

Supplement 3 : Site of infection and microorganisms identified

Site of Infection	Culture Organism(n)	Culture Organism(%)
Blood	240	41.52%
Escherechia coli	58	10.03%
Klebsiella pneumonia	51	8.82%
Staphylococcus aureus	22	3.81%
Acinetobacter spp	19	3.29%
Pseudomonas aeruginosa	12	2.08%
Enterococcus faecium	11	1.90%
Candida auris	9	1.56%
Staphylococcus epidermidis	9	1.56%
Staphylococcus haemolyticus	5	0.87%
Elizabethkingia meningoseptica	4	0.69%
Candida parapsilosis	3	0.52%
Enterobacter aerogen	3	0.52%
Burkholderia pseudomallei	2	0.35%
Candida glabrata	2	0.35%
Candida tropicalis	2	0.35%
Chryseobacterium indologenes	2	0.35%
Enterobacter cloacae	2	0.34%
Enterococcus faecalis	2	0.35%
Staphylococcus hominis	2	0.35%
Streptococcus pyogen	2	0.35%
Achromobacter xylosoxidans	1	0.17%
Aeromonous hydrophila	1	0.17%
Candida guilliermondii	1	0.17%
Candida Krusei	1	0.17%
Cryptococcus neoformans	1	0.17%
Enerococcus faecalis	1	0.17%
Enterococcus gallinarum	1	0.17%
Proteus mirabilis	1	0.17%
Sphingomonas paucimobilis	1	0.17%
Stenotrophomonas maltophilia	1	0.17%
Respiratory	139	24.05%
Klebsiella pneumonia	45	7.79%
Acinetobacter spp	35	6.06%
Pseudomonas aeruginosa	17	2.94%
Escherechia coli	8	1.38%
Staphylococcus aureus	6	1.04%
streptococcus pneumoniae	5	0.87%
streptococcus agalactiae	4	0.69%
Enterobacter colacae	3	0.52%
Stenotrophomonas maltophilia	3	0.52%
Aspergillus spp	2	0.35%
Candida tropicalis	2	0.35%
Candida albicans	1	0.17%
Burkholderia cepacia	1	0.17%
Chryseobacterium indologenes	1	0.17%
Elizabethkingia meningoseptica	1	0.17%
Enterococcus faecium	1	0.17%

MTB	1	0.17%
Proteus mirabilis	1	0.17%
Serratia marcescens	1	0.17%
Streptococcus pyogen	1	0.17%
Urine	145	25.09%
Escherechia coli	54	9.34%
Klebsiella pneumonia	34	5.88%
Enterococcus faecalis	9	1.56%
Enterococcus faecium	9	1.56%
Pseudomonas aeruginosa	8	1.38%
Proteus mirabilis	7	1.21%
Candida glabrata	4	0.69%
Candida tropicalis	4	0.69%
Candida auris	2	0.35%
Enterococcus gallinarum	2	0.35%
Candida albicans	1	0.17%
Acinetobacter spp	1	0.17%
Enterobacter colacae	1	0.17%
Providencia rettgeri	1	0.17%
Staphylococcus aureus	1	0.17%
Trichosporon asahii	1	0.17%
Abdominar Source	12	2.08%
Escherechia coli	5	0.87%
Klebsiella pneumonia	3	0.52%
Achromobacter xylosoxidans	1	0.17%
Candida tropicalis	1	0.17%
Enerococcus faecalis	1	0.17%
Enterococcus faecium	1	0.17%
Wound	30	5.19%
Klebsiella pneumonia	8	1.38%
Escherechia coli	6	1.04%
Staphylococcus aureus	4	0.69%
Acinetobacter spp	3	0.52%
Pseudomonas aeruginosa	2	0.35%
Candida albicans	1	0.17%
Citrobacter koseri	1	0.17%
Enerococcus faecalis	1	0.17%
Proteus mirabilis	1	0.17%
Providencia rettgeri	1	0.17%
Staph epidermidis	1	0.17%
streptococcus agalactiae	1	0.17%
Others	12	2.08%
Acinetobacter spp	1	0.17%
Cryptococcal neoformans	1	0.17%
Escherechia coli	1	0.17%
H.influenzae	1	0.17%
Klebsiella pneumonia	5	0.87%
Neisseria meningitidis	1	0.17%
Staphylococcus aureus	1	0.17%
Streptococous sanguinis	1	0.17%

Grand Total

578

100.00%