

# Resource Summary Report

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## Combinatorial Extension (CE)

RRID:SCR\_007585

Type: Tool

### Proper Citation

Combinatorial Extension (CE) (RRID:SCR\_007585)

### Resource Information

**URL:** <http://source.rcsb.org/jfatcatserver/ceHome.jsp>

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**Description:** CE is a databases of alignments for all polypeptide chains. A representative set of proteins is available and kept current with the PDB, a method for calculating pairwise structure alignments. CE aligns two polypeptide chains using characteristics of their local geometry as defined by vectors between C alpha positions. Matches are termed aligned fragment pairs (AFPs). Heuristics are used in defining a set of optimal paths joining AFPs with gaps as needed. The path with the best RMSD is subject to dynamic programming to achieve an optimal alignment. For specific families of proteins additional characteristics are used to weight the alignment. Complete details are described in the paper (PDF format). Databases of alignments for all polypeptide chains and a representative set of proteins is available and kept current with the PDB

**Abbreviations:** CE

**Synonyms:** Combinatorial extension

**Resource Type:** database, data or information resource

**Keywords:** polypeptide, polypeptide chain, protein, protein alignment, protein structure

**Resource Name:** Combinatorial Extension (CE)

**Resource ID:** SCR\_007585

**Alternate IDs:** nif-0000-02648

**Old URLs:** <http://cl.sdsc.edu/ce.html>

**Record Creation Time:** 20220129T080242+0000

**Record Last Update:** 20260803T040514+0000

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## Ratings and Alerts

No rating or validation information has been found for Combinatorial Extension (CE).

No alerts have been found for Combinatorial Extension (CE).

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [ASWG](#) .

Mohamed NA, et al. (2012) Homology Modeling of Coagulase in Staphylococcus aureus. Bioinformation, 8(9), 412.

Sahay A, et al. (2010) Structure prediction of dihydroflavonol 4- reductase and anthocyanidin synthase from spinach. Bioinformation, 5(6), 259.

Hambarde S, et al. (2010) Predictive inference on cytoplasmic and mitochondrial thioredoxin peroxidases in the highly radioresistant Lepidopteran insect Spodoptera frugiperda. Bioinformation, 4(9), 399.

Sierk ML, et al. (2010) Improving pairwise sequence alignment accuracy using near-optimal protein sequence alignments. BMC bioinformatics, 11, 146.

Cherkasov A, et al. (2004) An approach to large scale identification of non-obvious structural similarities between proteins. BMC bioinformatics, 5, 61.