

Yanagisawa *et al.*, Fig. S4

HT1125	1	MNTPPFVCWIFCKVIDNFGDIGVSLRLARVLHRELGWQVHLWTDDVSALRALCPDLPDVP	60
H44/76	1	MNTPPFVCWIFCKVIDNFGDIGVSWRLARVLHRELGWQVHLWTDDVSALRALCPDLPDVP	60
MC58	1	MNTPPFVCWIFCKVIDNFGDIGVSWRLARVLHRELGWQVHLWTDDVSALRALCPDLPDVP	60
HT1125	61	CVHQDIHVRTWHSDAADIDTAPVPDAVIETFACDLPENVLHIIRRHKPLWLNWEYLSAEE	120
H44/76	61	CVHQDIHVRTWHSDAADIDTAPVPDVVIETFACDLPENVLHIIRRHKPLWLNWEYLSAEE	120
MC58	61	CVHQDIHVRTWHSDAADIDTAPVPDVVIETFACDLPENVLHIIRRHKPLWLNWEYLSAEE	120
HT1125	121	SNERLHLMPSPQEGVQKYFWFMGFSEKSGGLIRERDYRDAVRFDTEALRQRLMLPEKNAP	180
H44/76	121	SNERLHLMPSPQEGVQKYFWFMGFSEKSGGLIRERDYCEAVRFDTEALRERLMLPEKNAS	180
MC58	121	SNERLHLMPSPQEGVQKYFWFMGFSEKSGGLIRERDYCEAVRFDTEALRERLMLPEKNAS	180
HT1125	181	EWLLFGYRSDVWAKWLEMWQQAGSPMTLLLAGAQIIDSLKQSGIIPQNALQNDGDVFTA	240
H44/76	181	EWLLFGYRSDVWAKWLEMWRQAGSPMTLLLAGTQIIDSLKQSGVIPQDALQNDGDVFTA	240
MC58	181	EWLLFGYRSDVWAKWLEMWRQAGSPMTLLLAGTQIIDSLKQSGVIPQDALQNDGDVFTA	240
HT1125	241	SVRLVKIPFVPQQDFDQLLHLADCAVIRGEDSFVRAQLAGKPPFFWHIYPQDEHVHLDKLH	300
H44/76	241	SVRLVKIPFVPQQDFDQLLHLADCAVIRGEDSFVRAQLAGKPPFFWHIYPQDENVHLDKLH	300
MC58	241	SVRLVKIPFVPQQDFDQLLHLADCAVIRGEDSFVRAQLAGKPPFFWHIYPQDENVHLDKLH	300
HT1125	301	AFWDKAHGFYTPETA SAHRCLSDDLNGGEALSATQRLECWQILQQHQNGWRQGA GAWSRY	360
H44/76	301	AFWDKAHGFYTPETVSAHRRLSDDLNGGEALSATQRLECWQTLQQHQNGWRQGA EDWSRY	360
MC58	301	AFWDKAHGFYTPETVSAHRRLSDDLNGGEALSATQRLECWQTLQQHQNGWRQGA EDWSRY	360
HT1125	361	LFGQPSASEKLAAFVSKHQKIR	382
H44/76	361	LFGQPSAPEKLAAFVSKHQKIR	382
MC58	361	LFGQPSAPEKLAAFVSKHQKIR	382

Fig. S4. Sequence alignment of EarP of *N. meningitidis* strains HT1125, H44/76, and MC58

EarP of *N. meningitidis* HT1125 has 14 different residues from those of *N. meningitidis* H44/76 and MC58.