

Pfam 34.0 (March 2021, 19179 entries)

The Pfam database is a large collection of protein families, each represented by **multiple sequence alignments** and **hidden Markov models (HMMs)**. [More...](#)

配列からドメインを検索する
(指定すると入力の枠が表示される)

UniProtなどの配列ID
からドメインを検索する

PDBの構造IDから
ドメインを検索する

キーワードから検索する

QUICK LINKS

[SEQUENCE SEARCH](#)

[VIEW A PFAM ENTRY](#)

[VIEW A CLAN](#)

[VIEW A SEQUENCE](#)

[VIEW A STRUCTURE](#)

[KEYWORD SEARCH](#)

[JUMP TO](#)

ANALYZE YOUR PROTEIN SEQUENCE FOR PFAM MATCHES

Paste your protein sequence here to find matching Pfam entries.

Go

Example

This search will use an E-value of 1.0. You can set your own search parameters and perform a range of other searches [here](#).

Recent Pfam [blog](#) posts

Hide this

[Google Research Team bring Deep Learning to Pfam](#) (posted 24 March 2021)

We are delighted to announce the first fruits of a collaboration between the Pfam team and a Google Research team led by Dr Lucy Colwell, with Maxwell Bileschi and David Belanger. In 2019, Colwell's team published a preprint describing a new deep learning method that was trained on Pfam data, and which improves upon the [...]

図3.16 Pfamのトップページ