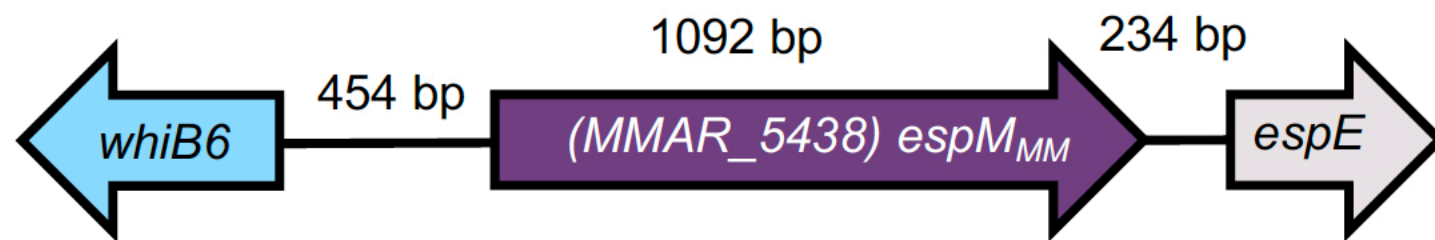


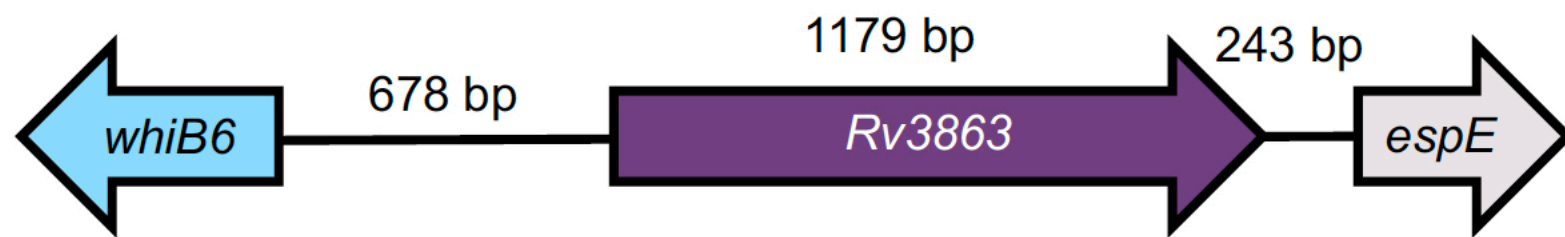
Figure S3

A.

*M. marinum*



*M. tb*



*M. smegmatis*



B.

### Predicted FHA Domain

MSMEG_0052	1	-----
MMAR_5438	1	<b>MPDAESTARPALRVARGGDSPLVTP--GHRPVGRGALTNARLDDPVLSQTHVRAVSDGG</b>
ERDMAN_4236	1	-----MIEPRRGVAIIGHSCRVTQIDDSRISQTHLRAVSDDG
Rv3863	1	<b>MSKAGSTVGPAPLVACSGGTSDVIEPRRGVAIIGHSCRVTQIDDSRISQTHLRAVSDDG</b>
consensus	1	.....

MSMEG_0052	1	-----
MMAR_5438	59	<b>QRRIVTNSPNGMFVDGTRKSSVAVSDKTIVRFGDPTGGKALTFEVVRPSNSPEEDSREQR</b>
ERDMAN_4236	39	<b>RWRIVGNIPRGMFVGGRRGSSVTVSDKTLIRFGDPPGGKALTFEVVRPSDSAAQHGRVQP</b>
Rv3863	61	<b>RWRIVGNIPRGMFVGGRRGSSVTVSDKTLIRFGDPPGGKALTFEVVRPSDSAAQHGRVQP</b>
consensus	61	.....

MSMEG_0052	1	----MTDAEFDLATGEFDVGLVVRAGAAAAARRRELDISQRS LAADGIINAGALIAFEKGR
MMAR_5438	119	<b>PAEQSDSQ-----TNEADPGVVRAGAAAAARRRELDISQRS LAADGIINAGALIAFEKGR</b>
ERDMAN_4236	99	<b>SADLSDDPAHNAAPVAPDPGVVRAGAAAAARRRELDISQRS LAADGIINAGALIAFEKGR</b>
Rv3863	121	<b>SADLSDDPAHNAAPVAPDPGVVRAGAAAAARRRELDISQRS LAADGIINAGALIAFEKGR</b>
consensus	121	.....*

MSMEG_0052	57	<b>SWPRERTRKLEEVLRWPPGTIARLRQGGSVPTTSAPVAPPPEPPAAAPVTSVPAA</b>
MMAR_5438	174	<b>SWPRERTRKLEEVLRWPPGTIARLRQGGSVPTTSAPVAPPPEPPAAAPVTSVPAA</b>
ERDMAN_4236	159	<b>SWPRERTRKLEEVLRWPPGTIARLRQGGSVPTTSAPVAPPPEPPAAAPVTSVPAA</b>
Rv3863	181	<b>SWPRERTRKLEEVLRWPPGTIARLRQGGSVPTTSAPVAPPPEPPAAAPVTSVPAA</b>
consensus	181	*****.*

MSMEG_0052	117	<b>DEVPLIAQAVLTAVHTLETTINAMPPESDPDFVPRVTAIIGDLRQLEAVASRAARISMVT</b>
MMAR_5438	221	<b>GPASLIAQAVAAAVDTCSLAIAALPAPPEPDEFTERAAPILADLRQLEGIQAVQATRISRIT</b>
ERDMAN_4236	206	<b>GPASLIAQAVTAAVDGCSLAIAALPATEDPEDEFTERAAPILADLRQLEAIQAVQATRISRIT</b>
Rv3863	228	<b>GPASLIAQAVTAAVDGCSLAIAALPATEDPEDEFTERAAPILADLRQLEAIQAVQATRISRIT</b>
consensus	241	.....*

MSMEG_0052	177	<b>PPLIKALSAVRRQIDELTMRAANAPGATLQRLYAARRQANLTVAEQAQAAGVSEDAIAR</b>
MMAR_5438	281	<b>PELIKALGAVRRYHDKLMTLSATAPGATLAQRLYAARRRANLSTSETAQAQAAGVTEELIVR</b>
ERDMAN_4236	266	<b>PELIKALGAVRRHDELMLRLGATAPGATLAQRLYAARRRANLSTLETAQAQAAGVAEEMIVG</b>
Rv3863	288	<b>PELIKALGAVRRHDELMLRLGATAPGATLAQRLYAARRRANLSTLETAQAQAAGVAEEMIVG</b>
consensus	301	*****.*

MSMEG_0052	237	<b>TEAEYVPVDAAAVHAIEALIDSLR</b>
MMAR_5438	341	<b>AEAEELHAEAAEAIEALIRQIN</b>
ERDMAN_4236	326	<b>AEAEELPAAEAIEALIRQIN</b>
Rv3863	348	<b>AEAEELPAAEAIEALIRQIN</b>
consensus	361	*****.*