Pfam #	Description	PD-(D/E)xK	*P*-value	HHsvm4
PF03008	Archaea bacterial proteins of unknown function	PF02021	3.1E-08	0.998
PF03838	Recombination protein U	PF01870	6.1E-06	0.883
PF04257	Exodeoxyribonuclease V, gamma subunit	PF06023	1.5E-18	1.000
PF04556	DpmII restriction endonuclease	PF02646	1.6E-03	0.709
PF05367	Phage endonuclease I	PF06356	2E-07	0.996
PF08696	DNA replication factor Dna2	PF06023	1.3E-15	1.000
PF08814	XisH protein	PF04471	6.1E-04	1.000
PF09002	Domain of unknown function (DUF1887)	PF10356	8E-07	0.998
PF09019	EcoRII C terminal	PF01870	1.1E-03	0.626
PF09254	Restriction endonuclease FokI, C terminal	PF10356	3.5E-04	0.576
PF09563	LlaJI restriction endonuclease	PF04411	2.5E-09	0.983
PF09588	YqaJ viral recombinase family	PF01771	1.8E-33	1.000
PF09810	Defects in morphology protein 1, mitochondrial precursor	PF06023	8E-19	1.000
PF09903	Uncharacterized protein conserved in bacteria (DUF2130)	PF02646	4.6E-06	1.000
PF10117	McrBC 5-methylcytosine restriction system component	PF04411	2E-13	1.000

Supplementary Table II. The list and descriptions of new Pfam families predicted to be members of the PD-(D/E)xK clan (CL0236) (Finn *et al.*, 2008). Values on the right represent the best evidence for this assignment based on profile-profile score to a known member of the PD-(D/E)xK clan. *P*-values were taken directly from HHsearch outputs and HHsvm4 column shows the probabilities that these hits are true homologues.