

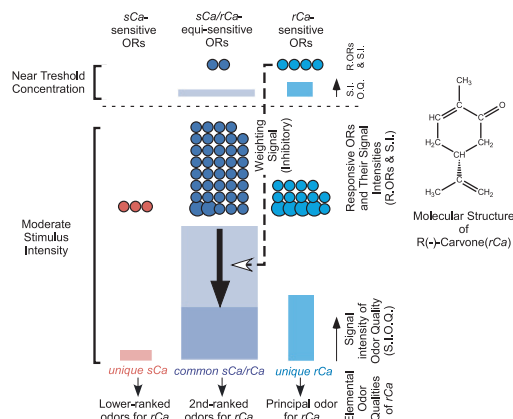
# Hierarchical Odor Coding in Receptors

- Biological system may be designed to extract common or unique information of objects -

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The basic question is what mechanism enables us to discriminate different odors. We suppose that the brain genetically functions to find common information and unique information between different objects, based on an informational factorization at receptors. Here, we describe a sensitivity-dependent hierarchical odor coding in receptors. The most-sensitive receptors encode the principal odor qualities, and the less-sensitive receptors encode supplementary odor qualities of the odorant. The receptors preferably sensitive to either S(+)-carvone (sCa) or R(-)-carvone (rCa) could represent the unique odor qualities of caraway or spearmint, respectively; those equally sensitive to both enantiomers could represent the fresh herbal quality common to both. In the hierarchical receptor codes, multiple subordinate odor qualities encoded by common receptors or less-sensitive receptors are reduced in an overall odor identity representation by signal weighting governed by the most-sensitive receptors. (OR: Odorant receptor.)



Schematic diagram of receptor-sensitivity-dependent hierarchical odor coding

# Development of a Novel Profile-Profile Comparison System, FORTE1

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We have developed a novel profile-profile comparison technique to increase the sensitivity of fold recognition and improve alignment accuracy. The FORTE1 program has distinct features of measuring similarity between two profiles as compared with other published methods which exploit alignment information. The FORTE1 program utilizes the sequence profiles of both a target and templates to predict the structure of target sequence. With the Magi cluster (<http://www.cbrc.jp/magi/>), we performed PSI-BLAST iterations maximally 20 times to prepare the profiles of both target and templates with the NCBI non-redundant database. FORTE1 is available at <http://www.cbrc.jp/forte1/>.

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**FORTE1**

NOTE: This is an experimental version of FORTE server.  
The output format is designed for CAFASE3, now.

Upload your sequence file and then click "set" button:  
Set Clear Done

OR

Enter your sequence:  
Please use FASTA or pure amino acid format (1400 Residue Maximum).

Enter a one-line description of your sequence:

Enter your e-mail address (where the results will be sent to):

SEARCH! All Clear

Internet N. Tomii (in preparation)

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The submission form of FORTE1