**Supporting information data**

**Additional file 2**

**Table S1: General information about patients.**

|  |  |
| --- | --- |
| Characteristics |  |
| Age | Mean | 66.8 |
| Range | 4-82 |
| Gender | Male | 5 (31%) |
| Female | 11 (69%) |
|  | Outpatients | 15 (94%) |
|  | Urine catheter | 4 (25%) |

**Table S2: Results of conventional urine culture and urine dipstick analysis for 16 urine samples.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| N.o. | Species (urine culture) | CFU/mL | Leukocyte | Nitrite | Urobilinogen | Protein | pH | Blood |
| UR1 | *Klebsiella pneumoniae ESBL* | > 100000 | ++ | - | - | +++ | 8,5 | - |
| UR2 | *Klebsiella oxytoca* | > 100000 | - | + | - | ++ | 8,5 | - |
| UR3 | *Klebsiella pneumoniae ESBL* | > 100000 | + | + | - | + | 8 | +++ |
| UR4 | *Proteus mirabilis* | > 100000 | ++ | + | - | ++ | 8 | +++ |
| UR5 | *Enterococcus faecalis* | > 100000 | - | - | -- | - | 7 | - |
| UR6 | *Enterococcus faecalis* | > 100000 | - | - | - | - | 7,5 | + |
| UR7 | *Enterobacter cloaceae ESBL* | > 100000 | ++ | - | --- | ++ | 8 | +++ |
| UR8 | *Citrobacter koseri* | > 100000 | - | - | - | + | 6 | - |
| UR9 | *Proteus mirabilis* | > 100000 | - | - | - | ++ | 8,5 | - |
| UR10 | *Proteus mirabilis* | > 100000 | ++ | ++ | - | - | 8,5 | - |
| UR11 | *Escherichia coli; Proteus mirabilis ESBL* | > 100000; > 100000; | - | - | - | + | 8 | ++ |
| UR12 | *Proteus mirabilis* | >100000 | ++ | - | - | +++ | 7 | - |
| UR13 | *Enterobacter aerogenes* | > 100000 | ++ | - | - | - | 5 | - |
| UR14 | *Enterobacter cloacae* | > 100000 | ++ | ++ | - | ++ | 6,5 | +++ |
| UR15 | *Enterobacter cloacae; Enterococcus faecalis; E coli; Proteus mirabilis* | 10000; > 10000 < 100000; 100000; > 100000; | - | - | - | ++ | 7,5 | +++ |
| UR16 | *Escherichia coli; Klebsiella pneumoniae* | >100000; >100000 | ++ | - | - | + | 6 | + |

**Table S3: Uropathogenic bacteria in urine samples (standard urine culture)**

1. Monomicrobial urine samples

|  |  |  |
| --- | --- | --- |
| **Bacterial species**  | **Sample** | **Number of samples** |
| *Citrobacter koseri* | UR8 | 1 |
| *Enterobacter aerogenes* | UR13 | 1 |
| *Enterobacter cloaceae* | UR7, UR14 | 2 |
| *Enterococcus faecalis* | UR5, UR6 | 2 |
| *Klebsiella oxytoca* | UR2 | 1 |
| *Klebsiella pneumoniae* | UR1, UR3 | 2 |
| *Proteus mirabilis* | UR4, UR9, UR10, UR12 | 4 |

1. Polymicrobial urine samples

|  |  |  |
| --- | --- | --- |
| **Bacterial species** | **Sample**  | **Number of samples** |
| *Enterococcus faecalis* | UR15 | 1 |
| *Escherichia coli* | UR11, UR15, UR16 | 3 |
| *Klebsiella pneumoniae* | UR16 | 1 |
| *Proteus mirabilis* |  UR11, UR15 | 2 |

**Table S4: Summary reports of identified bacterial proteins for each urine sample sorted by “MASCOT summa score”.**

***Sample UR1***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | YP\_002920498.1 | outer membrane porin protein C | 4 | 40008 | 830 | ***Klebsiella pneumoniae***  |
| 2 | YP\_001335792.1 | murein lipoprotein | 4 | 8381 | 483 | *Klebsiella pneumoniae*  |
| 3 | ACM07444.1 | OmpK36 porin | 1 | 39854 | 274 | *Klebsiella pneumoniae*  |
| 4 | 1006243A | lipoprotein mutant | 1 | 8265 | 233 | *Escherichia coli* |
| 5 | YP\_001334652.1 | outer membrane protein A | 2 | 38021 | 203 | *Klebsiella pneumoniae*  |
| 6 | WP\_004133882.1 | outer membrane porin protein C | 1 | 40676 | 198 | *Klebsiella oxytoca*  |
| 7 | WP\_016189672.1 | pyruvate formate-lyase | 1 | 85234 | 147 | *Erwinia tracheiphila*  |
| 8 | YP\_001334597.1 | formate acetyltransferase 1 | 1 | 85092 | 144 | *Klebsiella pneumoniae*  |
| 9 | 2K0L\_A | Chain A, Nmr Structure Of The Transmembrane Domain Of The Outer Membrane Protein A  | 1 | 23355 | 141 | *Klebsiella pneumoniae* |
| 10 | YP\_007872516.1 | outer membrane porin protein C | 1 | 40486 | 133 | *Raoultella ornithinolytica*  |
| 11 | WP\_016809062.1 | outer membrane porin protein C | 1 | / | 102 | *Klebsiella oxytoca*  |
| 12 | P02938.1 | RecName: Full=Major outer membrane lipoprotein; AltName: Full=Murein-lipoprotein; Flags: Precursor | 1 | 8234 | 100 | *Serratia marcescens* |
| 13 | AAD32649.1 | EF-Tu | 1 | 39423 | 96 | *Coxiella burnetii*  |
| 14 | YP\_007504946.1 | Pyruvate formate-lyase | 1 | 85227 | 93 | *Morganella morganii*  |
| 15 | WP\_006820044.1 | outer membrane porin protein C | 1 | / | 77 | *Yokenella regensburgei*  |
| 16 | WP\_006707774.1 | murein lipoprotein | 1 | 8805 | 75 | *Candidatus Regiella insecticola*  |
| 17 | ABS84845.1 | translation elongation factor Tu | 1 | 21970 | 73 | *Bacillus subtilis*  |
| 18 | NP\_872680.1 | elongation factor Tu | 1 | 43400 | 73 | *Haemophilus ducreyi*  |
| 19 | NP\_299905.1 | elongation factor Tu | 1 | 42849 | 70 | *Xylella fastidiosa*  |
| 20 | YP\_001453698.1 | outer membrane protein F | 1 | / | 67 | *Citrobacter koseri*  |
| 21 | NP\_667815.1 | elongation factor Tu | 1 | / | 67 | *Yersinia pestis*  |
| 22 | P09146.1 | RecName: Full=Outer membrane protein A; Flags: Precursor | 1 | 37552 | 67 | *Klebsiella aerogenes* |
| 23 | YP\_003755150.1 | translation elongation factor Tu | 1 | / | 65 | *Hyphomicrobium denitrificans*  |
| 24 | YP\_001334418.1 | peptidoglycan-associated outer membrane lipoprotein | 1 | 18851 | 64 | *Klebsiella pneumoniae*  |
| 25 | YP\_004393584.1 | major outer membrane protein OmpAII | 1 | / | 64 | *Aeromonas veronii*  |
| 26 | NP\_455305.1 | peptidoglycan-associated lipoprotein | 1 | 18853 | 64 | *Salmonella enterica*  |
| 27 | NP\_669338.1 | bifunctional acetaldehyde-CoA/alcohol dehydrogenase | 1 | 96527 | 64 | *Yersinia pestis*  |
| 28 | YP\_001335857.1 | bifunctional acetaldehyde-CoA/alcohol dehydrogenase | 1 | 95834 | 62 | *Klebsiella pneumoniae*  |

***Sample UR2***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | YP\_001338507.1 | molecular chaperone  | 3 | 21493 | 372 | *Klebsiella pneumoniae*  |
| 2 | YP\_001335792.1 | murein lipoprotein | 2 | 8381 | 289 | *Klebsiella pneumoniae*  |
| 3 | WP\_000350438.1 | heat shock protein Hsp20 | 2 | 21465 | 253 | *Escherichia coli* |
| 4 | 1006243A | lipoprotein mutant | 1 | 8265 | 227 | *Escherichia coli* |
| 5 | WP\_004103993.1 | outer membrane porin protein C | 1 | 40047 | 196 | ***Klebsiella oxytoca*** |
| 6 | EWF64901.1 | outer membrane protein C | 1 | 40621 | 185 | *Klebsiella oxytoca*  |
| 7 | WP\_004133882.1 | outer membrane porin protein C | 1 | 40676 | 174 | *Klebsiella oxytoca* |
| 8 | YP\_002920498.1 | outer membrane porin protein C | 1 | 40008 | 159 | *Klebsiella pneumoniae*  |
| 9 | YP\_005018909.1 | peptidoglycan-associated outer membrane lipoprotein | 1 | 18833 | 116 | *Klebsiella oxytoca*  |
| 10 | WP\_016809062.1 | outer membrane porin protein C | 1 | 41545 | 110 | *Klebsiella oxytoca* |
| 11 | YP\_001334652.1 | outer membrane protein A | 1 | 38021 | 98 | *Klebsiella pneumoniae*  |
| 12 | P09146.1 | RecName: Full=Outer membrane protein A; Flags: Precursor | 1 | 37552 | 98 | *Klebsiella aerogenes* |
| 13 | YP\_004393584.1 | major outer membrane protein OmpAII | 1 | / | 95 | *Aeromonas veronii*  |
| 14 | ABM66811.1 | OmpE36 | 1 | 40538 | 86 | *Enterobacter aerogenes* |
| 15 | WP\_006820044.1 | outer membrane porin protein C | 1 | 40792 | 81 | *Yokenella regensburgei* |
| 16 | YP\_005016763.1 | hypothetical protein KOX\_03925 | 1 | 15018 | 76 | *Klebsiella oxytoca*  |
| 17 | YP\_001175110.1 | 30S ribosomal protein S6 | 1 | 15096 | 74 | *Enterobacter sp.*  |
| 18 | AAL56004.1 | GroEL | 1 | 52000 | 73 | *Escherichia coli* |
| 19 | YP\_001453698.1 | outer membrane protein F | 1 | / | 70 | *Citrobacter koseri*  |
| 20 | YP\_004517370.1 | thioredoxin | 1 | 11419 | 65 | *Desulfotomaculum kuznetsovii*  |
| 21 | YP\_960652.1 | heat shock protein Hsp20 | 1 | 21458 | 62 | *Marinobacter aquaeolei*  |
| 22 | P02938.1 | RecName: Full=Major outer membrane lipoprotein; AltName: Full=Murein-lipoprotein; Flags: Precursor | 1 | 8234 | 62 | *Serratia marcescens* |

***Sample UR3***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | YP\_001335857.1 | bifunctional acetaldehyde-CoA/alcohol dehydrogenase  | 3 | 95834 | 308 | ***Klebsiella pneumoniae***  |
| 2 | YP\_001335792.1 | murein lipoprotein  | 1 | 8381 | 187 | *Klebsiella pneumoniae*  |
| 3 | 1006243A | lipoprotein mutant | 1 | 8265 | 187 | *Escherichia coli* |
| 4 | WP\_006777698.1 | major outer membrane lipoprotein  | 1 | 11702 | 142 | *Salmonella enterica*  |
| 5 | YP\_001177024.1 | bifunctional acetaldehyde-CoA/alcohol dehydrogenase  | 1 | 96203 | 74 | *Enterobacter sp.*  |
| 6 | ERE53009.1 | 30S ribosomal protein S2, partial  | 1 | 25562 | 67 | *Enterococcus gallinarum*  |
| 7 | BAA32342.1 | ribosomal protein S2  | 1 | 31289 | 67 | *Pseudomonas aeruginosa*  |
| 8 | YP\_001334860.1 | glyceraldehyde-3-phosphate dehydrogenase  | 1 | 35449 | 65 | *Klebsiella pneumoniae*  |
| 9 | YP\_007344897.1 | alcohol dehydrogenase, class IV  | 1 | 95701 | 64 | *Serratia marcescens*  |

***Sample UR4***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | WP\_004244438.1 | peptidoglycan-associated outer membrane lipoprotein  | 1 | 19482 | 263 | ***Proteus mirabilis***  |
| 2 | YP\_002150530.1 | outer membrane porin  | 2 | 40796 | 185 | *Proteus mirabilis*  |
| 3 | YP\_002150547.1 | outer membrane protein A  | 2 | 38994 | 146 | *Proteus mirabilis*  |
| 4 | WP\_017827341.1 | outer membrane porin protein C  | 1 | 41648 | 106 | *Proteus mirabilis*  |
| 5 | YP\_001334418.1 | peptidoglycan-associated outer membrane lipoprotein  | 1 | 18851 | 89 | *Klebsiella pneumoniae*  |
| 6 | NP\_455305.1 | peptidoglycan-associated lipoprotein  | 1 | 18853 | 89 | *Salmonella enterica*  |
| 7 | YP\_002987255.1 | porin Gram-negative type  | 1 | 39618 | 71 | *Dickeya dadantii*  |
| 8 | WP\_022633981.1 | Outer membrane porin 1a  | 1 | 40140 | 69 | *Dickeya*  |
| 9 | WP\_004256113.1 | membrane protein  | 1 | 39141 | 69 | *Providencia rettgeri*  |
| 10 | ADO64273.1 | porin 1  | 1 | 41193 | 69 | *Providencia stuartii*  |

***Sample UR5***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | NP\_815088.1 | cold-shock domain-contain protein  | 3 | 7181 | 267 | ***Enterococcus faecalis***  |
| 2 | NP\_814901.1 | 50S ribosomal protein L31  | 2 | 10119 | 240 | *Enterococcus faecalis*  |
| 3 | NP\_814526.1 | cold shock domain-contain protein  | 1 | 7109 | 136 | *Enterococcus faecalis*  |
| 4 | NP\_814417.1 | hypothetical protein EF0665  | 2 | 6666 | 132 | *Enterococcus faecalis*  |
| 5 | BAI53110.1 | elongation factor Tu  | 1 | 28690 | 91 | *Carnobacterium maltaromaticum*  |
| 6 | AAF17305.1 | putative elongation factor Tu  | 1 | 27433 | 91 | *Enterococcus avium*  |
| 7 | ABS84849.1 | translation elongation factor Tu  | 1 | 21843 | 91 | *Serratia rubidaea*  |
| 8 | NP\_814237.1 | OsmC/Ohr family protein  | 1 | 14371 | 90 | *Enterococcus faecalis*  |
| 9 | WP\_016173398.1 | general stress protein  | 1 | 22194 | 86 | *Enterococcus dispar*  |
| 10 | NP\_813885.1 | gls24 protein  | 1 | 20540 | 86 | *Enterococcus faecalis*  |
| 11 | NP\_267752.1 | 50S ribosomal protein L31  | 1 | / | 83 | *Lactococcus lactis*  |
| 12 | EUJ37103.1 | cold-shock DNA-binding domain-containing protein  | 1 | 7459 | 74 | *Brochothrix thermosphacta*  |
| 13 | WP\_010765440.1 | hypothetical protein  | 1 | 7260 | 70 | *Enterococcus moraviensis*  |
| 14 | EUK53620.1 | 50S ribosomal protein L31 type B  | 1 | / | 68 | *Staphylococcus aureus*  |
| 15 | NP\_372644.1 | 50S ribosomal protein L31  | 1 | / | 68 | *Staphylococcus aureus*  |
| 16 | NP\_815637.1 | enolase  | 1 | 46482 | 67 | *Enterococcus faecalis*  |
| 17 | NP\_816504.1 | acyl carrier protein  | 1 | 8610 | 67 | *Enterococcus faecalis*  |
| 18 | NP\_816831.1 | Dps family protein  | 1 | 17877 | 67 | *Enterococcus faecalis*  |
| 19 | WP\_002568043.1 | cold shock protein  | 1 | 7270 | 66 | *Clostridium*  |
| 20 | WP\_002586010.1 | cold-shock protein  | 1 | 7305 | 66 | *Clostridium*  |

***Sample UR6***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | NP\_814526.1 | cold-shock DNA-binding domain-containing protein  | 4 | 7109 | 497 | ***Enterococcus faecalis***  |
| 2 | NP\_815088.1 | cold-shock domain-contain protein  | 2 | 7181 | 142 | *Enterococcus faecalis*  |
| 3 | AAC80242.1 | major cold-shock protein, partial  | 1 | 4967 | 88 | *Enterococcus faecalis*  |

***Sample UR7***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | P24016.1 | RecName: Full=Outer membrane protein A; AltName: Full=Outer membrane protein II | 3 | 25648 | 283 | *Citrobacter freundii* |
| 2 | YP\_001335792.1 | murein lipoprotein  | 1 | 8381 | 208 | *Klebsiella pneumoniae*  |
| 3 | 1006243A | lipoprotein mutant | 1 | 8265 | 208 | *Escherichia coli* |
| 4 | YP\_049963.1 | major outer membrane lipoprotein  | 1 | 8396 | 148 | *Pectobacterium atrosepticum*  |
| 5 | AHF77098.1 | Major outer membrane lipoprotein  | 1 | 8327 | 148 | *Sodalis sp.*  |
| 6 | WP\_007664753.1 | Outer membrane protein A precursor  | 1 | 38294 | 113 | *Cronobacter condimenti*  |
| 7 | AAA24807.1 | outer membrane protein II, partial  | 1 | 25538 | 113 | ***Enterobacter*** *aerogenes*  |
| 8 | ERE53009.1 | 30S ribosomal protein S2, partial  | 1 | 25562 | 72 | *Enterococcus gallinarum*  |
| 9 | BAA32342.1 | ribosomal protein S2  | 1 | 31289 | 72 | *Pseudomonas aeruginosa*  |

***Sample UR8***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | P24016.1 |  RecName: Full=Outer membrane protein A; AltName: Full=Outer membrane protein II | 3 | 25648 | 391 | *Citrobacter freundii* |
| 2 | YP\_001335792.1 |  murein lipoprotein  | 2 | 8381 | 290 | *Klebsiella pneumoniae*  |
| 3 | YP\_001452149.1 |  outer membrane porin protein C  | 2 | 40804 | 242 | ***Citrobacter koseri***  |
| 4 | 1006243A |  lipoprotein mutant | 1 | 8265 | 204 | *Escherichia coli* |
| 5 | YP\_001334418.1 |  peptidoglycan-associated outer membrane lipoprotein  | 2 | 18851 | 165 | *Klebsiella pneumoniae*  |
| 6 | YP\_001337990.1 |  50S ribosomal protein L7/L12  | 1 | 12334 | 163 | *Klebsiella pneumoniae*  |
| 7 | NP\_290617.1 |  50S ribosomal protein L7/L12  | 1 | 12288 | 163 | *Escherichia coli*  |
| 8 | WP\_002438624.1 |  50S ribosomal protein L7/L12  | 1 | 12334 | 151 | *Escherichia hermannii*  |
| 9 | YP\_049963.1 |  major outer membrane lipoprotein  | 1 | 8396 | 146 | *Pectobacterium atrosepticum*  |
| 10 | AHF77098.1 |  Major outer membrane lipoprotein  | 1 | 8327 | 146 | *Sodalis sp.*  |
| 11 | WP\_002438592.1 |  outer membrane phosphoporin protein E  | 1 | 38178 | 143 | *Escherichia hermannii*  |
| 12 | WP\_023490706.1 |  50S ribosomal protein L7/L12  | 1 | 12320 | 139 | *Serratia sp.*  |
| 13 | YP\_001453952.1 |  peptidoglycan-associated outer membrane lipoprotein  | 1 | 18655 | 132 | *Citrobacter koseri*  |
| 14 | YP\_001570436.1 |  hypothetical protein SARI\_01396  | 1 | 41232 | 124 | *Salmonella enterica*  |
| 15 | NP\_456260.1 |  heat shock protein  | 1 | 17671 | 113 | *Salmonella enterica*  |
| 16 | YP\_005196338.1 |  outer membrane pore protein F  | 1 | / | 112 | *Pantoea ananatis*  |
| 17 | AAQ96078.1 |  outer membrane protein II  | 1 | 17424 | 108 | *Hafnia alvei*  |
| 18 | YP\_001455345.1 |  hypothetical protein CKO\_03833  | 1 | 85023 | 106 | *Citrobacter koseri*  |
| 19 | ERE43463.1 |  alkyl hydroperoxide reductase subunit C, partial  | 1 | 20509 | 91 | *Enterococcus gallinarum*  |
| 20 | NP\_455184.1 |  alkyl hydroperoxide reductase c22 protein  | 1 | 20734 | 91 | *Salmonella enterica*  |
| 21 | NP\_455305.1 |  peptidoglycan-associated lipoprotein  | 1 | 18853 | 88 | *Salmonella enterica*  |
| 22 | ADK27722.1 |  outer membrane protein F  | 1 | / | 86 | *Yersinia aldovae*  |
| 23 | P02938.1 |  RecName: Full=Major outer membrane lipoprotein; AltName: Full=Murein-lipoprotein; Flags: Precursor | 1 | 8234 | 86 | *Serratia marcescens* |
| 24 | YP\_003883508.1 |  outer membrane protein F  | 1 | 39421 | 85 | *Dickeya dadantii*  |
| 25 | YP\_001336542.1 |  autonomous glycyl radical cofactor GrcA  | 1 | 14234 | 84 | *Klebsiella pneumoniae*  |
| 26 | P18953.2 |  RecName: Full=Autonomous glycyl radical cofactor | 1 | 14366 | 84 | *Serratia liquefaciens* |
| 27 | NP\_460044.1 |  outer membrane protein A  | 1 | 37492 | 83 | *Salmonella enterica*  |
| 28 | YP\_001175971.1 |  peptidoglycan-associated outer membrane lipoprotein  | 1 | 18801 | 79 | *Enterobacter sp.*  |
| 29 | YP\_538610.1 |  hypothetical protein UTI89\_P011  | 1 | 19211 | 79 | *Escherichia coli*  |
| 30 | YP\_001454596.1 |  hypothetical protein CKO\_03069  | 1 | 9501 | 76 | *Citrobacter koseri*  |
| 31 | WP\_021542859.1 |  hypothetical protein  | 1 | 9376 | 75 | *Escherichia coli*  |
| 32 | YP\_004116947.1 |  enolase  | 1 | 45393 | 74 | *Pantoea sp.*  |
| 33 | WP\_006176733.1 |  autonomous glycyl radical cofactor GrcA  | 1 | 14432 | 71 | *Enterobacter*  |
| 34 | NP\_457121.1 |  autonomous glycyl radical cofactor GrcA  | 1 | 14335 | 71 | *Salmonella enterica*  |
| 35 | YP\_001338188.1 |  RNA-binding protein Hfq  | 1 | 10996 | 69 | *Klebsiella pneumoniae*  |
| 36 | AAA24175.1 |  ORF, partial  | 1 | 8848 | 69 | *Escherichia coli*  |
| 37 | YP\_006588965.1 |  RNA chaperone Hfq  | 1 | 11375 | 69 | *secondary endosymbiont of Heteropsylla cubana*  |
| 38 | YP\_454193.1 |  phosphopyruvate hydratase  | 1 | 45803 | 68 | *Sodalis glossinidius*  |
| 39 | EUD03787.1 |  outer membrane protein C  | 1 | / | 67 | *Providencia alcalifaciens*  |
| 40 | WP\_019677784.1 |  50S ribosomal protein L7/L12  | 1 | 12157 | 67 | *Rheinheimera perlucida*  |
| 41 | 1LR1\_A |  Chain A, Solution Structure Of The Oligomerization Domain Of The Bacterial Chromatin-Structuring Protein H-Ns | 1 | 7005 | 67 | *Escherichia coli* |
| 42 | WP\_024131942.1 | membrane protein  | 1 | 37713 | 65 | *Salmonella enterica*  |
| 43 | YP\_001338154.1 | chaperonin GroEL  | 1 | 57090 | 64 | *Klebsiella pneumoniae*  |
| 44 | BAA25225.1 | similar to GroEL protein  | 1 | 56351 | 64 | *Klebsiella pneumoniae*  |
| 45 | ERE50858.1 | outer membrane porin protein C  | 1 | 40831 | 62 | *Enterococcus gallinarum*  |
| 46 | YP\_001336754.1 | phosphopyruvate hydratase  | 1 | 45521 | 62 | *Klebsiella pneumoniae subsp. pneumoniae*  |
| 47 | YP\_002932251.1 | Gram-negative porin family protein  | 1 | / | 62 | *Edwardsiella ictaluri*  |
| 48 | YP\_001336083.1 | outer membrane pore protein  | 1 | / | 62 | *Klebsiella pneumoniae*  |

***Sample UR9***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | YP\_002150354.1 | peptidoglycan-associated outer membrane lipoprotein  | 4 | 18118 | 650 | ***Proteus mirabilis***  |
| 2 | YP\_001334418.1 | peptidoglycan-associated outer membrane lipoprotein  | 2 | 18851 | 184 | *Klebsiella pneumoniae*  |
| 3 | AAB86977.1 | peptidoglycan associated lipoprotein  | 1 | 6732 | 76 | *Allochromatium vinosum*  |
| 4 | YP\_003147027.1 | peptidoglycan-associated lipoprotein  | 1 | 19050 | 76 | *Kangiella koreensis*  |
| 5 | WP\_017628417.1 | outer membrane porin protein C  | 1 | 41496 | 74 | *Proteus mirabilis*  |
| 6 | NP\_290617.1 | 50S ribosomal protein L7/L12  | 1 | 12288 | 60 | *Escherichia coli*  |
| 7 | WP\_017842506.1 | peptidoglycan-associated lipoprotein  | 1 | / | 60 | *Methylomicrobium buryatense*  |
| 8 | YP\_048349.1 | 50S ribosomal protein L7/L12  | 1 | 12424 | 60 | *Pectobacterium atrosepticum*  |

***Sample UR10***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | YP\_002151979.1 | DL-methionine transporter substrate-binding subunit  | 2 | 29682 | 295 | ***Proteus mirabilis***  |
| 2 | YP\_002150354.1 | peptidoglycan-associated outer membrane lipoprotein  | 1 | 18118 | 225 | *Proteus mirabilis*  |
| 3 | YP\_001334418.1 | peptidoglycan-associated outer membrane lipoprotein  | 2 | 18851 | 161 | *Klebsiella pneumoniae*  |
| 4 | YP\_002150599.1 | outer membrane receptor  | 2 | 73933 | 160 | *Proteus mirabilis*  |
| 5 | P09461.1 | RecName: Full=Major outer membrane lipoprotein; AltName: Full=Murein-lipoprotein; Flags: Precursor | 1 | 8246 | 119 | *Proteus mirabilis* |
| 6 | NP\_455305.1 | peptidoglycan-associated lipoprotein  | 1 | 18853 | 104 | *Salmonella enterica*  |
| 7 | YP\_051614.1 | DL-methionine transporter substrate-binding subunit  | 1 | 29463 | 73 | *Pectobacterium atrosepticum*  |
| 8 | YP\_001333901.1 | DL-methionine transporter substrate-binding subunit  | 1 | 29366 | 72 | *Klebsiella pneumoniae*  |
| 9 | AAA24507.1 | lipoprotein 28, partial  | 1 | 10781 | 72 | *Escherichia coli*  |
| 10 | NP\_670405.1 | DL-methionine transporter substrate-binding subunit  | 1 | / | 72 | *Yersinia pestis*  |
| 11 | AAB86977.1 | peptidoglycan associated lipoprotein  | 1 | 6732 | 57 | *Allochromatium vinosum*  |
| 12 | YP\_003147027.1 | peptidoglycan-associated lipoprotein  | 1 | / | 56 | *Kangiella koreensis*  |

***Sample UR11***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | AAA24232.1 | outer membrane protein II, partial  | 1 | 26114 | 164 | *Escherichia fergusonii*  |
| 2 | NP\_287228.1 | acyl carrier protein  | 2 | 8634 | 134 | ***Escherichia coli***  |
| 3 | ERE53009.1 | 30S ribosomal protein S2, partial  | 1 | 25562 | 82 | *Enterococcus gallinarum*  |
| 4 | BAA32342.1 | ribosomal protein S2  | 1 | 31289 | 82 | *Pseudomonas aeruginosa*  |
| 5 | YP\_001335792.1 | murein lipoprotein  | 1 | 8381 | 68 | *Klebsiella pneumoniae*  |
| 6 | P02938.1 | RecName: Full=Major outer membrane lipoprotein; AltName: Full=Murein-lipoprotein; Flags: Precursor | 1 | 8234 | 68 | *Serratia marcescens* |
| 7 | 1BXW\_A | Chain A, Outer Membrane Protein A (Ompa) Transmembrane Domain | 1 | 18864 | 67 | *Escherichia coli*  |
| 8 | YP\_001336542.1 | autonomous glycyl radical cofactor GrcA  | 1 | 14234 | 65 | *Klebsiella pneumoniae*  |
| 9 | P18953.2 | RecName: Full=Autonomous glycyl radical cofactor | 1 | 14366 | 65 | *Serratia liquefaciens* |
| 10 | CAA57795.1 | enolase  | 1 | 46417 | 63 | *Escherichia coli*  |
| 11 | YP\_001334138.1 | adenylate kinase  | 1 | 23533 | 61 | *Klebsiella pneumoniae*  |
| 12 | BAA14303.1 | adenylate kinase  | 1 | 12103 | 61 | *Escherichia coli*  |

***Sample UR12***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | YP\_002150599.1 | outer membrane receptor  | 3 | 73933 | 382 | ***Proteus mirabilis***  |
| 2 | YP\_002150354.1 | peptidoglycan-associated outer membrane lipoprotein  | 1 | 18118 | 275 | *Proteus mirabilis*  |
| 3 | YP\_002152262.1 | molecular chaperone GroEL  | 1 | 57615 | 150 | *Proteus mirabilis*  |
| 4 | NP\_927927.1 | molecular chaperone DnaK  | 2 | 68818 | 142 | *Photorhabdus luminescens*  |
| 5 | WP\_021710396.1 | chaperone protein DnaK  | 2 | 69029 | 142 | *Vibrio azureus*  |
| 6 | YP\_002150023.1 | phosphoglycerate kinase  | 1 | 41197 | 121 | *Proteus mirabilis*  |
| 7 | YP\_858397.1 | outer membrane receptor  | 1 | 71927 | 72 | *Aeromonas hydrophila*  |
| 8 | YP\_002152488.1 | 50S ribosomal protein L10  | 1 | 17640 | 72 | *Proteus mirabilis*  |

***Sample UR13***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | YP\_004593040.1 | peptidoglycan-associated outer membrane lipoprotein  | 1 | 18865 | 160 | ***Enterobacter aerogenes***  |
| 2 | 1OEL\_A | Chain A, Conformational Variability In The Refined Structure Of The Chaperonin  | 1 | 57031 | 157 | *Escherichia coli* |
| 3 | YP\_001337379.1 | elongation factor G  | 1 | 77494 | 98 | *Klebsiella pneumoniae*  |
| 4 | NP\_289887.1 | elongation factor G  | 1 | 77532 | 98 | *Escherichia coli*  |
| 5 | YP\_001334507.1 | DNA starvation/stationary phase protection protein Dps  | 1 | 18697 | 89 | *Klebsiella pneumoniae*  |
| 6 | AAB49426.1 | PexB, partial  | 1 | 5584 | 89 | *Salmonella enterica*  |
| 7 | YP\_001334652.1 | outer membrane protein A  | 1 | 38021 | 85 | *Klebsiella pneumoniae*  |
| 8 | P09146.1 | RecName: Full=Outer membrane protein A; Flags: Precursor | 1 | 37552 | 85 | *Klebsiella aerogenes* |
| 9 | YP\_004393584.1 | major outer membrane protein OmpAII  | 1 | 36565 | 83 | *Aeromonas veronii*  |
| 10 | WP\_021015441.1 | Ferritin Dps family protein  | 1 | / | 74 | *Serratia sp.*  |

***Sample UR14***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | YP\_001335792.1 |  murein lipoprotein  | 1 | 8381 | 188 | *Klebsiella pneumoniae*  |
| 2 | P02938.1 |  RecName: Full=Major outer membrane lipoprotein; AltName: Full=Murein-lipoprotein; Flags: Precursor | 1 | 8234 | 188 | *Serratia marcescens* |
| 3 | AAA24807.1 |  outer membrane protein II, partial  | 2 | 25538 | 140 | ***Enterobacter*** *aerogenes*  |
| 4 | YP\_049963.1 |  major outer membrane lipoprotein  | 1 | 8396 | 139 | *Pectobacterium atrosepticum*  |
| 5 | AHF77098.1 |  Major outer membrane lipoprotein  | 1 | 8327 | 139 | *Sodalis sp.*  |
| 6 | P24016.1 |  RecName: Full=Outer membrane protein A; AltName: Full=Outer membrane protein II | 1 | 25648 | 77 | *Citrobacter freundii* |

***Sample UR15***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | NP\_814526.1 | cold shock domain-contain protein  | 1 | 7109 | 94 | ***Enterococcus faecalis***  |
| 2 | YP\_001335792.1 | murein lipoprotein  | 1 | 8381 | 90 | *Klebsiella pneumoniae*  |
| 3 | P02938.1 | RecName: Full=Major outer membrane lipoprotein; AltName: Full=Murein-lipoprotein; Flags: Precursor | 1 | 8234 | 90 | *Serratia marcescens* |
| 4 | WP\_005297706.1 | glyceraldehyde-3-phosphate dehydrogenase  | 1 | 40057 | 64 | *Photobacterium damselae*  |
| 5 | WP\_009972002.1 | hypothetical protein  | 1 | 4391 | 59 | *Burkholderia pseudomallei*  |
| 6 | YP\_002602369.1 | protein FeoB1  | 1 | / | 55 | *Desulfobacterium autotrophicum*  |
| 7 | ETT00120.1 | TcdA/TcdB pore forming domain protein  | 1 | / | 55 | *Providencia alcalifaciens*  |
| 8 | NP\_643074.1 | PmbA protein  | 1 | / | 54 | *Xanthomonas axonopodis*  |
| 9 | WP\_020491921.1 | UDP-N-acetylenolpyruvoylglucosamine reductase  | 1 | 31795 | 53 | *Dehalobacter sp.*  |

***Sample UR16***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Σ Peptides | MW (Da) | ∑ Score | Bacteria |
| 1 | YP\_049963.1 | major outer membrane lipoprotein | 1 | 8396 | 212 | *Pectobacterium atrosepticum* |
| 2 | AHF77098.1 | Major outer membrane lipoprotein | 2 | 8327 | 212 | *Sodalis sp.* |
| 3 | YP\_001335792.1 | murein lipoprotein | 1 | 8381 | 161 | ***Klebsiella pneumoniae*** |
| 4 | P02938.1 | RecName: Full=Major outer membrane lipoprotein; AltName: Full=Murein-lipoprotein; Flags: Precursor | 1 | 8234 | 161 | *Serratia marcescens* |
| 5 | YP\_001463566.1 | outer membrane porin protein C | 1 | 40070 | 102 | ***Escherichia coli*** |
| 6 | ABS84845.1 | translation elongation factor Tu | 1 | 21970 | 85 | *Bacillus subtilis* |
| 7 | NP\_299905.1 | elongation factor Tu | 1 | 42849 | 85 | *Xylella fastidiosa* |
| 8 | 0803214A | elongation factor Tu 59-263 | 1 | 22630 | 85 | *Escherichia coli* |
| 9 | NP\_667815.1 | elongation factor Tu | 1 | / | 84 | *Yersinia pestis* |
| 10 | AAQ96088.1 | outer membrane protein II | 1 | 17373 | 62 | *Klebsiella pneumoniae* |
| 11 | YP\_003929643.1 | hypothetical protein Pvag\_pPag10133 | 1 | / | 61 | *Pantoea vagans* |
| 12 | YP\_001337372.1 | 50S ribosomal protein L4 | 1 | 22100 | 59 | *Klebsiella pneumoniae* |
| 13 | NP\_289880.1 | 50S ribosomal protein L4 | 1 | 22073 | 59 | *Escherichia coli* |

**Supplementary table 5: The comparative view of urine culture, proteomics and genomic results.**

|  |  |  |  |
| --- | --- | --- | --- |
| **N.o.** | **Urine culture identification** | **MALDI TOF/TOF IDENTIFICATION** | **16S rRNA sequencing identification** |
| UR1 | *Klebsiella pneumoniae*  | *Klebsiella pneumoniae*  | *100% Enterobacteriaceae* |
| UR2 | *Klebsiella oxytoca* | *Klebsiella pneumoniae*  | *97% Enterobacteriaceae* |
| UR3 | *Klebsiella pneumoniae*  | *Klebsiella pneumoniae*  | *90% Enterobacteriaceae, 5.1% Granulicatella, 1,1% Anaerococcus* |
| UR4 | *Proteus mirabilis* | *Proteus mirabilis*  | *97.7% Proteus, 1% Enterobacteriaceae* |
| UR5 | *Enterococcus faecalis* | *Enterococcus faecalis*  | *21,8% Pseudomonas; 13,7% Propionibacterium acnes; 11% Lactobacillus helvetisus; 8,1% Adhaeribacter; 8% Acinetobacter; 5,9% Staphylococcus; 4,9% Stenotrophomonas; 3,8% Hydrogenophaga; 3,6% Erysipelotrichaceae; 3,1% Corynebacterium; 3,1% Cellulomonas; 2,3% Aerococcus; 2% Acidovorax; 1,9% Lachnospiraceae; 1,6% Sphingobium* |
| UR6 | *Enterococcus faecalis* | *Enterococcus faecalis*  | *51,4% Enterococcus, 46,5% Enterococcaceae* |
| UR7 | *Enterobacter cloaceae*  | *Citrobacter freundii* | *98% Enterobacter; 0,9% Proteus* |
| UR8 | *Citrobacter koseri* | *Citrobacter freundii* | *57,5% Citrobacter koseri; 4,5% Bacteroides; 3,7% Dysgonomonas; 2,7% Bacteroides; 2,6% Rikenellaceae; 2,3% Parabacteroides; 2% Desulfovibrionaceae; 2% Lachnospiraceae; 2% Ruminococcaceae; 1,9% Enterobacteriaceae; 1,3% Ruminococcus; 1,3% Erysipelotrichaceae; 1,2% Enterococcus; 1,1% Clostridiales* |
| UR9 | *Proteus mirabilis* | *Proteus mirabilis*  | *96.7% Proteus; 2,4% Enterobacteriaceae; 1,2% Prevotella* |
| UR10 | *Proteus mirabilis* | *Proteus mirabilis*  | *97% Proteus; 1,3% Enterobacteriaceae* |
| UR11 | *Escherichia coli;Proteus mirabilis*  | *Escherichia fergusonii*  | *93% Enterobacteriaceae; 3,5% Proteus* |
| UR12 | *Proteus mirabilis* | *Proteus mirabilis*  | *99,2% Proteus* |
| UR13 | *Enterobacter aerogenes* | *Enterobacter aerogenes*  | *75,4% Enterobacteriaceae; 14% Lactobacillus delbrueckii; 4,2% Kluyvera; 4% Enterobacter; 1% Lactobacillus helveticus* |
| UR14 | *Enterobacter cloacae* | *Klebsiella pneumoniae* | *95,4% Enterobacteriaceae; 1,2% Clostridium perfringens; 1% Bifidobacterium pseudolongum* |
| UR15 | *Enterobacter cloacae; Enterococcus faecalis; E coli; Proteus mirabilis* | *Enterococcus faecalis* | *86,9% Proteus; 7,2% Enterobacteriaceae; 2,2% Enterobacter; 1% Rhodospirillaceae* |
| UR16 | *Escherichia coli; Klebsiella pneumoniae* | *Pectobacterium atrosepticum* | *91,2% Enterobacteriaceae; 8,6% Klebsiella* |

**Supplementary table 6: Identified human proteins ranked by MASCOT score for each urine sample.**

***Sample UR1***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | BAG59381.1 |  unnamed protein product  | 140 | 1 |
| 2 | CAA34982.1 |  alpha-1 antitrypsin  | 99 | 1 |
| 3 | CAA26677.1 |  alpha-1-antitrypsin (aa 268-394)  | 70 | 1 |
| 4 | NP\_000691.1 |  annexin A1  | 67 | 1 |
| 5 | 740525A |  lipoprotein Gln I | 66 | 1 |
| 6 | 2A01\_A |  Chain A, Crystal Structure Of Lipid-Free Human Apolipoprotein A-I | 66 | 1 |
| 7 | CAA37116.1 |  unnamed protein product  | 55 | 1 |

***Sample UR2***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | CAA23759.1 | unnamed protein product  | 325, 200, 105 | 3 |
| 2 | 2YRS\_B | Chain B, Human Hemoglobin D Los Angeles: Crystal Structure | 325 | 1 |
| 3 | AAN84548.1 |  beta globin chain variant | 283 | 1 |
| 4 | 1NQP\_B | Chain B, Crystal Structure Of Human Hemoglobin E At 1.73 A Resolution | 239 | 1 |
| 5 | AAY46275.1 |  beta globin chain | 214 | 1 |
| 6 | AAY51976.1 |  hemoglobin beta chain  | 200 | 1 |
| 7 | AAA36799.1 |  uromodulin  | 170, 51 | 2 |
| 8 | CAA23749.1 |  alpha globin  | 152 | 1 |
| 9 | AAA51747.1 |  proapolipoprotein, partial  | 105, 76 | 2 |
| 10 | 740525A |  lipoprotein Gln I | 100 | 1 |
| 11 | 2A01\_A | Chain A, Crystal Structure Of Lipid-Free Human Apolipoprotein A-I | 100 | 1 |
| 12 | ACF16774.1 |  beta globin  | 85 | 1 |
| 13 | AAA35597.1 |  beta-globin  | 64 | 1 |
| 14 | 1Y5K\_B | Chain B, T-to-t(high) Quaternary Transitions In Human Hemoglobin: Betad99a Deoxy Low-salt (10 Test Sets) | 64 | 1 |

***Sample UR3***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | AAA36799.1 |  uromodulin  | 121, 91 | 2 |
| 2 | NP\_002956.1 |  protein S100-A9  | 101, 86 | 2 |
| 3 | AAB50880.1 |  anitubulin IgG1 kappa VL chain {N-terminal} [human, serum, immunocytic sarcom patient PER isolate, Peptide Partial, 219 aa] | 89 | 1 |
| 4 | 1COH\_A |  Chain A, Structure Of Haemoglobin In The Deoxy Quaternary State With Ligand Bound At The Alpha Haems | 82 | 1 |
| 5 | CAA23759.1 |  unnamed protein product  | 75 | 1 |
| 6 | 3KR3\_L |  Chain L, Crystal Structure Of Igf-Ii Antibody Complex | 70 | 1 |
| 7 | BAG59381.1 |  unnamed protein product  | 65 | 1 |
| 8 | AAA51747.1 |  proapolipoprotein, partial  | 55 | 1 |
| 9 | 740525A |  lipoprotein Gln I | 54 | 1 |

***Sample UR4***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | NP\_002956.1 |  protein S100-A9  | 89 | 1 |
| 2 | CAA68390.1 |  unnamed protein product  | 61 | 1 |
| 3 | AAH13767.1 |  VASN protein  | 58 | 1 |

***Sample UR5***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | AAA36799.1 |  uromodulin  | 148, 74 | 2 |
| 2 | CAA23749.1 |  alpha globin  | 52 | 1 |

***Sample UR6***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | AAA51747.1 |  proapolipoprotein, partial  | 475, 344, 195 | 3 |
| 2 | 740525A |  lipoprotein Gln I | 354, 234, 195, 69 | 4 |
| 3 | AAB59495.1 |  alpha-1-antitrypsin  | 132, 59 | 2 |
| 4 | 1OR3\_A |  Chain A, Apolipoprotein E3 (Apoe3), Trigonal Truncation Mutant 165 | 131 | 1 |
| 5 | AAA51547.1 |  alpha-1-antitrypsin precursor  | 104 | 1 |
| 6 | AAB59372.1 |  apolipoprotein C-III  | 91 | 1 |
| 7 | AAB59518.1 |  apolipoprotein E  | 71, 60 | 2 |
| 8 | CAA23749.1 |  alpha globin  | 65 | 1 |
| 9 | 1506383A |  apolipoprotein E mutant E3K | 52 | 1 |

***Sample UR7***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | CAA23749.1 |  alpha globin  | 95 | 1 |
| 2 | NP\_002956.1 |  protein S100-A9  | 91 | 1 |
| 3 | 2CMR\_L |  Chain L, Crystal Structure Of The Hiv-1 Neutralizing Antibody D5 Fab Bound To The Gp41 Inner-Core Mimetic 5-Helix | 84 | 1 |
| 4 | CAA23759.1 |  unnamed protein product  | 70 | 1 |
| 5 | 3KR3\_L |  Chain L, Crystal Structure Of Igf-Ii Antibody Complex | 66 | 1 |
| 6 | 4JFY\_A |  Chain A, Apo Structure Of Phosphotyrosine (pyab) Scaffold | 77 | 1 |

***Sample UR8***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | AAM13690.1 |  delta 2-isopentenyl pyrophosphate transferase-like protein  | 69 | 1 |

***Sample UR9***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | AAA51747.1 |  proapolipoprotein, partial  | 212, 87 | 2 |
| 2 | CAA34982.1 |  alpha-1 antitrypsin  | 68 | 1 |
| 3 | AAA36799.1 |  uromodulin  | 50 | 1 |

***Sample UR10***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | AAA36799.1 |  uromodulin  | 119 | 1 |
| 2 | A37927 |  Ig kappa chain C region (allotype Inv(1,2)) - human (fragment) | 114 | 1 |
| 3 | 3KR3\_L |  Chain L, Crystal Structure Of Igf-Ii Antibody Complex | 114 | 1 |
| 4 | NP\_002956.1 |  protein S100-A9  | 86 | 1 |
| 5 | CAA33438.1 |  unnamed protein product  | 61 | 1 |
| 6 | CAA40416.1 |  histone H2A.2  | 57 | 1 |
| 7 | 740525A |  lipoprotein Gln I | 56 | 1 |
| 8 | CAA68390.1 |  unnamed protein product  | 44 | 1 |
| 9 | CAA37116.1 |  unnamed protein product  | 42 | 1 |

***Sample UR11***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | AAA36799.1 |  uromodulin  | 119 | 1 |
| 2 | AAF00488.1 |  hemoglobin beta subunit variant  | 43 | 1 |

***Sample UR12***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | 1AU8\_A |  Chain A, Human Cathepsin G | 71 | 1 |
| 2 | AAB57795.1 |  lactoferrin  | 53 | 1 |
| 3 | NP\_001148.1 |  annexin A11 isoform 1  | 41 | 1 |

***Sample UR13***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | AAA36799.1 |  uromodulin  | 149 | 1 |
| 2 | NP\_002956.1 |  protein S100-A9  | 85 | 1 |

***Sample UR14***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | CAA23759.1 |  unnamed protein product  | 104, 69 | 2 |
| 2 | CAA23749.1 |  alpha globin  | 99, 77 | 2 |

***Sample UR15***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 | CAA23759.1 |  unnamed protein product  | 244, 138, 119 | 3 |
| 2 | AAF00488.1 |  hemoglobin beta subunit variant  | 220 | 1 |
| 3 | BAA33580.1 |  anti-HBsAg immunoglobulin Fab kappa chain  | 123 | 1 |
| 4 | CAA23749.1 |  alpha globin  | 112 | 1 |
| 5 | AAY46275.1 |  beta globin chain  | 104 | 1 |
| 6 | AAA35597.1 |  beta-globin  | 104, 71 | 2 |
| 7 | 3KR3\_L |  Chain L, Crystal Structure Of Igf-Ii Antibody Complex | 103 | 1 |
| 8 | AAA36799.1 |  uromodulin  | 66 | 1 |
| 9 | H7BZ55.3 |  RecName: Full=Putative ciliary rootlet coiled-coil protein-like 3 protein | 39 | 1 |

***Sample UR16***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accession | Protein\_description | Score | ∑ Peptide |
| 1 |  protein S100-A9  | NP\_002956.1 | 97, 68 | 2 |