

KPC-3	MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYR	60
KPC-46	MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYR	60
KPC-92	MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYR	60
KPC-66	MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYR *****	60
KPC-3	AERFPLCSSFKGFLLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTGTMVAE	120
KPC-46	AERFPLCSSFKGFLLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTGTMVAE	120
KPC-92	AERFPLCSSFKGFLLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTGTMVAE	120
KPC-66	AERFPLCSSFKGFLLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTGTMVAE *****	120
KPC-3	LSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDITFRLD	180
KPC-46	LSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDITFRLD	180
KPC-92	LSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDITFRLD	178
KPC-66	LSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDITFRLD *****	178
KPC-3	SPRAVTESLQKLTLSALAAPQRQQFVDWLKGNITGNHRIRAAVPADWAVGDKTGTGCVY	240
KPC-46	SPRAVTESLQKLTLSALAAPQRQQFVDWLKGNITGNHRIRAAVPADWAVGDKTGTGCVY	240
KPC-92	SPRAVTESLQKLTLSALAAPQRQQFVDWLKGNITGNHRIRAAVPADWAVGDKTGTGCVY	238
KPC-66	SPRAVTESLQKLTLSALAAPQRQQFVDWLKGNITGNHRIRAAVPADWAVGDKTGTGCVY *****	238
KPC-3	GTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAAARLALEGLGVNGQ	293
KPC-46	GTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAAARLALEGLGVNGQ	293
KPC-92	GTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAAARLALEGLGVNGQ	291
KPC-66	GTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAAARLALEGLGVNGQ *****	291

Figure S1. Alignment of the amino acid sequences of KPC-3 and novel KPC-46, KPC-66 and KPC-92 enzymes. Red box indicates the Ω -loop region (Arg164 to Asp179). The gray shading shows the mutated positions in KPC-46, KPC-66 and KPC-92 variants.