

**URINE CULTURE  
COMMON ISOLATES  
AND  
INTERPRETIVE GUIDELINES**



**Table 1. URINE CULTURE - COMMON ISOLATES**

<u>Potential Pathogens</u>	<u>Probable Contaminants</u>
Gram negative bacilli <i>Enterococcus</i> <i>Staphylococcus aureus</i> <i>Staphylococcus saprophyticus</i> * Other coag neg <i>Staph</i> (immunocompromised) Beta <i>Streptococcus</i> * <i>Gardnerella vaginalis</i> , $\geq 50,000$ * Yeast*	Gram positive bacilli Alpha and gamma streptococci Coag negative <i>Staphylococcus</i> , except <i>S. saprophyticus</i> Saprophytic <i>Neisseria</i> Gram positive cocci, not Staph or Strep
*No routine sens.	

Table 2. URINE CULTURE INTERPRETIVE GUIDELINES			
Quantitation (col/ml)	Organism	Ident Level/Susceptibilities (ID/S) URINE CULTURE	Ident Level/Susceptibilities (ID/S) URINE CULTURE, ADDITIONAL WORKUP
<10,000	Pathogens, except <i>Gardnerella</i>	<b>Void:</b> Multiple organisms <b>Cath:</b> Descriptive ID, except Staph in mixed culture	<b>Pure:</b> ID and S <b>Mixed:</b> Void - Multiple organisms Cath – Descriptive ID, except Staph in mixed culture.
	Contaminants	<b>Void:</b> Multiple organisms <b>Cath:</b> Multiple organisms; probable contaminants	<b>Void:</b> Multiple organisms <b>Cath:</b> Multiple organisms; probable contaminants.
<b>1-2 Organisms <math>\geq 10,000</math></b>			
10-50,000	Pathogens, except <i>Gardnerella</i>	If $\geq 50,000$ contaminant, descriptive ID of pathogen. <b>Void:</b> ID <b>Cath:</b> ID and S (see Staph below) <i>S.aureus:</i> ID/S (pure) or ID (mixed) <b>Coag neg Staph:</b> <b>Void: Pure</b> - “Staph” <b>Mixed</b> - Multiple organisms; probable contaminants <b>Cath:</b> <i>S.saprophyticus:</i> ID* Coag neg Staph: ID (S if pure)	If $\geq 50,000$ contaminant, descriptive ID of pathogen. <u>ID and S</u> <b>Coag neg Staph:</b> <b>Void: Pure</b> - <i>S.saprophyticus:</i> ID* Other coag neg Staph: ID/S <b>Mixed</b> - Multiple organisms; probable contaminants <b>Cath:</b> <i>S.saprophyticus:</i> ID* Coag neg Staph: ID/S
	Contaminants	Multiple organisms; probable contaminants	<b>Pure:</b> Descriptive ID <b>Mixed:</b> Multiple organisms; probable contaminants.
50 - 100,000 >100,000	Pathogens	ID and S <i>S. saprophyticus:</i> ID* Other coag neg Staph: ID (S if pure)	ID and S <i>S. saprophyticus:</i> ID* Other coag neg Staph: ID/ S
	Contaminants	Multiple organisms; probable contaminants	<b>Pure:</b> Descriptive ID. <b>Mixed:</b> Multiple organisms; probable contaminants.
<b>3 Organisms <math>\geq 10,000</math></b>			
	Pathogens	1. If one pathogen clearly predominates, ID and S. 2. <b>Void:</b> Descriptive ID. "Specimen appears contaminated; no further workup pending" 3. <b>Cath:</b> Descriptive ID. "May represent colonization; no further workup pending"	ID and S. ( <i>S.saprophyticus:</i> ID* Other coag neg Staph: ID) <b>If contaminants = or &gt; than pathogens, descriptive ID, with comment:</b> <b>Void:</b> "Specimen appears contaminated; no further workup pending" <b>Cath:</b> "May represent colonization; no further workup pending"
	Contaminants	Multiple organisms; probable contaminants	Multiple organisms; probable contaminants

\* *Staphylococcus saprophyticus* typically responds to urine concentrations of agents commonly used to treat acute uncomplicated UTIs (nitrofurantoin, trimeth plus or minus sulfa, or a fluoroquinolone. Routine susceptibility testing is not recommended.