

MICROORGANISM LOW-UVC SUSCEPTIBILITY FACTORS

Assuming first-order rate constant and kinetics,¹ microorganism susceptibility to low-UVC is characterized by:

$$C(t) = C_0 \bullet \exp(-Kd)$$

where C(t) is the concentration of active microorganisms surviving after low-UVC exposure, C₀ is the initial concentration, K is the microorganism susceptibility factor (m²/J), and d is the delivered low-UVC dose (J/m²). The following table includes 254 nm low-UVC susceptibility factors, K (m²/J) for various microorganisms:

Microorganism *	Type	K, m ² /J	Microorganism *	Type	K, m ² /J
SARS-CoV-2 (COVID-19) (agar)	Virus	0.098-0.23	Sarcina lutea	Bacteria	0.012
MS2 (agar/aerosol)	Virus	0.099-0.56	Serratia marcescens	Bacteria	0.095
phi X174 (agar/aerosol)	Virus	0.099-0.56	Shigella paradysenteriae	Bacteria	0.141
Influenza A (aerosol)	Virus	0.26	Shigella sonnei	Bacteria	0.077
H1N1 (aerosol)	Virus	0.26	Spirillum rubrum	Bacteria	0.053
phi 6 (aerosol)	Virus	0.31	Staphylococcus albus	Bacteria	0.126
T7 (aerosol)	Virus	0.31	Staphylococcus aureus	Bacteria	0.086
Hepatitis A	Virus	0.032	Streptococcus faecalis	Bacteria	0.052
Polio virus	Virus	0.040	Streptococcus hemolyticus	Bacteria	0.106
Rotavirus	Virus	0.028	Streptococcus lactus	Bacteria	0.037
Bacillus anthracis	Bacteria	0.051	Streptococcus viridans	Bacteria	0.115
B. megatherium sp. (spores)	Bacteria	0.084	Sentertidis	Bacteria	0.057
B. megatherium sp. (veg)	Bacteria	0.178	Vibrio cholerae (V.comma)	Bacteria	0.066
B. paratyphosus	Bacteria	0.072	Yersinia enterocolitica	Bacteria	0.209
B. subtilis	Bacteria	0.032	Bakers' yeast	Yeast	0.060
B. subtilis spores	Bacteria	0.019	Brewers' yeast	Yeast	0.070
Campylobacter jejuni	Bacteria	0.209	Common yeast cake	Yeast	0.038
Clostridium tetani	Bacteria	0.019	Saccharomyces cerevisiae	Yeast	0.038
Corynebacterium diphtheriae	Bacteria	0.069	Saccharomyces ellipsoideus	Yeast	0.038
Dysentery bacilli	Bacteria	0.105	Saccharomyces sp.	Yeast	0.029
Eberthella typhosa	Bacteria	0.108	Aspergillus flavus	Mold	0.003
Escherichia coli	Bacteria	0.077	Aspergillus glaucus	Mold	0.004
Klebsiella terrifani	Bacteria	0.089	Aspergillus niger	Mold	0.0014
Legionella pneumophila	Bacteria	0.256	Mucor racemosus A	Mold	0.013
Micrococcus candidus	Bacteria	0.038	Mucor racemosus B	Mold	0.013
Micrococcus sphaeroides	Bacteria	0.023	Oospora lactis	Mold	0.046
Mycobacterium tuberculosis	Bacteria	0.038	Penicillium digitatum	Mold	0.004
Neisseria catarrhalis	Bacteria	0.053	Penicillium expansum	Mold	0.018
Phytomonas tumefaciens	Bacteria	0.053	Penicillium roqueford	Mold	0.018
Pseudomonas aeruginosa	Bacteria	0.042	Rhizopus nigricans	Mold	0.002
Pseudomonas fluorescens	Bacteria	0.065	Rhizopus nigricans	Mold	0.002
Proteus vulgaris	Bacteria	0.086	Cryptosporidium parvum	Protozoa	0.092
Salmonella enteritidis	Bacteria	0.058	Giardia lamblia	Protozoa	0.209
Salmonella paratyphi	Bacteria	0.072	Blue green	Algae	0.0008
Salmonella typhimurium	Bacteria	0.029	Chlorella vulgaris	Algae	0.019

* Higher K values mean more susceptible. **Bold entries with shaded cells** are from Table 6 in Preventing respiratory infections: A unified dose model and IAQ risk assessment tool by LUV Systems, Inc. (December 2021). All others are from Section 2.2 in Ultraviolet purification application information by Koninklijke Philips Electronics N.V. (November 2006). K values that are provided as ranges represent different substrates including aerosols or various surfaces. As the substrate can significantly affect microorganism susceptibility to low-UVC light (due to shielding), it is noted the Philips reference does not identify the substrate associated with each K value. This is an important qualifier as the measured dose is not necessarily the same as the dose physically received by a given pathogen.

¹ <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7176239/#po=17.0588>

