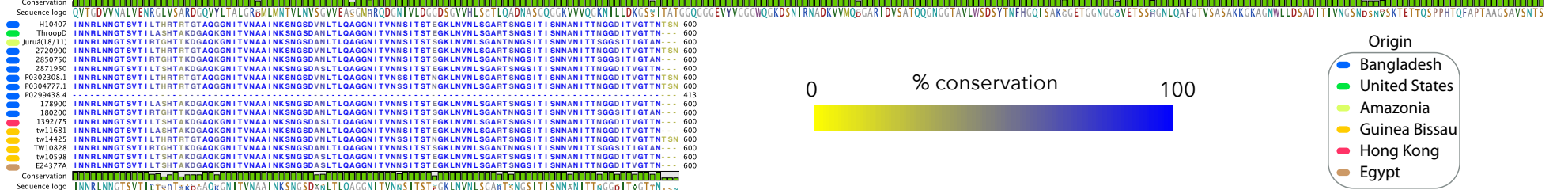


# EtpA\_ (residues 1-600) Alignment

H10407	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSV	250
ThroopD	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSA	250
Jurua(18,11)	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSA	250
2720900	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSV	250
2850750	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSA	250
2871950	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSA	250
P0302308.1	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSV	250
P0304777.1	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSV	250
P0299438.4	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSV	250
178900	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSA	250
180200	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSA	250
1392/75	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSA	250
tw11681	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSA	250
tw14425	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSV	250
tw10828	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSA	250
tw10598	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSA	250
E24377A	MNRIYKLFKDKRRNELVVVSEITTVGNAKATGSVGEKSPRRGVRAMALSLSGMMIMAHMPANSANLPTGGQIVAGSGSIQTPSGNQMNIHQNSQNMVANWNSFDIKGKNTVQFQDPSSSAVALNRRVVGGGESQIMGNLKANGQVFLVNPNGVLFEGEASVSTSGFVASTRIDIKNDDFMNRRYTFSGGQKAGAAIVNQGLTNNAGGYVLAADRVSNSGTRTPGGKTVLAAASERVTLQLDNGLGMSV	250



- Origin
- Bangladesh
  - United States
  - Amazonia
  - Guinea Bissau
  - Hong Kong
  - Egypt

0 % conservation 100