## Figure 1 - figure supplement 1

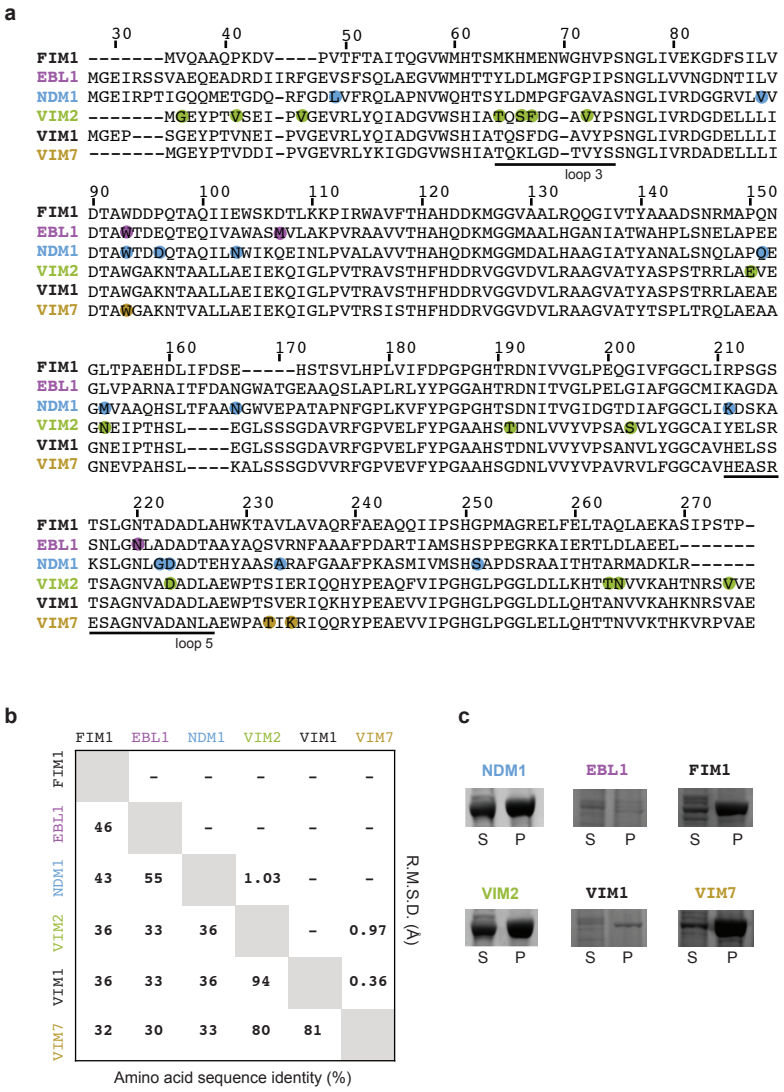


**Figure 1-figure supplement 1.** Sequence comparison between metallo-β-lactamases. (**A**) Sequence alignment of selected metallo-β-lactamases. Residue number is based on the NDM1 sequence (PDB-ID 3spu). Positions that were mutated and selected during the directed evolution of PMH activities are highlighted in color. Actual mutations are listed in **Supplementary File 1B**. (**B**) Sequence identity and structure similarity among selected B1 β-lactamases. A multiple sequence alignment of the nine B1 β-lactamases using ClustalW2 (standard parameters), which was then used to calculate the pairwise sequence identities using the web based program SIAS (hcp://imed.med.ucm.es/Tools/sias.html) with gaps taken into account. To determine pairwise structural similarity, we computed the root mean standard deviation (RMSD) between all structure pairs using the align command PyMOL. (**C**) SDS-PAGE images of protein expression in the supernatant (S) and pellet (P) fractions of the cell lysate. Images for NDM1 and Vim2 are the same as the ones used in **Figure 3-figure supplement 1**.