wwPDB EM Validation Summary Report

Sep 13, 2023 – 11:49 am BST

PDB ID	:	7ZVW
EMDB ID	:	EMD-14989
Title	:	NuA4 Histone Acetyltransferase Complex
Authors	:	Schultz, P.; Ben-Shem, A.; Frechard, A.
Deposited on	:	2022-05-17
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:

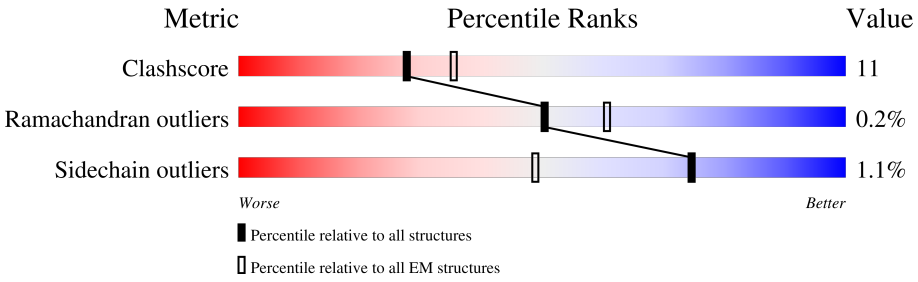
EMDB validation analysis	:	0.0.1.dev50
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.40 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)
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	A	3825	5% 67% 17% 16%
2	B	376	8% 66% 27% 7%
3	G	468	5% 66% 24% 10%
4	E	1051	5% 34% 12% 54%
4	H	1051	98%
5	F	565	24% 12% 61%
6	C	752	7% 23% 6% 70%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 37905 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 Transcription-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	3226	24052	15394	4173	4395	90	0	0

- Molecule 2 is a protein called Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	350	2735	1740	457	522	16	0	0

- Molecule 3 is a protein called Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	G	422	3310	2110	557	633	10	0	0

- Molecule 4 is a protein called Chromatin modification-related protein EAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	488	3952	2521	696	724	11	0	0
			Total	C	N	O			
4	H	22	110	66	22	22		0	0

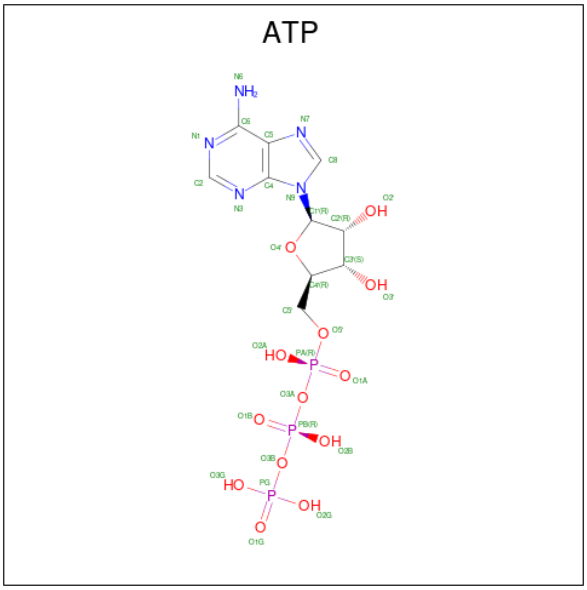
- Molecule 5 is a protein called SWR1-complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	223	1877	1189	321	362	5	0	0

- Molecule 6 is a protein called Enhancer of polycomb-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	224	Total	C	N	O	S	0	0
			1805	1135	314	347	9		

- Molecule 7 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
7	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
7	G	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

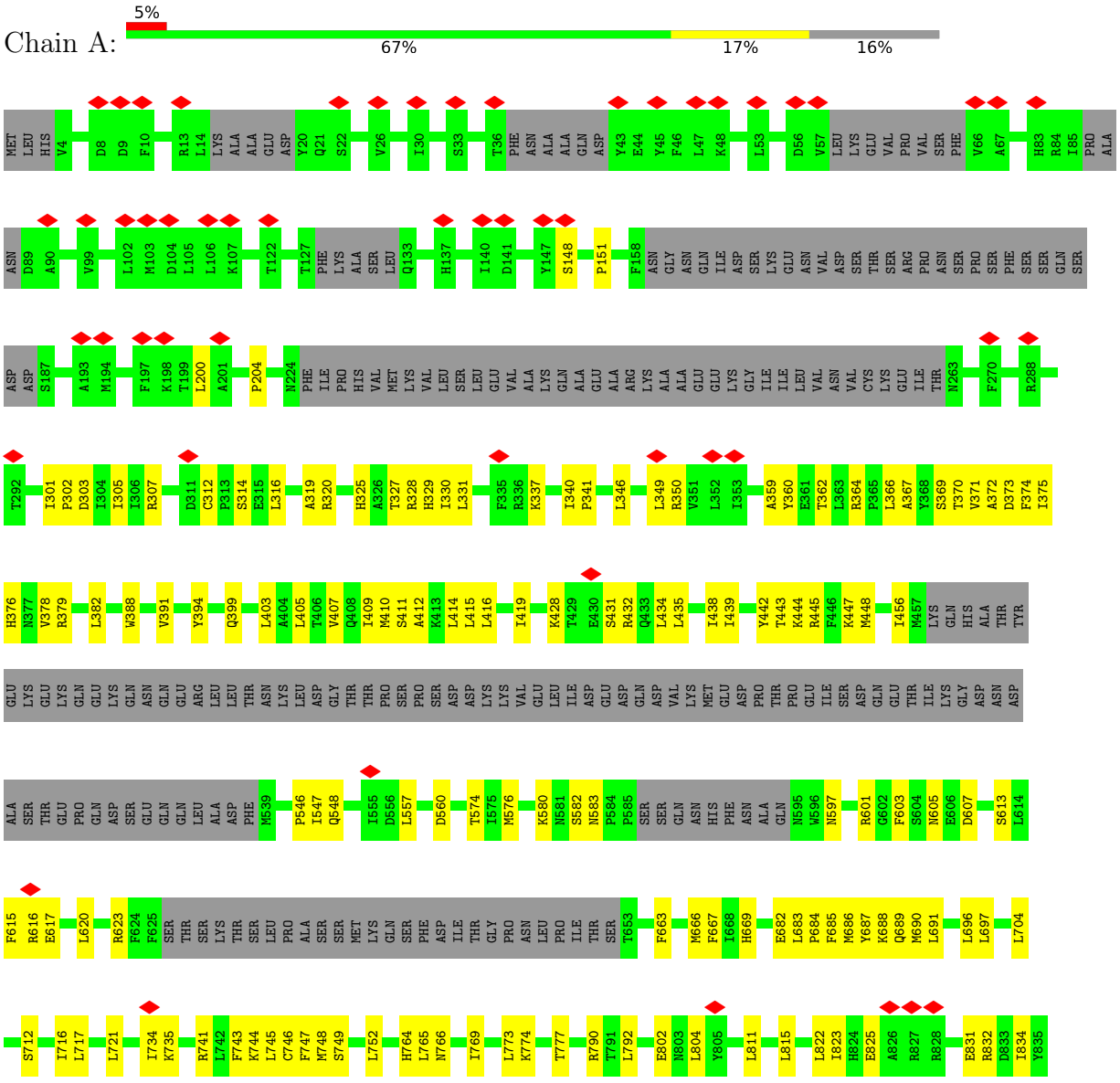
Mol	Chain	Residues	Atoms		AltConf
8	B	1	Total	Mg	0
			1	1	
8	G	1	Total	Mg	0
			1	1	

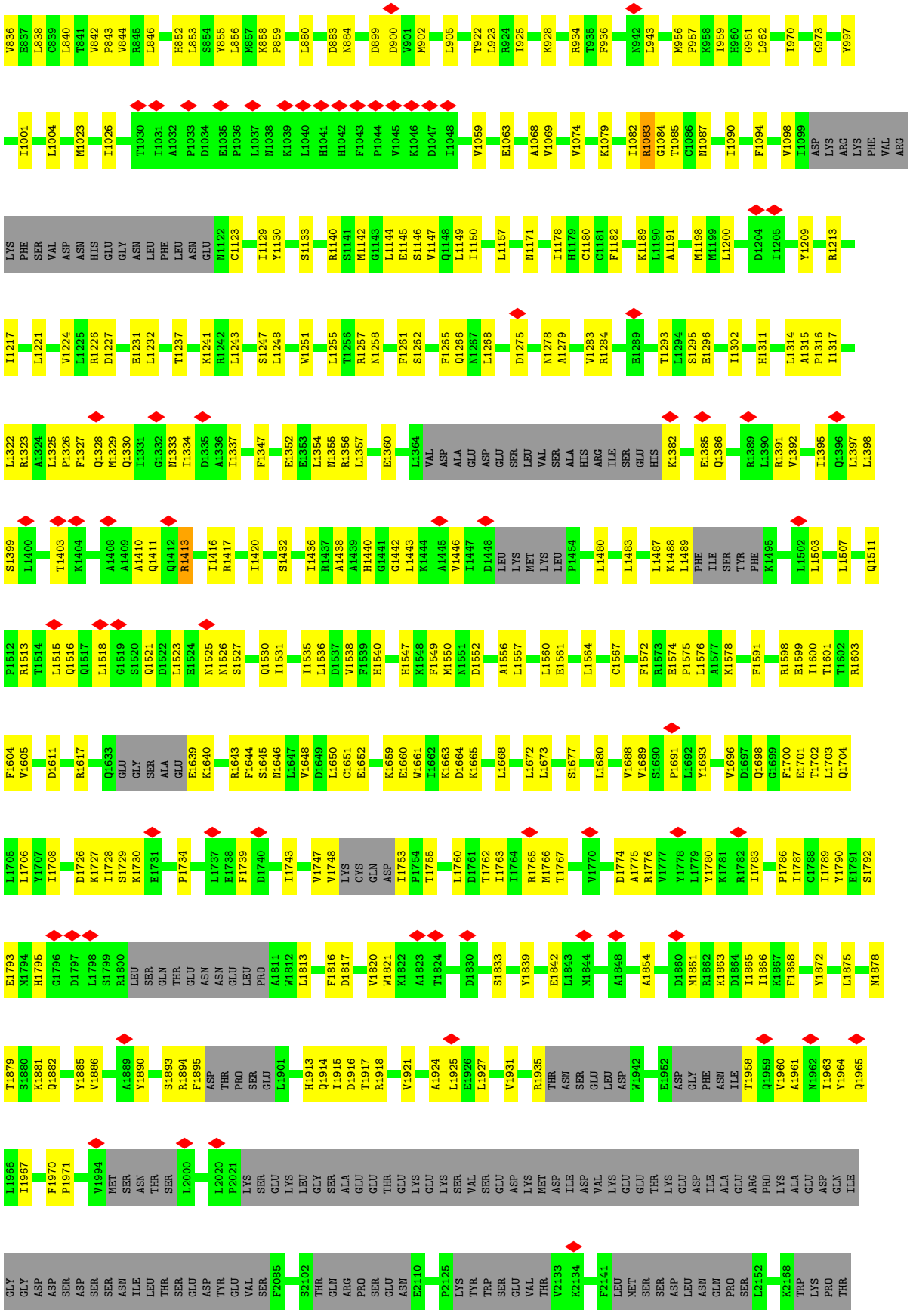
3 Residue-property plots (i)

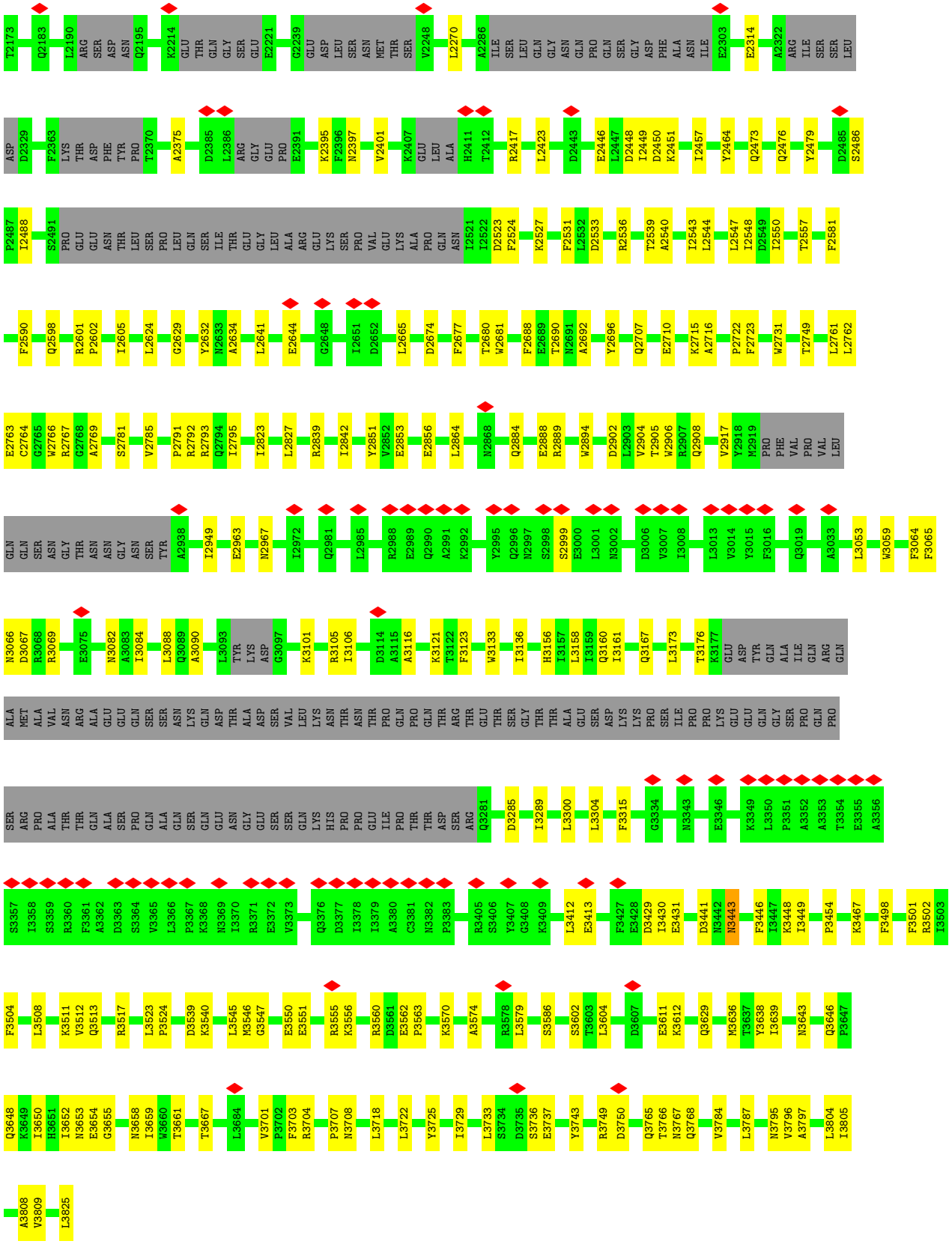
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

Chain A:

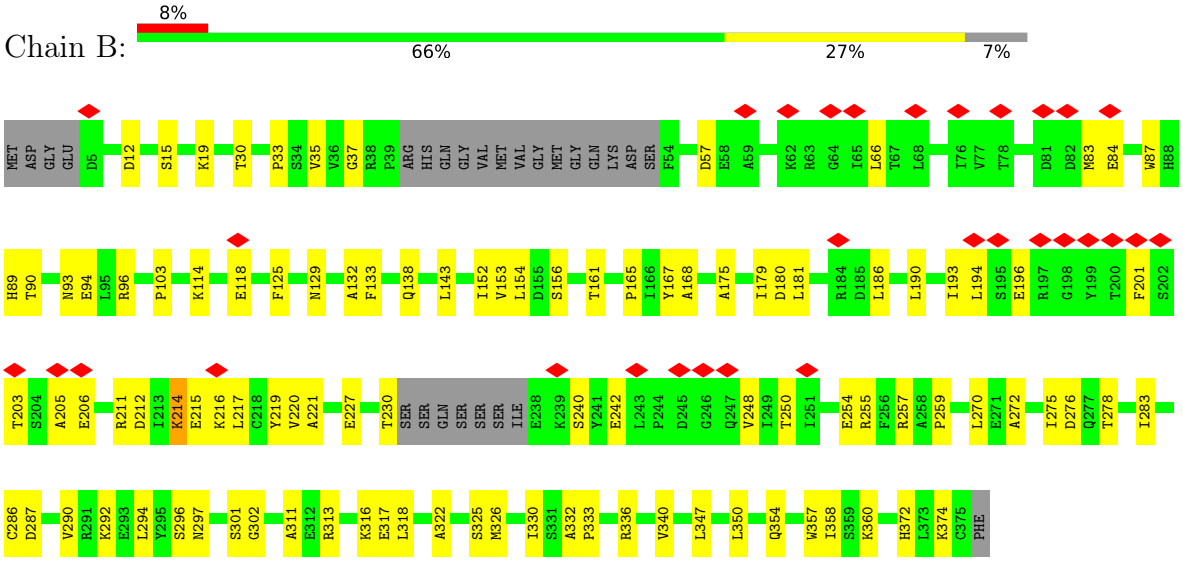



V836 E837 L838 C839 L840 T841 V842 P843 V844 R845 L846 H852 L853 S854 Y855 L856 M857 K858 P859 L880 D883 N884 D899 D900 V901 M902 L905 T922 L923 R924 I925 K928 R934 T935 F936 N942 L943 M956 F957 K958 I959 H960 G961 L962 I970 G973 Y997
I1001 L1004 M1023 I1026 T1030 I1031 A1032 P1033 D1034 E1035 P1036 L1037 N1038 K1039 L1040 H1041 H1042 F1043 P1044 V1045 K1046 D1047 I1048 V1059 E1063 A1068 V1069 V1074 K1079 I1082 R1083 G1084 T1085 C1086 N1087 I1090 F1094 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 C1123 I1129 Y1130 S1133 R1140 S1141 M1142 G1143 L1144 E1145 S1146 V1147 Q1148 L1149 I1150 L1157 N1171 I1178 H1179 C1180 C1181 F1182 K1189 L1190 A1191 M1198 M1199 L1200 D1204 I1205 Y1209 R1213
I1217 L1221 V1224 L1225 R1226 D1227 E1231 L1232 T1237 K1241 R1242 L1243 S1247 L1248 W1251 L1255 T1256 R1257 N1258 F1261 S1262 F1265 Q1266 N1267 L1268 D1275 N1278 A1279 V1283 R1284 E1289 T1293 L1294 S1295 E1296 I1302 H1311 L1314 A1315 P1316 I1317
L1322 R1323 A1324 L1325 P1326 F1327 Q1328 M1329 Q1330 I1331 G1332 N1333 I1334 D1335 A1336 I1337 F1347 E1352 E1353 L1354 N1355 R1356 L1357 E1360 L1364 VAL ASP ALA GLU ASP GLU SER LEU VAL SER ALA HIS ARG ILE SER GLU HIS K1382 E1385 Q1386 R1389 L1390 R1391 V1392 I1395 Q1396 L1397 L1398
S1399 L1400 T1403 K1404 A1408 A1409 A1410 Q1411 Q1412 R1413 I1416 R1417 I1420 S1432 I1436 R1437 A1438 A1439 H1440 G1441 G1442 L1443 K1444 A1445 V1446 T1447 D1448 LEU LYS MET LYS LEU P1454 L1480 L1483 L1487 K1488 L1489 PHE ILE SER TYR PHE K1495 L1502 L1503 L1507 Q1511
P1512 R1513 T1514 L1515 Q1516 Q1517 L1518 G1519 S1520 Q1521 D1522 L1523 E1524 N1525 N1526 S1527 Q1530 I1531 I1535 L1536 D1537 V1538 F1539 H1540 H1547 K1548 F1549 M1550 N1551 D1552 A1556 L1557 L1560 E1561 L1564 C1567 F1572 R1573 E1574 P1575 L1576 A1577 K1578 F1591 R1598 E1599 I1600 T1601 T1602 R1603
F1604 V1605 D1611 R1617 Q1633 GLU GLY SER ALA GLU E1639 K1640 R1643 F1644 S1645 N1646 L1647 V1648 D1649 L1650 C1651 E1652 K1659 E1660 W1661 I1662 K1663 D1664 K1665 L1668 L1672 L1673 S1677 L1680 V1688 V1689 S1690 P1691 L1692 Y1693 V1696 D1697 D1698 G1699 F1700 E1701 T1702 L1703 Q1704
L1705 L1706 Y1707 I1708 D1726 K1727 I1728 S1729 K1730 E1731 P1734 L1737 E1738 F1739 D1740 I1743 V1747 V1748 LYS CYS GLN ASP I1753 P1754 T1755 L1760 D1761 T1762 I1763 I1764 R1765 M1766 T1767 V1770 D1774 A1775 R1776 V1777 Y1778 L1779 Y1780 K1781 R1782 I1783 P1786 I1787 C1788 I1789 Y1790 E1791 S1792
E1793 M1794 H1795 G1796 D1797 L1798 S1799 R1800 LEU SER GLN THR GLU ASN ASN GLU GLU LEU PRO A1811 W1812 L1813 F1816 D1817 V1820 W1821 K1822 A1823 T1824 D1830 S1833 Y1839 E1842 L1843 M1844 A1848 A1854 D1860 M1861 R1862 K1863 D1864 I1865 I1866 K1867 F1868 Y1872 L1875 N1878
T1879 S1880 K1881 Q1882 Y1885 V1886 A1889 Y1890 S1893 R1894 F1895 ASP THR PRO SER GLU L1901 H1913 Q1914 I1915 D1916 T1917 R1918 V1921 A1924 L1925 E1926 L1927 V1931 R1935 THR ASN SER GLU LEU ASP W1942 E1952 ASP GLY PHE ASN ILE T1958 Q1959 V1960 A1961 N1962 I1963 Y1964 Q1965
L1966 I1967 F1970 P1971 V1994 MET SER ASN THR SER L2000 L2020 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 LEU ASP GLU THR LYS GLU ASP ILE ASP ARG PRO LYS ALA GLU ASP GLN ILE
GLY GLY ASP ASP SER ASP SER SER ASN ILE LEU THR SER GLU ASP TYR GLU VAL SER F2085 S2102 THR GLN ARG PRO SER GLU ASN E2110 P2125 LYS TYR TRP SER GLU VAL THR V2133 K2134 F2141 LEU MET SER SER ASP LEU ASN GLN PRO SER L2152 K2168 TRP LYS PRO THR



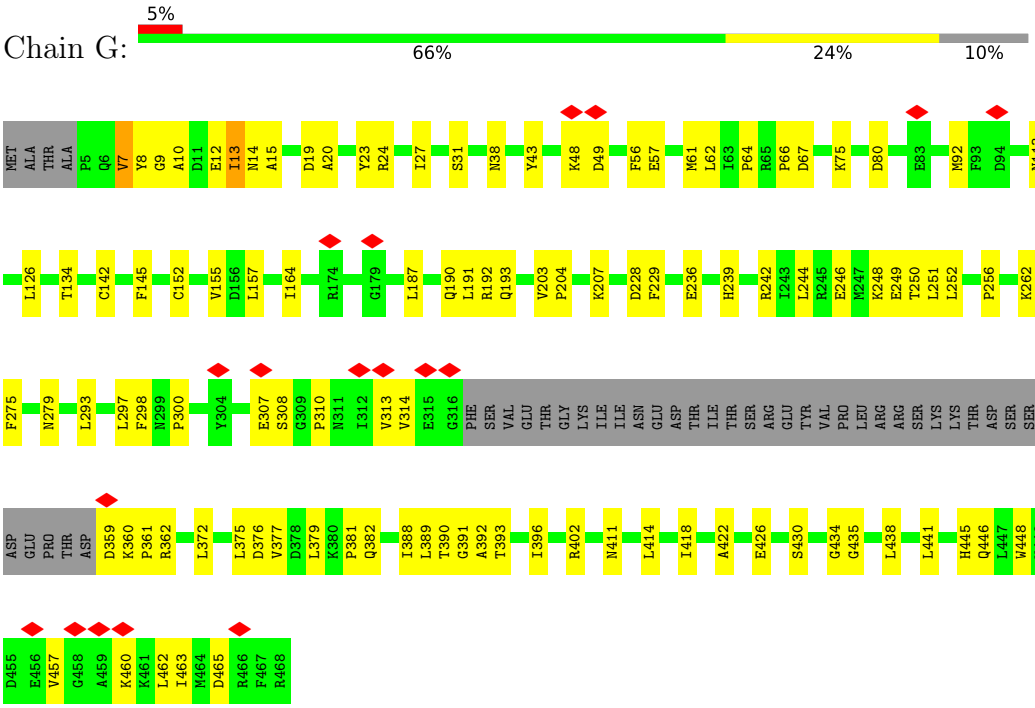
• Molecule 2: Actin

Chain B:



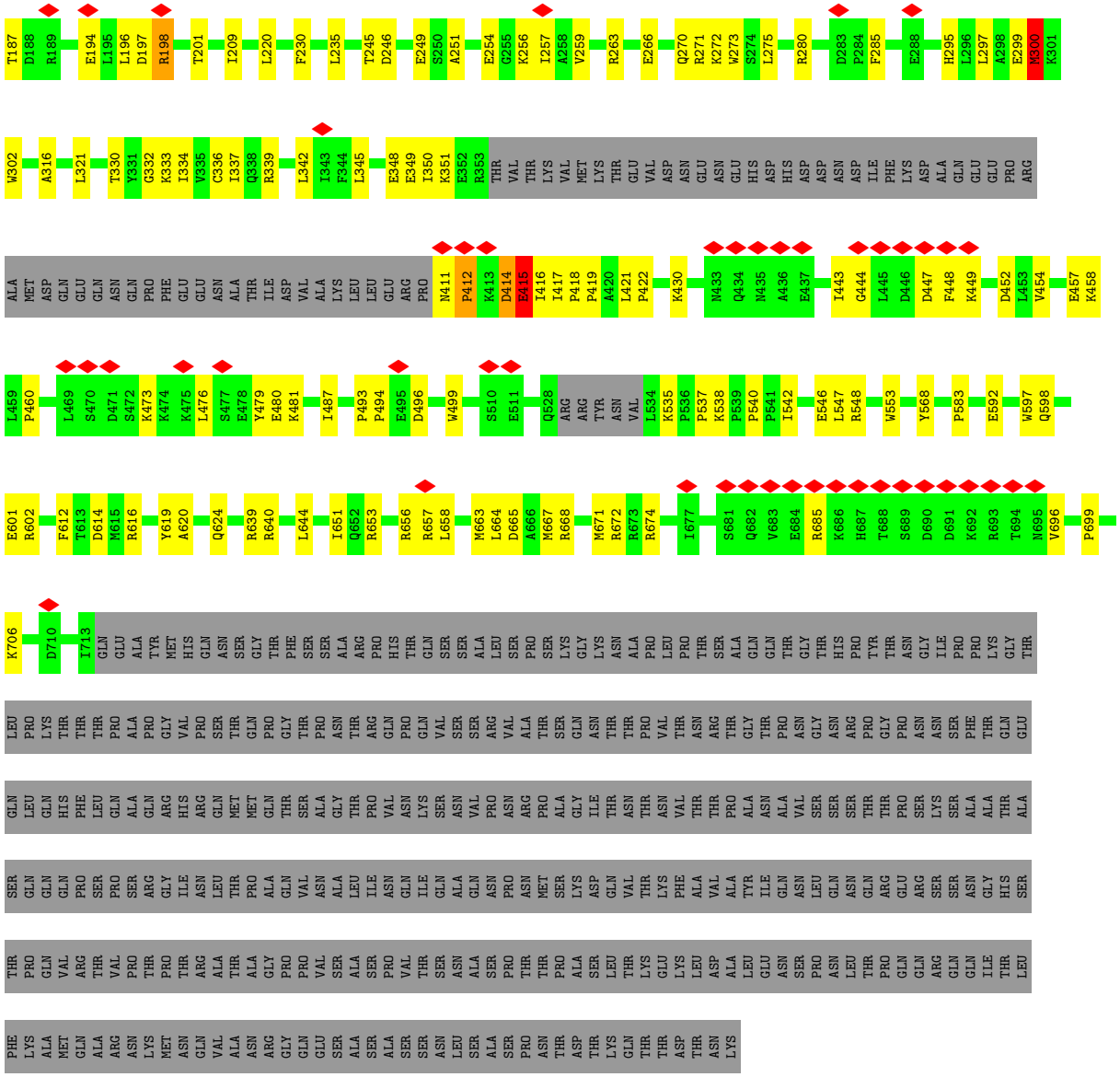
• Molecule 3: Actin

Chain G:



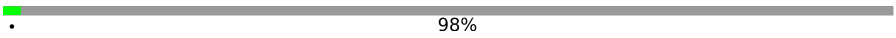
• Molecule 4: Chromatin modification-related protein EAF1

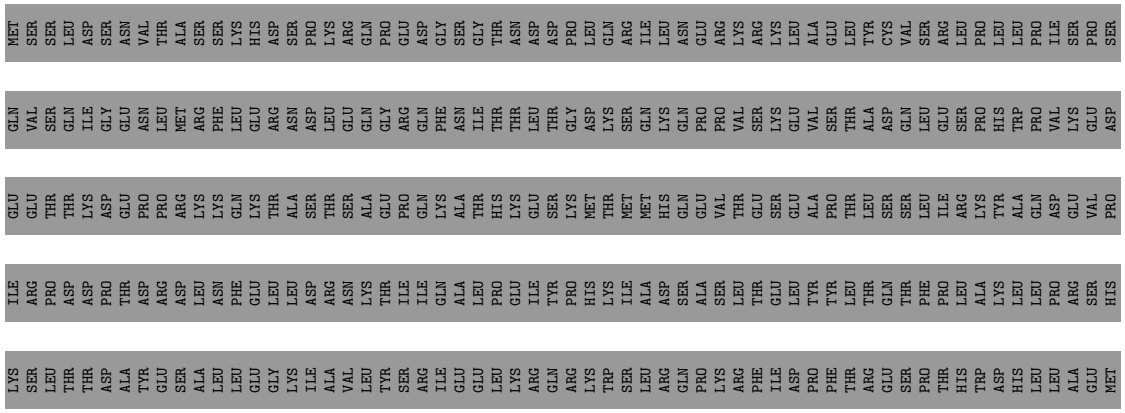
Chain E:

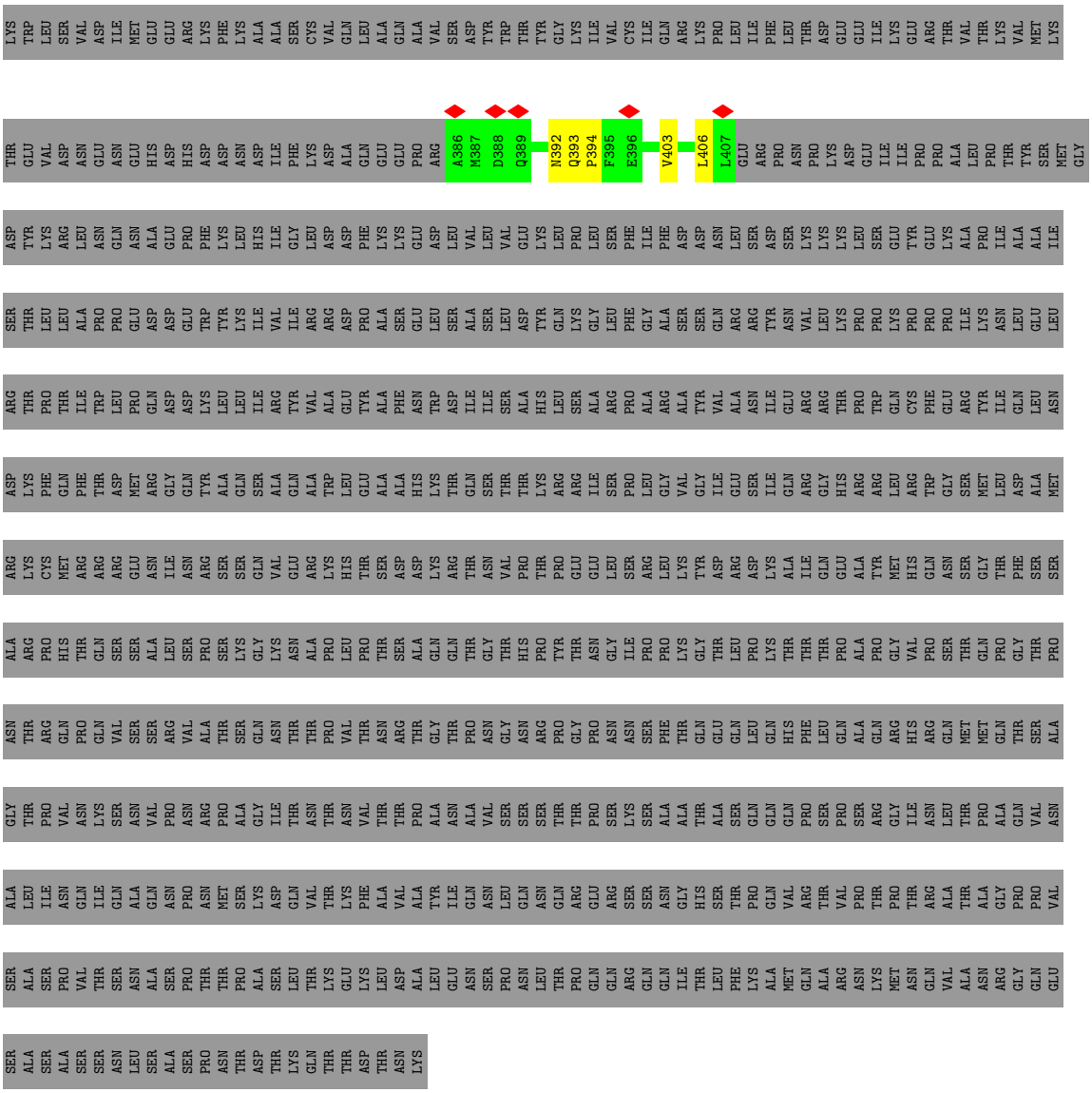


• Molecule 4: Chromatin modification-related protein EAF1

Chain H:

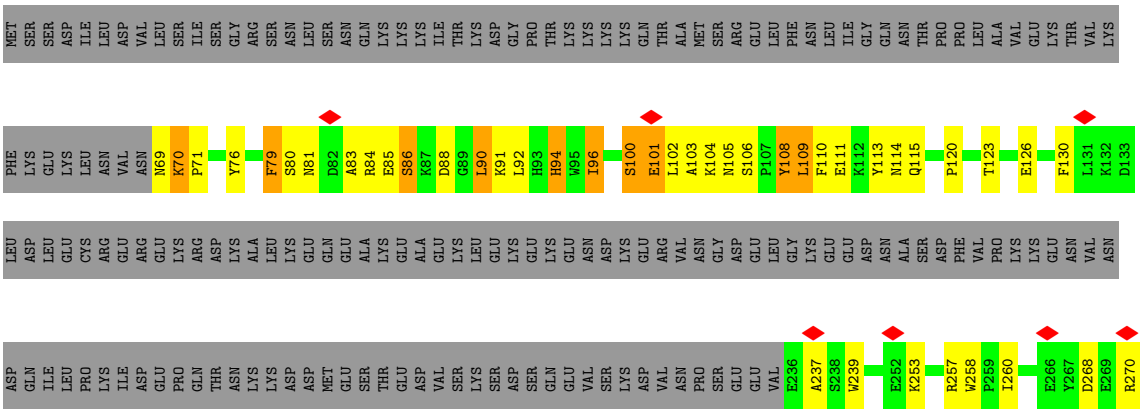


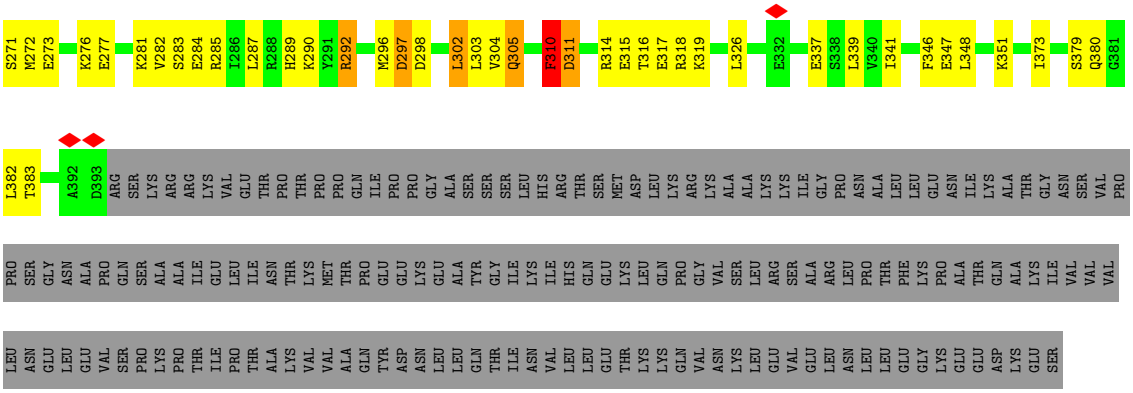




• Molecule 5: SWR1-complex protein 4

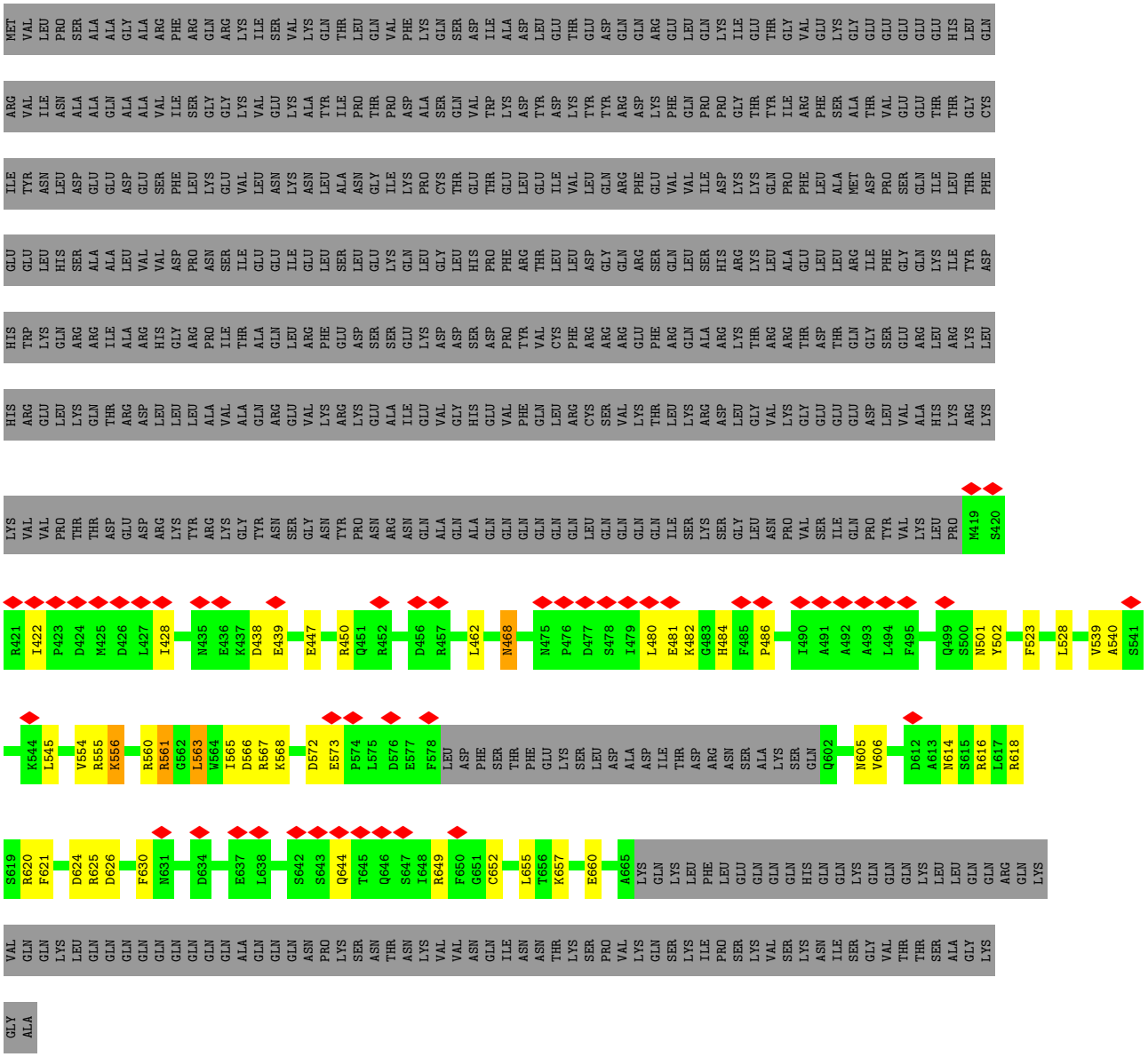
Chain F:





• Molecule 6: Enhancer of polycomb-like protein

Chain C:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	518386	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	52.8	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.005	Depositor
Minimum map value	-2.188	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.062	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	386.176, 386.176, 386.176	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.862, 0.862, 0.862	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.25	0/24505	0.47	0/33321
2	B	0.25	0/2795	0.50	0/3788
3	G	0.28	0/3377	0.52	1/4577 (0.0%)
4	E	0.31	0/4044	0.57	2/5478 (0.0%)
4	H	0.68	0/109	1.37	1/151 (0.7%)
5	F	0.45	0/1916	0.80	2/2579 (0.1%)
6	C	0.27	0/1842	0.54	0/2495
All	All	0.28	0/38588	0.52	6/52389 (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
4	E	0	1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	412	PRO	N-CA-CB	8.17	113.10	103.30
3	G	10	ALA	N-CA-CB	-6.94	100.38	110.10
4	H	394	PRO	N-CA-C	-6.54	95.08	112.10
5	F	297	ASP	CB-CA-C	-5.73	98.95	110.40
5	F	310	PHE	N-CA-CB	-5.44	100.81	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	E	300	MET	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	A	24052	0	22457	476	0
2	B	2735	0	2704	81	0
3	G	3310	0	3269	80	0
4	E	3952	0	3937	104	0
4	H	110	0	51	1	0
5	F	1877	0	1848	75	0
6	C	1805	0	1782	39	0
7	B	31	0	12	2	0
7	G	31	0	12	3	0
8	B	1	0	0	0	0
8	G	1	0	0	0	0
All	All	37905	0	36072	790	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 790 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)
4:E:411:ASN:CB	4:E:444:GLY:H	1.57	1.17
4:E:411:ASN:CB	4:E:444:GLY:N	2.17	1.07
1:A:1872:TYR:HA	1:A:1875:LEU:HD23	1.56	0.86
2:B:129:ASN:HD21	5:F:70:LYS:HB3	1.40	0.85
1:A:2894:TRP:HA	1:A:3512:VAL:HG23	1.56	0.84

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	3148/3825 (82%)	3050 (97%)	98 (3%)	0	100 100
2	B	344/376 (92%)	330 (96%)	14 (4%)	0	100 100
3	G	418/468 (89%)	404 (97%)	14 (3%)	0	100 100
4	E	482/1051 (46%)	448 (93%)	29 (6%)	5 (1%)	15 46
4	H	20/1051 (2%)	16 (80%)	2 (10%)	2 (10%)	0 4
5	F	219/565 (39%)	201 (92%)	15 (7%)	3 (1%)	11 37
6	C	220/752 (29%)	211 (96%)	9 (4%)	0	100 100
All	All	4851/8088 (60%)	4660 (96%)	181 (4%)	10 (0%)	50 78

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E	333	LYS
4	E	412	PRO
5	F	311	ASP
4	H	393	GLN
4	E	300	MET

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	2299/3450 (67%)	2296 (100%)	3 (0%)	93 98
2	B	300/322 (93%)	299 (100%)	1 (0%)	92 97

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	G	362/419 (86%)	358 (99%)	4 (1%)	73 86
4	E	422/940 (45%)	418 (99%)	4 (1%)	78 90
5	F	209/520 (40%)	187 (90%)	22 (10%)	7 25
6	C	206/682 (30%)	199 (97%)	7 (3%)	37 65
All	All	3798/6333 (60%)	3757 (99%)	41 (1%)	74 86

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	F	296	MET
6	C	556	LYS
5	F	302	LEU
5	F	314	ARG
6	C	561	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
5	F	114	ASN
5	F	94	HIS
3	G	14	ASN
5	F	93	HIS
2	B	89	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
7	ATP	G	501	8	26,33,33	0.61	0	31,52,52	0.73	2 (6%)
7	ATP	B	401	8	26,33,33	0.59	0	31,52,52	0.74	2 (6%)

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
7	ATP	G	501	8	-	8/18/38/38	0/3/3/3
7	ATP	B	401	8	-	5/18/38/38	0/3/3/3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	B	401	ATP	C5-C6-N6	2.32	123.87	120.35
7	G	501	ATP	C5-C6-N6	2.30	123.85	120.35
7	B	401	ATP	PB-O3B-PG	2.05	139.85	132.83
7	G	501	ATP	PB-O3B-PG	2.04	139.82	132.83

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	401	ATP	PB-O3B-PG-O3G
7	B	401	ATP	C3'-C4'-C5'-O5'
7	G	501	ATP	PB-O3B-PG-O2G
7	G	501	ATP	C5'-O5'-PA-O1A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
7	G	501	ATP	C5'-O5'-PA-O2A

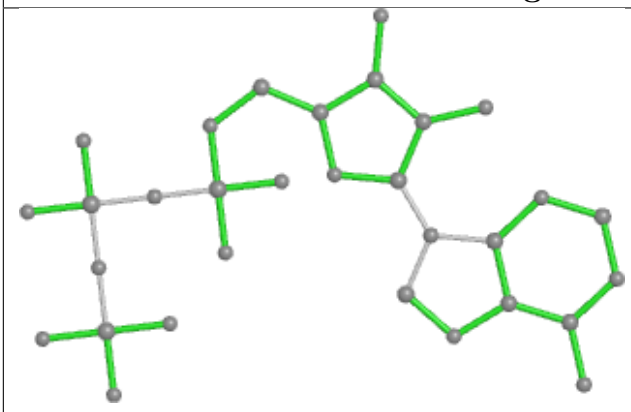
There are no ring outliers.

2 monomers are involved in 5 short contacts:

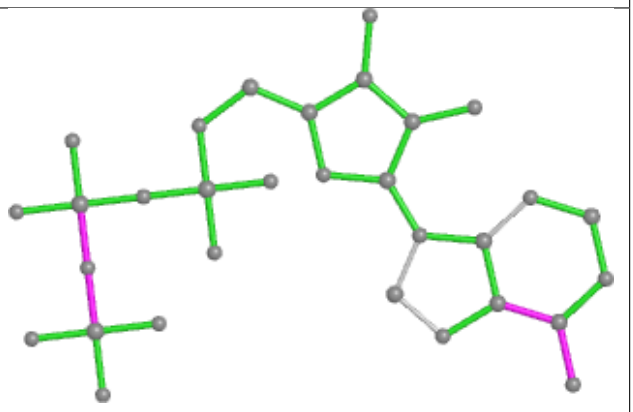
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	G	501	ATP	3	0
7	B	401	ATP	2	0

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

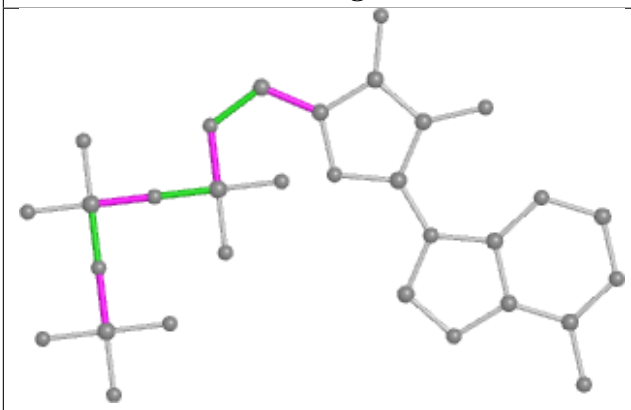
Ligand ATP G 501



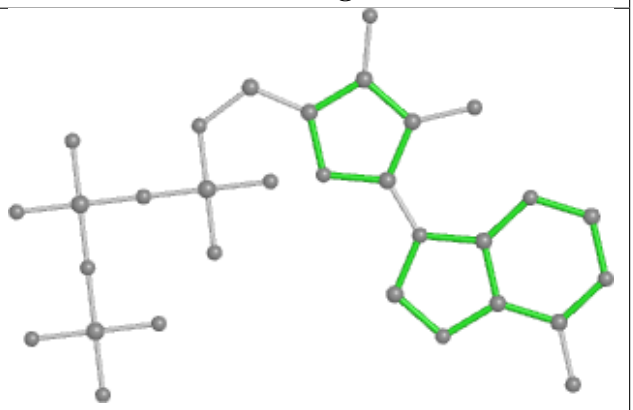
Bond lengths



Bond angles

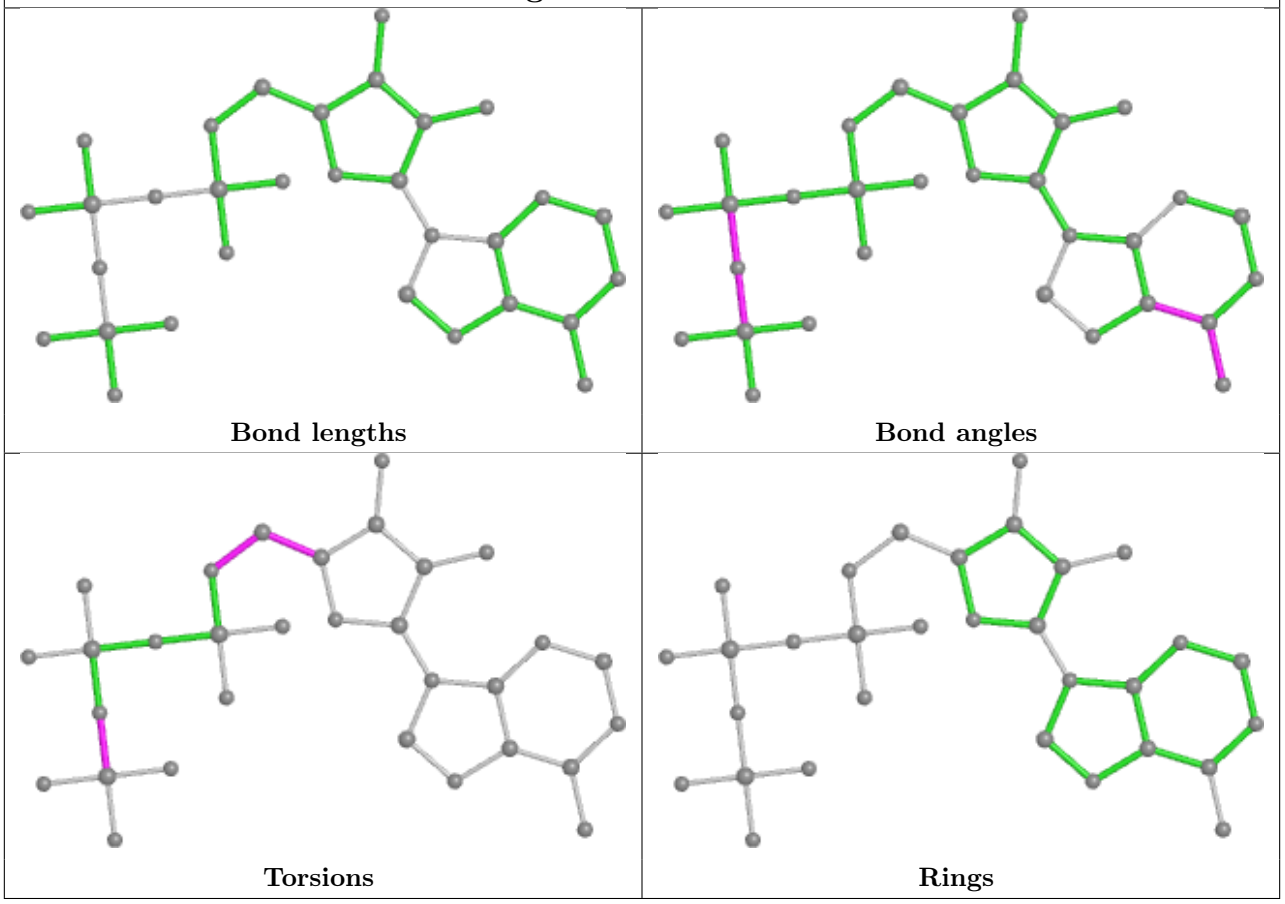


Torsions



Rings

Ligand ATP B 401



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.

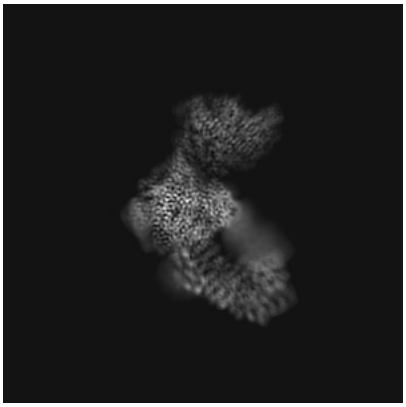
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-14989. These allow visual inspection of the internal detail of the map and identification of artifacts.

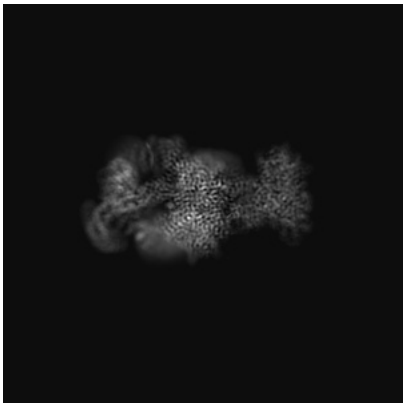
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

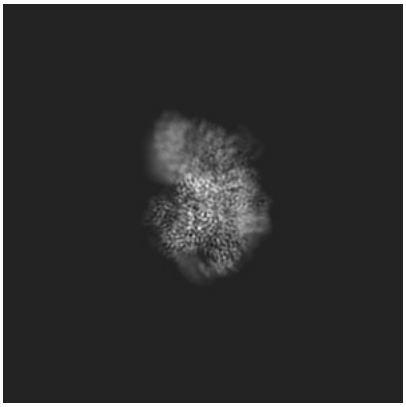
6.1.1 Primary map



X



Y

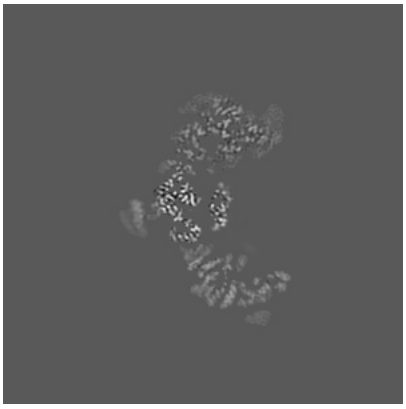


Z

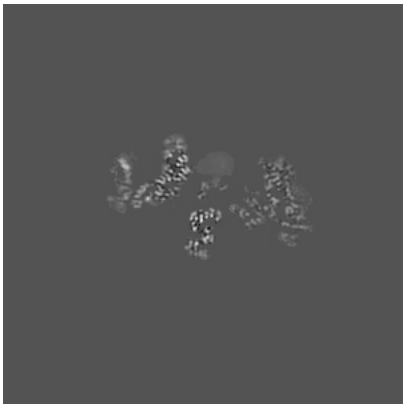
The images above show the map projected in three orthogonal directions.

6.2 Central slices

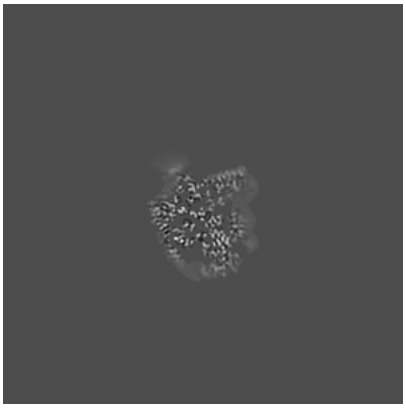
6.2.1 Primary map



X Index: 224



Y Index: 224

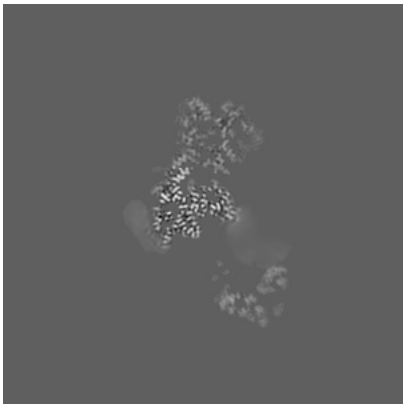


Z Index: 224

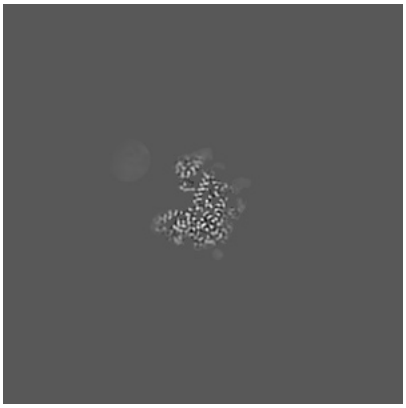
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

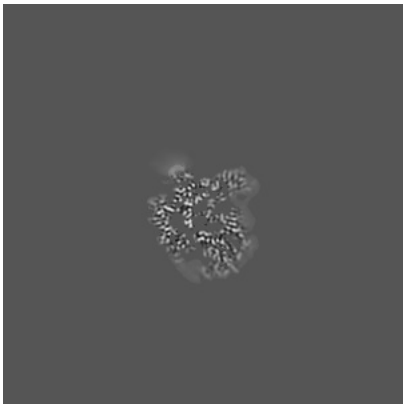
6.3.1 Primary map



X Index: 209



Y Index: 182

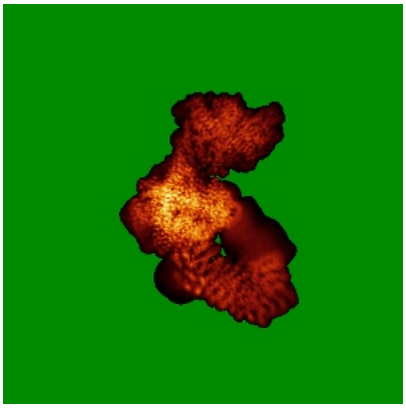


Z Index: 221

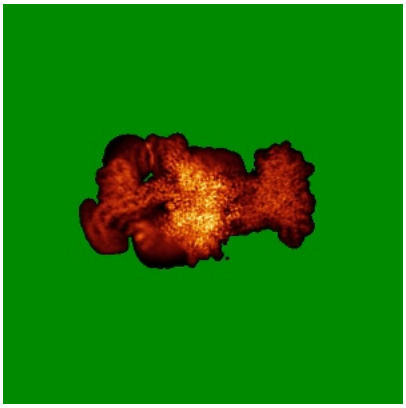
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

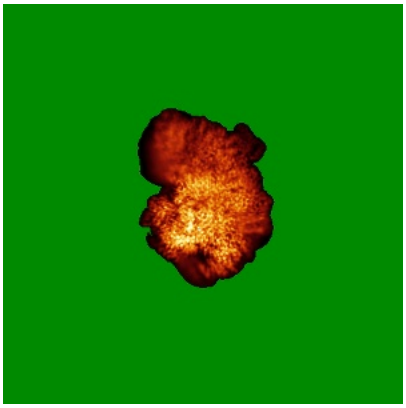
6.4.1 Primary map



X



Y

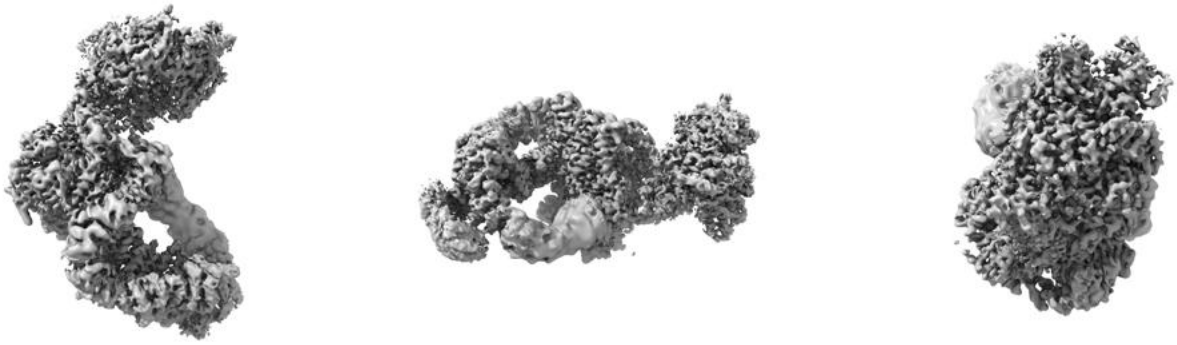


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

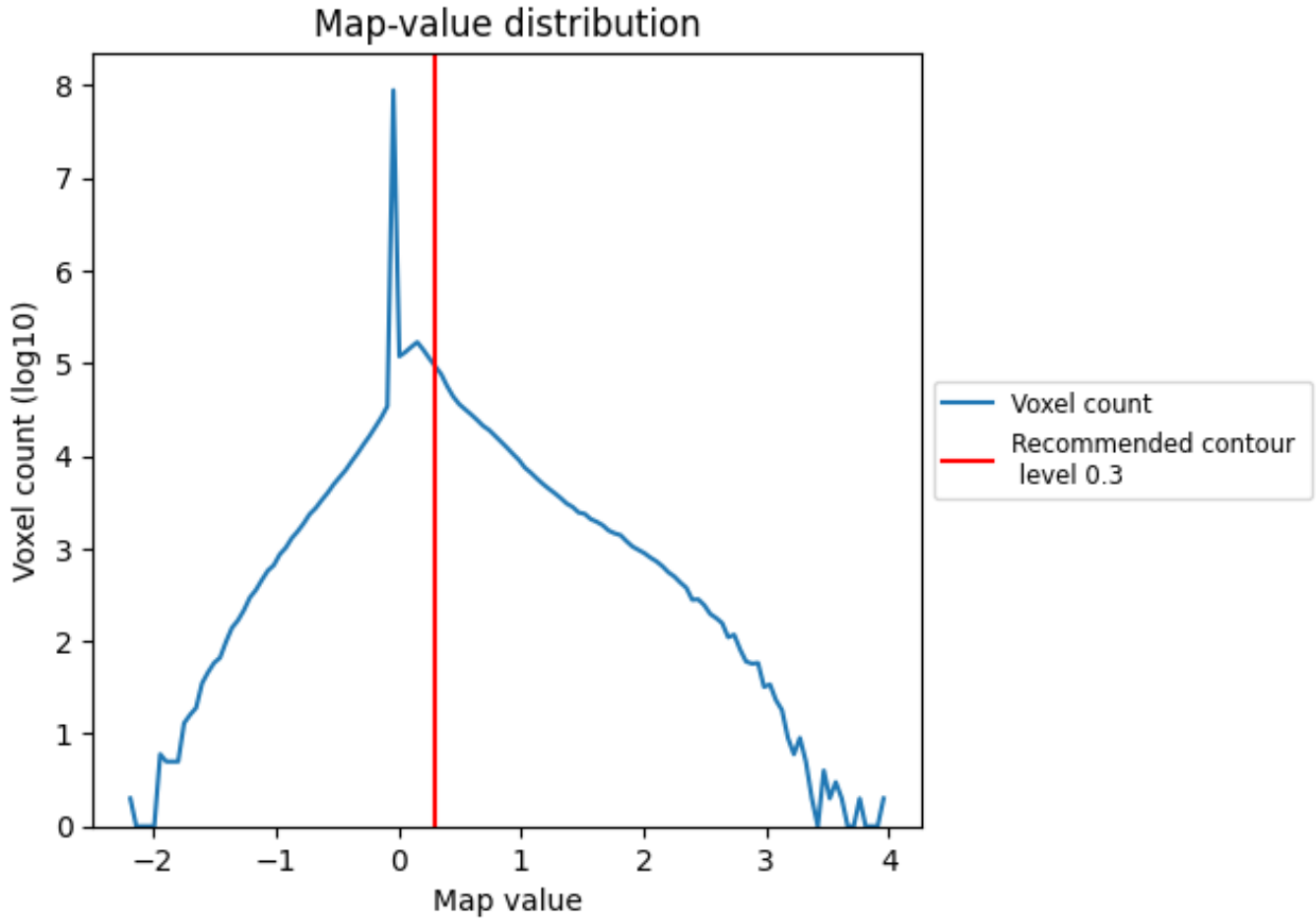
6.6 Mask visualisation (i)

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

7 Map analysis

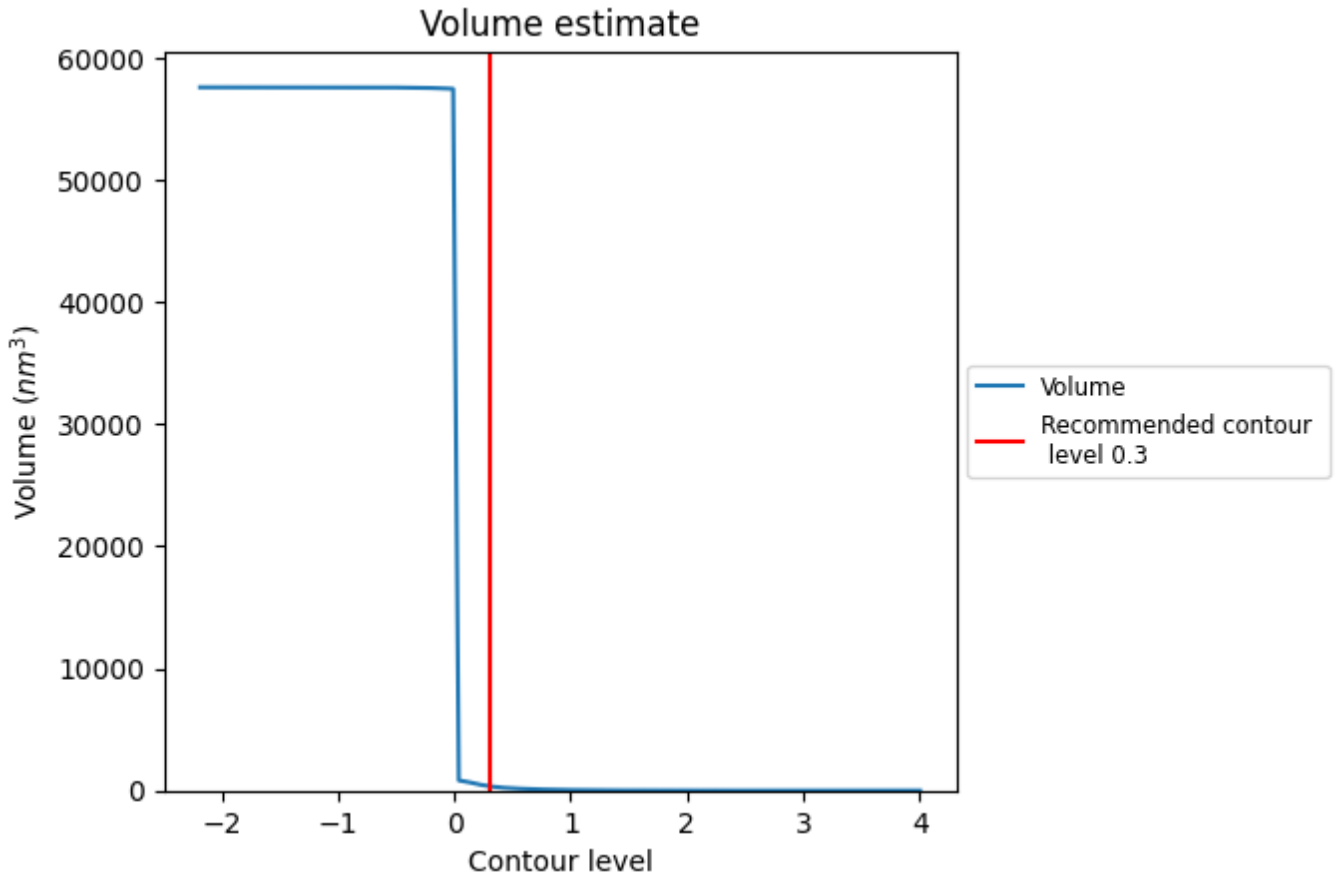
This section contains the results of statistical analysis of the map.

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.

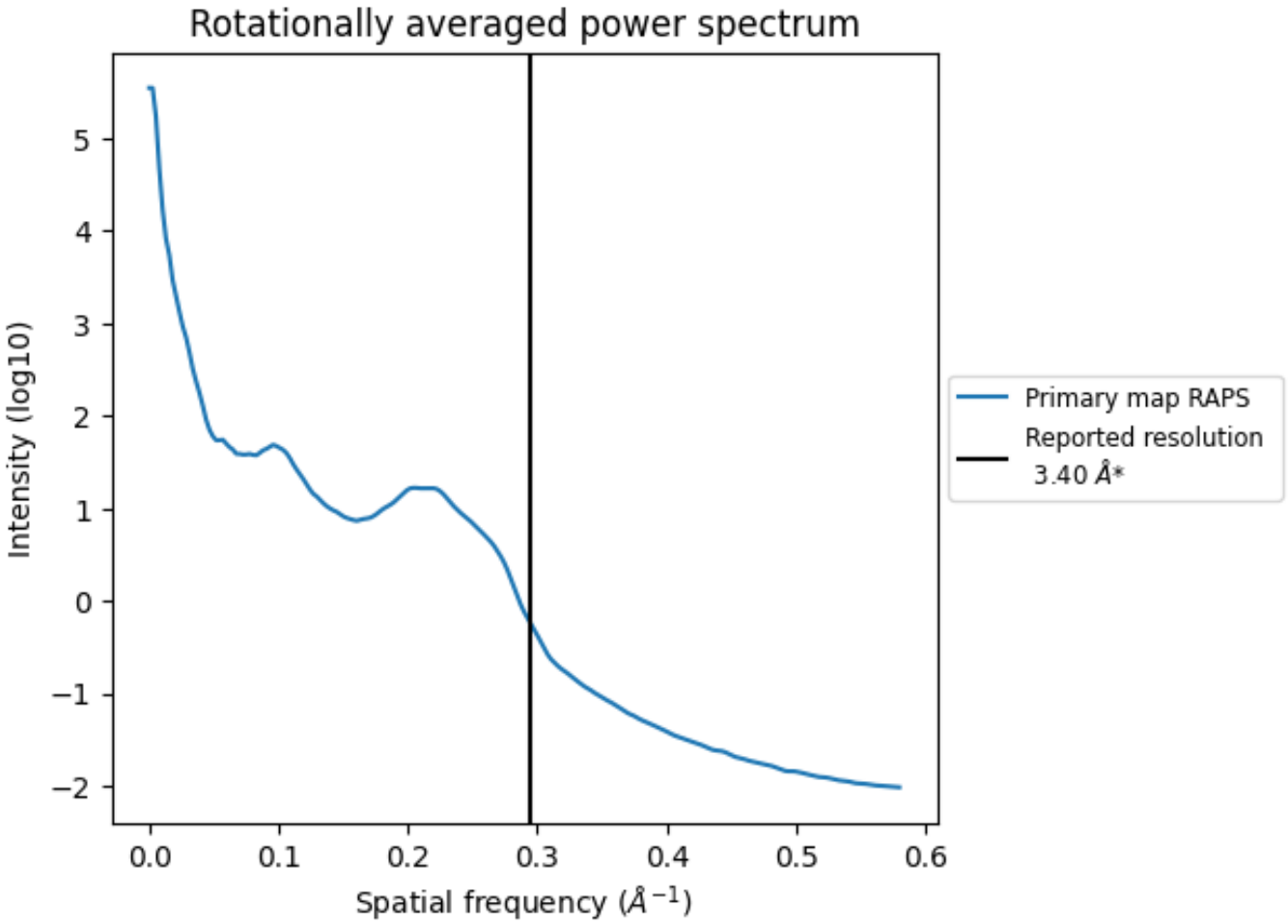
7.2 Volume estimate (i)



The volume at the recommended contour level is 358 nm^3; this corresponds to an approximate mass of 323 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 0.294 Å^{-1}

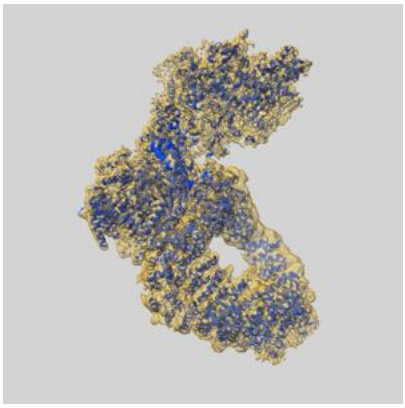
8 Fourier-Shell correlation

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

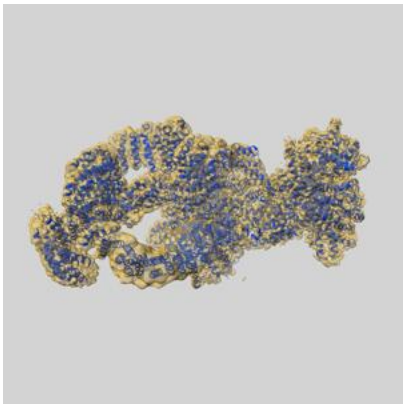
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-14989 and PDB model 7ZVW. Per-residue inclusion information can be found in section 3 on page 5.

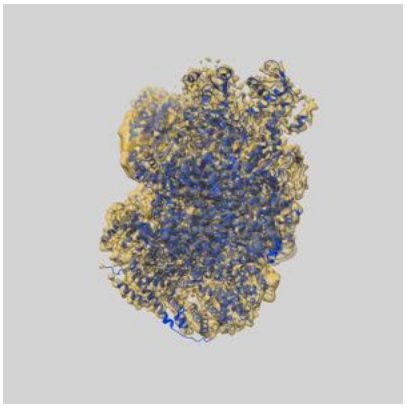
9.1 Map-model overlay



X



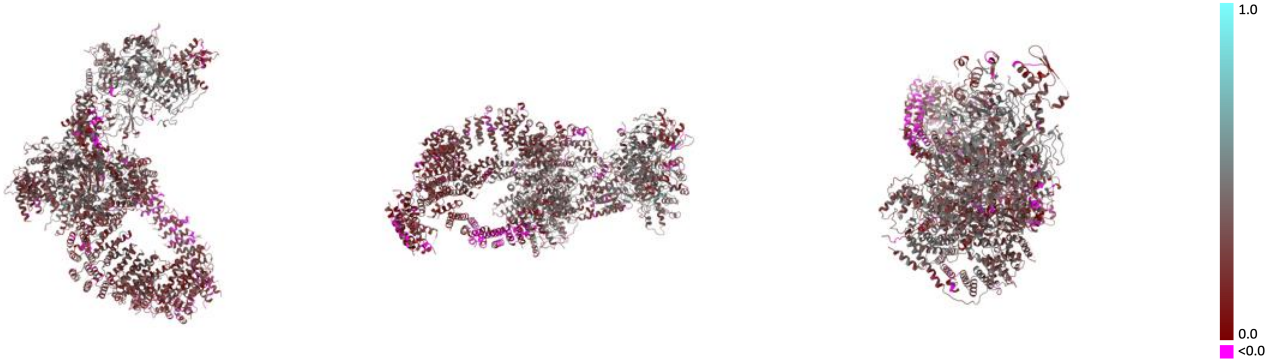
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3 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.

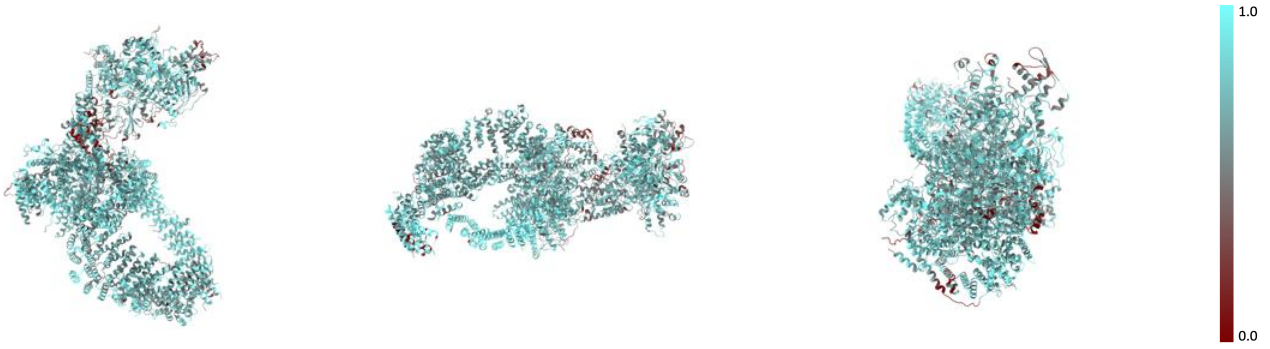
9.2 Q-score mapped to coordinate model



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.

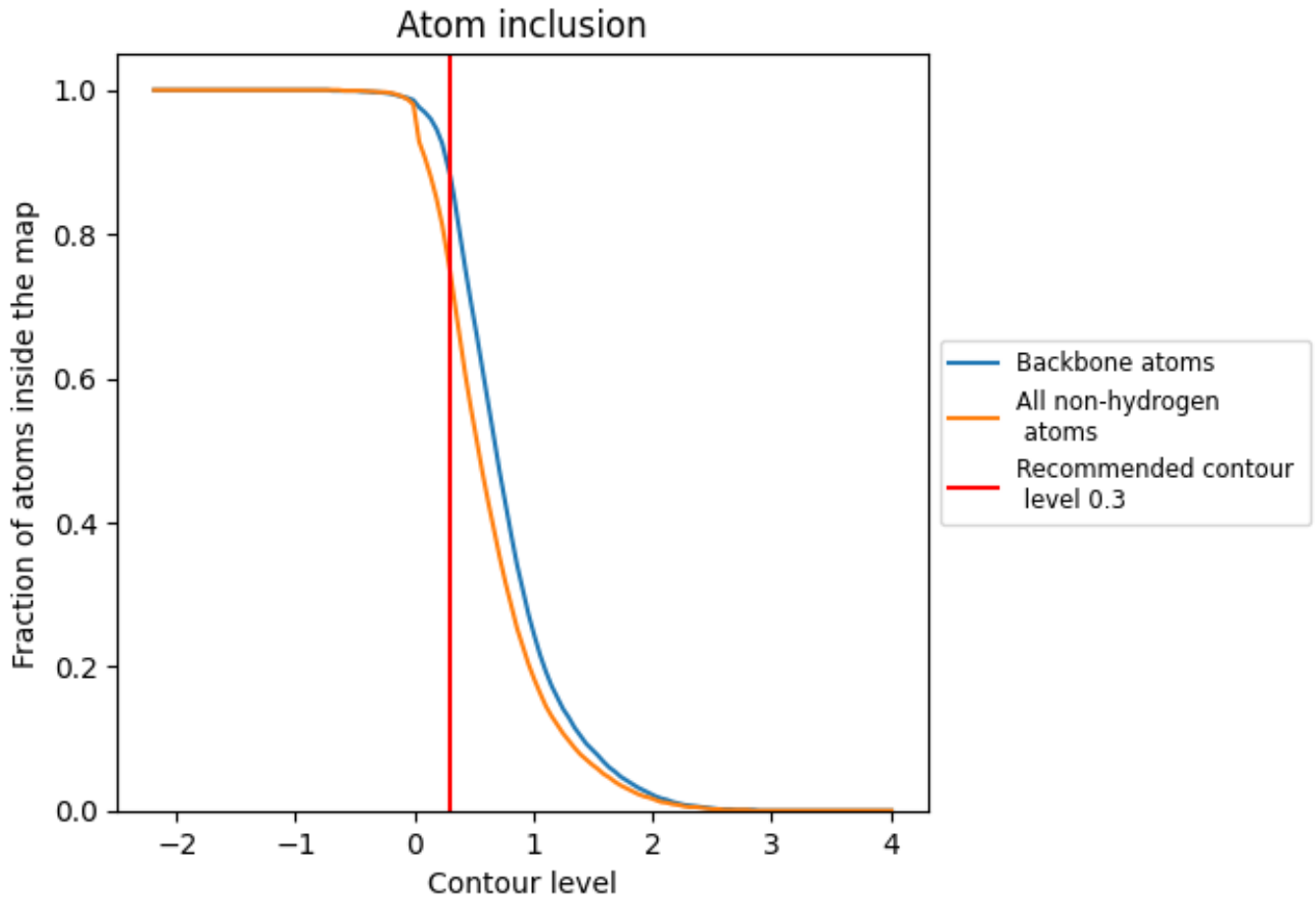
9.3 Atom inclusion mapped to coordinate model



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 (0.3).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 75% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7460	0.3090
A	0.7740	0.2840
B	0.6900	0.3500
C	0.5820	0.2910
E	0.6980	0.3340
F	0.7400	0.3760
G	0.7390	0.3920
H	0.7000	0.4500