

ANEXO

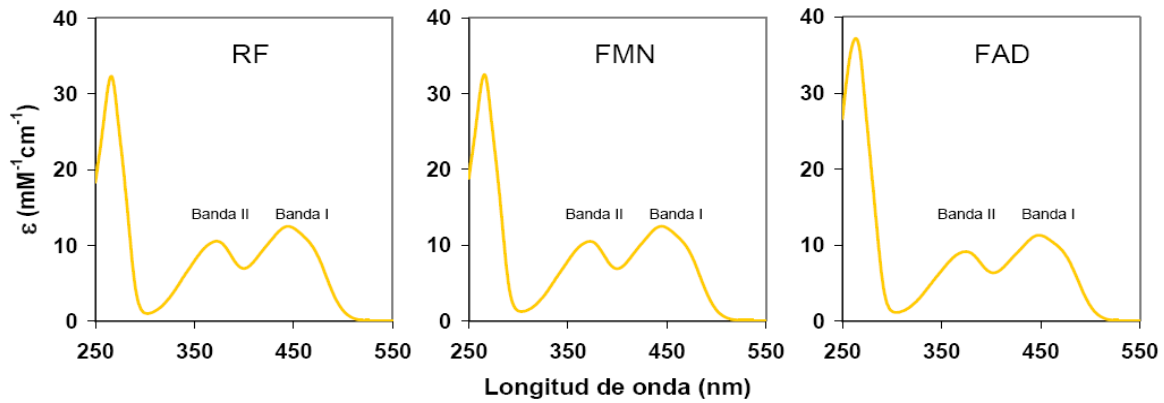


FIGURA 1.1.3. ESPECTROS DE ABSORCIÓN DE RF, FMN Y FAD EN ESTADO OXIDADO NEUTRO.



FIGURA 1.2.1. MODELO ESTRUCTURAL DE LA FADS DE *STREPTOCOCCUS PNEUMONIAE* (SPFADS). EL PREGAMIENTO DEL MÓDULO FMNAT SE MUESTRA EN ROJO Y EL DEL MÓDULO RFK EN AZUL.

The image shows a screenshot of the SWISSDOCK web interface with three main sections: Target selection, Ligand selection, and Description. Red arrows point from specific input fields to labels on the right side of the page.

Target selection

Search for targets:

ie. PDB code, protein name, sequence, or URL
or upload file (max 5MB)

Ligand selection

Search for ligands:

ie. ZINC AC, ligand name or category (like scaffolds or sidechains), or URL
or upload file (max 5MB)

Description

Job name (required):

E-mail address (optional):

Hide extra parameters

Docking type

Definition of the region of interest

X center: Y center: Z center:
X size: Y size: Z size:

Flexibility

Labels on the right side of the page:

- Proteína
- Ligando/molécula pequeña
- Nombre trabajo
- E-Mail

Red arrows indicate the following connections:

- From the 'Search' button in the 'Target selection' section to 'Proteína'.
- From the 'Search' button in the 'Ligand selection' section to 'Ligando/molécula pequeña'.
- From the 'Job name' input field to 'Nombre trabajo'.
- From the 'E-mail address' input field to 'E-Mail'.

FIGURA 3.2.2 DE LA PAGINA DEL SWISSDOCK DONDE SE MUESTRAN CADA UNA DE LAS PARTES PARA ENVIAR UN DOCKING.

CLUSTAL O(1.2.1) multiple sequence alignment

```

CaFADs      --MDIWYGTAAVPKDLNSAVTIGVFDGVHRGHQKLINATVEKAREVGAKAIMVTFDHPH
SpFADs      MIITIPKIQKDIGTPSDSVVVLGYFDGIHKGHQELFRVANKAARKDLLPIVVMTFNESP
              : *      .      .:*.*.:* ***:*:***:*.:.: : **:      :*:*: *

CaFADs      VSVFLPRRAPLG--ITTLAERFALAESFGIDGVLVIDFTRELSGTSPEKYVEFLLEDTLH
SpFADs      KIALEPYHPDLFLHILNPAERERKLRKREGVEELYLLDFSSQFASLTAQEFFATYI-KAMN
              .: * : * * . ***      : *:: :*:*: :*: . : :*: . :*.

CaFADs      ASHVVGANFTFGENAAGTADSLRQICQSRLTVDVIDLLDDEGVRISSSTTVREFLSEGDV
SpFADs      AKIIVAGFDYTFGSDKKAED-LKNYFDG--EVIIVPPVEDEKKGKISSSTRIRQAILDGNV
              *. :*. * :*:*.: : * *:: :. * : : :*: :**** :*: : :*:

CaFADs      ARANWALGRHFYVTGPVVRGAGRGGKELGFPTANQYFHDTVALPADGVYAGWLTILPTEA
SpFADs      KEAGKLLGAPLPSRGMVVHGNAE-GRTIGYPTANLVLLDRTYMPADGVYVVDVEIQ----
              .* ** : * **:* .* *: :*:*** : * . :*****. : *

CaFADs      PVSGNMEPEVAYAAAI SVGTNPTFGDEQRSVESFVLDLRDADLYGHDVKVEFVDHVRAMEK
SpFADs      -----RQKYRAMASVGKNVTFDGEARFEVNI FDFNQDIYGETVMVYWLDRI RDMTK
              . * * ***.* ** *: .* :*: :*:*. * * :*:*: * *

CaFADs      FDSVEQLLEVMAKDVQKTRTLLAQDVQAHKMAPETYFLQAES
SpFADs      FDSVDQLVDQLKADEEVTRNWS-----
              ****:***: : * : **
    
```

FIGURA 4.1.1.2 : ALINEAMIENTO ESTRUCTURAL ENTRE LA SPFADS Y CAFADS.