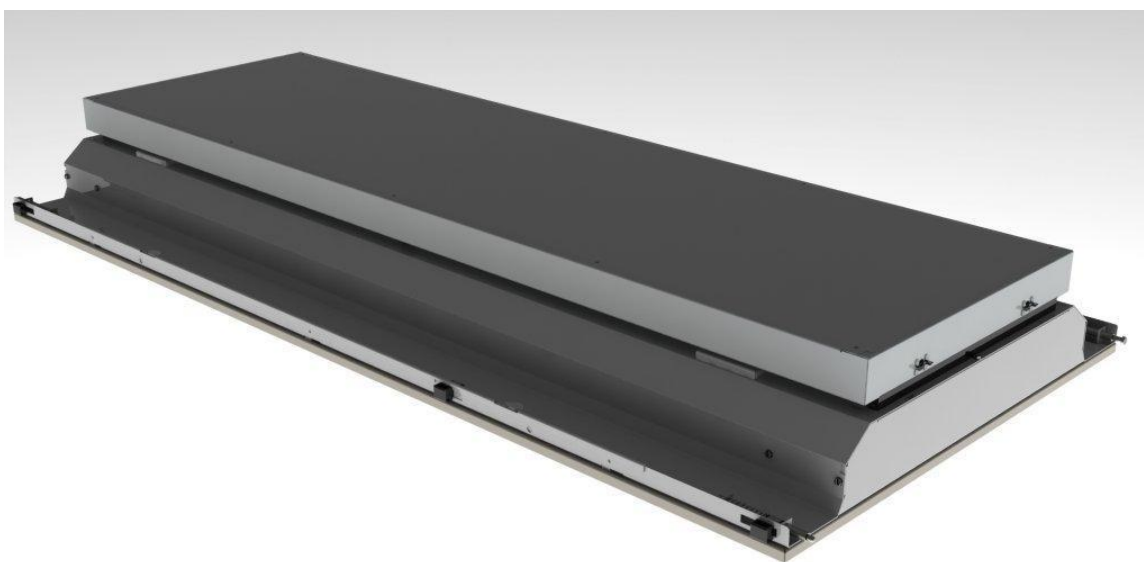


Report on the Performance of the VidaShield™ System



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Executive Summary

The superior performance of the VidaShield (formerly known as HRMS) will enable high levels of air disinfection to be achieved as well as a consequent reduction in the risk of airborne nosocomial infection in any health care environment. This report evaluates the performance of the VidaShield in terms of the removal rates of known airborne nosocomial or hospital-acquired pathogens, including bacteria, viruses, and fungi. Removal rates due to filtration and UV irradiation are evaluated using computer models and tabulated for various operating conditions. These removal rates, which will reduce concentrations of airborne pathogens, are used to estimate the risk of infection to occupants and this risk is presented in terms of the Zonal Protection Factor (ZPF). The ZPF is a measure of the percentage of occupants protected from infection. Removal rates for most pathogens are in excess of 90% in the primary configurations. At the nominal design airflow of **50 cfm**, and with a **MERV 6** filter and a UV lamp with **15 W** of UV output, the VidaShield System provides overall **single pass removal rates of approximately 97%** on the average for the 44 airborne nosocomial pathogens in the database. For the nominal design floor area of 100 ft², the unit will provide Zonal Protection Factors that exceed 91% for most of the pathogens in the database, with an **average ZPF of 90%**. ZPF data is provided for alternate airflows ranging from 50 ft² to 300 ft² as shown in Table 6. Both the single pass removal rates and the ZPFs are close to the limits of what can be achieved with a combined UV and filtration system, and this unit should outperform other similar units while consuming the least amount of energy as it has been optimized for both high performance and low power consumption. Quiet operation also makes this unit suitable for any hospital environment and it can be used in general wards, procedure rooms, hallways, laboratories, and other facilities.

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Introduction

The VidaShield is a UV air disinfection system incorporated into a ceiling light fixture such that it has no visible profile. It is intended to disinfect the air of bacteria, viruses, and fungi in hospital environments. The system includes an ultraviolet (UV) lamp, a filter, and a fan that will recirculate air locally, such as in a hallway or procedure room. Light baffles ensure that no hazardous levels of UV will escape into the local area. The system is designed to operate quietly while delivering air of the highest purity, with disinfection rates approaching 100%. Targeted microorganisms include MRSA, VRE, *Acinetobacter*, *Streptococcus* species, Influenza, VZV, *Pseudomonas*, *Clostridium difficile*, and other causative agents of hospital-acquired infections (HAIs). This report summarizes the predicted performance of the unit in terms of UV dose, filter removal rates, and overall disinfection or kill rates of pathogenic nosocomial microbes. Comparative predictions are provided for reductions of airborne concentrations of microbes for particular floor areas and room volumes. These airborne reductions are related to the risk of reduced infections. This unit will also remove fungal and bacterial spores at rates that are specified in this report.

System Description

The VidaShield consists of a ceiling light fixture that includes a UV lamp, a filter, light baffles, and a UV irradiation chamber. Air is drawn into the unit, filtered and disinfected, and then exhausted back into the local airspace. A MERV 6 filter is included to keep dust off the UV lamp, but this filter also serves to remove a percentage of airborne pathogens. Figure 1 shows a partially exploded view of the major components of the system. From top to bottom are shown the UV irradiation chamber, the lighting components, and the bottom grille.

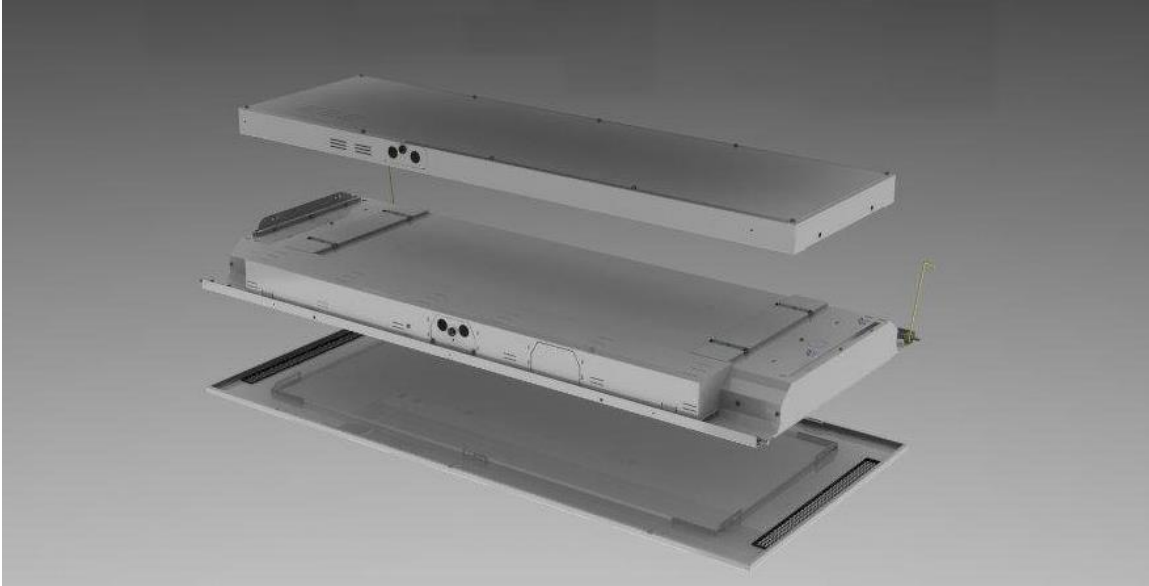


Figure 1: Partially exploded view of the VidaShield™ System showing major components.

Figure 2 shows the internal arrangement of the UV irradiation chamber, including the UV lamps and the fans at the outlet. The irradiation chamber is lined or coated with reflective materials to increase the total irradiance.

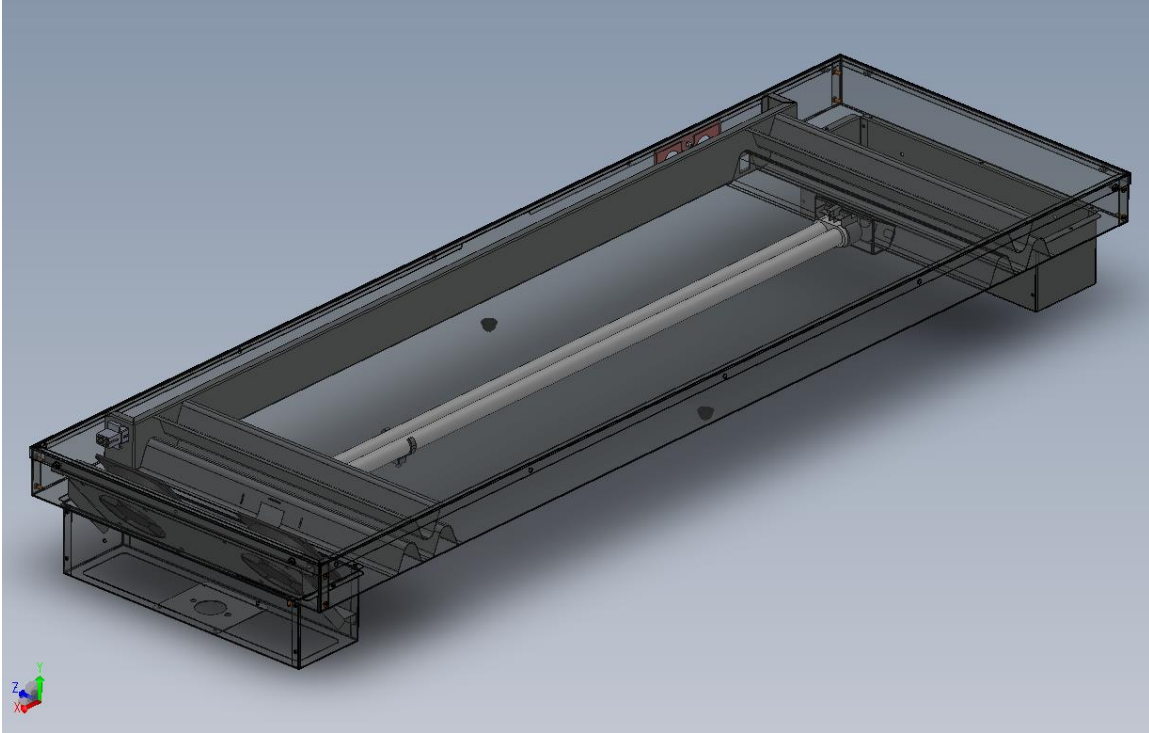


Figure 2: Schematic image of VidaShield™ showing internal UV lamps and irradiation chamber.

The properties of the reflective material were provided in the manufacturer's documents. The reflectivity of the aluminum surface is approximately 75-85% in the UV spectrum. Dimensions and design specifications are summarized in Table 1. These dimensions have been adjusted from those shown in the previous figure. The two configurations represent two different UV lamp sizes. The nominal airflow is 50 cfm. The airflow affects the air velocity and the exposure time (Et). Lamp dimensions and coordinates are unchanged from Table 1. At the nominal airflow of 50 scfm the air velocity is approximately 252 fpm. This is an acceptable airflow and will not decrease filter performance – in fact, filter performance will be slightly improved over the results given in the tables. The normal operating design airflow for a UV lamp is about 400-600 fpm.

Table 1: Specifications for VidaShield™

| | |
|---|--------|
| Lamp Type | T5 |
| # Lamps | 1 |
| Lamp UV Output, W | 15 |
| Width, in | 14.5 |
| Length, in | 30.979 |
| Height, in | 1.97 |
| Width, ft | 1.21 |
| Length, ft | 2.58 |
| Height, ft | 0.16 |
| Width, cm | 36.83 |
| Length, cm | 78.69 |
| Height, cm | 5.0038 |
| Nominal Airflow, Q, cfm | 50 |
| Nominal Airflow, Q, m ³ /min | 1.42 |
| Velocity, fpm | 252 |
| Velocity, fps | 4.20 |
| Velocity, cm/s | 128.04 |
| Velocity, m/s | 1.28 |
| Face Area, in ² | 28.57 |
| Face Area, ft ² | 0.1984 |
| Face Area, cm ² | 184.29 |
| Face Area, m ² | 0.0184 |
| Exposure Time, Et, s | 0.6145 |
| lamp end coordinate, x1, cm | 18.42 |
| lamp end coordinate, x2, cm | 18.42 |
| lamp end coordinate, y1, cm | 2.50 |
| lamp end coordinate, y2, cm | 2.50 |
| lamp end coordinate, z1, cm | 10.77 |
| lamp end coordinate, z2, cm | 67.92 |
| lamp arc length, arcl, cm | 57.15 |
| lamp radius, r, cm | 0.79 |

A MERV 6 filter is included in the unit and a representative filter performance curve is adapted from Kowalski and Bahnfleth (2002). Figure 3 shows the filter performance curve. The removal efficiency at any microbial particle size can be estimated from this curve.

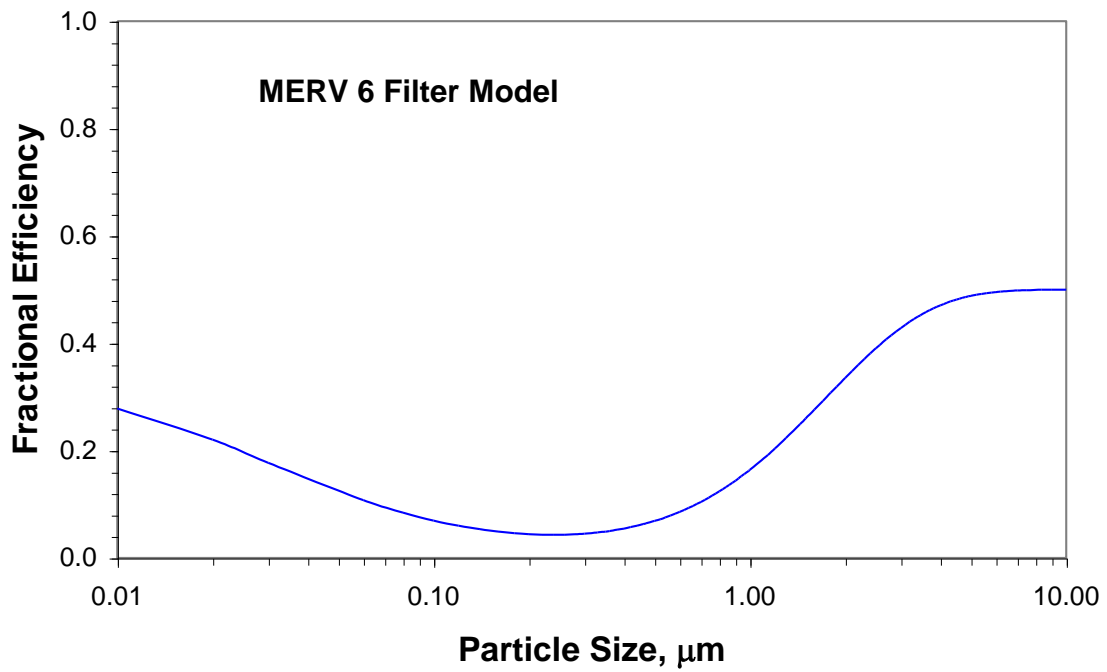


Figure 3: Performance of a generic MERV 6 filter. Based on modeling per Kowalski & Bahnfleth (2002).

Fan Pressure Loss and Noise

One of the design criteria for the VidaShield is that it must have quiet operation and produce the lowest possible level of noise. Noise is produced by the airflow as it moves through the fan and from turbulence inside the unit. The higher the pressure drop through the system the higher the fan static pressure and noise level. The unit includes smooth baffles to reduce turbulence inside the unit and fans have been selected for quiet operation. In order to minimize pressure losses a low pressure drop MERV 6 filter has been selected.

Analysis Results

Table 2 lists all nosocomial or HAI microbes that are known or suspected of having an airborne opponent in their transmission cycle. These include bacteria, viruses, fungal spores, and bacterial spores. Table 2 identifies the predicted filter removal rate for all these microbes based on the Figure 3 filter model. These filter removal rates will be combined with the UV disinfection rates to develop the overall removal rates of the pathogens. The filter removal rates are computed based on the log mean diameter of each pathogen. The size range of any microbe in nature will have a lognormal distribution, or a normal distribution (bell curve) on a logarithmic scale. The log mean diameter is an adequate representation of the mean size of any microbial population (Kowalski et al 1999). The log mean diameter will therefore be an adequate predictor of removal rates through any filter with a known performance curve.

Table 2: MERV 6 Filter Removal Rates of Airborne Nosocomial Pathogens

| Microbe | Type | Size µm | MERV 6 Removal Rate | |
|---------------------------------|----------|------------|---------------------|------|
| | | | fraction | % |
| Acinetobacter | Bacteria | 1.225 | 0.2089 | 20.9 |
| Adenovirus | Virus | 0.079 | 0.0853 | 8.5 |
| Aspergillus spores | Fungi | 3.354 | 0.4476 | 44.8 |
| Blastomyces dermatitidis spores | Fungi | 12.649 | 0.5000 | 50.0 |
| Bordetella pertussis | Bacteria | 0.245 | 0.0431 | 4.3 |
| Clostridium difficile spores | Bacteria | 2 | 0.3353 | 33.5 |
| Clostridium perfringens spores | Bacteria | 1 | 0.1643 | 16.4 |
| Coronavirus (SARS) | Virus | 0.11 | 0.0643 | 6.4 |
| Corynebacterium diphtheriae | Bacteria | 0.698 | 0.1040 | 10.4 |
| Coxsackievirus | Virus | 0.027 | 0.1886 | 18.9 |
| Cryptococcus neoformans spores | Fungi | 4.899 | 0.4872 | 48.7 |
| Enterobacter cloacae | Bacteria | 1.414 | 0.2442 | 24.4 |
| Enterococcus | Bacteria | 1.414 | 0.2442 | 24.4 |
| Fusarium spores | Fungi | 11.225 | 0.5000 | 50.0 |
| Haemophilus influenzae | Bacteria | 0.285 | 0.0443 | 4.4 |
| Haemophilus parainfluenzae | Bacteria | 1.732 | 0.2973 | 29.7 |
| Influenza A virus | Virus | 0.098 | 0.0709 | 7.1 |
| Klebsiella pneumoniae | Bacteria | 0.671 | 0.0988 | 9.9 |
| Legionella pneumophila | Bacteria | 0.52 | 0.0721 | 7.2 |
| Measles virus | Virus | 0.158 | 0.0493 | 4.9 |
| Mucor spores | Fungi | 7.071 | 0.4983 | 49.8 |
| Mumps virus | Virus | 0.164 | 0.0483 | 4.8 |
| Mycobacterium avium | Bacteria | 1.118 | 0.1879 | 18.8 |
| Mycobacterium tuberculosis | Bacteria | 0.637 | 0.0925 | 9.3 |
| Mycoplasma pneumoniae | Bacteria | 0.177 | 0.0464 | 4.6 |
| Neisseria meningitidis | Bacteria | 0.775 | 0.1190 | 11.9 |
| Nocardia asteroides | Bacteria | 1.118 | 0.1879 | 18.8 |
| Norwalk virus | Virus | 0.029 | 0.1809 | 18.1 |
| Parainfluenza virus | Virus | 0.194 | 0.0447 | 4.5 |
| Parvovirus B19 | Virus | 0.022 | 0.2104 | 21.0 |
| Proteus mirabilis | Bacteria | 0.494 | 0.0680 | 6.8 |
| Pseudomonas aeruginosa | Bacteria | 0.494 | 0.0680 | 6.8 |
| Reovirus | Virus | 0.075 | 0.0892 | 8.9 |
| RSV | Virus | 0.19 | 0.0450 | 4.5 |
| Rhinovirus | Virus | 0.023 | 0.2057 | 20.6 |
| Rhizopus spores | Fungi | 6.928 | 0.4981 | 49.8 |
| Rotavirus | Virus | 0.073 | 0.0913 | 9.1 |
| Rubella virus | Virus | 0.061 | 0.1062 | 10.6 |
| Serratia marcescens | Bacteria | 0.632 | 0.0916 | 9.2 |
| Staphylococcus aureus | Bacteria | 0.866 | 0.1372 | 13.7 |
| Staphylococcus epidermis | Bacteria | 0.866 | 0.1372 | 13.7 |
| Streptococcus pneumoniae | Bacteria | 0.707 | 0.1057 | 10.6 |
| Streptococcus pyogenes | Bacteria | 0.894 | 0.1428 | 14.3 |
| VZV | Virus | 0.173 | 0.0469 | 4.7 |

Appendix A reproduces the information in Table 2 but arranges the microbes in order of decreasing removal rates. Figure 4 illustrates how the pathogen removal rates correlate with the microbe size. This chart essentially duplicates Figure 4, the performance curve for a MERV 6 filter.

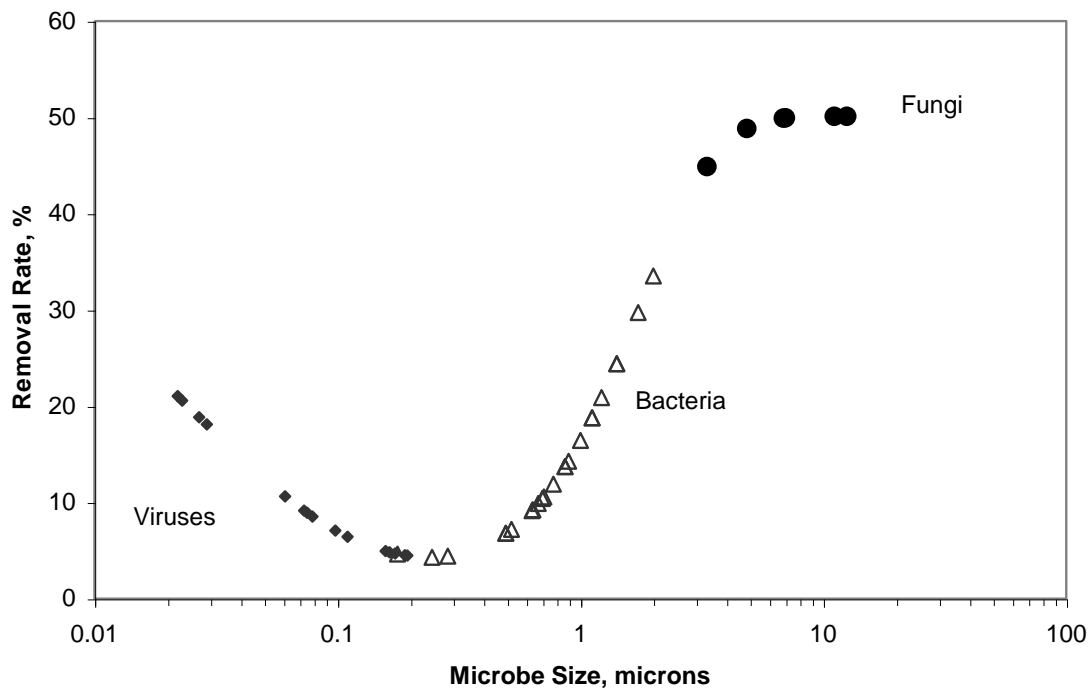


Figure 4: Removal rates for nosocomial pathogens arranged in a MERV 6 filter performance curve format (see Figure 3).

Table 3 lists the disinfection rates for airborne nosocomial pathogens based on the dose produced by the UV lamp. The 15 W lamp has been modeled (using the methods from Kowalski 2009) and found to produce a UV dose of 198 J/m² at 50 cfm. This dose is used to compute the disinfection rate based on the indicated UV rate constants listed in Table 3. Table 3 is reproduced in Appendix B where the pathogens are listed in order of decreasing removal rates.

Table 3: UV Disinfection Rates of Airborne Nosocomial Pathogens

| Microbe | Type | UV k m ² /J | UV D90 J/m ² | Disinfection Rate, % |
|---------------------------------|----------|---------------------------|----------------------------|----------------------|
| | | | | 15 W |
| Acinetobacter | Bacteria | 0.16 | 14 | 100 |
| Adenovirus | Virus | 0.054 | 43 | 100 |
| Aspergillus spores | Fungi | 0.00894 | 258 | 83 |
| Blastomyces dermatitidis spores | Fungi | 0.01645 | 140 | 96 |
| Bordetella pertussis* | Bacteria | 0.0364 | 63 | 100 |
| Clostridium difficile spores | Bacteria | 0.0385 | 60 | 100 |
| Clostridium perfringens spores | Bacteria | 0.0385 | 60 | 100 |
| Coronavirus (SARS) | Virus | 0.377 | 6 | 100 |
| Corynebacterium diphtheriae | Bacteria | 0.0701 | 33 | 100 |
| Coxsackievirus | Virus | 0.111 | 21 | 100 |
| Cryptococcus neoformans spores | Fungi | 0.0167 | 138 | 96 |
| Enterobacter cloacae | Bacteria | 0.03598 | 64 | 100 |
| Enterococcus* | Bacteria | 0.0822 | 28 | 100 |
| Fusarium spores | Fungi | 0.00855 | 269 | 82 |
| Haemophilus influenzae | Bacteria | 0.11845 | 19 | 100 |
| Haemophilus parainfluenzae* | Bacteria | 0.03 | 77 | 100 |
| Influenza A virus | Virus | 0.119 | 19 | 100 |
| Klebsiella pneumoniae | Bacteria | 0.04435 | 52 | 100 |
| Legionella pneumophila | Bacteria | 0.2024 | 11 | 100 |
| Measles virus | Virus | 0.1051 | 22 | 100 |
| Mucor spores | Fungi | 0.01012 | 228 | 87 |
| Mumps virus* | Virus | 0.0766 | 30 | 100 |
| Mycobacterium avium | Bacteria | 0.04387 | 52 | 100 |
| Mycobacterium tuberculosis | Bacteria | 0.4721 | 5 | 100 |
| Mycoplasma pneumoniae | Bacteria | 0.2791 | 8 | 100 |
| Neisseria meningitidis* | Bacteria | 0.1057 | 22 | 100 |
| Nocardia asteroides | Bacteria | 0.0822 | 28 | 100 |
| Norwalk virus* | Virus | 0.0116 | 198 | 90 |
| Parainfluenza virus* | Virus | 0.1086 | 21 | 100 |
| Parvovirus B19 | Virus | 0.092 | 25 | 100 |
| Proteus mirabilis | Bacteria | 0.289 | 8 | 100 |
| Pseudomonas aeruginosa | Bacteria | 0.5721 | 4 | 100 |
| Reovirus | Virus | 0.01459 | 158 | 94 |
| RSV* | Virus | 0.0917 | 25 | 100 |
| Rhinovirus* | Virus | 0.0142 | 162 | 94 |
| Rhizopus spores | Fungi | 0.00861 | 267 | 82 |
| Rotavirus | Virus | 0.02342 | 98 | 99 |
| Rubella virus* | Virus | 0.0037 | 622 | 52 |
| Serratia marcescens | Bacteria | 0.221 | 10 | 100 |
| Staphylococcus aureus | Bacteria | 0.5957 | 4 | 100 |
| Staphylococcus epidermis | Bacteria | 0.09703 | 24 | 100 |
| Streptococcus pneumoniae | Bacteria | 0.00492 | 468 | 62 |
| Streptococcus pyogenes | Bacteria | 0.8113 | 3 | 100 |
| VZV (Varicella surrogate k) | Virus | 0.1305 | 18 | 100 |
| UV Dose, J/m ² | | 198 | | |

Note: Asterisk means the UV rate constant is a predicted value based on the complete genome.

Table 4 lists the combined single pass removal rates for the array of nosocomial pathogens in the previous tables. This table is shown again in Appendix C where they have been rearranged in order of most susceptible to least susceptible.

Given the removal rates as listed in Table 4, the Zonal Protection Factor (ZPF) can be computed assuming the floor area coverage is 100 ft² and the zone has 15% outside air (from the normal ventilation system). The ZPF (aka BPF or Building Protection Factor) represents the theoretical protection offered to occupants by the VidaShield System. It must be computed for each individual pathogen since each pathogen has a different removal rate (RR). The ZPF is computed by transient analysis of the airborne concentrations in the zone and is based on eight hours of breathing air in the occupied zone. The ZPF is the percentage of occupants likely to be protected from infection. The converse of the ZPF (1-ZPF) represents the number of likely infections. It is computed by assuming that the baseline condition has no air cleaning. The baseline condition assumes a release rate of pathogens sufficient to cause 99% infections. See Kowalski (2009) or Kowalski (2006) for more specific details on the computation of the BPF or ZPF.

Table 5 summarizes the predicted ZPF for each of the nosocomial pathogens under consideration and it indicates that very high protection factors are possible with the VidaShield System, which could be expected since the removal rates are high for most pathogens and the airflow rate (50 cfm) is appropriate for the subject floor area (100 ft²). The maximum ZPF is 93% and this cannot be increased further without increasing airflow. The minimum acceptable ZPF for any system is about 50%, which means that half the occupants are protected from infection. Based on the results in Table 5, the ZPF is above the minimum for all pathogens, including bacterial and fungal spores.

The results in Table 5 are based on the nominal airflow rate of 50 cfm. The results will be proportionally lower for lower airflow rates, since the combined removal rates (filters plus UV) are largely maxed out. Table 5 is reproduced in Appendix C but rearranged in order of decreasing ZPF.

Table 4: Combined Single Pass Removal Rates

| Microbe | Component Removal Rates | | Overall Removal Rates |
|---------------------------------|-------------------------|----------|-----------------------|
| | MERV 6 | 15 W | MERV 6 + 15 W |
| | fraction | fraction | % |
| Acinetobacter | 0.2089 | 1.0000 | 100.0 |
| Adenovirus | 0.0853 | 1.0000 | 100.0 |
| Aspergillus spores | 0.4476 | 0.8297 | 90.6 |
| Blastomyces dermatitidis spores | 0.5000 | 0.9615 | 98.1 |
| Bordetella pertussis | 0.0431 | 0.9993 | 99.9 |
| Clostridium difficile spores | 0.3353 | 0.9995 | 100.0 |
| Clostridium perfringens spores | 0.1643 | 0.9995 | 100.0 |
| Coronavirus (SARS) | 0.0643 | 1.0000 | 100.0 |
| Corynebacterium diphtheriae | 0.1040 | 1.0000 | 100.0 |
| Coxsackievirus | 0.1886 | 1.0000 | 100.0 |
| Cryptococcus neoformans spores | 0.4872 | 0.9634 | 98.1 |
| Enterobacter cloacae | 0.2442 | 0.9992 | 99.9 |
| Enterococcus | 0.2442 | 1.0000 | 100.0 |
| Fusarium spores | 0.5000 | 0.8160 | 90.8 |
| Haemophilus influenzae | 0.0443 | 1.0000 | 100.0 |
| Haemophilus parainfluenzae | 0.2973 | 0.9974 | 99.8 |
| Influenza A virus | 0.0709 | 1.0000 | 100.0 |
| Klebsiella pneumoniae | 0.0988 | 0.9998 | 100.0 |
| Legionella pneumophila | 0.0721 | 1.0000 | 100.0 |
| Measles virus | 0.0493 | 1.0000 | 100.0 |
| Mucor spores | 0.4983 | 0.8652 | 93.2 |
| Mumps virus | 0.0483 | 1.0000 | 100.0 |
| Mycobacterium avium | 0.1879 | 0.9998 | 100.0 |
| Mycobacterium tuberculosis | 0.0925 | 1.0000 | 100.0 |
| Mycoplasma pneumoniae | 0.0464 | 1.0000 | 100.0 |
| Neisseria meningitidis | 0.1190 | 1.0000 | 100.0 |
| Nocardia asteroides | 0.1879 | 1.0000 | 100.0 |
| Norwalk virus | 0.1809 | 0.8994 | 91.8 |
| Parainfluenza virus | 0.0447 | 1.0000 | 100.0 |
| Parvovirus B19 | 0.2104 | 1.0000 | 100.0 |
| Proteus mirabilis | 0.0680 | 1.0000 | 100.0 |
| Pseudomonas aeruginosa | 0.0680 | 1.0000 | 100.0 |
| Reovirus | 0.0892 | 0.9444 | 94.9 |
| RSV | 0.0450 | 1.0000 | 100.0 |
| Rhinovirus | 0.2057 | 0.9399 | 95.2 |
| Rhizopus spores | 0.4981 | 0.8182 | 90.9 |
| Rotavirus | 0.0913 | 0.9903 | 99.1 |
| Rubella virus | 0.1062 | 0.5193 | 57.0 |
| Serratia marcescens | 0.0916 | 1.0000 | 100.0 |
| Staphylococcus aureus | 0.1372 | 1.0000 | 100.0 |
| Staphylococcus epidermis | 0.1372 | 1.0000 | 100.0 |
| Streptococcus pneumoniae | 0.1057 | 0.6225 | 66.2 |
| Streptococcus pyogenes | 0.1428 | 1.0000 | 100.0 |
| VZV | 0.0469 | 1.0000 | 100.0 |

Table 5: Zonal Protection Factors for Nosocomial Pathogens

| Pathogen | Type | MERV6+15W | FA 100 ft ² |
|------------------------------------|----------|-----------|------------------------|
| | | Removal % | ZPF % |
| Acinetobacter | Bacteria | 100.0 | 91 |
| Adenovirus | Virus | 100.0 | 91 |
| Aspergillus spores | Fungi | 90.6 | 89 |
| Blastomyces dermatitidis spores | Fungi | 98.1 | 90 |
| Bordetella pertussis | Bacteria | 99.9 | 91 |
| Clostridium difficile spores | Bacteria | 100.0 | 91 |
| Clostridium perfringens spores | Bacteria | 100.0 | 91 |
| Coronavirus (SARS) | Virus | 100.0 | 91 |
| Corynebacterium diphtheriae | Bacteria | 100.0 | 91 |
| Coxsackievirus | Virus | 100.0 | 91 |
| Cryptococcus neoformans spores | Fungi | 98.1 | 90 |
| Enterobacter cloacae | Bacteria | 99.9 | 91 |
| Enterococcus | Bacteria | 100.0 | 91 |
| Fusarium spores | Fungi | 90.8 | 89 |
| Haemophilus influenzae | Bacteria | 100.0 | 91 |
| Haemophilus parainfluenzae | Bacteria | 99.8 | 91 |
| Influenza A virus | Virus | 100.0 | 91 |
| Klebsiella pneumoniae | Bacteria | 100.0 | 91 |
| Legionella pneumophila | Bacteria | 100.0 | 91 |
| Measles virus | Virus | 100.0 | 91 |
| Mucor spores | Fungi | 93.2 | 89 |
| Mumps virus | Virus | 100.0 | 91 |
| Mycobacterium avium | Bacteria | 100.0 | 91 |
| Mycobacterium tuberculosis | Bacteria | 100.0 | 91 |
| Mycoplasma pneumoniae | Bacteria | 100.0 | 91 |
| Neisseria meningitidis | Bacteria | 100.0 | 91 |
| Nocardia asteroides | Bacteria | 100.0 | 91 |
| Norwalk virus | Virus | 91.8 | 89 |
| Parainfluenza virus | Virus | 100.0 | 91 |
| Parvovirus B19 | Virus | 100.0 | 91 |
| Proteus mirabilis | Bacteria | 100.0 | 91 |
| Pseudomonas aeruginosa | Bacteria | 100.0 | 91 |
| Reovirus | Virus | 94.9 | 90 |
| Rhinovirus | Virus | 100.0 | 91 |
| Rhizopus spores | Virus | 95.2 | 90 |
| Rotavirus | Fungi | 90.9 | 89 |
| RSV | Virus | 99.1 | 91 |
| Rubella virus | Virus | 57.0 | 73 |
| Serratia marcescens | Bacteria | 100.0 | 91 |
| Staphylococcus aureus | Bacteria | 100.0 | 91 |
| Staphylococcus epidermis | Bacteria | 100.0 | 91 |
| Streptococcus pneumoniae | Bacteria | 66.2 | 79 |
| Streptococcus pyogenes | Bacteria | 100.0 | 91 |
| VZV | Virus | 100.0 | 91 |
| Average Protection Factor % | | | 90 |

Table 6 provides the Zonal Protection Factors for a range of alternate airflows from 50 ft² to 300 ft², arranged in order of descending ZPF.

Table 6: Zonal Protection Factors for Nosocomial Pathogens at Alternate Room Areas

| Pathogen | MERV6+15W | Zonal Protection Factor % | | | | | | |
|------------------------------------|-----------|---------------------------|--------------------|---------------------|---------------------|---------------------|---------------------|---------------------|
| | Removal | Area | Area | Area | Area | Area | Area | Area |
| | % | 50 ft ² | 75 ft ² | 100 ft ² | 125 ft ² | 150 ft ² | 200 ft ² | 300 ft ² |
| Coronavirus (SARS) | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Legionella pneumophila | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Mycobacterium tuberculosis | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Mycoplasma pneumoniae | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Proteus mirabilis | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Pseudomonas aeruginosa | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Serratia marcescens | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Staphylococcus aureus | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Streptococcus pyogenes | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Acinetobacter | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| VZV | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Influenza A virus | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Haemophilus influenzae | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Coxsackievirus | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Parainfluenza virus | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Neisseria meningitidis | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Measles virus | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Staphylococcus epidermis | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Parovirus B19 | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Rhinovirus | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Enterococcus | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Nocardia asteroides | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Mumps virus | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Corynebacterium diphtheriae | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Adenovirus | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Mycobacterium avium | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Klebsiella pneumoniae | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Clostridium difficile spores | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Clostridium perfringens spores | 100.0 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Enterobacter cloacae | 99.9 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Bordetella pertussis | 99.9 | 93 | 92 | 91 | 90 | 88 | 85 | 80 |
| Haemophilus parainfluenzae | 99.8 | 93 | 92 | 91 | 90 | 88 | 85 | 79 |
| RSV | 99.1 | 93 | 92 | 91 | 89 | 88 | 85 | 79 |
| Cryptococcus neoformans spores | 98.1 | 93 | 92 | 90 | 89 | 88 | 85 | 79 |
| Blastomyces dermatitidis spores | 98.1 | 93 | 92 | 90 | 89 | 88 | 85 | 79 |
| Rhizopus spores | 95.2 | 92 | 91 | 90 | 88 | 87 | 84 | 78 |
| Reovirus | 94.9 | 92 | 91 | 90 | 88 | 87 | 84 | 78 |
| Mucor spores | 93.2 | 92 | 91 | 89 | 88 | 86 | 83 | 77 |
| Norwalk virus | 91.8 | 92 | 90 | 89 | 87 | 86 | 83 | 76 |
| Rotavirus | 90.9 | 91 | 90 | 89 | 87 | 86 | 82 | 76 |
| Fusarium spores | 90.8 | 91 | 90 | 89 | 87 | 86 | 82 | 76 |
| Aspergillus spores | 90.6 | 91 | 90 | 89 | 87 | 86 | 82 | 76 |
| Streptococcus pneumoniae | 66.2 | 83 | 81 | 79 | 77 | 74 | 69 | 61 |
| Rubella virus | 57.0 | 78 | 75 | 73 | 70 | 67 | 62 | 53 |
| Average Protection Factor % | | 92.2 | 91.1 | 90.0 | 88.8 | 86.9 | 83.8 | 78.3 |

Summary and Discussion of Analysis Results

The analysis presented herein indicates that the VidaShield will produce high removal rates of all nosocomial pathogens including bacteria, fungi, and viruses. Analysis also shows that the risk of infection in areas where the unit is installed will be considerably reduced, based on predicted reduction in airborne concentrations of microbes. The combination of a 15 W UV lamp, a MERV 6 filter, and an airflow rate of 50 cfm will produce an average removal rates in excess of 97%, in a single pass, for all but two of the pathogens listed in Table 5. Table 7 provides a comparison of unitary UV systems operating between 30-100 cfm arranged in order of UV dose. The VidaShield provides a higher UV dose than most of these systems and has more efficient filtration than all but one of these systems.

Table 7: Comparison of Unitary UV Systems between 30-100 cfm

| Manufacturer | Model | Airflow/CADR | | Prefilter | Primary Filter | UVP W | Dose J/m ² | URV | Notes |
|----------------|----------------------|--------------|---------------------|------------|----------------|-----------|-----------------------|-----------|-------------|
| | | cfm | m ³ /min | | | | | | |
| Virobuster | Steritube | 44 | 1.25 | G4 | none | 57 | 592 | 23 | multispeed |
| Virobuster | Steritube | 59 | 1.67 | G4 | none | 57 | 443 | 22 | multispeed |
| Virobuster | Steritube | 74 | 2.083 | G4 | none | 57 | 355 | 21 | multispeed |
| sterilAir AG | LSK2036-U | 29.2 | 0.83 | none | none | 30 | 315 | 21 | |
| Arcalux | HR Mgt System | 50 | 1.42 | Yes | MERV6 | 15 | 198 | 19 | |
| sterilAir AG | UVR2250-1 | 88 | 2.50 | optional | none | 27 | 190 | 19 | |
| sterilAir AG | LSK2018 | 11.8 | 0.33 | none | none | 7 | 173 | 19 | |
| Holmes Group | BAP920-U | 100 | 2.83 | none | MERV15 | 22 | 69.2 | 17 | PCO |
| Sanuvox | P-900 | 35 | 0.99 | Yes | none | 4.76 | 48 | 15 | multispeed |
| Amcor | AM-45 | 30 | 0.85 | none | none | 1.96 | 26.9 | 13 | |
| Amcor | AM-45C | 31 | 0.88 | Yes | none | 25 | 23.2 | 13 | PCO, carbon |
| Amcor | AM-45C | 40 | 1.13 | Yes | none | 25 | 17.8 | 12 | PCO, carbon |
| Amcor | AM-45C | 45 | 1.27 | Yes | none | 25 | 15.9 | 12 | PCO, carbon |
| Amcor | AM-45 | 60 | 1.70 | none | none | 1.96 | 13.5 | 11 | |

NOTE: CADR is approximately equal to the airflow for all systems.

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Appendix A: Filter Removal Rates of Airborne Nosocomial Pathogens

| Microbe | Type | Size µm | Removal Rate % |
|---------------------------------|----------|------------|----------------|
| | | | MERV 6 |
| Blastomyces dermatitidis spores | Fungi | 12.649 | 50.0 |
| Fusarium spores | Fungi | 11.225 | 50.0 |
| Mucor spores | Fungi | 7.071 | 49.8 |
| Rhizopus spores | Fungi | 6.928 | 49.8 |
| Cryptococcus neoformans spores | Fungi | 4.899 | 48.7 |
| Aspergillus spores | Fungi | 3.354 | 44.8 |
| Clostridium difficile spores | Bacteria | 2 | 33.5 |
| Haemophilus parainfluenzae | Bacteria | 1.732 | 29.7 |
| Enterobacter cloacae | Bacteria | 1.414 | 24.4 |
| Enterococcus | Bacteria | 1.414 | 24.4 |
| Acinetobacter | Bacteria | 1.225 | 20.9 |
| Mycobacterium avium | Bacteria | 1.118 | 18.8 |
| Nocardia asteroides | Bacteria | 1.118 | 18.8 |
| Clostridium perfringens spores | Bacteria | 1 | 16.4 |
| Streptococcus pyogenes | Bacteria | 0.894 | 14.3 |
| Staphylococcus aureus | Bacteria | 0.866 | 13.7 |
| Staphylococcus epidermis | Bacteria | 0.866 | 13.7 |
| Neisseria meningitidis | Bacteria | 0.775 | 11.9 |
| Streptococcus pneumoniae | Bacteria | 0.707 | 10.6 |
| Corynebacterium diphtheriae | Bacteria | 0.698 | 10.4 |
| Klebsiella pneumoniae | Bacteria | 0.671 | 9.9 |
| Mycobacterium tuberculosis | Bacteria | 0.637 | 9.3 |
| Serratia marcescens | Bacteria | 0.632 | 9.2 |
| Legionella pneumophila | Bacteria | 0.52 | 7.2 |
| Proteus mirabilis | Bacteria | 0.494 | 6.8 |
| Pseudomonas aeruginosa | Bacteria | 0.494 | 6.8 |
| Haemophilus influenzae | Bacteria | 0.285 | 4.4 |
| Bordetella pertussis | Bacteria | 0.245 | 4.3 |
| Parainfluenza virus | Virus | 0.194 | 4.5 |
| RSV | Virus | 0.19 | 4.5 |
| Mycoplasma pneumoniae | Bacteria | 0.177 | 4.6 |
| VZV | Virus | 0.173 | 4.7 |
| Mumps virus | Virus | 0.164 | 4.8 |
| Measles virus | Virus | 0.158 | 4.9 |
| Coronavirus (SARS) | Virus | 0.11 | 6.4 |
| Influenza A virus | Virus | 0.098 | 7.1 |
| Adenovirus | Virus | 0.079 | 8.5 |
| Reovirus | Virus | 0.075 | 8.9 |
| Rotavirus | Virus | 0.073 | 9.1 |
| Rubella virus | Virus | 0.061 | 10.6 |
| Norwalk virus | Virus | 0.029 | 18.1 |
| Coxsackievirus | Virus | 0.027 | 18.9 |
| Rhinovirus | Virus | 0.023 | 20.6 |
| Parvovirus B19 | Virus | 0.022 | 21.0 |

Appendix B: UV Disinfection Rates of Airborne Nosocomial Pathogens

| Microbe | Type | UV k m ² /J | UV D90 J/m ² | Disinfection Rate, % |
|---------------------------------|----------|---------------------------|----------------------------|----------------------|
| | | | | 15 W |
| Coronavirus (SARS) | Virus | 0.377 | 6 | 100 |
| Legionella pneumophila | Bacteria | 0.2024 | 11 | 100 |
| Mycobacterium tuberculosis | Bacteria | 0.4721 | 5 | 100 |
| Mycoplasma pneumoniae | Bacteria | 0.2791 | 8 | 100 |
| Proteus mirabilis | Bacteria | 0.289 | 8 | 100 |
| Pseudomonas aeruginosa | Bacteria | 0.5721 | 4 | 100 |
| Serratia marcescens | Bacteria | 0.221 | 10 | 100 |
| Staphylococcus aureus | Bacteria | 0.5957 | 4 | 100 |
| Streptococcus pyogenes | Bacteria | 0.8113 | 3 | 100 |
| Acinetobacter | Bacteria | 0.16 | 14 | 100 |
| VZV (Varicella surrogate k) | Virus | 0.1305 | 18 | 100 |
| Influenza A virus | Virus | 0.119 | 19 | 100 |
| Haemophilus influenzae | Bacteria | 0.11845 | 19 | 100 |
| Coxsackievirus | Virus | 0.111 | 21 | 100 |
| Parainfluenza virus* | Virus | 0.1086 | 21 | 100 |
| Neisseria meningitidis* | Bacteria | 0.1057 | 22 | 100 |
| Measles virus | Virus | 0.1051 | 22 | 100 |
| Staphylococcus epidermis | Bacteria | 0.09703 | 24 | 100 |
| Parvovirus B19 | Virus | 0.092 | 25 | 100 |
| RSV* | Virus | 0.0917 | 25 | 100 |
| Enterococcus* | Bacteria | 0.0822 | 28 | 100 |
| Nocardia asteroides | Bacteria | 0.0822 | 28 | 100 |
| Mumps virus* | Virus | 0.0766 | 30 | 100 |
| Corynebacterium diphtheriae | Bacteria | 0.0701 | 33 | 100 |
| Adenovirus | Virus | 0.054 | 43 | 100 |
| Klebsiella pneumoniae | Bacteria | 0.04435 | 52 | 100 |
| Mycobacterium avium | Bacteria | 0.04387 | 52 | 100 |
| Clostridium difficile spores | Bacteria | 0.0385 | 60 | 100 |
| Clostridium perfringens spores | Bacteria | 0.0385 | 60 | 100 |
| Bordetella pertussis* | Bacteria | 0.0364 | 63 | 100 |
| Enterobacter cloacae | Bacteria | 0.03598 | 64 | 100 |
| Haemophilus parainfluenzae* | Bacteria | 0.03 | 77 | 100 |
| Rotavirus | Virus | 0.02342 | 98 | 99 |
| Cryptococcus neoformans spores | Fungi | 0.0167 | 138 | 96 |
| Blastomyces dermatitidis spores | Fungi | 0.01645 | 140 | 96 |
| Reovirus | Virus | 0.01459 | 158 | 94 |
| Rhinovirus* | Virus | 0.0142 | 162 | 94 |
| Norwalk virus* | Virus | 0.0116 | 198 | 90 |
| Mucor spores | Fungi | 0.01012 | 228 | 87 |
| Aspergillus spores | Fungi | 0.00894 | 258 | 83 |
| Rhizopus spores | Fungi | 0.00861 | 267 | 82 |
| Fusarium spores | Fungi | 0.00855 | 269 | 82 |
| Streptococcus pneumoniae | Bacteria | 0.00492 | 468 | 62 |
| Rubella virus* | Virus | 0.0037 | 622 | 52 |
| UV Dose, J/m ² | | 198 | | |

Note: Asterisk means the UV rate constant is a predicted value based on the complete genome.

Appendix C: Combined Single Pass Removal Rates

| Microbe | Component Removal Rates | | Overall Removal Rates |
|---------------------------------|-------------------------|----------|-----------------------|
| | MERV 6 | 15 W | MERV 6 + 15 W |
| | fraction | fraction | % |
| Coronavirus (SARS) | 0.0643 | 1.0000 | 100.0 |
| Legionella pneumophila | 0.0721 | 1.0000 | 100.0 |
| Mycobacterium tuberculosis | 0.0925 | 1.0000 | 100.0 |
| Mycoplasma pneumoniae | 0.0464 | 1.0000 | 100.0 |
| Proteus mirabilis | 0.0680 | 1.0000 | 100.0 |
| Pseudomonas aeruginosa | 0.0680 | 1.0000 | 100.0 |
| Serratia marcescens | 0.0916 | 1.0000 | 100.0 |
| Staphylococcus aureus | 0.1372 | 1.0000 | 100.0 |
| Streptococcus pyogenes | 0.1428 | 1.0000 | 100.0 |
| Acinetobacter | 0.2089 | 1.0000 | 100.0 |
| VZV | 0.0469 | 1.0000 | 100.0 |
| Influenza A virus | 0.0709 | 1.0000 | 100.0 |
| Haemophilus influenzae | 0.0443 | 1.0000 | 100.0 |
| Coxsackievirus | 0.1886 | 1.0000 | 100.0 |
| Parainfluenza virus | 0.0447 | 1.0000 | 100.0 |
| Neisseria meningitidis | 0.1190 | 1.0000 | 100.0 |
| Measles virus | 0.0493 | 1.0000 | 100.0 |
| Staphylococcus epidermis | 0.1372 | 1.0000 | 100.0 |
| Parovirus B19 | 0.2104 | 1.0000 | 100.0 |
| RSV | 0.0450 | 1.0000 | 100.0 |
| Enterococcus | 0.2442 | 1.0000 | 100.0 |
| Nocardia asteroides | 0.1879 | 1.0000 | 100.0 |
| Mumps virus | 0.0483 | 1.0000 | 100.0 |
| Corynebacterium diphtheriae | 0.1040 | 1.0000 | 100.0 |
| Adenovirus | 0.0853 | 1.0000 | 100.0 |
| Mycobacterium avium | 0.1879 | 0.9998 | 100.0 |
| Klebsiella pneumoniae | 0.0988 | 0.9998 | 100.0 |
| Clostridium difficile spores | 0.3353 | 0.9995 | 100.0 |
| Clostridium perfringens spores | 0.1643 | 0.9995 | 100.0 |
| Enterobacter cloacae | 0.2442 | 0.9992 | 99.9 |
| Bordetella pertussis | 0.0431 | 0.9993 | 99.9 |
| Haemophilus parainfluenzae | 0.2973 | 0.9974 | 99.8 |
| Rotavirus | 0.0913 | 0.9903 | 99.1 |
| Cryptococcus neoformans spores | 0.4872 | 0.9634 | 98.1 |
| Blastomyces dermatitidis spores | 0.5000 | 0.9615 | 98.1 |
| Rhinovirus | 0.2057 | 0.9399 | 95.2 |
| Reovirus | 0.0892 | 0.9444 | 94.9 |
| Mucor spores | 0.4983 | 0.8652 | 93.2 |
| Norwalk virus | 0.1809 | 0.8994 | 91.8 |
| Rhizopus spores | 0.4981 | 0.8182 | 90.9 |
| Fusarium spores | 0.5000 | 0.8160 | 90.8 |
| Aspergillus spores | 0.4476 | 0.8297 | 90.6 |
| Streptococcus pneumoniae | 0.1057 | 0.6225 | 66.2 |
| Rubella virus | 0.1062 | 0.5193 | 57.0 |