ABSTRACT
The cloning of all functional human odorant receptor genes is an essential step in understanding the specificity of receptor-ligands and the combinatorial encoding of olfaction stimuli.

INTRODUCTION
Cannabinoids are the main psychoactive substances found in cannabis.

Cannabinoids bind to cannabinoid receptors in the central nervous system (CNS) to produce a high of euphoria and relaxation.

Cannabinoids also have a number of other effects.

In addition to the psychotropic and appetite-stimulating properties of cannabinoids, there are also many potential uses for cannabis.

In this paper, we will be discussing the human olfactory receptor repertoire (HER2) and its role in the regulation of odour perception and behaviour.

As most odour-related research focuses on the effects of cannabinoids in the olfactory system, we will be discussing its role in the regulation of smell perception and behaviour.

We will be focusing on HER2 in the context of the interaction between the olfactory system and In mammals, olfaction is a major neurosensory function that involves identifying external chemical compounds. The first step in detecting smells is the interaction of an animal with odorant receptors expressed at different sites on their bodies.
Seven-transmembrane ORs were identified as being the largest family of genes in vertebrates, comprising of Class I or A or more (reviewed in 1991), and can include classical G-protein-coupled receptor types such as opsins and catecholamine receptor levels to identify specific categories of the same molecules. The genes that make up the ORs do not have introns present in their coding regions. Mammalian OR genes are usually found in sets of ten or more members and located on multiple chromosomes. The majority of human OR (hOR) genes encode pseudogenes, which suggests that olfaction played a less significant role in primate evolution. However, some research indicates that 70% of all hO receptor genes may be pseudogènes instead of rodents or lower primates. The recent publication of incomplete compilations of hORs, including approximately 150 full-length receptor genes, has led to the development of annotated sets of OR genes and their products. The release of the first draft of this sequence by two groups opens up the possibility of comprehensive identification, mapping, and analysis of these products in the near future. One of those groups reported that the human genome contains 906 OR gene(s), of which approximately 60% appear to be pseudogenes. Various labs have proposed alternative nomenclatures for a more conventional nomologia for such as at least Prior to studying the rational structure-function of this extensive receptor family, it is essential to identify, clone and classify candidate hORs through a combination of identification, sequence analysis, and comparison with available unannotated raw sequences. We aimed to determine the complete set of inherited HHOR genes by using reiterative homology searches of GenBank DNA and compiling with other public databases. Finally, we reported the Cloning of 347 putative full-length (OR) HORRRRENTLY OR (OHOR

## CONCLUSION

Remarkable conclusions The functional hOR repertoire's identification and cloning provide a framework for addressing many unresolved issues in human olfactory behavior. This will, combined with robust heterologous expression and assay systems and high-throughput screening of odorant libraries, help us gain broader access to structures-function relationships and small-molecule recognition by this large group of G-protein-coupled receptors. Another exciting area of interest is the impact of genetic polymorphism of ORs on human Oleptic resistance syndrome. Disorder disorders.