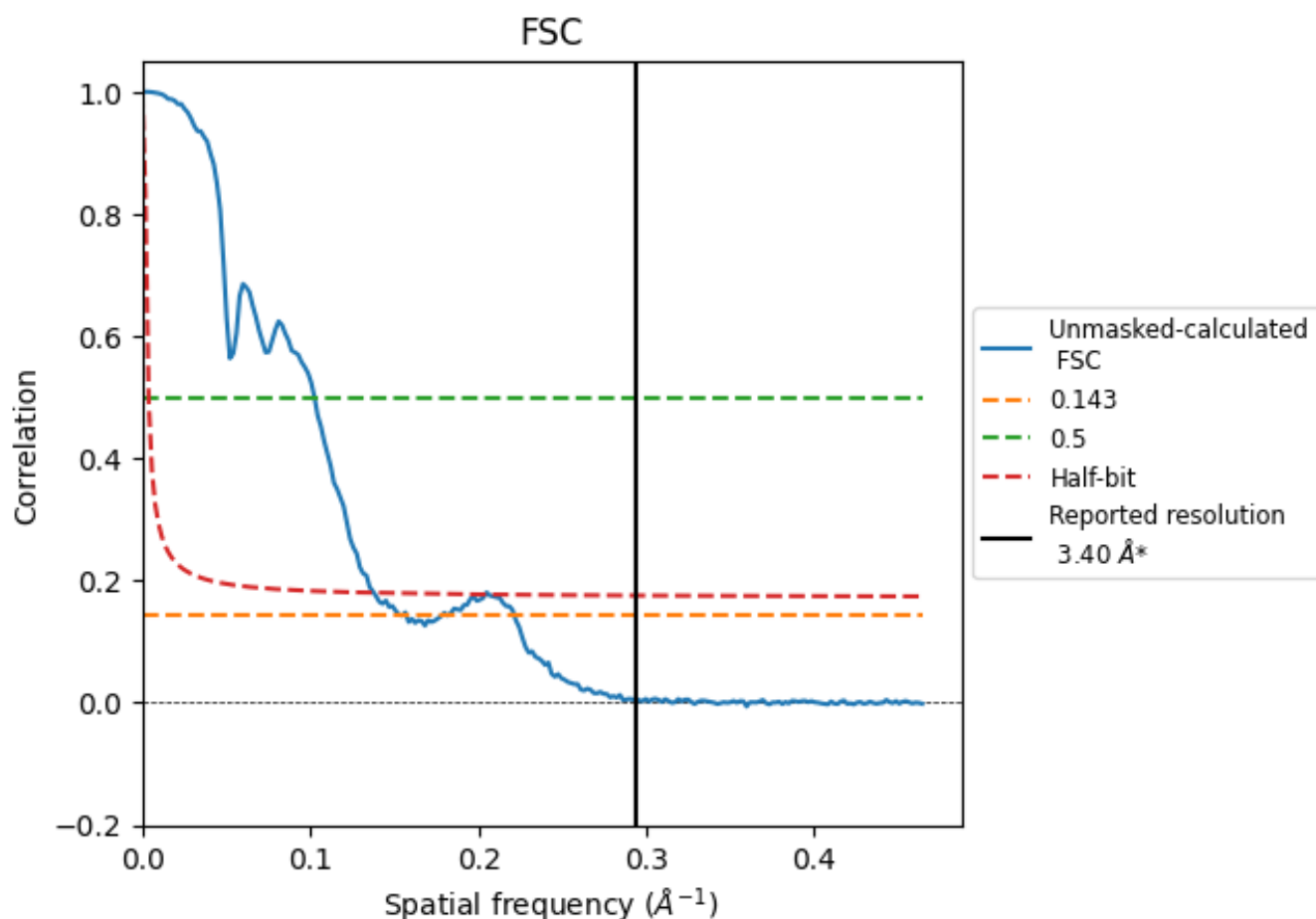


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

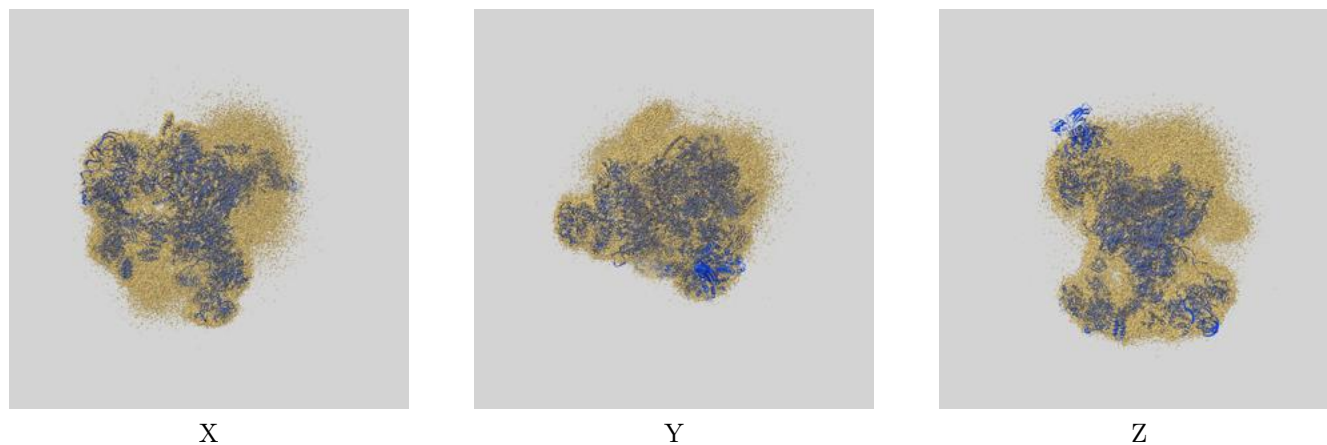
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.48	9.75	7.25

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.48 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

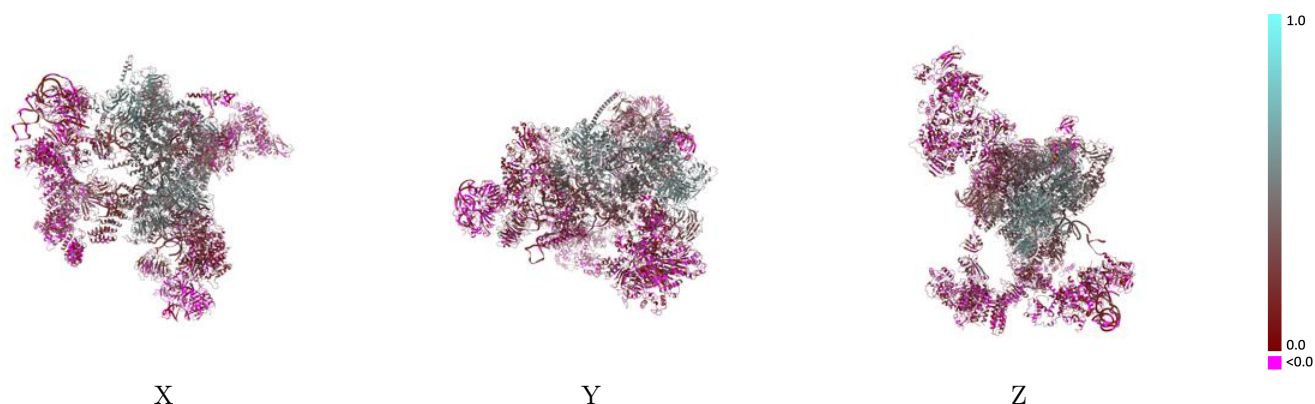
This section contains information regarding the fit between EMDB map EMD-35105 and PDB model 8I0P. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



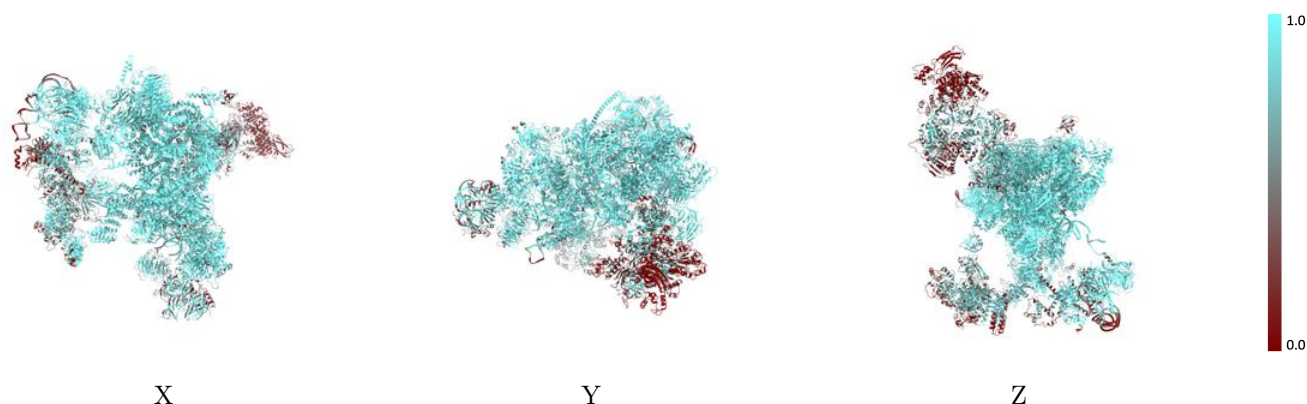
The images above show the 3D surface view of the map at the recommended contour level 0.19 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



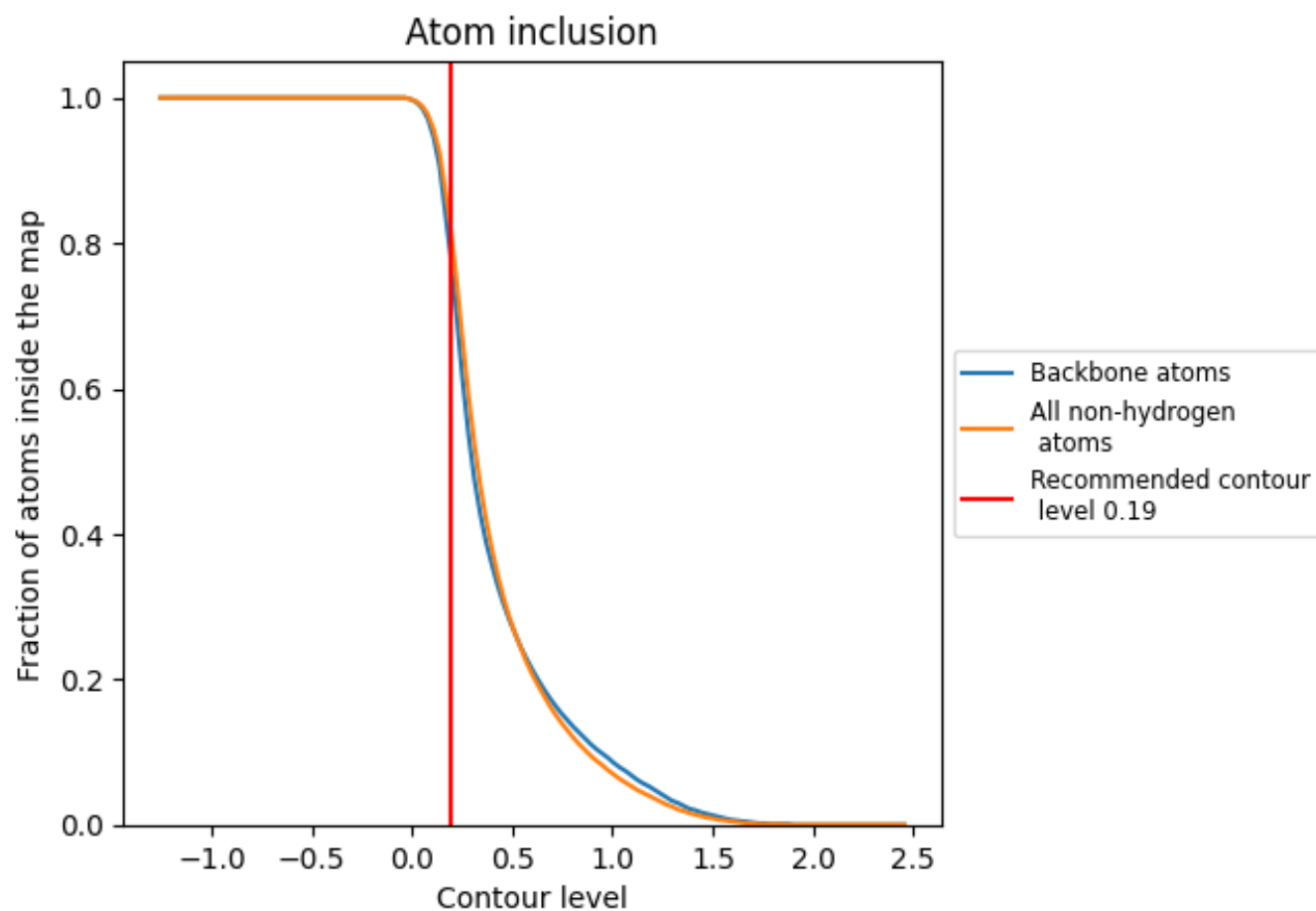
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.19).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 83% 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 (0.19) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8270	 0.2870
1	 0.9710	 0.4690
2	 0.9300	 0.3980
3	 0.9870	 0.4850
4	 0.9420	 0.2370
5	 0.9340	 0.5140
6	 0.9910	 0.3740
7	 0.9520	 0.4660
8	 0.9720	 0.4140
9	 0.9100	 0.2660
A	 0.8960	 0.3530
B	 0.9040	 0.1640
C	 0.9010	 0.1980
D	 0.3650	 0.1400
E	 0.8420	 0.1810
F	 0.8960	 0.2350
G	 0.9640	 0.2930
H	 0.7850	 0.2110
I	 0.7100	 0.1150
J	 0.9590	 0.2620
K	 0.8650	 0.2550
L	 0.9840	 0.4810
N	 0.8340	 0.1620
O	 0.8730	 0.1820
P	 0.9520	 0.4780
Q	 0.5540	 0.1340
R	 0.9420	 0.4120
T	 0.9860	 0.4700
X	 0.9680	 0.3540
Y	 0.9680	 0.4810
Z	 0.9670	 0.4700
a	 0.6700	 0.0550
b	 0.5760	 0.0140
c	 0.6260	 0.0030
d	 0.6420	 0.0290



Continued on next page...

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Chain	Atom inclusion	Q-score
e	 0.6430	 0.0390
f	 0.5850	 0.0300
g	 0.6480	 -0.0220
h	 0.8420	 0.1220
i	 0.8660	 0.1030
j	 0.9280	 0.1720
k	 0.9340	 0.1280
l	 0.8940	 0.1710
m	 0.8860	 0.1450
n	 0.7760	 0.1740
o	 0.8330	 0.1390
p	 0.9010	 0.1850
u	 0.5620	 0.1590
v	 0.7330	 0.2950
w	 0.6850	 0.2220
y	 0.7640	 0.1920
z	 0.9760	 0.3290