

'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. RNAmaps are generated across all PASs of a certain PAS type.

Value

RNAmap plot

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