Poultry processing plants and slaughterhouses produce huge quantities of feathers and hair/bristle waste annually. These keratinaceous wastes are highly resistant to degradation. *Onygena corvina*, a non-pathogenic fungus, grows specifically on feathers, hooves, horn, and hair in nature. Hence, the proteases secreted by *O. corvina* are interesting in view of their potential relevance for industrial decomposition of keratinaceous wastes. We sequenced and assembled the genome of *O. corvina* and used a method called peptide pattern recognition to identify 73 different proteases. Comparative genome analysis of proteases in keratin-degrading and non-keratin-degrading fungi indicated that 18 putative secreted proteases from four protease families (M36, M35, M43, and S8) may be responsible for keratin decomposition. Twelve of the 18 predicted protease genes could be amplified from *O. corvina* grown on keratinaceous materials and were transformed into *Pichia pastoris*. One of the recombinant proteases belonging to the S8 family showed high keratin-degrading activity. Furthermore, 29 different proteases were identified by mass spectrometry in the culture broth of *O. corvina* grown on feathers and bristle. The culture broth was fractionated by ion exchange chromatography to isolate active fractions with five novel proteases belonging to three protease families (S8, M28, and M3). Enzyme blends composed of three of these five proteases, one from each family, showed high degree of degradation of keratin in vitro. A blend of novel proteases, such as those we discovered, could possibly find a use for degrading keratinaceous wastes and provide proteins, peptides, and amino acids as valuable ingredients for animal feed.