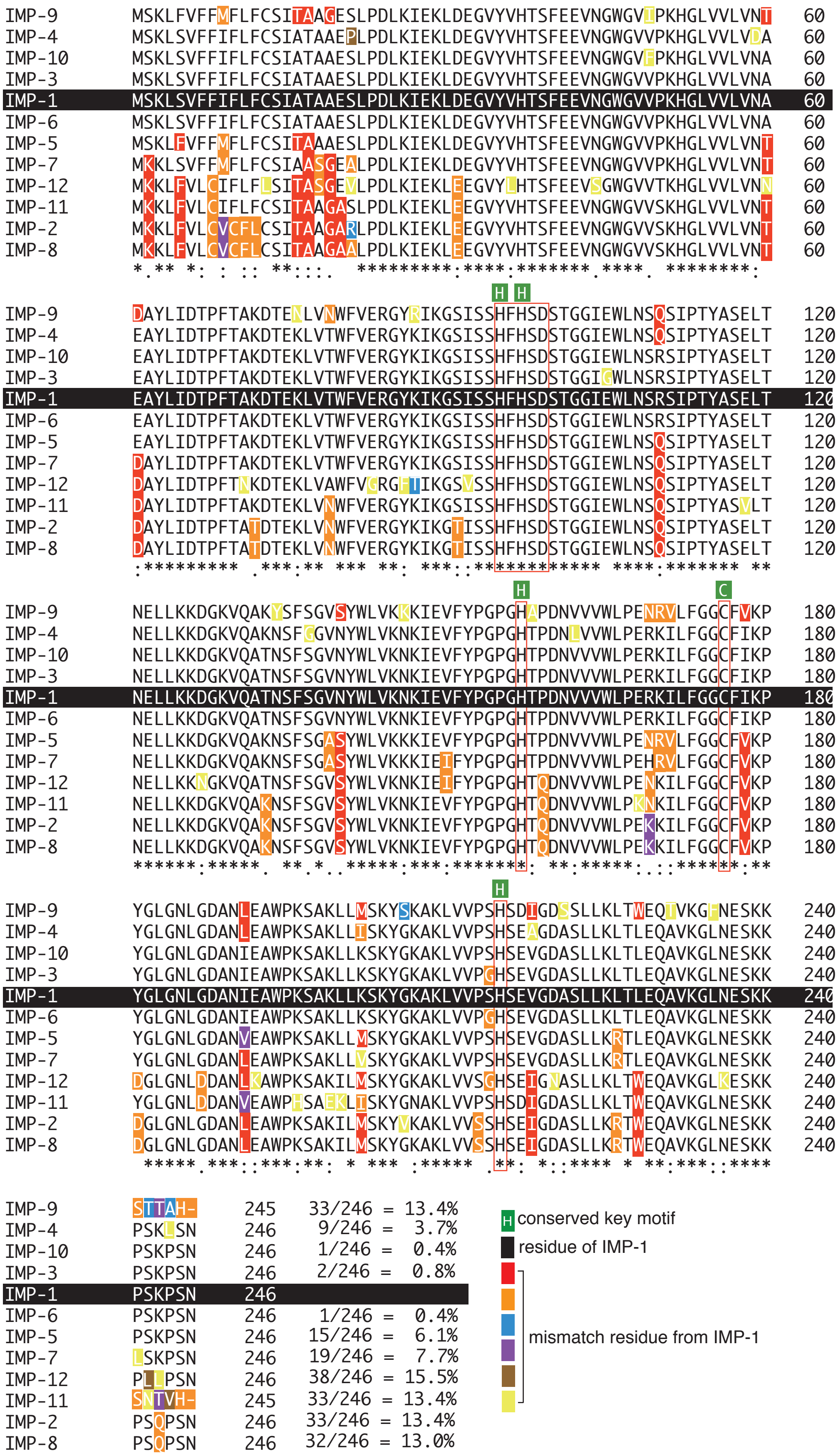
* indicates positions which have a single, fully conserved residue
: indicates that one of the following 'strong' groups is fully conserved (>0.5 Gonnet Pam250 matrix)
. indicates that one of the following 'weaker' groups is fully conserved (=<0.5 Gonnet Pam250 matrix)



```
IMP-9         MSKLFVFFMFLFCSITAAGESLPDLKIEKLDEGVYVHTSFEEVNGWGVIPKHGLVVLVNT    60
IMP-4         MSKLSVFFIFLFCSIATAAEPLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVDA    60
IMP-10        MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVFPKHGLVVLVNA    60
IMP-3         MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVNA    60
IMP-1         MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVNA    60
IMP-6         MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVNA    60
IMP-5         MSKLFVFFMFLFCSITAAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVNT    60
IMP-7         MKKLSVFFMFLFCSIAASGEALPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVNT    60
IMP-12        MKKLFVLCIFLFLSITASGEVLPDLKIEKLEEGVYLHTSFEEVSGWGVVTKHGLVVLVNN    60
IMP-11        MKKLFVLCIFLFCSITAAGASLPDLKIEKLEEGVYVHTSFEEVNGWGVVSKHGLVVLVNT    60
IMP-2         MKKLFVLCVCFLCSITAAGARLPDLKIEKLEEGVYVHTSFEEVNGWGVVSKHGLVVLVNT    60
IMP-8         MKKLFVLCVCFLCSITAAGAALPDLKIEKLEEGVYVHTSFEEVNGWGVVSKHGLVVLVNT    60
              *.** *: : :: **:::.  *********:****:*******.****. ********:

IMP-9         DAYLIDTPFTAKDTENLVNWFVERGYRIKGSISSHFHSDSTGGIEWLNSQSIPTYASELT    120
IMP-4         EAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTYASELT    120
IMP-10        EAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYASELT    120
IMP-3         EAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIGWLNSRSIPTYASELT    120
IMP-1         EAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYASELT    120
IMP-6         EAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYASELT    120
IMP-5         EAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTYASELT    120
IMP-7         DAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTYASELT    120
IMP-12        DAYLIDTPFTNKDTEKLVAWFVGRGFTIKGSVSSHFHSDSTGGIEWLNSQSIPTYASELT    120
IMP-11        DAYLIDTPFTAKDTEKLVNWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTYASVLT    120
IMP-2         DAYLIDTPFTATDTEKLVNWFVERGYKIKGTISSHFHSDSTGGIEWLNSQSIPTYASELT    120
IMP-8         DAYLIDTPFTATDTEKLVNWFVERGYKIKGTISSHFHSDSTGGIEWLNSQSIPTYASELT    120
              :********* .***:** *** **: ***::************ ****:******* **

IMP-9         NELLKKDGKVQAKYSFSGVSYWLVKKKIEVFYPGPGHAPDNVVVWLPENRVLFGGCFVKP    180
IMP-4         NELLKKDGKVQAKNSFGGVNYWLVKNKIEVFYPGPGHTPDNLVVWLPERKILFGGCFIKP    180
IMP-10        NELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKILFGGCFIKP    180
IMP-3         NELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKILFGGCFIKP    180
IMP-1         NELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKILFGGCFIKP    180
IMP-6         NELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKILFGGCFIKP    180
IMP-5         NELLKKDGKVQAKNSFSGASYWLVKKKIEVFYPGPGHTPDNVVVWLPENRVLFGGCFVKP    180
IMP-7         NELLKKDGKVQAKNSFSGASYWLVKKKIEIFYPGPGHTPDNVVVWLPEHRVLFGGCFVKP    180
IMP-12        NELLKKNGKVQATNSFSGVSYWLVKNKIEIFYPGPGHTQDNVVVWLPENKILFGGCFVKP    180
IMP-11        NELLKKDGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPKNKILFGGCFVKP    180
IMP-2         NELLKKDGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPEKKILFGGCFVKP    180
IMP-8         NELLKKDGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPEKKILFGGCFVKP    180
              ******:*****. **.*..*****:***:*******: **:*****:.::******:**

IMP-9         YGLGNLGDANLEAWPKSAKLLMSKYSKAKLVVPSHSDIGDSSLLKLTWEQTVKGFNESKK    240
IMP-4         YGLGNLGDANLEAWPKSAKLLISKYGKAKLVVPSHSEAGDASLLKLTLEQAVKGLNESKK    240
IMP-10        YGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPSHSEVGDASLLKLTLEQAVKGLNESKK    240
IMP-3         YGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPGHSEVGDASLLKLTLEQAVKGLNESKK    240
IMP-1         YGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPSHSEVGDASLLKLTLEQAVKGLNESKK    240
IMP-6         YGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPGHSEVGDASLLKLTLEQAVKGLNESKK    240
IMP-5         YGLGNLGDANVEAWPKSAKLLMSKYGKAKLVVPSHSEVGDASLLKRTLEQAVKGLNESKK    240
IMP-7         YGLGNLGDANLEAWPKSAKLLVSKYGKAKLVVPSHSEVGDASLLKRTLEQAVKGLNESKK    240
IMP-12        DGLGNLDDANLKAWPKSAKILMSKYGKAKLVVSGHSEIGNASLLKLTWEQAVKGLKESKK    240
IMP-11        YGLGNLDDANVEAWPHSAEKLISKYGNAKLVVPSHSDIGDASLLKLTWEQAVKGLNESKK    240
IMP-2         DGLGNLGDANLEAWPKSAKILMSKYVKAKLVVSSHSEIGDASLLKRTWEQAVKGLNESKK    240
IMP-8         DGLGNLGDANLEAWPKSAKILMSKYGKAKLVVSSHSEIGDASLLKRTWEQAVKGLNESKK    240
               *****.***::***:**: * *** :***** .**: *::**** * **:***::****

IMP-9         STTAH-    245     33/246 = 13.4%
IMP-4         PSKLSN    246      9/246 =  3.7%
IMP-10        PSKPSN    246      1/246 =  0.4%
IMP-3         PSKPSN    246      2/246 =  0.8%
IMP-1         PSKPSN    246
IMP-6         PSKPSN    246      1/246 =  0.4%
IMP-5         PSKPSN    246     15/246 =  6.1%
IMP-7         LSKPSN    246     19/246 =  7.7%
IMP-12        PLLPSN    246     38/246 = 15.5%
IMP-11        SNTVH-    245     33/246 = 13.4%
IMP-2         PSQPSN    246     33/246 = 13.4%
IMP-8         PSQPSN    246     32/246 = 13.0%
```

Supplemental Fig. 6. The alignment of primary sequences of the class B metallo-β-lactamase IMP family

Primary sequence variations as evidenced by the alignment of IMP-type MBLs. The binding site for Zn^{2+} at the enzymatic active site involves three histidines at the amino-terminal side. Based on the primary sequences, the alignment was generated using Clustal Omega [32, 33, 34] of GenomeNet at Kyoto University Bioinformatics Center (https://www.genome.jp/tools-bin/clustalw).