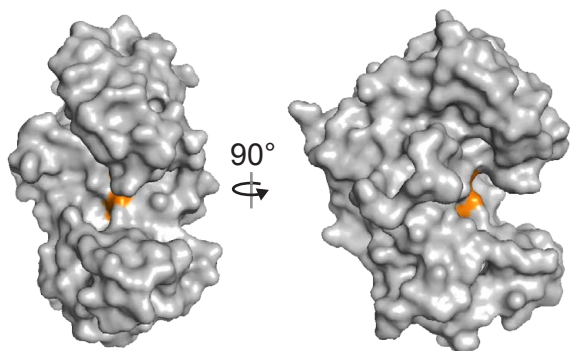


S1A

M. tuberculosis PE_PGRS16 structure



M. marinum MMAR_28540 model

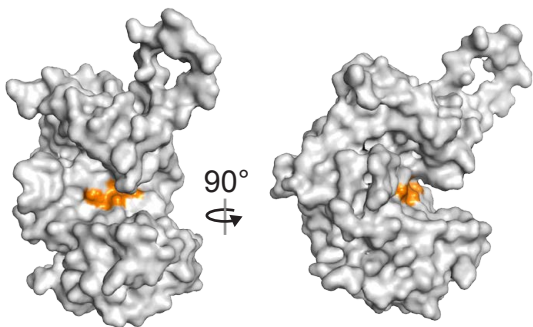


Figure S1B

PGA3
HIV-PR
PE_PGRS35 (Rv1983)
MMARE11_28540 (MMARE_2933)
MMAR_2272
PE_PGRS16 (Rv0977)
PE26 (Rv2519)
MMAR_1538

WKAPTIVDEQPLENYLDMEYFGTIGI-GTPAQDFTVVFDTGSSNLWVPS-----VYCS
-----PQVTLWQRPLVTIKI-GGQLKE--ALLDTGADDTV-----LEE
-----DGRVTPLEIIHVTEPTVHANVNGGPTST--ILVDTGSAGLVVSPEDVGGILGLVLH
-----**TVPLEVNVTEPVVNVVNGGHSTP--VLIDTGSAGLVMQVKDVGGLGLLR**
-----PVVVISVGGGGPIA--VTVDTCASGLLVRPQDV----NLQS
-STTLTNATVPLQLVNTTEPVVVISLNGGQMPV--VLLDTGSTGLVMDS-QF----LTQN
---DPVNVAVPLRVENNF-PLVNLVNRGPTVP--ILLDTGSSSLVPIFWKI----GWQN
-----NASVPLYLDNNF-PAVNVSINGGPSVP--VLLDTGSAGLVVPIWDI----GLQN
:
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PGA3
HIV-PR
PE_PGRS35 (Rv1983)
MMARE11_28540 (MMARE_2933)
MMAR_2272
PE_PGRS16 (Rv0977)
PE26 (Rv2519)
MMAR_1538

SLACTNHNRFNPEDSS----TYQSTSETVSIYGTGSMTGILGYDVTQVGGISDTNQIFG
MSLP-GRWPKPMIGGI-----GGFIK-----VRQYDQILIE
MGLPTGLSISGYSGLL----YYIFATYTTTVDGNGIVTAPTA---VNVVLLSIPSPFA
MGLPSGISMSAYSGLL----TYLFATYPTTVDFGNGIVTSTTG---VDVVLFSIPTSPYA
LGTPTGSGAVTYGNSSYAFNTVQYQYQTTVNFNGIVTNPNTN---VAVATSATQT-ING
FGPVIGTGAGYAGGL----TYNYNTYSTTVDFGNGLLTLPTS---VNVVTSSSPGTL--
LGLPTGFDVVHYGNGV---SIVYADVPTTVDFGGAATTPTS---VHVGIPLPYPRNLDS
LGVPTGFDVIRYNGV---NILYADFNTTVDFGSGAVTAPTS---VQVGILPFPTSLQG
:
:***:

PGA3
HIV-PR
PE_PGRS35 (Rv1983)
MMARE11_28540 (MMARE_2933)
MMAR_2272
PE_PGRS16 (Rv0977)
PE26 (Rv2519)
MMAR_1538

LS-----ETEPGSFLYYAPFDGILGLAYPSISS---SGATPVFDNIWNQGLVSO
IC-----GHKAIG-TVLVG---PTPVNII-----
ISTYFALLADPTTTTPEAYFGAVGVDGVLGVG-PNAV---PGP-SIPTMALPGDLNQG
LTTWLNALWSNPLTFPDAYFQSAGVDGVLGVG-PNAV---PGP-SIPTQALGGGLGQG
VT-----TSIPLSSLPL-----YLGIG-PNNDF---PLP-DQVTAALPGDLNQG
-----GNFLRSRGAVGVLGIG-PNNGF---PGTSSIV-TAMPGLLNNG
LV-----LIASGGAFGPNG-NGILGIG-PNVGSYAVSGPNNVTTDLPGQLNEG
LT-----LIAMNGFGPTG-HGVLGIG-PNINA-ATGGHGNVTTALPGQLNEG
:
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PGA3
HIV-PR
PE_PGRS35 (Rv1983)
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MMAR_2272
PE_PGRS16 (Rv0977)
PE26 (Rv2519)
MMAR_1538

DLFSVYLSADDQSGSVVIFGGIDSSYYTGSNLWVPTVEGYWQITVDSITMNGEAIACAE
-----GRNLLTQIGCTLNFPQVTL---WQRPLVTIKIGGQLKE---
VLI-----DAPAGELVFGPNPLPAPNVVEVVGSPITT---LYVKID---GGTPIPVV
LLI-----DMKGELVFGPNPL-TPEFSISGAPIAT---LWVSVN---GGAPVAVP-
VLI-----NTNLGYLQFGANPL-TPVASVTGSPVTD---LQIQIN---NGPLQPATG
VLI-----DESAGILQFGPNTL-TGGITISGAPIST---VAVQID---NGPLQQAP-
TLI-----DIPGGYMQFGPNTG-TPITSVTGAPITV---LNVQIGGYDPNGGYWSLP-
ELI-----NIPQGYMQFGPNTG-TPITSVSGVPITT---LDVQFGGYDPLGTYYVPT-
:
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PGA3
HIV-PR
PE_PGRS35 (Rv1983)
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MMAR_2272
PE_PGRS16 (Rv0977)
PE26 (Rv2519)
MMAR_1538

GCQAIVDTGTSLLTGPTSPIANIQSDIGASENSD-GDMVVSCSAISSLPDIVFTINGVQY
---ALLDTGADDTVLEEMSLP---GRWPKPMIGGIGGFIKVRQYDQILIEICGHKAIGT
---SIIDSGGVTGTIPSYVIG---SGTLP---ANTNIEVYTPG-GDRLYAFNTNDY
---**SIIDSGVMGTIPSSVIG---GSTLP---ANTNITVYTDNTMTTEVYHYSTNDY**
---SFIIDSGGLYGTIPSSLI PGVPVGYVSVV---VGTITVYTTDQ--VQLYSQVTVGS
---VMFDSGGINGTIPSA-LASLPSGGFV---AGTTISVYTSDG-QTLLYSYTTTAT
---SIFDSGGNHGTLPAVILGTGQTTGYAP---PGTVISISIHND-QTLLYQYTTTAS
---SIVDSGGNHGTLPGIILGTGQTSVGPV---PGTVISISTNDN-QTLLYSYTTTGT
:
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PGA3
HIV-PR
PE_PGRS35 (Rv1983)
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MMAR_2272
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MMAR_1538

PVPPSAYILQSEGCISGFGQMNLPTESEGLWILGDVVFIRQYFTVFDNRANQVGLAPVA-
-----VLVGPTPVN-----IIGR-----NLLTQIGCT-L
R-P---TVISSGLMNTGF---LP-----FRFQPVYID-----YSPSGIGTTVF
Q-P---TVISSGLMNTGF---LP-----FWNQPVYID-----YSPAGTGTTF
TNAPL--VVPSSNNPNTGN---YP-----FLLGPIYIS-----NSPTGGGQTIF
NTP---FVTSGGVMNTGH---VP-----FAQQPIYVS-----YSPTAIGTTTT
NSP---VVTADPRLNTGL---TP-----FLLGPVYIS-----NNPSGVGTVVV
DSP---VVTGNI PMNTGL---LP-----FALGPVYIS-----NSPSGVGTVVV
:
:***:

PGA3
HIV-PR
PE_PGRS35 (Rv1983)
MMARE11_28540 (MMARE_2933)
MMAR_2272
PE_PGRS16 (Rv0977)
PE26 (Rv2519)
MMAR_1538

NF---
DHPA-
DMP--
DF---
N---
NYPPP
NYPPP