wwPDB EM Validation Summary Report

Dec 11, 2022 – 10:23 pm GMT

PDB ID	:	6TB4
EMDB ID	:	EMD-10438
Title	:	Structure of SAGA bound to TBP
Authors	:	Papai, G.; Frechard, A.; Kolesnikova, O.; Crucifix, C.; Schultz, P.; Ben-Shem, A.
Deposited on	:	2019-10-31
Resolution	:	3.80 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:

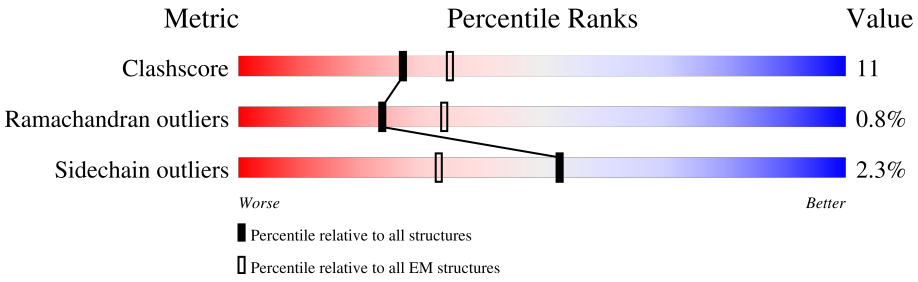
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	M	243	74% 37% 31% 6% 26%
2	A	448	28% 31% 7% 61%
3	C	698	9% 8% 91%
4	F	517	33% 33% 7% 59%
5	D	341	39% 37% 21% 39%
6	E	1191	6% 10% 87%
7	J	217	19% 36% 7% 56%
8	K	609	15% 17% 7% 75%

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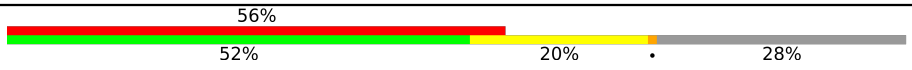
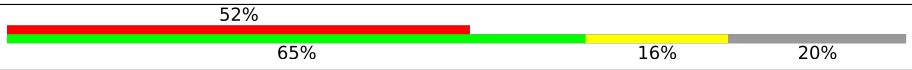
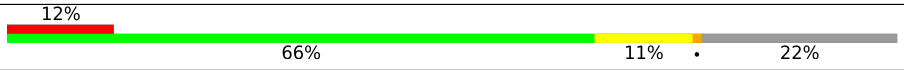
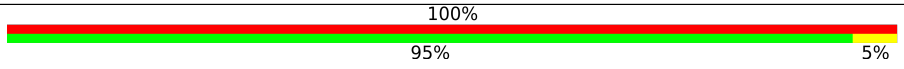
Mol	Chain	Length	Quality of chain
9	G	722	
10	H	485	
11	I	153	
12	L	3825	
13	B	76	

2 Entry composition (i)

There are 13 unique types of molecules in this entry. The entry contains 40740 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 TATA-box Binding Protein (TBP).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	M	180	1415	921	242	246	6	0	0

- Molecule 2 is a protein called Transcriptional coactivator HFI1/ADA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	173	1300	816	228	250	6	0	0

- Molecule 3 is a protein called SAGA-associated factor 73 (Sgf73).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	65	518	331	94	90	3	0	0

- Molecule 4 is a protein called Spt20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	F	210	1682	1071	292	315	4	0	0

- Molecule 5 is a protein called Subunit of the SAGA and SAGA-like transcriptional regulatory complexes, interacts with Spt15p to act.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	209	1616	1016	298	295	7	0	0

- Molecule 6 is a protein called Subunit of the SAGA transcriptional regulatory complex, involved in proper assembly of the complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	154	Total	C	N	O	S	0	0
			1232	784	208	233	7		

- Molecule 7 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	96	Total	C	N	O	S	0	0
			768	489	120	156	3		

- Molecule 8 is a protein called Subunit (61/68 kDa) of TFIID and SAGA complexes.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	154	Total	C	N	O	S	0	0
			1192	747	216	226	3		

- Molecule 9 is a protein called Subunit (90 kDa) of TFIID and SAGA complexes.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	522	Total	C	N	O	S	0	0
			4075	2581	719	756	19		

- Molecule 10 is a protein called Subunit (60 kDa) of TFIID and SAGA complexes.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	421	Total	C	N	O	S	0	0
			3263	2084	556	617	6		

- Molecule 11 is a protein called Subunit (17 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	123	Total	C	N	O	S	0	0
			981	632	169	178	2		

- Molecule 12 is a protein called Transcription-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	2968	Total	C	N	O	S	0	0
			22318	14296	3864	4071	87		

- Molecule 13 is a protein called Transcriptional adapter 3 (Ada3).

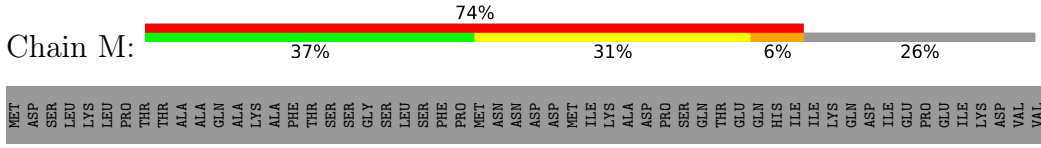
Mol	Chain	Residues	Atoms				AltConf	Trace
13	B	76	Total	C	N	O	0	0
			380	228	76	76		

3 Residue-property plots (i)

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.

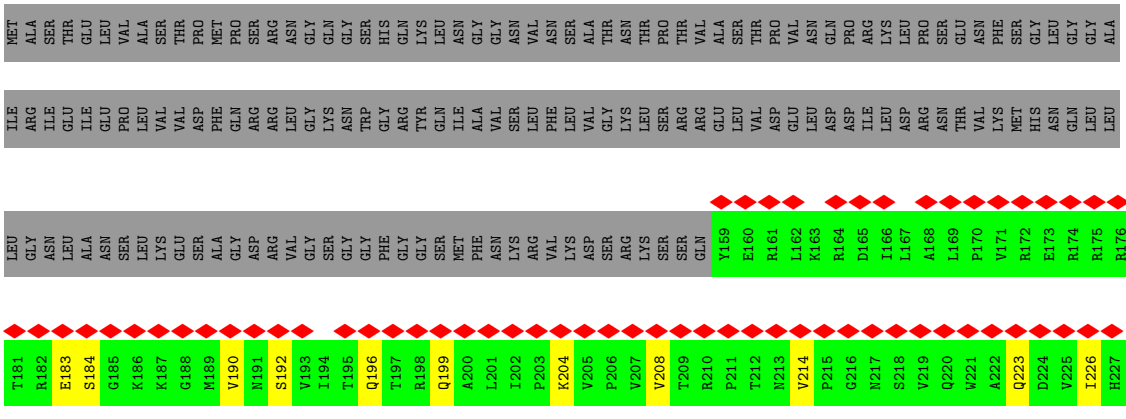
• Molecule 1: TATA-box Binding Protein (TBP)

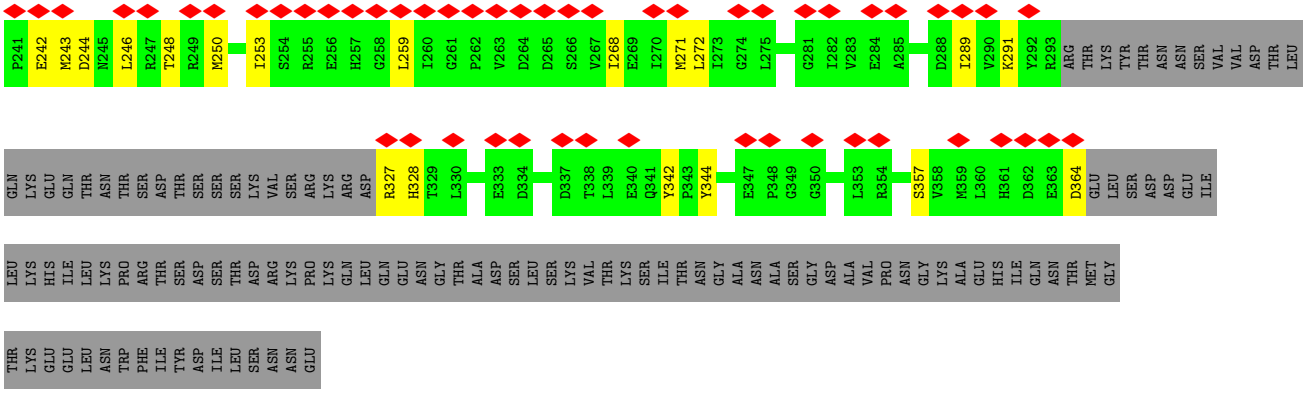
Chain M:



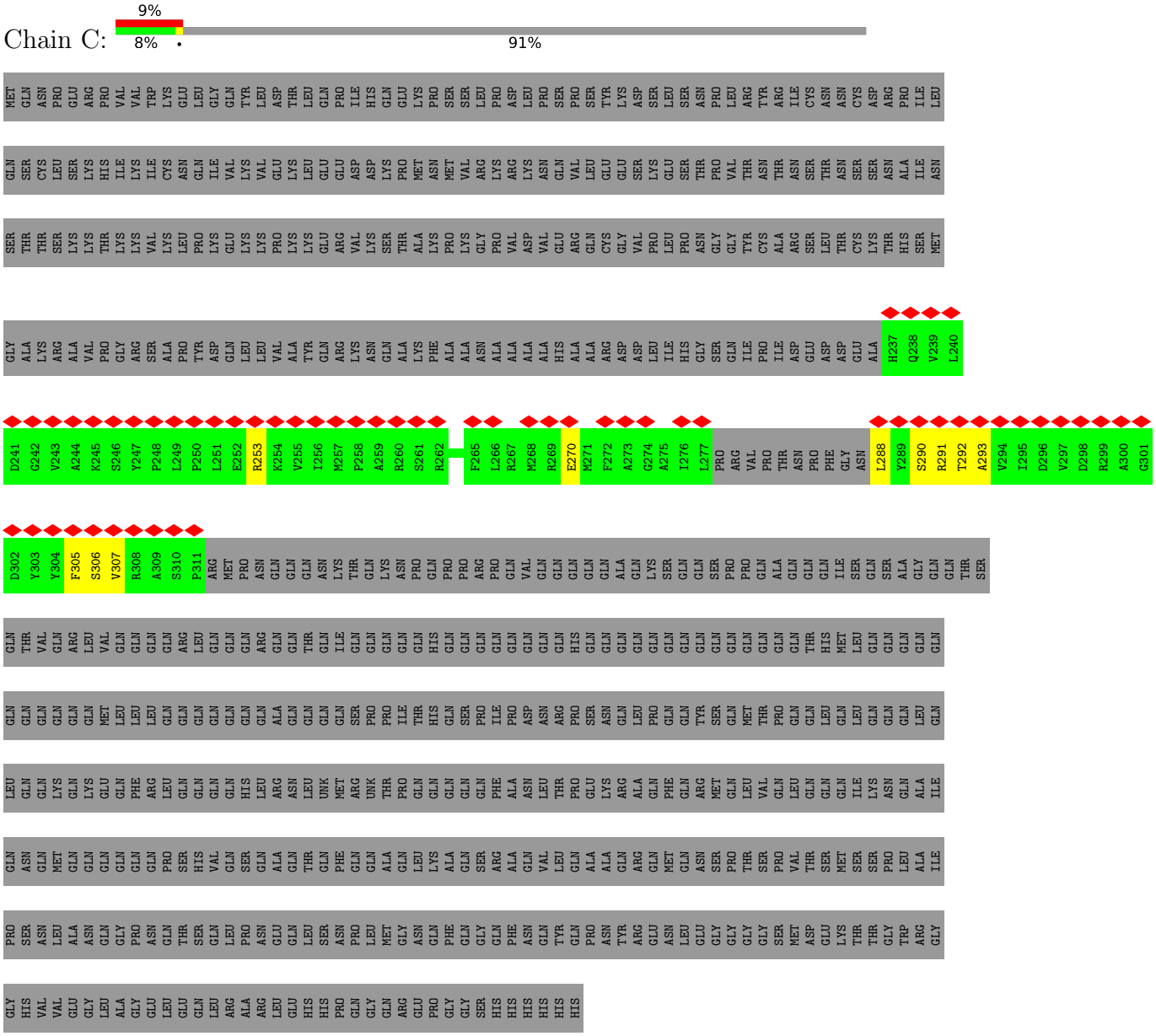
• Molecule 2: Transcriptional coactivator HFI1/ADA1

Chain A:



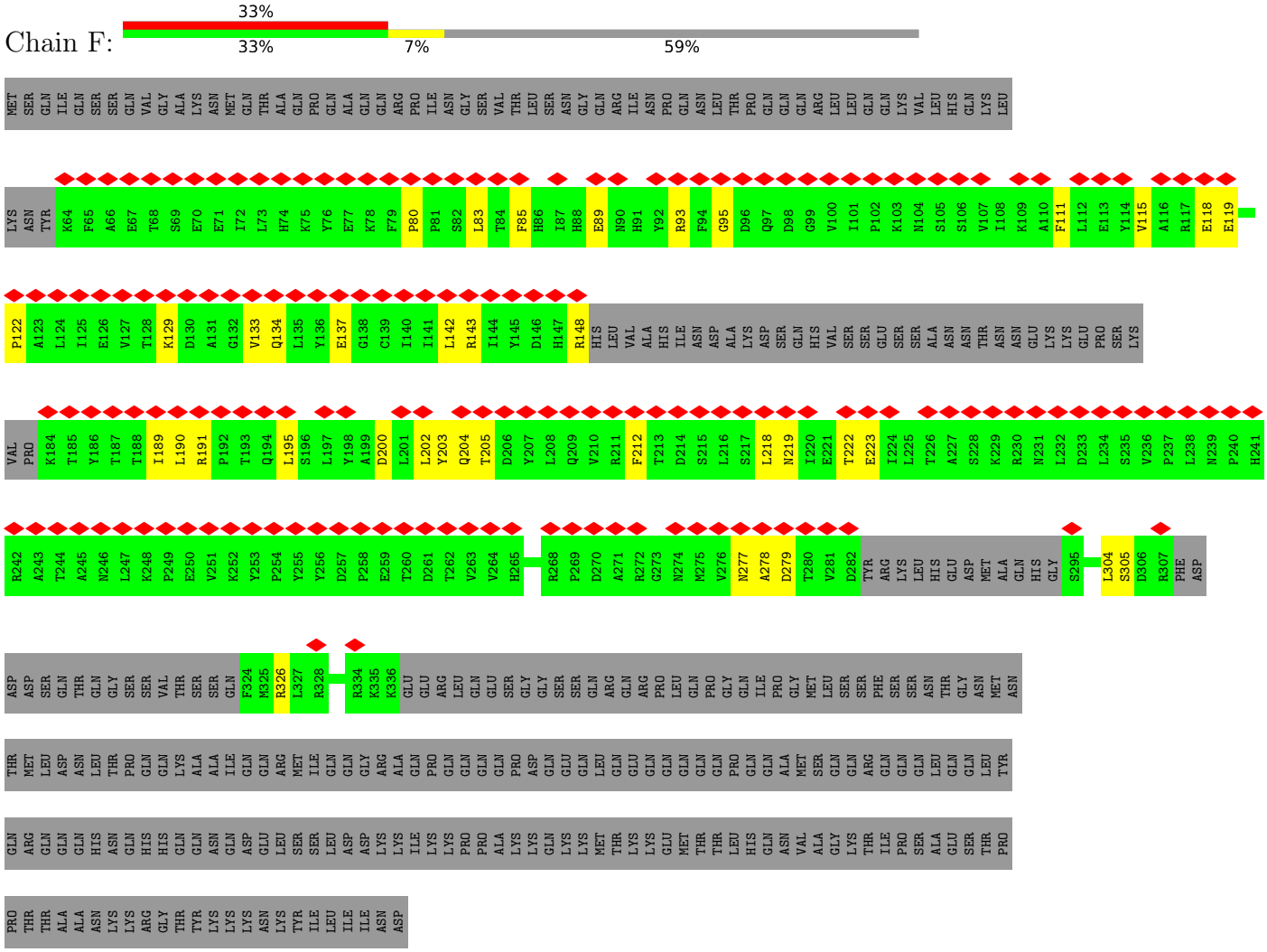


• Molecule 3: SAGA-associated factor 73 (Sgf73)



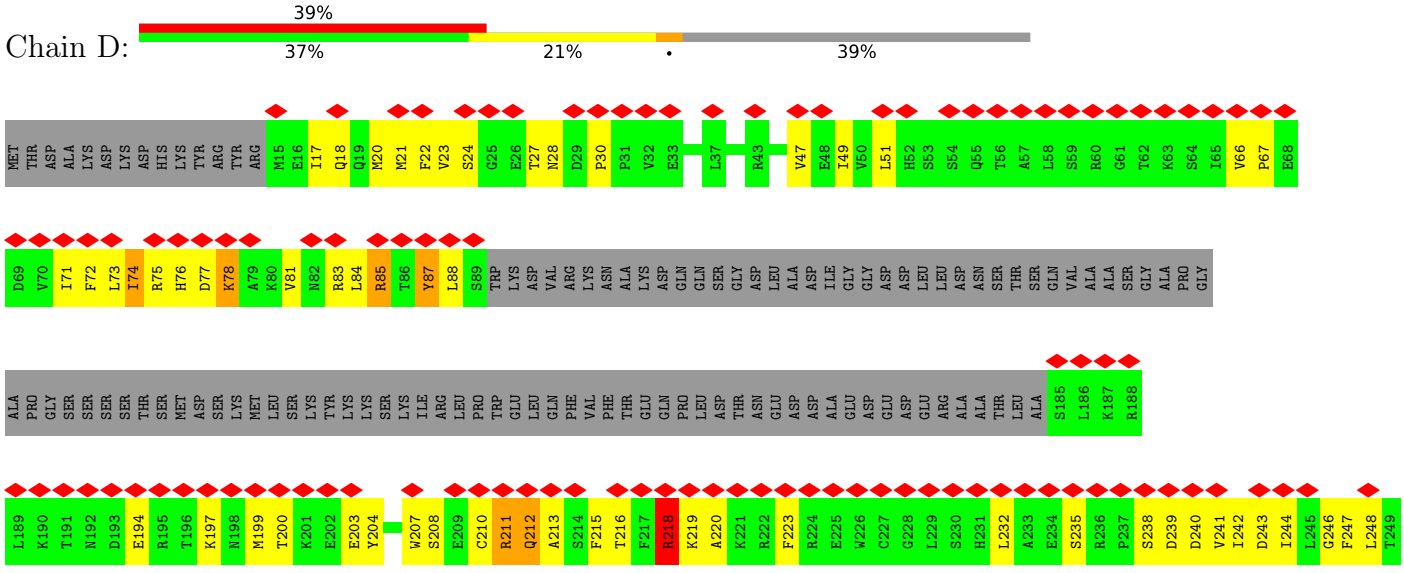
• Molecule 4: Spt20

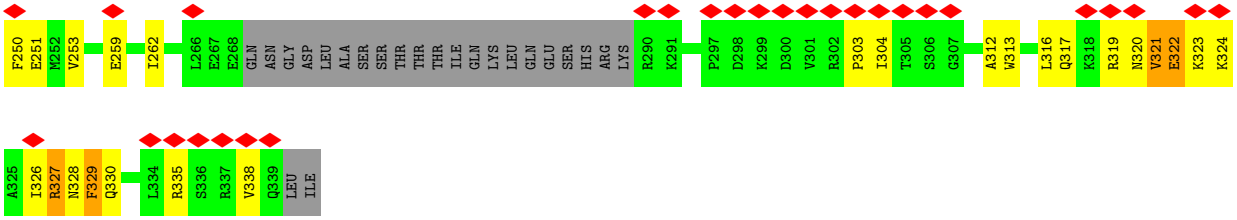
Chain F:



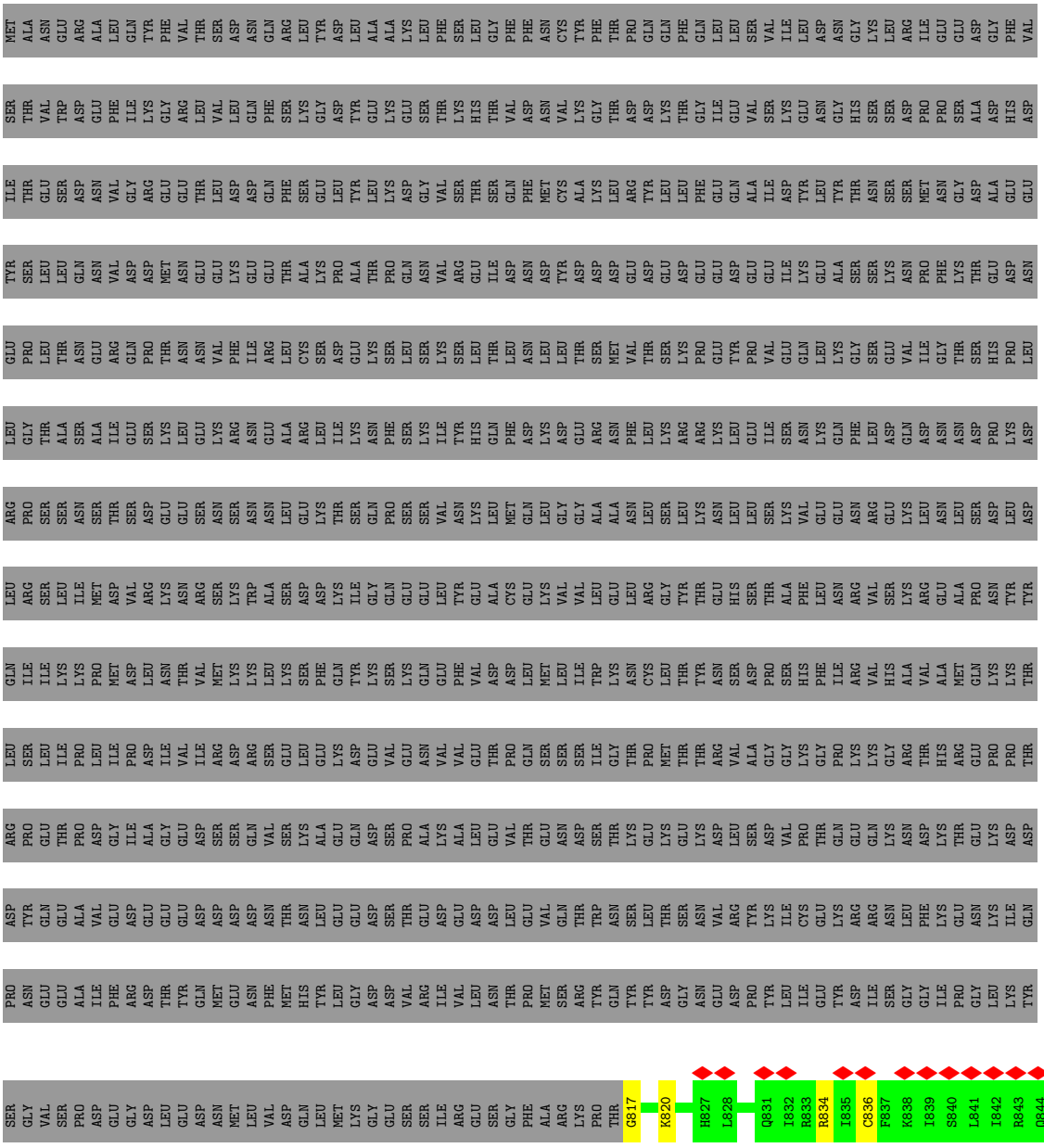
• Molecule 5: Subunit of the SAGA and SAGA-like transcriptional regulatory complexes, interacts with Spt15p to act

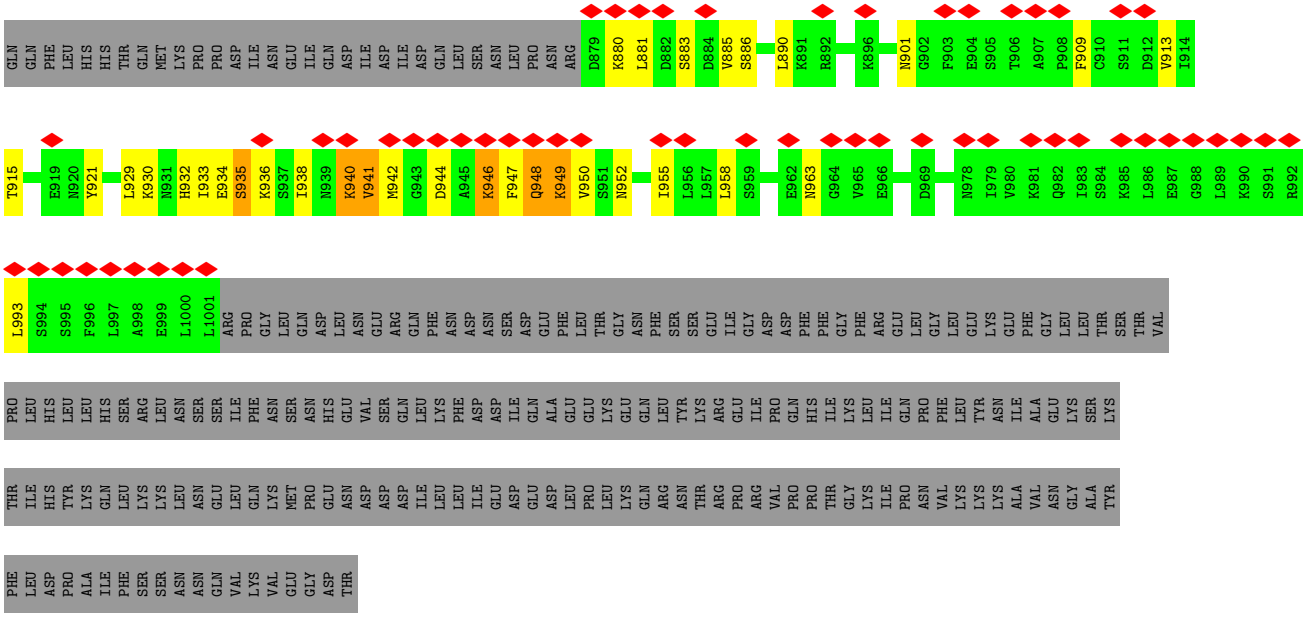
Chain D:





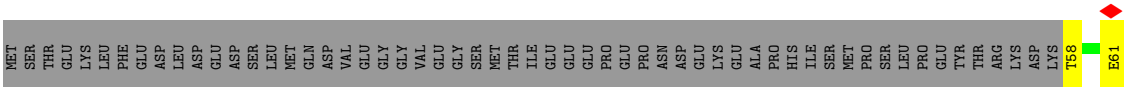
• Molecule 6: Subunit of the SAGA transcriptional regulatory complex, involved in proper assembly of the complex

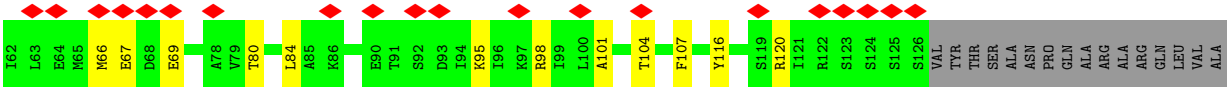


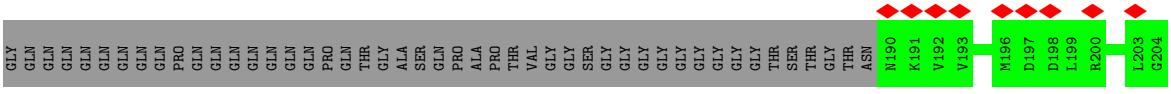


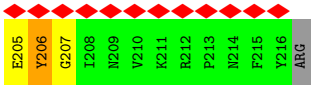
• Molecule 7: Transcription initiation factor TFIID subunit 10

Chain J:



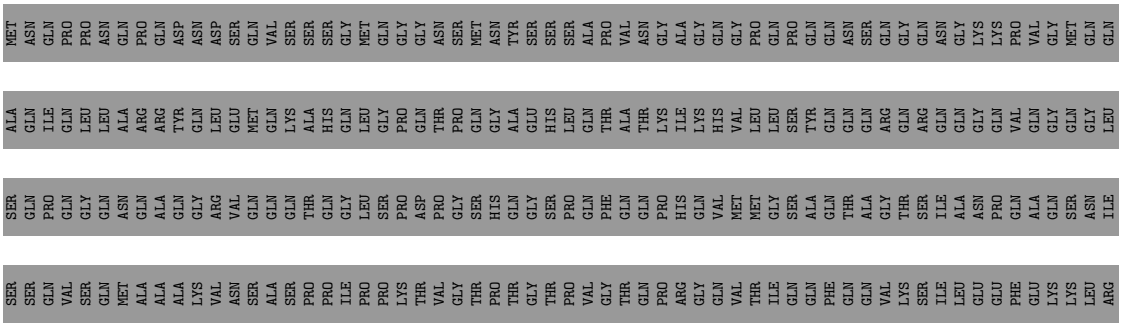


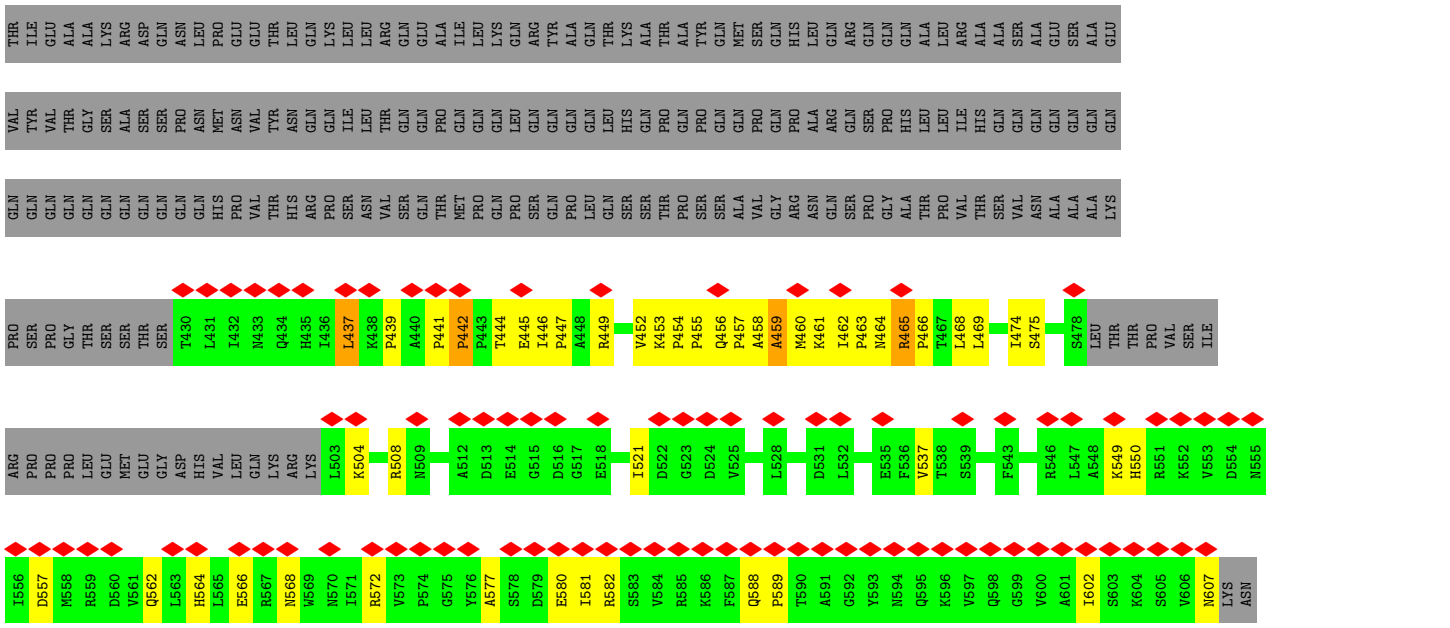




• Molecule 8: Subunit (61/68 kDa) of TFIID and SAGA complexes

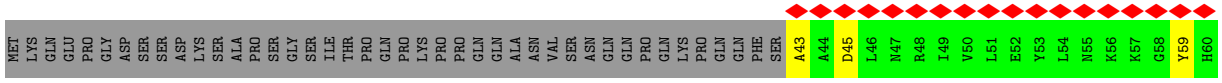
Chain K:

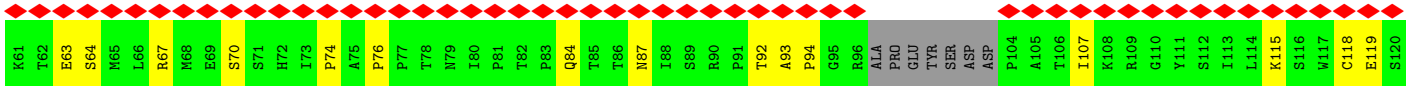


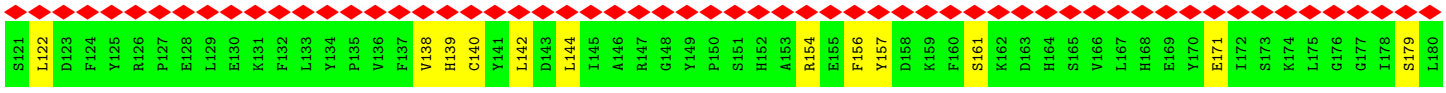


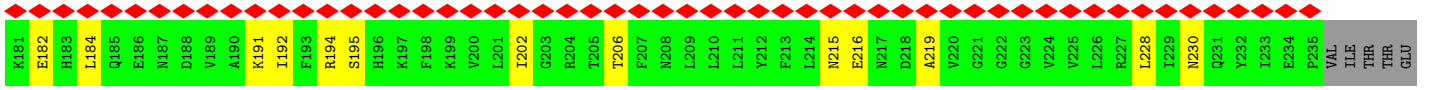
• Molecule 9: Subunit (90 kDa) of TFIID and SAGA complexes

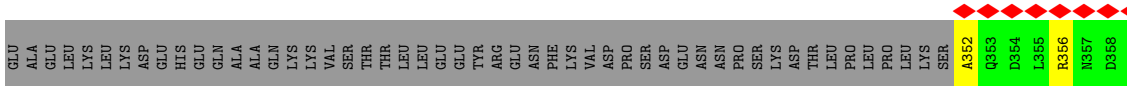
Chain G:

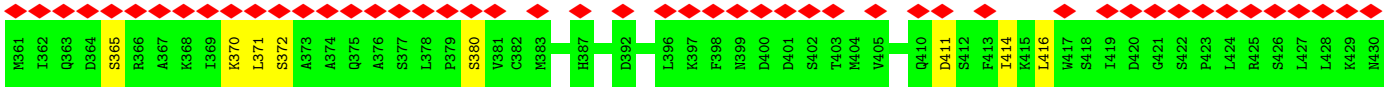


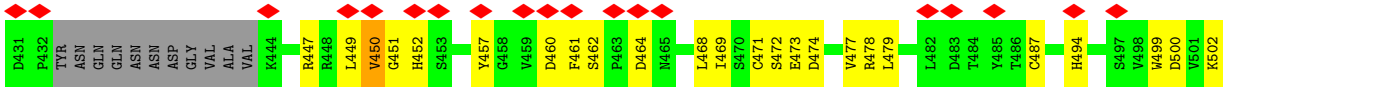


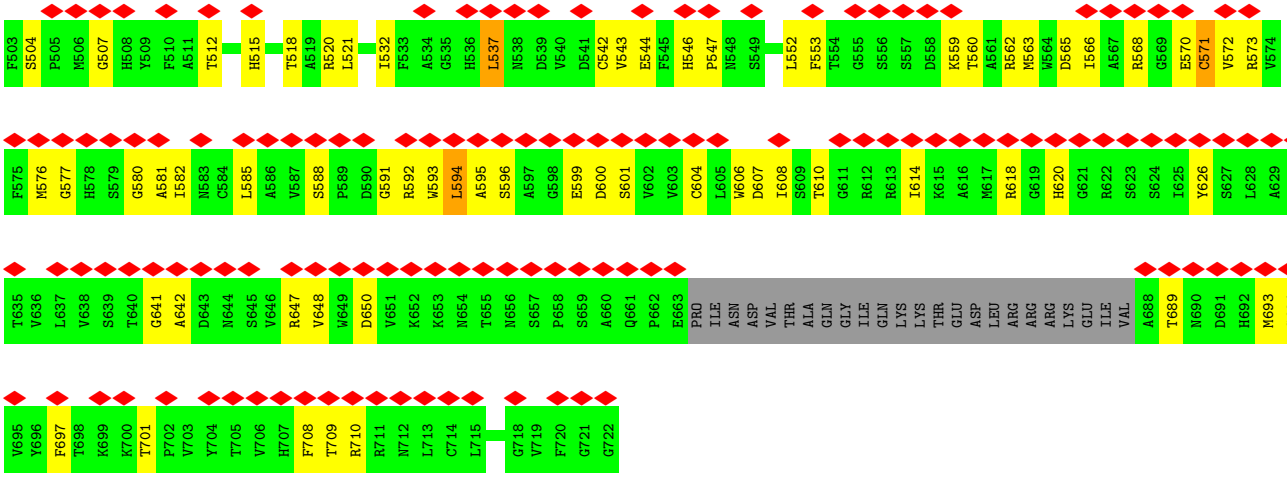






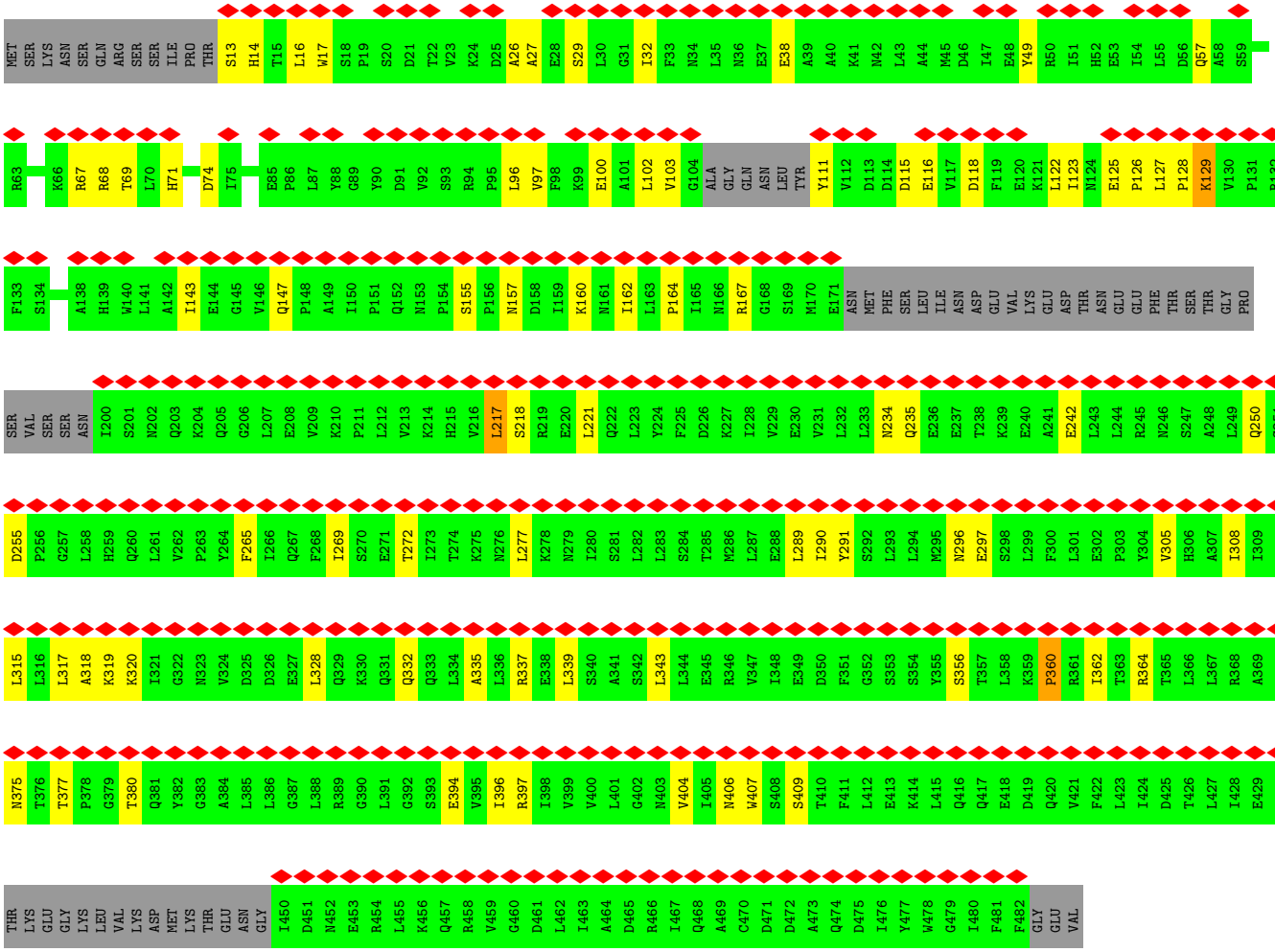






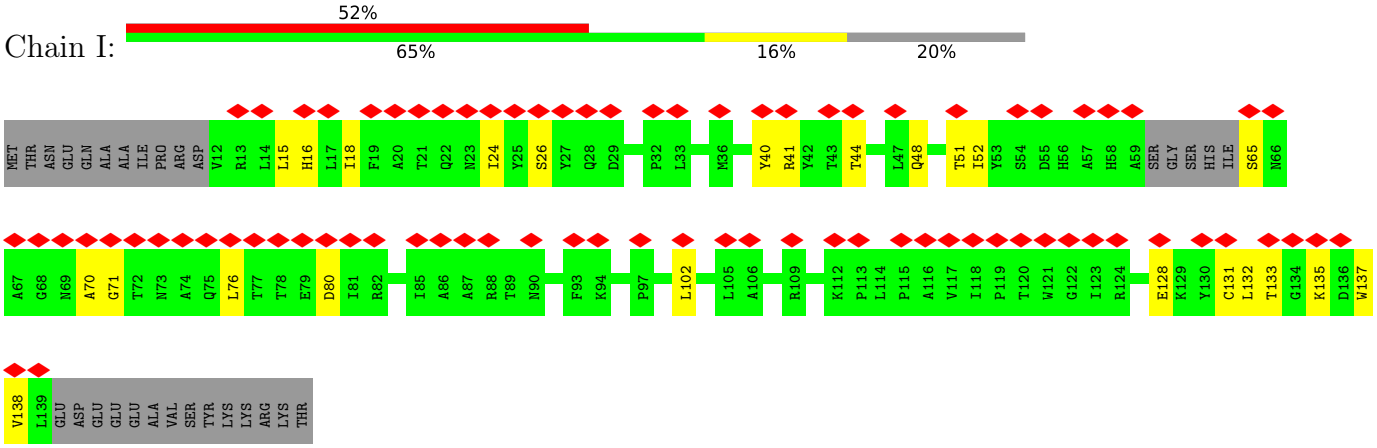
• Molecule 10: Subunit (60 kDa) of TFIID and SAGA complexes

Chain H:



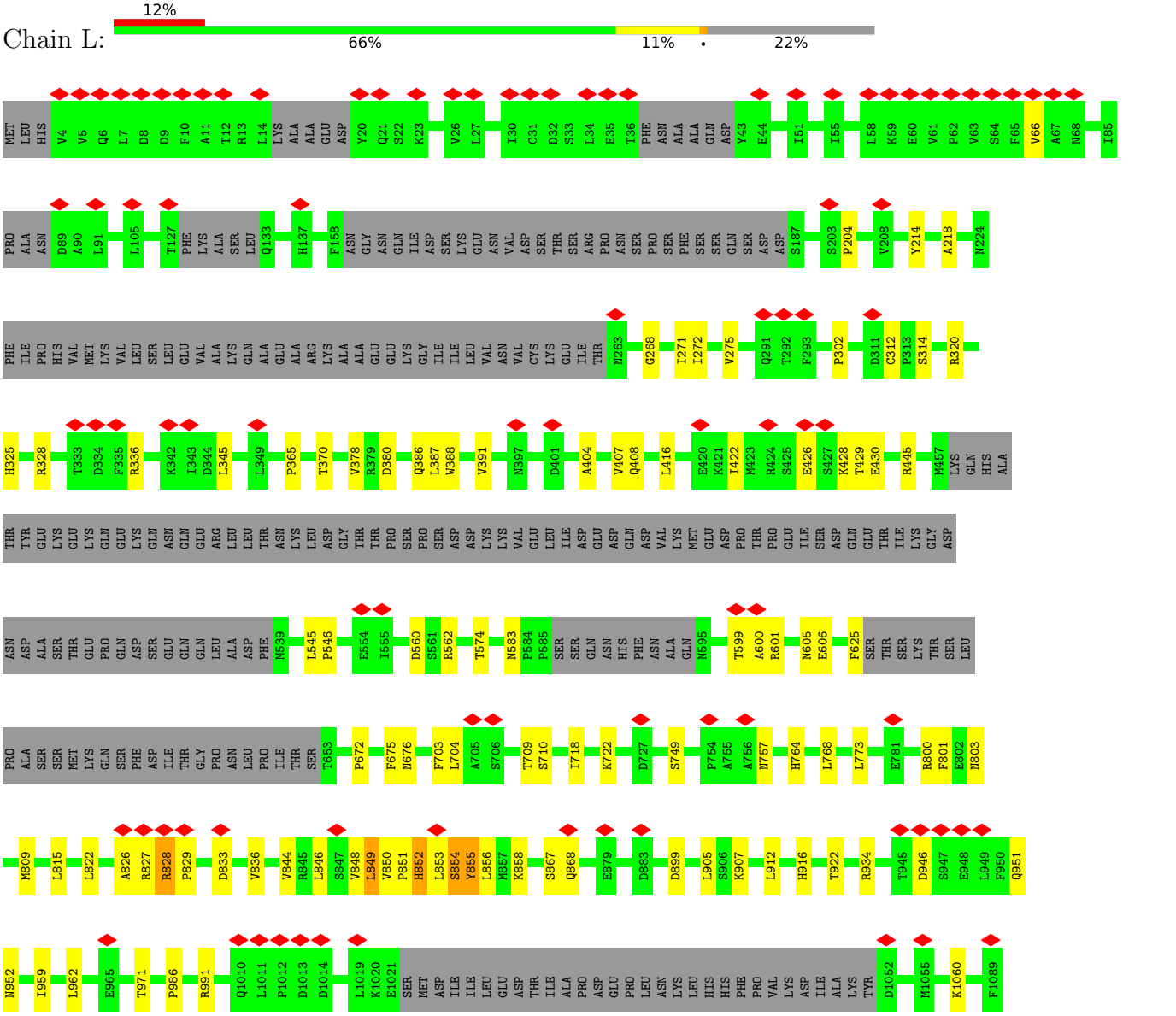
• Molecule 11: Subunit (17 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation

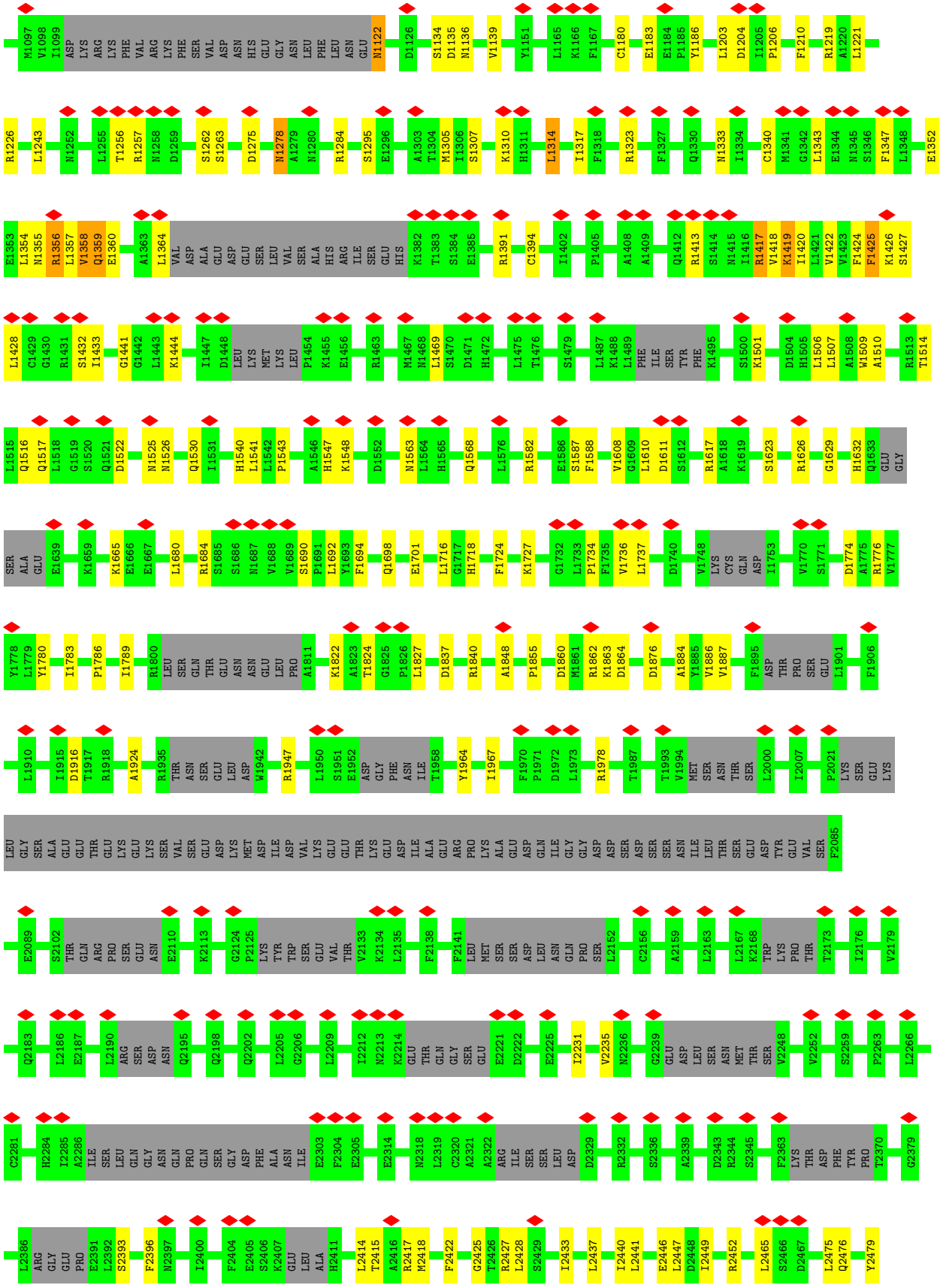
Chain I:



• Molecule 12: Transcription-associated protein

Chain L:




M1097 V1098 I1099 ASP LYS ARG LYS PHE VAL ARG LYS PHE SER VAL ASP ASN HIS GLU GLY ASN LEU PHE LEU ASN GLU N1122
D1126
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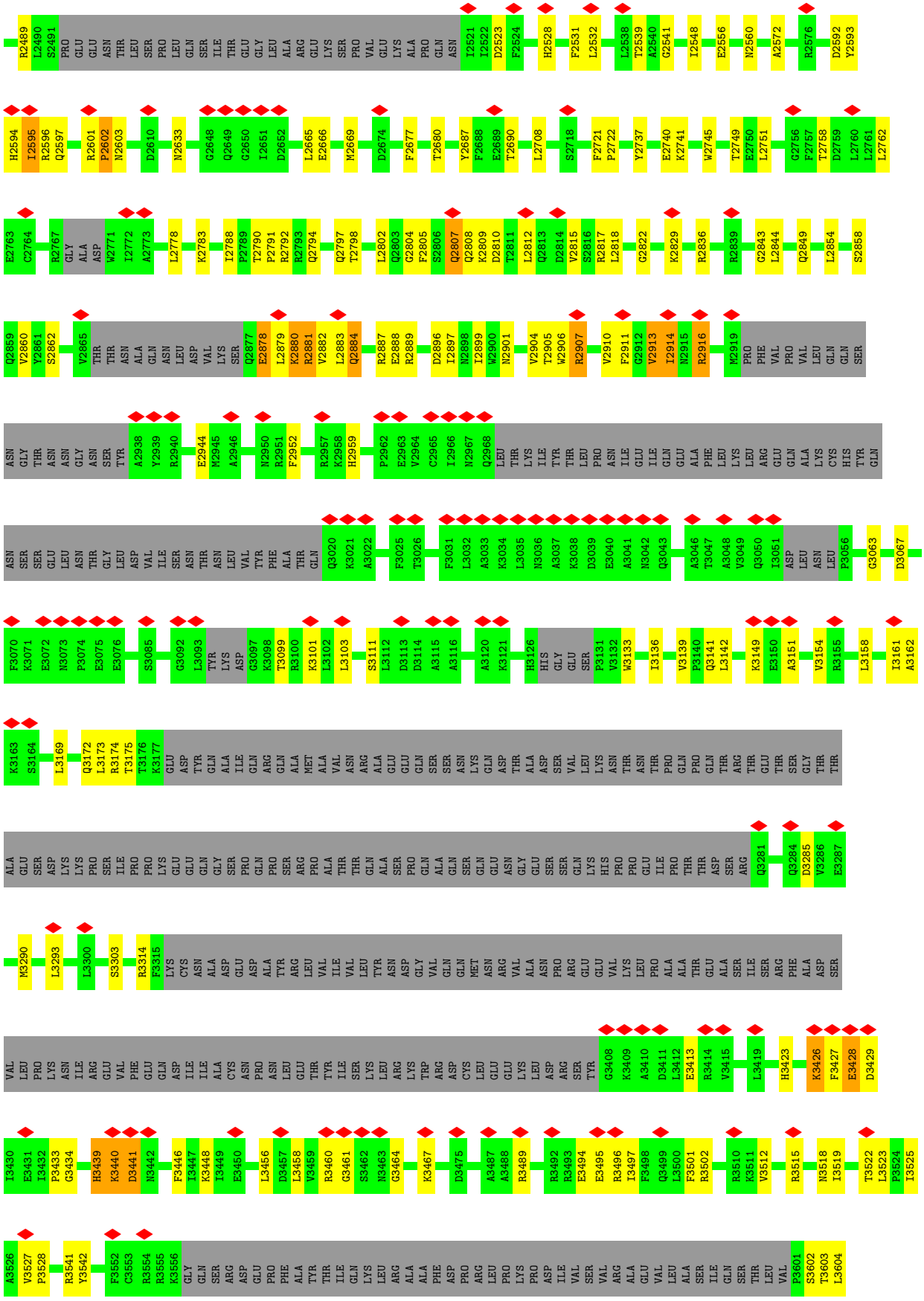
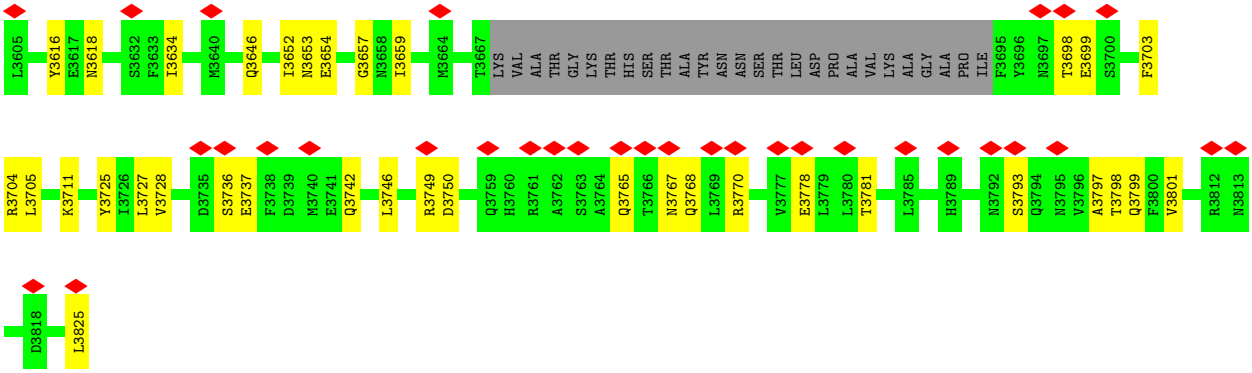
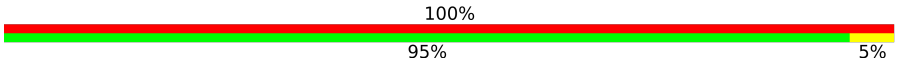
V1139
Y1151
L1165 K1166 F1167
C1180
E1183 E1184 P1185 Y1186
L1203 D1204 I1205 P1206
F1210
R1219 A1220 L1221
R1226 L1243 N1252 L1255 T1256 R1257 N1258 D1259 S1262 S1263 D1275 N1278 A1279 N1280 R1284 S1295 E1296 A1303 T1304 M1305 T1306 S1307 K1310 H1311 L1314 I1317 F1318 R1323 F1327 Q1330 N1333 I1334 C1340 M1341 G1342 L1343 E1344 N1345 S1346 F1347 L1348 E1352
E1353 L1354 N1355 R1356 L1357 V1358 Q1359 E1360 A1363 L1364 VAL ASP ALA GLU ASP GLU SER LEU VAL SER ALA HIS ARG ILE SER GLU HIS K1382 T1383 S1384 E1385 R1391 C1394 I1402 P1405 A1408 A1409 Q1412 R1413 S1414 N1415 I1416 R1417 V1418 K1419 I1420 L1421 V1422 V1423 F1424 F1425 K1426 S1427
L1428 C1429 G1430 R1431 S1432 I1433 G1441 G1442 L1443 K1444 I1447 D1448 LEU LYS MET LYS LEU P1454 K1455 E1456 R1463 M1467 N1468 L1469 S1470 D1471 H1472 L1475 T1476 S1479 L1487 K1488 L1489 PHE ILE SER TYR PHE K1495 S1500 K1501 D1504 H1505 L1506 L1507 A1508 W1509 A1510 R1513 T1514
L1515 Q1516 Q1517 L1518 G1519 S1520 Q1521 D1522 N1525 N1526 Q1530 I1531 H1540 L1541 L1542 P1543 A1546 H1547 K1548 D1552 N1563 L1564 H1565 Q1568 L1576 R1582 E1586 S1587 F1588 V1608 G1609 L1610 D1611 S1612 R1617 A1618 K1619 S1623 R1626 G1629 H1632 Q1633 GLU GLY
SER ALA GLU E1639 K1659 K1665 E1666 E1667 L1680 R1684 S1685 S1686 N1687 V1688 V1689 S1690 P1691 L1692 Y1693 F1694 Q1698 E1701 L1716 G1717 H1718 F1724 K1727 G1732 L1733 P1734 F1735 V1736 L1737 D1740 V1748 LYS CYS GLN ASP I1753 V1770 S1771 D1774 A1775 R1776 V1777
Y1778 L1779 Y1780 I1783 P1786 I1789 R1800 LEU SER GLN THR GLU ASN ASN GLU LEU PRO A1811 K1822 A1823 T1824 G1825 P1826 L1827 D1837 R1840 A1848 P1855 D1860 M1861 R1862 K1863 D1864 D1876 A1884 Y1885 V1886 V1887 F1895 ASP THR PRO SER GLU L1901 F1906
L1910 T1915 D1916 T1917 R1918 A1924 R1935 THR ASN SER GLU LEU ASP W1942 R1947 L1950 S1951 E1952 ASP GLY PHE ASN ILE T1958 Y1964 I1967 F1970 P1971 D1972 L1973 R1978 T1987 T1993 V1994 MET SER ASN THR SER L2000 I2007 P2021 LYS SER GLU LYS
LEU GLY SER ALA GLU GLU THR GLU LYS GLU LYS SER VAL SER GLU ASP LYS MET ASP ILE ASP VAL LYS GLU GLU THR LYS GLU ASP ILE ALA GLU ARG PRO LYS ALA GLU ASP GLN ILE GLY GLY ASP SER ASP SER SER ASN ILE LEU THR SER GLU ASP TYR GLU VAL SER F2085
E2089 S2102 THR GLN ARG PRO SER GLU ASN E2110 K2113 G2124 P2125 LYS TYR TRP SER GLU VAL THR V2133 K2134 L2135 F2138 F2141 LEU MET SER SER ASP LEU ASN GLN PRO SER L2152 C2156 A2159 L2163 L2167 K2168 TRP LYS PRO THR T2173 I2176 V2179
Q2183 L2186 E2187 L2190 ARG SER ASP ASN Q2195 Q2198 Q2202 L2205 G2206 L2209 I2212 N2213 K2214 GLU THR GLN GLY SER GLU E2221 D2222 E2225 I2231 V2235 N2236 G2239 GLU ASP LEU SER ASN MET THR SER V2248 V2252 S2259 P2263 L2266
C2281 H2284 I2285 A2286 ILE SER LEU GLN GLY ASN GLN PRO GLN SER GLY ASP PHE ALA ASN ILE E2303 F2304 E2305 E2314 N2318 L2319 C2320 A2321 A2322 ARG ILE SER SER LEU ASP D2329 R2332 S2336 A2339 D2343 R2344 S2345 F2363 LYS THR ASP PHE TYR PRO T2370 G2379
L2386 ARG GLY GLU PRO E2391 L2392 S2393 F2396 N2397 I2400 F2404 E2405 S2406 K2407 GLU LEU ALA H2411 L2414 T2415 A2416 R2417 M2418 F2422 G2425 T2426 R2427 L2428 S2429 I2433 L2437 I2440 L2441 E2446 L2447 D2448 I2449 R2452 L2465 S2466 D2467 L2475 Q2476 Y2479

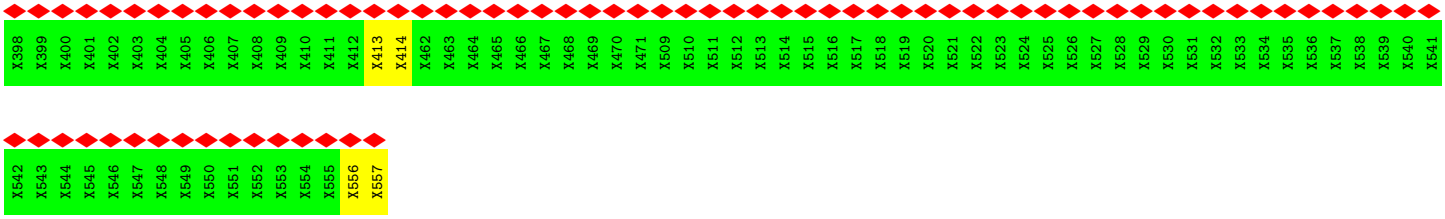




• Molecule 13: Transcriptional adapter 3 (Ada3)

Chain B:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	354104	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 ($e^-/Å^2$)	52.8	Depositor
Minimum defocus (nm)	0.8	Depositor
Maximum defocus (nm)	4.5	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	3.125	Depositor
Minimum map value	-1.547	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	558.08, 558.08, 558.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality

5.1 Standard geometry

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	M	0.88	2/1442 (0.1%)	0.78	2/1942 (0.1%)
2	A	0.44	0/1319	0.60	0/1794
3	C	0.35	0/528	0.61	0/710
4	F	0.34	0/1718	0.58	0/2335
5	D	0.51	0/1641	0.65	0/2213
6	E	0.45	0/1246	0.62	0/1667
7	J	0.47	0/779	0.60	0/1051
8	K	0.42	0/1213	0.66	0/1647
9	G	0.52	0/4177	0.60	0/5661
10	H	0.38	0/3315	0.60	0/4500
11	I	0.44	0/1006	0.63	0/1374
12	L	0.33	0/22712	0.54	0/30825
All	All	0.41	2/41096 (0.0%)	0.58	2/55719 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	M	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	194	ILE	C-N	27.38	1.97	1.34
1	M	183	SER	C-N	6.38	1.48	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	M	62	GLY	N-CA-C	6.94	130.46	113.10
1	M	194	ILE	CA-C-N	-6.13	103.71	117.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	M	183	SER	Mainchain

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	M	1415	0	1492	88	0
2	A	1300	0	1254	30	0
3	C	518	0	528	9	0
4	F	1682	0	1622	30	0
5	D	1616	0	1558	122	0
6	E	1232	0	1276	40	0
7	J	768	0	754	11	0
8	K	1192	0	1214	89	0
9	G	4075	0	3934	102	0
10	H	3263	0	3258	69	0
11	I	981	0	982	18	0
12	L	22318	0	20960	376	0
13	B	380	0	85	2	0
All	All	40740	0	38917	865	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 865 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)
8:K:469:LEU:HD13	12:L:2788:ILE:CG2	1.31	1.51
8:K:469:LEU:CD1	12:L:2788:ILE:HG21	1.57	1.34
12:L:828:ARG:H	12:L:829:PRO:HD3	1.06	1.20
1:M:194:ILE:HG22	1:M:195:TYR:N	1.57	1.19
1:M:194:ILE:C	1:M:195:TYR:N	1.97	1.17

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	M	178/243 (73%)	147 (83%)	24 (14%)	7 (4%)	3 28
2	A	169/448 (38%)	151 (89%)	18 (11%)	0	100 100
3	C	61/698 (9%)	56 (92%)	5 (8%)	0	100 100
4	F	202/517 (39%)	177 (88%)	24 (12%)	1 (0%)	29 66
5	D	203/341 (60%)	177 (87%)	19 (9%)	7 (3%)	3 31
6	E	150/1191 (13%)	135 (90%)	13 (9%)	2 (1%)	12 48
7	J	92/217 (42%)	82 (89%)	9 (10%)	1 (1%)	14 51
8	K	150/609 (25%)	125 (83%)	23 (15%)	2 (1%)	12 48
9	G	512/722 (71%)	448 (88%)	63 (12%)	1 (0%)	47 79
10	H	413/485 (85%)	365 (88%)	48 (12%)	0	100 100
11	I	119/153 (78%)	98 (82%)	21 (18%)	0	100 100
12	L	2874/3825 (75%)	2623 (91%)	233 (8%)	18 (1%)	25 62
All	All	5123/9449 (54%)	4584 (90%)	500 (10%)	39 (1%)	24 57

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	77	GLY
1	M	99	PHE
1	M	110	LYS
5	D	200	THR
5	D	327	ARG

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	M	152/208 (73%)	138 (91%)	14 (9%)	9 35
2	A	134/394 (34%)	132 (98%)	2 (2%)	65 81
3	C	55/627 (9%)	55 (100%)	0	100 100
4	F	179/471 (38%)	179 (100%)	0	100 100
5	D	166/306 (54%)	154 (93%)	12 (7%)	14 45
6	E	142/1101 (13%)	136 (96%)	6 (4%)	30 58
7	J	85/183 (46%)	84 (99%)	1 (1%)	71 84
8	K	133/524 (25%)	130 (98%)	3 (2%)	50 72
9	G	439/635 (69%)	430 (98%)	9 (2%)	53 74
10	H	352/438 (80%)	348 (99%)	4 (1%)	73 85
11	I	104/130 (80%)	103 (99%)	1 (1%)	76 86
12	L	2156/3450 (62%)	2114 (98%)	42 (2%)	57 76
All	All	4097/8467 (48%)	4003 (98%)	94 (2%)	53 72

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	L	1122	ASN
12	L	2489	ARG
12	L	1314	LEU
12	L	1419	LYS
12	L	2878	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
10	H	64	HIS
10	H	157	ASN
12	L	2884	GLN
12	L	2633	ASN
12	L	2698	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
13	B	2
1	M	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	414:UNK	C	462:UNK	N	28.86
1	B	471:UNK	C	509:UNK	N	23.98
1	M	194:ILE	C	195:TYR	N	1.97

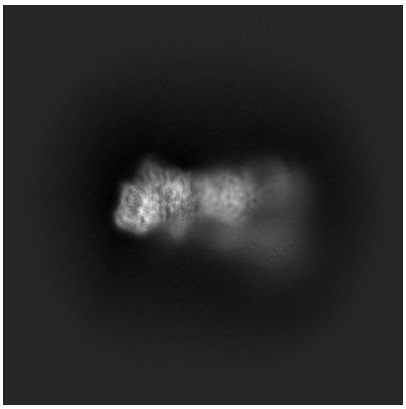
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10438. These allow visual inspection of the internal detail of the map and identification of artifacts.

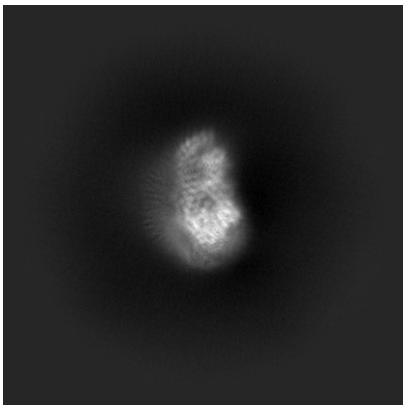
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

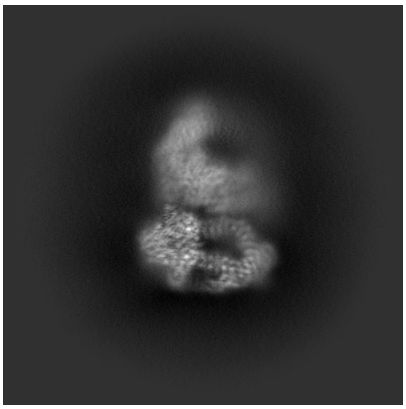
6.1.1 Primary map



X

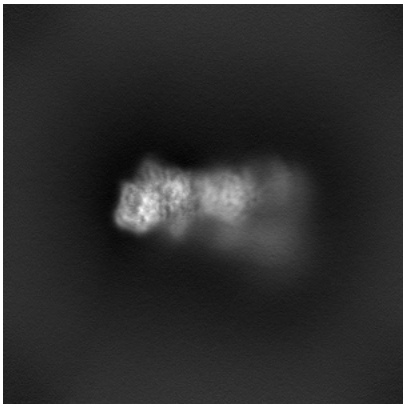


Y

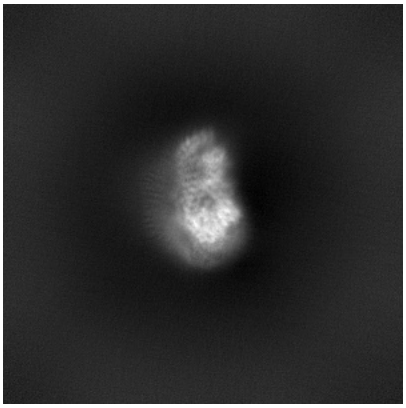


Z

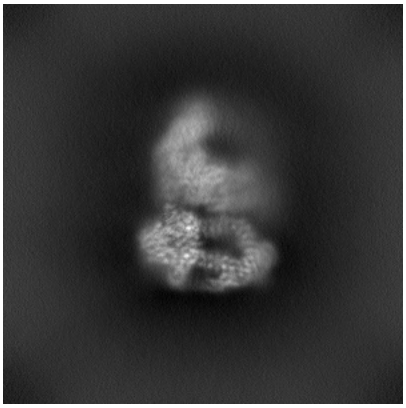
6.1.2 Raw map



X



Y

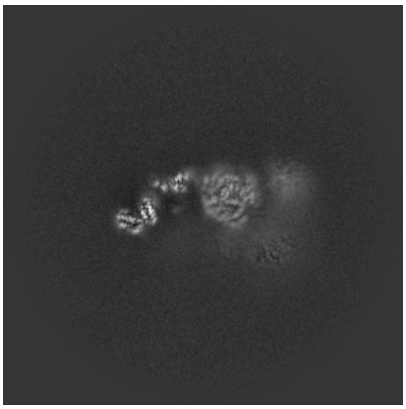


Z

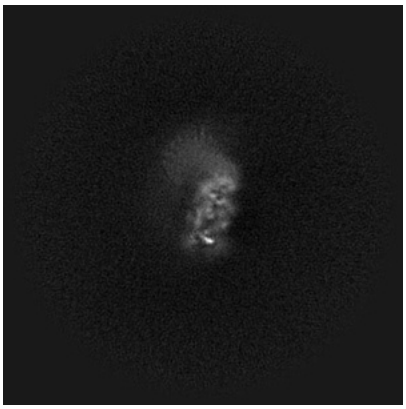
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

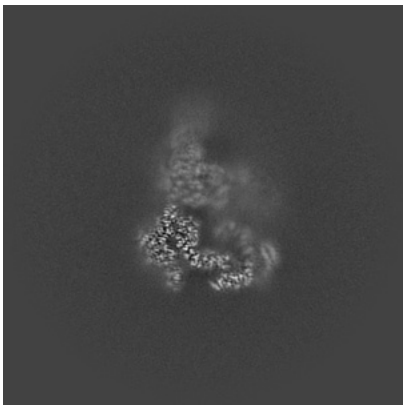
6.2.1 Primary map



X Index: 256

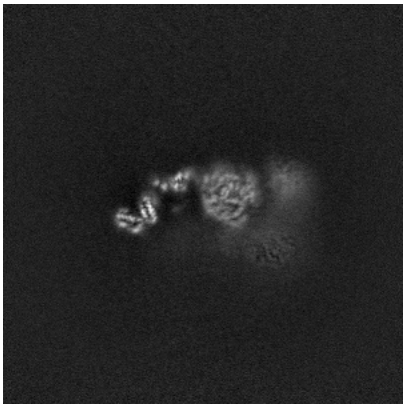


Y Index: 256

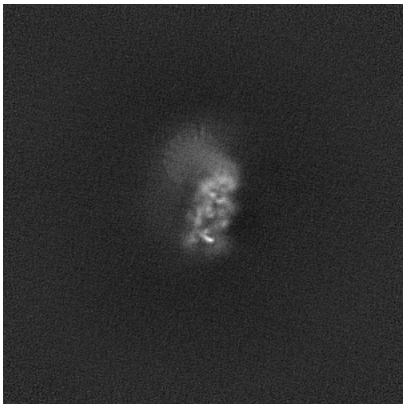


Z Index: 256

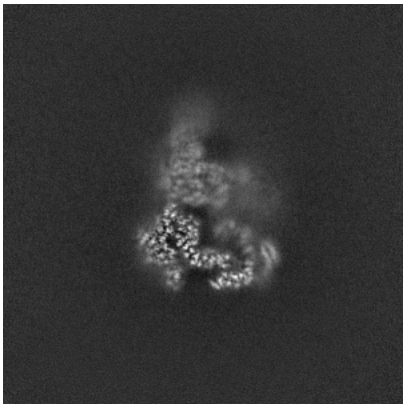
6.2.2 Raw map



X Index: 256



Y Index: 256

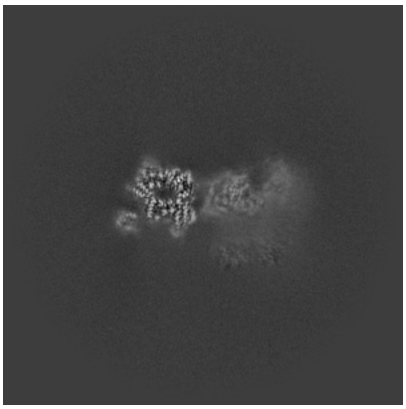


Z Index: 256

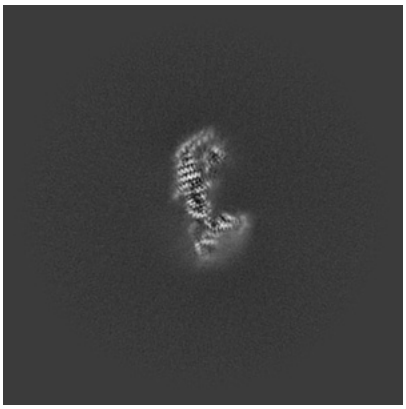
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

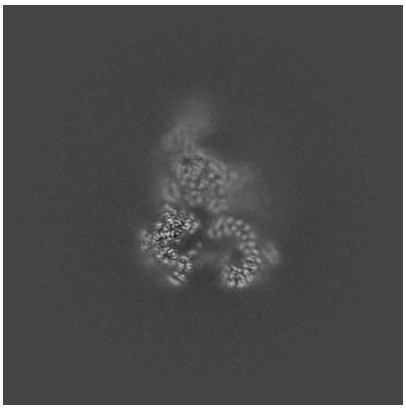
6.3.1 Primary map



X Index: 236

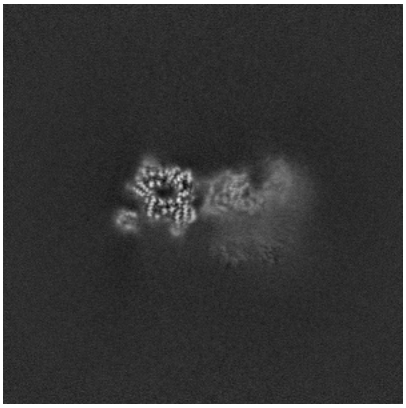


Y Index: 182

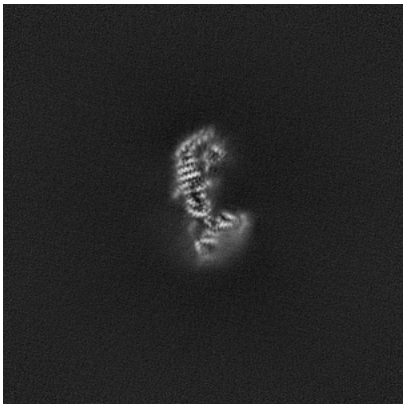


Z Index: 268

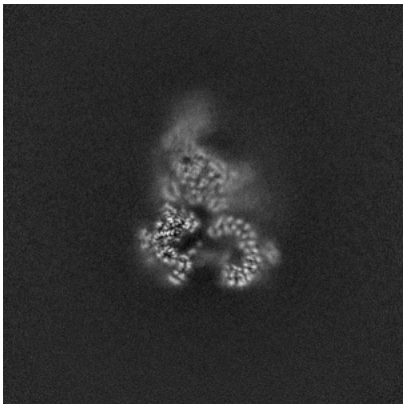
6.3.2 Raw map



X Index: 236



Y Index: 182

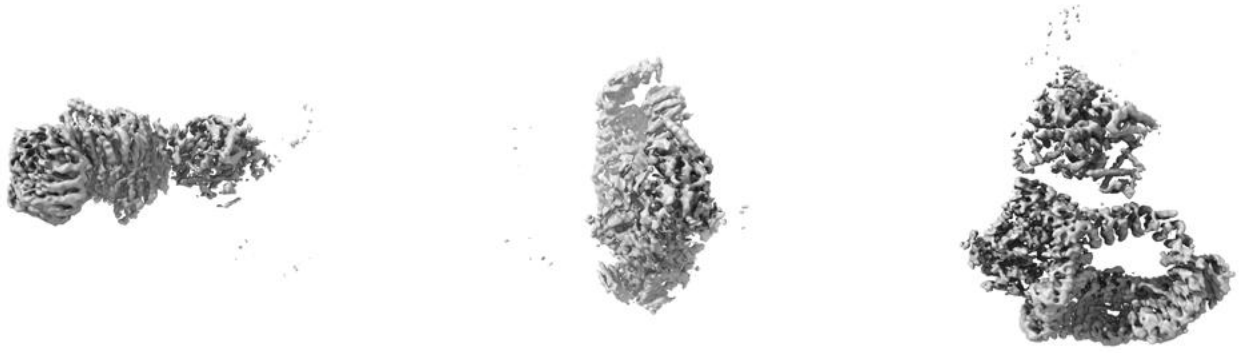


Z Index: 268

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

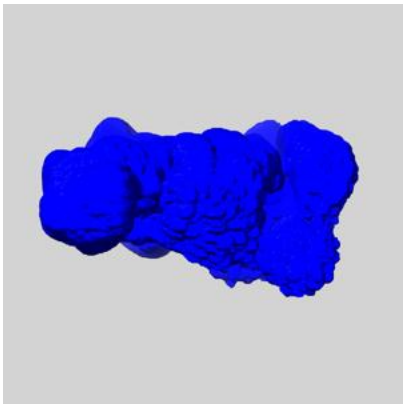
6.5 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

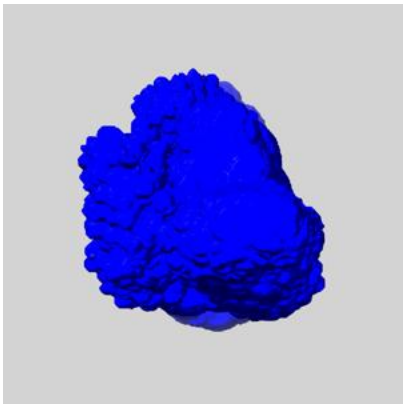
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

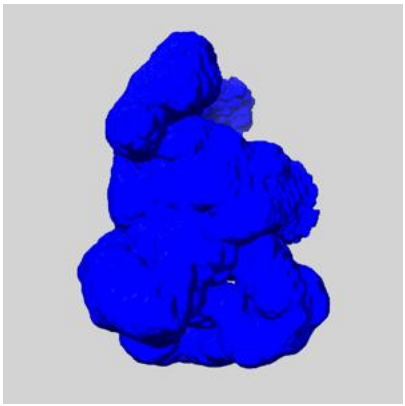
6.5.1 emd_10438_msk_1.map (i)



X



Y

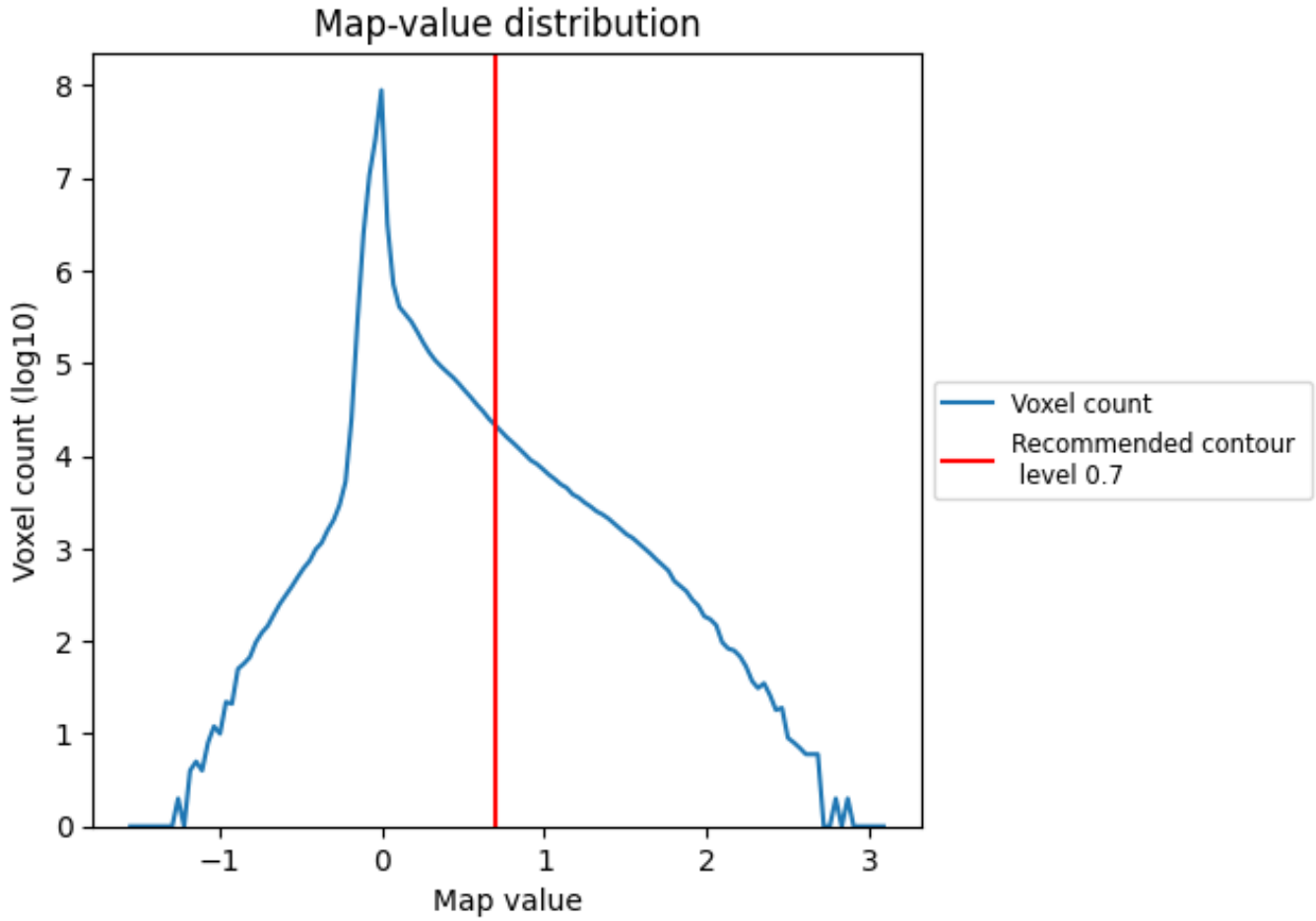


Z

7 Map analysis

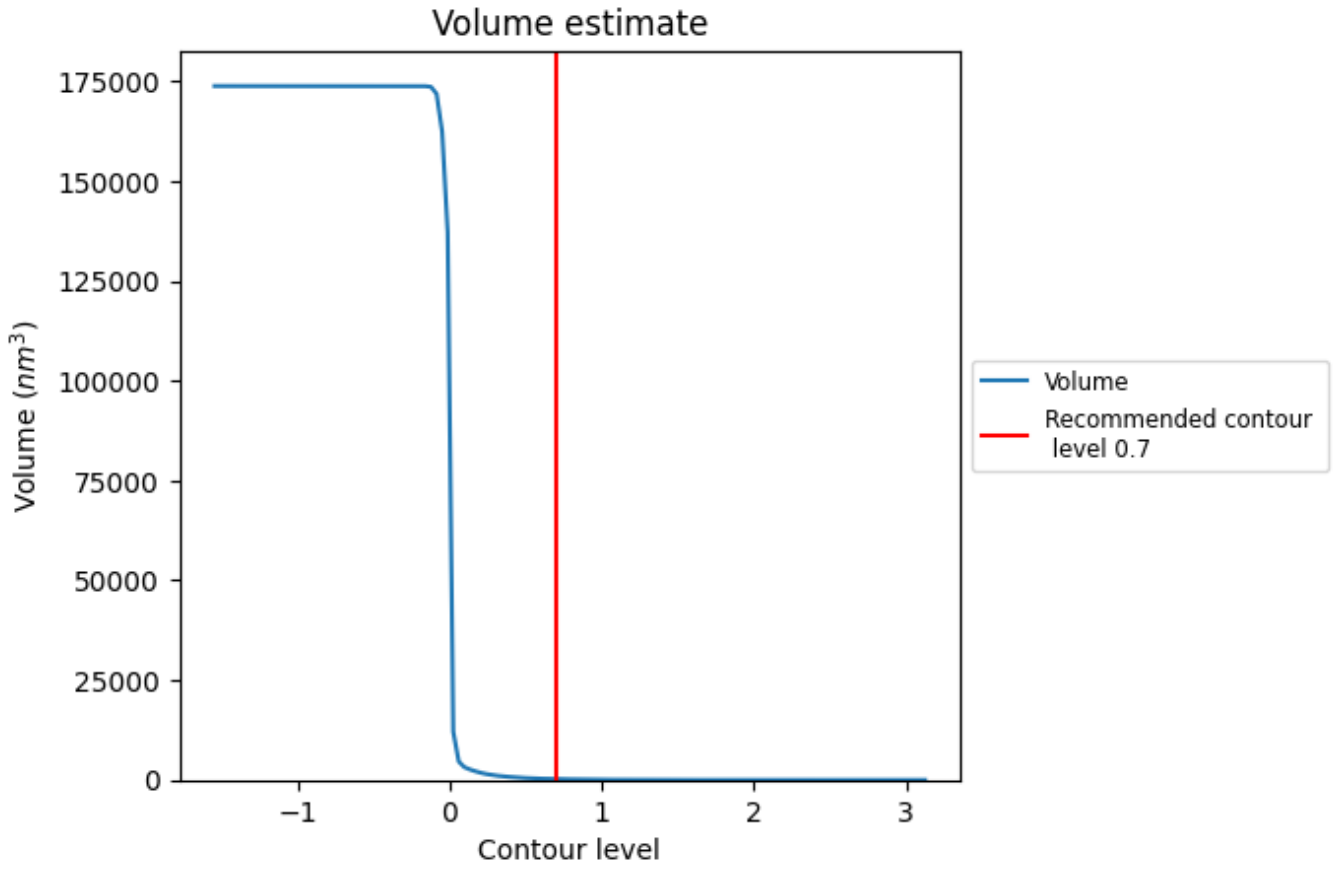
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

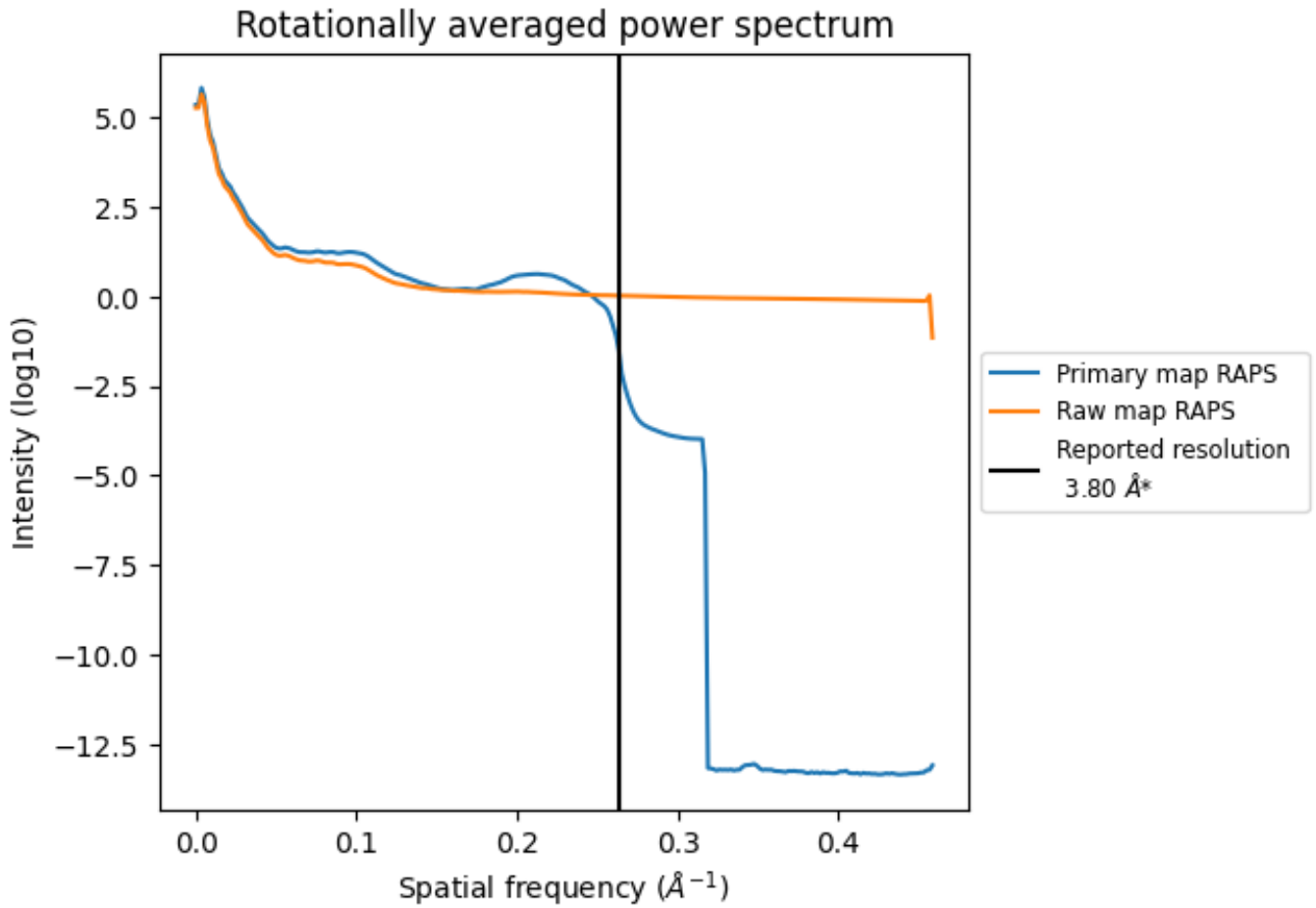
7.2 Volume estimate (i)



The volume at the recommended contour level is 221 nm^3; this corresponds to an approximate mass of 199 kDa.

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

7.3 Rotationally averaged power spectrum (i)

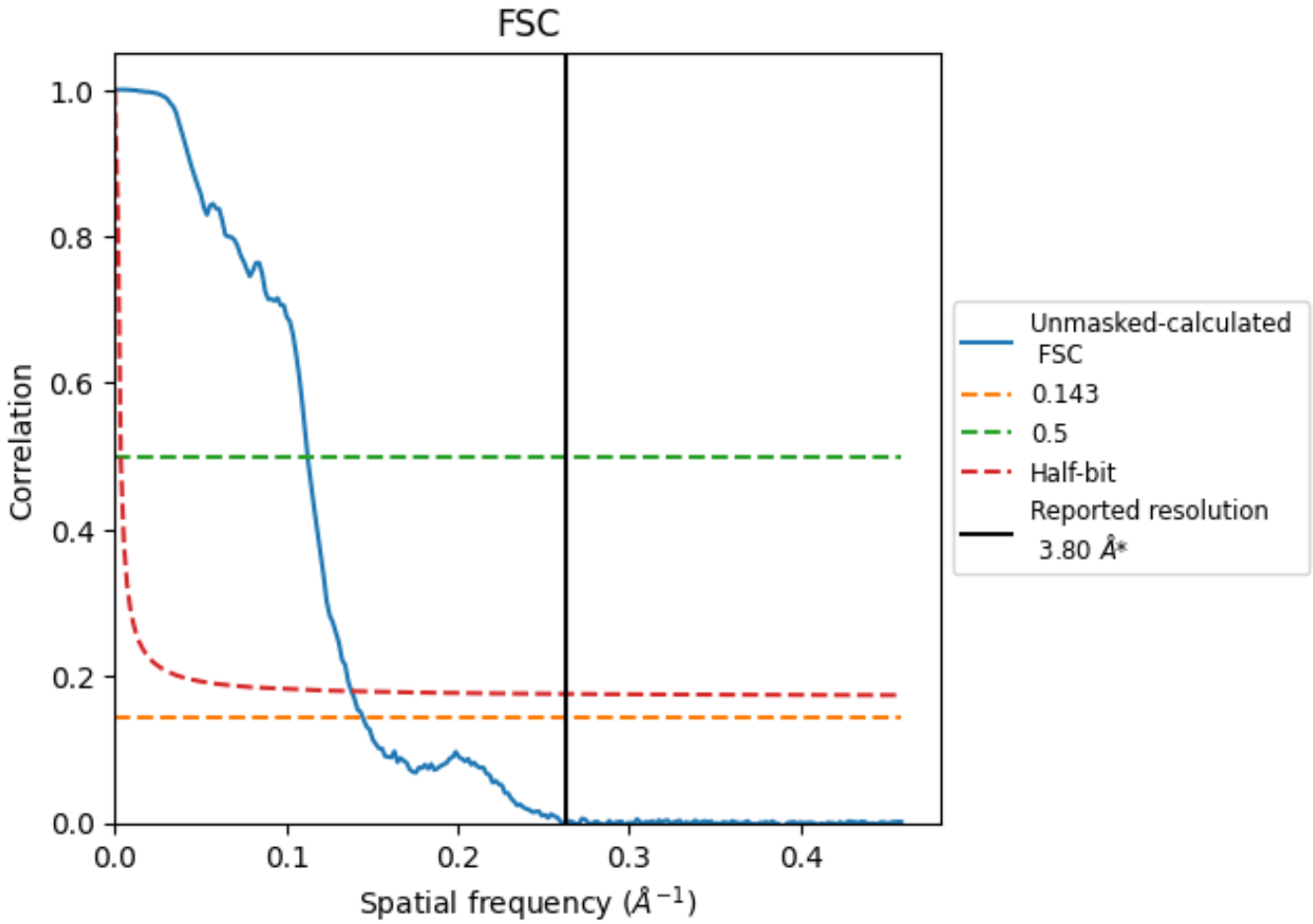


*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

8.2 Resolution estimates (i)

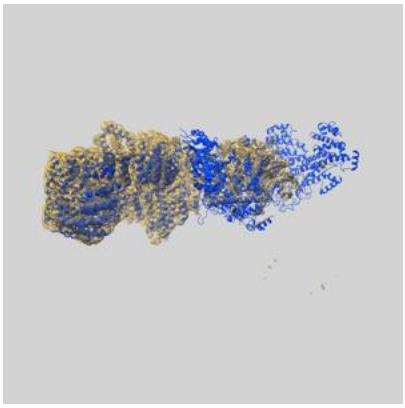
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.91	8.89	7.24

*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 6.91 differs from the reported value 3.8 by more than 10 %

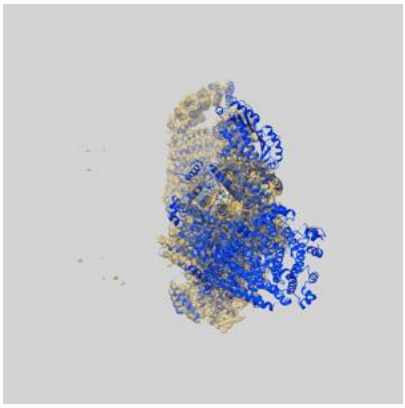
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-10438 and PDB model 6TB4. Per-residue inclusion information can be found in section 3 on page 7.

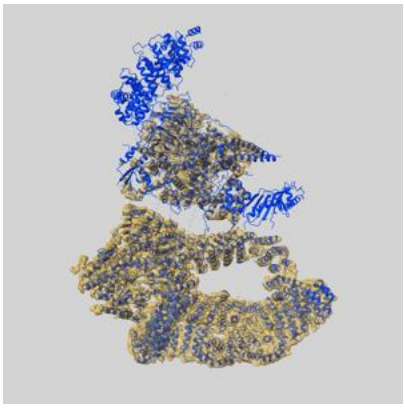
9.1 Map-model overlay



X



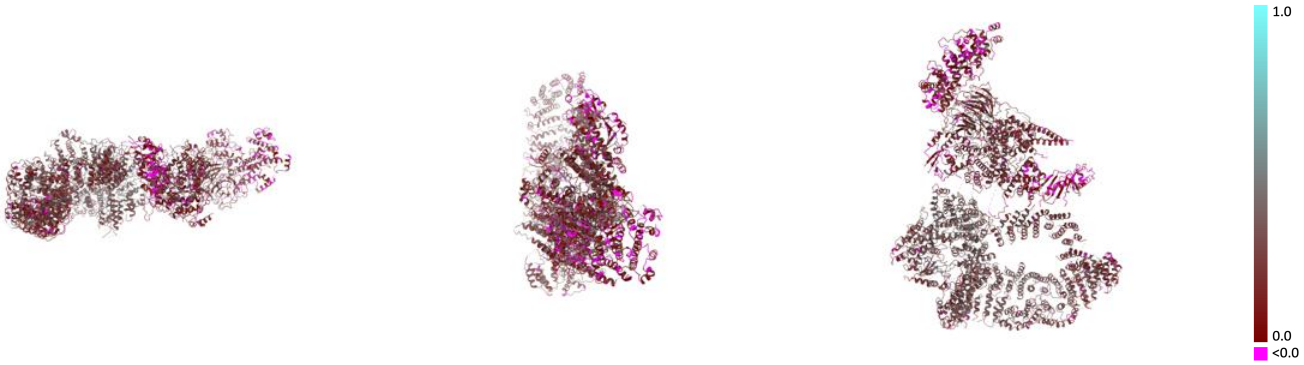
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.7 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.

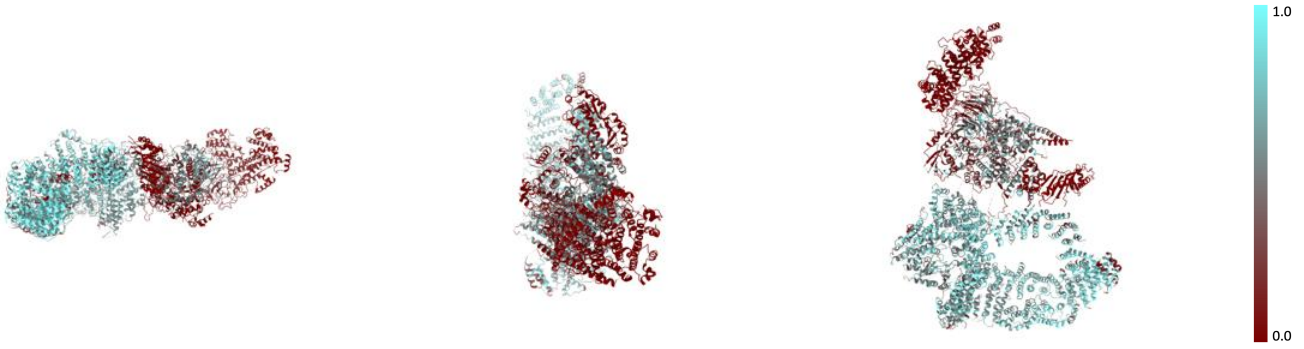
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

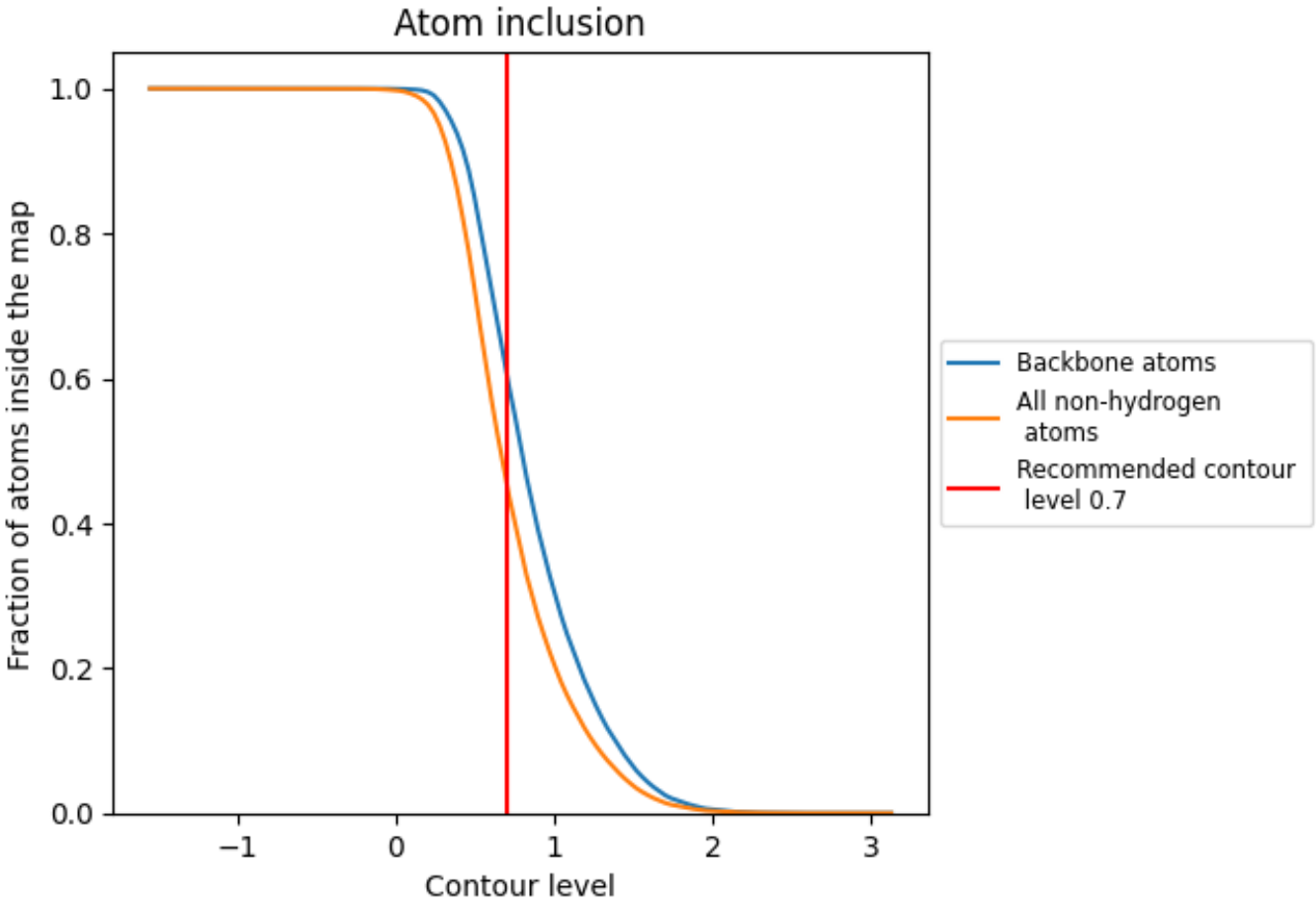
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.7).

9.4 Atom inclusion (i)



At the recommended contour level, 61% of all backbone atoms, 46% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4562	0.2310
A	0.2351	0.1830
B	0.0026	0.1280
C	0.0904	0.1570
D	0.2949	0.1690
E	0.4002	0.1980
F	0.1989	0.1540
G	0.1955	0.1800
H	0.0853	0.1350
I	0.2927	0.1750
J	0.4019	0.2060
K	0.3293	0.2160
L	0.6655	0.2880
M	0.0022	0.0490