ARO:3003761 - MEG\_2694 - Reg:T450I\_PAELY\_WDEPL (mt instead of wt – eatAv gene saved in CARD is mutated variant of the eatA gene isolated from Enterococcus faecium)

ARO:3003326 - MEG\_2710 - Reg:T630I\_RMAFL\_ALFFL (not a T, but an A; conserved domain shows same context) |Mult:Reg:A314G\_VADHA\_YMSNY;Reg:Y322C\_SNYFR\_FGSPE (not correct pos, might be A313G and Y319C)

ARO:3003327 - MEG\_2712 - Reg:S244T\_ALTGA\_LVALH (wrong gene - <https://pubmed.ncbi.nlm.nih.gov/26417605/>)

ARO:3003735 - MEG\_3065 - Reg:F441Y\_TFHAH\_DEETG (not in sequence -> might be wrong pos)| Mult:Reg:T387I\_DTGTG\_TLCGE;Reg:E449K\_ETGQV\_IGGMG (not in sequence -> might be wrong pos)

ARO:3003901 - MEG\_3143 - Reg:V213I\_AAISY\_LIRDT (mt instead of wt – sequence is MRSA)| Reg:A100V\_LVLGL\_LTAIV (mt instead of wt - sequence is MRSA)

ARO:3004562 - MEG\_3241 - Reg:E467V\_LSSDE\_KNMIT (E466V, mistake in kargva)|Reg:E467K\_LSSDE\_KNMIT (E466K, mistake in kargva)|Reg:K444F\_NSQAI\_PLRGK (L, not K, mistake in CARD - <https://pubmed.ncbi.nlm.nih.gov/20226332/>)| Reg:R388P\_EAAKK\_RELTR (R389P, mistake in kargva) (no match -> not same organism, use <https://www.ncbi.nlm.nih.gov/protein/WP_003434229.1>)

ARO:3003459 - MEG\_3243 - Reg:N510D\_SAKSG\_DSMFQ (is actually N538D when using sequence from PubMed - <https://pubmed.ncbi.nlm.nih.gov/16377674/>) |Reg:E501D\_VVEGD\_AGGSA (not in sequence, might be E540D, PMID not found) |Reg:N499T\_LYVVE\_DSAGG (not in sequence, might be N538T, PMID not found)

ARO:3003302 - MEG\_3246 - Reg:T214I\_VHILL\_NQHHA|Reg:T214A\_VHILL\_NQHHA|Reg:R184Q\_LPSPE\_FTMVK|Reg:G125S\_SGGLH\_VGVSV (uses old version of sequence - <https://www.ncbi.nlm.nih.gov/protein/1766064>) (G124S, mistake in kargva)

ARO:3003392 - MEG\_3446 - Reg:A234G\_YVNPE\_PNGNP| Reg:A431V\_YLGPL\_PKQTL (mt instead of wt)|Mult:Reg:V431A\_YLGPL\_PKQTL (wait a sec?);Reg:G490S\_GSDKR\_GANGG -> (conserved domain shows that G and V are wild type in other organisms)

ARO:3003790 - MEG\_3591 - Reg:L39F\_IFGIF\_IYLAM (not in sequence -> MSA shows similar context)

ARO:3003028 - MEG\_3594 - Reg:Q52P\_VTVVN\_ALPAI (not same organism, use <https://www.ncbi.nlm.nih.gov/protein/16077337>)

ARO:3003319 - MEG\_4057 - Reg:I418N\_FFTYA\_YILIT (matches CARD sequence, but not correct sequence) (many unmatched -> not correct sequence, use <https://www.ncbi.nlm.nih.gov/protein/YP_499886.1>)

ARO:3003776 - MEG\_4094 - Reg:E291D\_VRAEG\_LQPVD (mt instead of wt – sequence is MRSA)|Reg:D278E\_MGVEL\_YQEDG (mt instead of wt – sequence is MRSA)

ARO:3003784 - MEG\_4096 - Reg:C117D\_ALPGG\_AIGSR (C is wt in E.coli; D is found in M.tuberculosis, making organism naturally resistant <https://pubmed.ncbi.nlm.nih.gov/10589726/>)

ARO:3003778 - MEG\_4132 - Reg:G84D\_AQVLL\_DVTHI (not a G, but a C (conserved domains shows that G is wt in E.coli; also found G in this sequence of M. smegmatis - <https://www.ncbi.nlm.nih.gov/protein/WP_003895076.1>))

ARO:3003702 - MEG\_5325 - Reg:S80L\_GDVLG\_FHPHG (not correct pos, might be S87L by looking at context of other parC genes)

ARO:3003042 - MEG\_5406 - Reg:T488A\_LRSTF\_EYGLG|Reg:E475G\_FVGTS\_LESAM|Reg:T445A\_TAVQA\_EYSSN (not correct pos; using conserved domains, might be T494A, E481G, and T451A)

ARO:3003043 - MEG\_5407 - Reg:R384G\_SLTGG\_MMTFS (mt instead of wt; also found R in this sequence of S. pneumoniae - <https://www.ncbi.nlm.nih.gov/protein/18266817?report=GenPept>)

ARO:3003394 - MEG\_5803 – Reg:A8G\_ALIIV\_VQNDF(D, not A, mistake in CARD - <https://pubmed.ncbi.nlm.nih.gov/11641519/>)| Reg:Y68D\_DYSSS\_PPHCV(W, not Y, mistake in CARD - <https://pubmed.ncbi.nlm.nih.gov/11641519/>))|Reg:H59D\_PGDHF\_GTPDY(not an H, but an S -> H59D mutation is found in specific strain)|Reg:A140S\_TDHCV\_QTAED(R, not A, mistake in CARD - <https://pubmed.ncbi.nlm.nih.gov/10681313/>)|Reg:L72P\_SWPPH\_VSGTP(L172P, mistake in CARD - <https://pubmed.ncbi.nlm.nih.gov/31910878/>)| Reg:R157W\_ATRVL\_DLTAG(V, not R, mistake in CARD - <https://pubmed.ncbi.nlm.nih.gov/31910878/>)|

ARO:3003283 - MEG\_6090 – (no match)

Reg:S531LFCWG\_TADEE\_RHVVA|Reg:N518TI\_VVDGV\_SDEIV|Reg:S522QLW\_VVSDE\_VYLTA|Reg:K527NQ\_IVYLT\_DEEDR|Reg:R528HP\_VYLTA\_EEDRH|Reg:S512RTIN\_ETPYR\_VVDGV|Reg:L521MP\_GVVSD\_IVYLT|Reg:H526GFQNTEDSYCLRP\_EIVYL\_ADEED|Reg:F505L\_VNPFG\_IETPY|Reg:S574L\_EVDYM\_VSPRQ|Reg:G507SD\_PFGFI\_TPYRK|Reg:T508PAHNS\_FGFIE\_PYRKV|Reg:Q513DEKLPR\_TPYRK\_VDGVV|Reg:S456WL\_ALGPG\_LSRER|Reg:D515HTYGNK\_YRKVV\_GVVSD|Reg:N519K\_VDGVV\_DEIVY|Reg:G523A\_VSDEI\_YLTAD|Reg:L511RVPM\_IETPY\_KVVDG|Reg:R529Q\_YLTAD\_EDRHV|Reg:L525S\_DEIVY\_TADEE|Reg:Q517LH\_KVVDG\_VSDEI|Reg:S509QR\_GFIET\_YRKVV|Reg:E672D\_RKFAR\_NHGTC|Reg:L533PR\_DEEDR\_VVAQA|Reg:P520T\_DGVVS\_EIVYL|Reg:M515IV\_YRKVV\_GVVSD|Reg:I572F\_SSEVD\_MDVSP|Reg:L538RP\_HVVAQ\_NSPID|Reg:V176F\_SQLVR\_PGVYF|Reg:Q438K\_FMDQN\_PLSGL|Reg:D441VY\_QNNPL\_GLTHK|Reg:S447Q\_GLTHK\_RLSAL|Reg:H451YCDR\_KRRLS\_LGPGG|Reg:S450LW\_HKRRL\_ALGPG|Reg:V146F\_IKSQT\_FMGDF|Reg:A381V\_GELIQ\_QIRVG|Reg:Q490H\_GPNIG\_IGSLS|Reg:E504A\_RVNPF\_FIETP|Reg:D518H\_VVDGV\_SDEIV|Reg:L545M\_SPIDA\_GRFVE|Reg:L571V\_PSSEV\_YMDVS|Reg:R633C\_AAIDA\_DVVVA|Non:Q513\*\_TPYRK\_VDGVV|Non:S522\*\_VVSDE\_VYLTA|Reg:I1106T\_VKGEN\_PEPGI|Reg:Q975H\_VFDGA\_EAELQ|Reg:G836S\_LKVPH\_ESGKV|Reg:H835R\_SLKVP\_GESGK|Reg:R827H\_KAREV\_DTSLK|Reg:L731P\_EDAII\_SNRLV|Reg:F503S\_ARVNP\_GFIET|Reg:I480V\_GRMCP\_ETPEG|Reg:P45L\_EPLEV\_GLLDV|Reg:H445RYD\_LSGLT\_KRRLS|Reg:D435VG\_LSQFM\_QNNPL|Reg:M434I\_QLSQF\_DQNNP|Reg:Q432P\_TSQLS\_FMDQN|Mult:Reg:S531L\_TADEE\_RHVVA;Reg:S622A\_APLVG\_GMELR|Mult:Reg:H526S\_EIVYL\_ADEED;Reg:M515V\_YRKVV\_GVVSD|Mult:Reg:H526S\_EIVYL\_ADEED;Reg:P535H\_EDRHV\_AQANS|Mult:Reg:H526Y\_EIVYL\_ADEED;Reg:E541G\_AQANS\_IDADG|Mult:Reg:D516Y\_RKVVD\_VVSDE;Reg:L511R\_IETPY\_KVVDG|Del:S512-\_ETPYR\_VVDGV|Mult:Reg:D516E\_RKVVD\_VVSDE;Reg:S522L\_VVSDE\_VYLTA|Mult:Reg:S531L\_TADEE\_RHVVA;Reg:H526C\_EIVYL\_ADEED|Mult:Reg:L511R\_IETPY\_KVVDG;Reg:D516V\_RKVVD\_VVSDE|Mult:Reg:L511P\_IETPY\_KVVDG;Reg:M515I\_YRKVV\_GVVSD|Mult:Reg:L524W\_SDEIV\_LTADE;Reg:T525P\_DEIVY\_TADEE;Reg:H526Q\_EIVYL\_ADEED;Del:K527-\_IVYLT\_DEEDR|Mult:Reg:Q513H\_TPYRK\_VDGVV;Del:F514-\_PYRKV\_DGVVS;Del:M515-\_YRKVV\_GVVSD;Del:D516-\_RKVVD\_VVSDE|Del:L519-\_VDGVV\_DEIVY|Mult:Reg:H526D\_EIVYL\_ADEED;Reg:S531\_LDVQT\_SFEWL|Mult:Reg:L511P\_IETPY\_KVVDG;Reg:S512T\_ETPYR\_VVDGV;Reg:D516V\_RKVVD\_VVSDE|Mult:Reg:T516I\_RKVVD\_VVSDE;Reg:G523W\_VSDEI\_YLTAD;Reg:D525Y\_DEIVY\_TADEE|Mult:Reg:H526D\_EIVYL\_ADEED;Reg:E541G\_AQANS\_IDADG;Reg:S553A\_FVEPR\_LVRRK|Mult:Reg:H526P\_EIVYL\_ADEED;Reg:K527Q\_IVYLT\_DEEDR|Mult:Reg:E562G\_RKAGE\_EYVPS;Reg:P564L\_AGEVE\_VPSSE|Del:N515-\_YRKVV\_GVVSDARO:3004153 - MEG\_7250 - Reg:I211V\_CHIYD\_HVEQV (not an I, but an N)

ARO:3003369 - MEG\_7301 – (no match -> wrong sequence, use <https://www.ncbi.nlm.nih.gov/protein/NP_417798.1>)

ARO:3003361 - MEG\_7305 - Reg:G261S\_TTTVT\_IEMFN|Reg:V295C\_VERGQ\_IIKPG|Reg:G279A\_AGDNA\_LLLRG|Reg:V278A\_HAGDN\_ALLLR (mt instead of wt; conserved domain shows same context)

ARO:3003359 - MEG\_7306 - Reg:A379T\_EGLRF\_IREGG (A is wt in other EF-Tu proteins; T is found in S. cinnamoneus, making organism naturally resistant - <https://pubmed.ncbi.nlm.nih.gov/9043138/>)

ARO:3003970 - MEG\_7333 - Reg:G98R\_VFPVL\_GPNGE (G99R, mistake in kargva) (not same organism, use <https://www.ncbi.nlm.nih.gov/protein/UPS54974.1>)