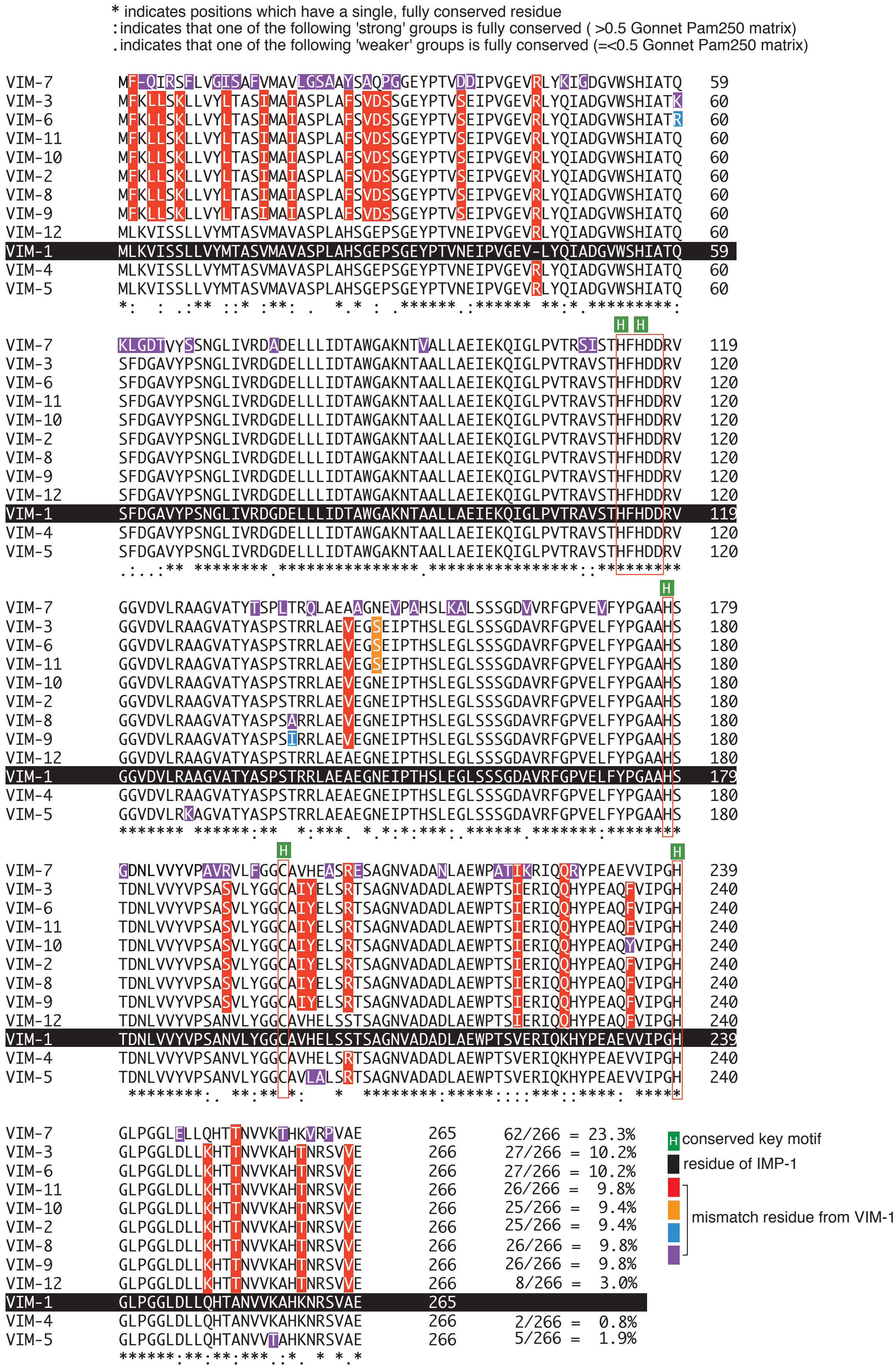

* indicates positions which have a single, fully conserved residue
: indicates that one of the following 'strong' groups is fully conserved (>0.5 Gonnet Pam250 matrix)
. indicates that one of the following 'weaker' groups is fully conserved (=<0.5 Gonnet Pam250 matrix)

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VIM-7           MF-QIRSFLVGISAFVMAVLGSAAYSAQPGGEYPTVDDIPVGEVRLYKIGDGVWSHIATQ   59
VIM-3           MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIATK   60
VIM-6           MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIATR   60
VIM-11          MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIATQ   60
VIM-10          MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIATQ   60
VIM-2           MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIATQ   60
VIM-8           MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIATQ   60
VIM-9           MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIATQ   60
VIM-12          MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHIATQ   60
VIM-1           MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEV-LYQIADGVWSHIATQ   59
VIM-4           MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHIATQ   60
VIM-5           MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHIATQ   60
                *:  : .:** ::* :**: .  *.* : .******.:****** **:*.*********:
                                                                   H H
VIM-7           KLGDTVYSSNGLIVRDADELLLIDTAWGAKNTVALLAEIEKQIGLPVTRSISTHFHDDRV   119
VIM-3           SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   120
VIM-6           SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   120
VIM-11          SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   120
VIM-10          SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   120
VIM-2           SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   120
VIM-8           SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   120
VIM-9           SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   120
VIM-12          SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   120
VIM-1           SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   119
VIM-4           SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   120
VIM-5           SFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRV   120
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VIM-7           GGVDVLRAAGVATYTSPLTRQLAEAAGNEVPAHSLKALSSSGDVVRFGPVEVFYPGAAHS   179
VIM-3           GGVDVLRAAGVATYASPSTRRLAEVEGSEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   180
VIM-6           GGVDVLRAAGVATYASPSTRRLAEVEGSEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   180
VIM-11          GGVDVLRAAGVATYASPSTRRLAEVEGSEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   180
VIM-10          GGVDVLRAAGVATYASPSTRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   180
VIM-2           GGVDVLRAAGVATYASPSTRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   180
VIM-8           GGVDVLRAAGVATYASPSARRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   180
VIM-9           GGVDVLRAAGVATYASPSIRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   180
VIM-12          GGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   180
VIM-1           GGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   179
VIM-4           GGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   180
VIM-5           GGVDVLRKAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVELFYPGAAHS   180
                ******* ******:**  *:***. *.*:*:***:.******.*******:********
                                 H                                         H
VIM-7           GDNLVVYVPAVRVLFGGCAVHEASRESAGNVADANLAEWPATIKRIQQRYPEAEVVIPGH   239
VIM-3           TDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHYPEAQFVIPGH   240
VIM-6           TDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHYPEAQFVIPGH   240
VIM-11          TDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHYPEAQFVIPGH   240
VIM-10          TDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHYPEAQYVIPGH   240
VIM-2           TDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHYPEAQFVIPGH   240
VIM-8           TDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHYPEAQFVIPGH   240
VIM-9           TDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHYPEAQFVIPGH   240
VIM-12          TDNLVVYVPSANVLYGGCAVHELSSTSAGNVADADLAEWPTSIERIQQHYPEAQFVIPGH   240
VIM-1           TDNLVVYVPSANVLYGGCAVHELSSTSAGNVADADLAEWPTSVERIQKHYPEAEVVIPGH   239
VIM-4           TDNLVVYVPSANVLYGGCAVHELSRTSAGNVADADLAEWPTSVERIQKHYPEAEVVIPGH   240
VIM-5           TDNLVVYVPSANVLYGGCAVLALSRTSAGNVADADLAEWPTSVERIQKHYPEAEVVIPGH   240
                 ********:. **:** *:   *  ********:*****::::***::****: *****

VIM-7           GLPGGLELLQHTTNVVKTHKVRPVAE       265     62/266 = 23.3%
VIM-3           GLPGGLDLLKHTTNVVKAHTNRSVVE       266     27/266 = 10.2%
VIM-6           GLPGGLDLLKHTTNVVKAHTNRSVVE       266     27/266 = 10.2%
VIM-11          GLPGGLDLLKHTTNVVKAHTNRSVVE       266     26/266 =  9.8%
VIM-10          GLPGGLDLLKHTTNVVKAHTNRSVVE       266     25/266 =  9.4%
VIM-2           GLPGGLDLLKHTTNVVKAHTNRSVVE       266     25/266 =  9.4%
VIM-8           GLPGGLDLLKHTTNVVKAHTNRSVVE       266     26/266 =  9.8%
VIM-9           GLPGGLDLLKHTTNVVKAHTNRSVVE       266     26/266 =  9.8%
VIM-12          GLPGGLDLLKHTTNVVKAHTNRSVVE       266      8/266 =  3.0%
VIM-1           GLPGGLDLLQHTANVVKAHKNRSVAE       265
VIM-4           GLPGGLDLLQHTANVVKAHKNRSVAE       266      2/266 =  0.8%
VIM-5           GLPGGLDLLQHTANVVTAHKNRSVAE       266      5/266 =  1.9%
                ******:**:**:***.:*. * *.*
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Supplemental Fig. 7. The alignment of primary sequences of the class B metallo-β-lactamase VIM family

Primary sequence variations as evidenced by the alignment of VIM-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).