

'Roxygen documentation for file motif_search.R '

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motif_search	<i>Motif search around PASs</i>
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Description

Enrichment of motifs around PASs

Usage

```
motif_search(PASs.gr, flanking = 550, motif = "GAY")
```

Arguments

PASs.gr	A GRanges object containing exact positions of PASs as single nucleotide region. A metadata column called "PAS.type" is required for each region and should be either sPAS, pPAS or dPAS.
flanking	The number of flanking nucleotides that should be included upstream and downstream.
motif	The motif to be searched.

Details

For each PAS of a certain PAS type a window is opened in which the desired motif is searched. RNAmaphs are generated across all PASs of a certain PAS type.

Value

RNAmaph plot

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