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 (is actually T494A, E481G, and T451A, using sequence <https://www.ncbi.nlm.nih.gov/protein/ACB14610.1> which covers residues 48-639 (<https://pubmed.ncbi.nlm.nih.gov/18394970/>))

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 – use MEG\_6090\_SNP\_list\_update2

ARO: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>)