

Table S5. The partitioning schemes and corresponding substitution models determined by PartitionFinder for the PCGAA dataset

Partitions	Models	Amino acid partitions
P1	mtART + I + G + F	ATP6, ND2, ND3, CYTB
P2	mtREV + I + G+ F	ATP8, ND6
P3	mtART + I + G	COX1
P4	mtART + I + G	COX2, COX3
P5	mtART + I + G + F	ND1, ND4, ND4L, ND5