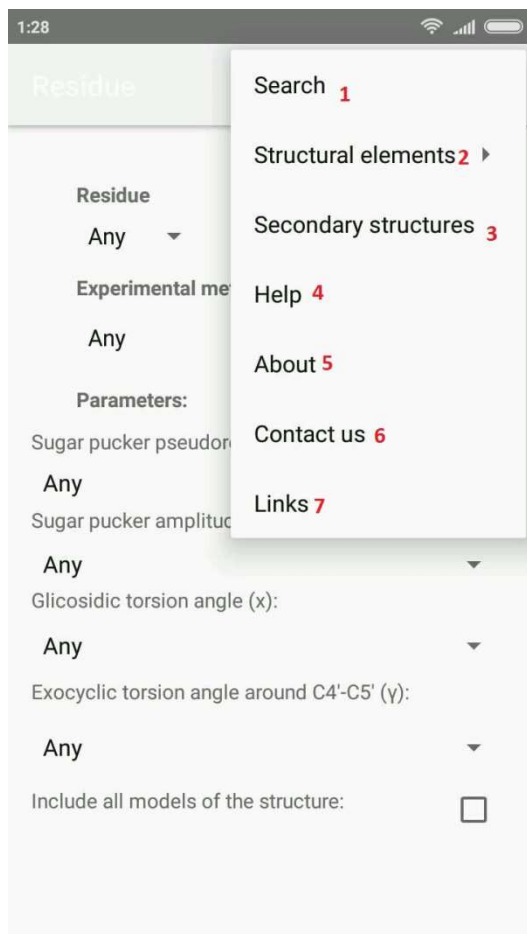


Interface RNA Frabase Instruction Manual

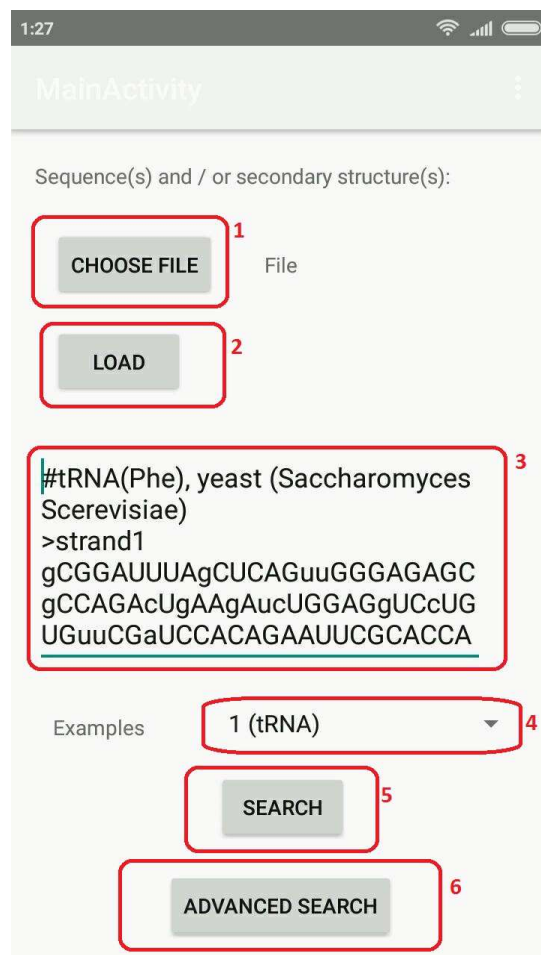


Menu:

- 1- Search – moves to Search Activity (I.)
- 2- Structural elements – Opens a submenu of structural elements(II).
- 3- Secondary Structures – Displays a complete list of secondary structures.
- 4- Help – Displays helpful information about the application and how to operate it
- 5- About – Displays other information about the app
- 6- Contact us – Allows you to send a message to RNA Frabase directly through the app
- 7- Links – displays a list of helpful and/or interesting links.

I. Search Activity:

- 1- Choose File button. Let u choose file.
- 2- Load button. Loads the chosen file. User must first choose(1) a file to load.
- 3- Text field. Input the sequence or secondary structure you want to process in this field.
- 4- Drop-down list of examples to choose.
- 5- Search button. Searches for the text in field (3) in the RNA Frabase.
- 6- Advanced Search button. Enables additional search options.



II. Structural elements.

-Residue, Base Pair, Loop, Multiplet, Dinuclear Step, Stem

1- Search button. Starts a search for specified data in the RNA Frabase

2- Drop-down list that allow for selection of an existing value or range of values

3- Checkboxes – check to enable corresponding option, uncheck to disable it

4- Text fields – enter specific values to search for

Residue

SEARCH 1

Residue 2

Any 2

Experimental method: 2

Any 2

Parameters:

Sugar pucker pseudorotation phase angle (P): 2

Any 2

Sugar pucker amplitude (Tm): 2

Any 2

Glicosidic torsion angle (x): 2

Any 2

Exocyclic torsion angle around C4'-C5' (y): 2

Any 2

Include all models of the structure: 3

☐

Basepair

SEARCH 1

Associated residues 1

Residue of the 1st strand: 2

Any 2

Residue of the 2nd strand: 2

Any 2

Experimental method:

Any

Base pairs classification

Westhof's notation: 2

Any 2

Saenger's notation: 2

Any 2

Base-base parameters

Shear (Sx): 2

Any 2

Stretch (Sy): 2

Any 2

Stagger (Sz): 2

Any 2

Buckle (κ): 2

Any 2

Propeller (ω): 2

Any 2

Opening (σ): 2

Any 2

Include all models of the structure: 3

☐

Loop

SEARCH 1

Experimental method 2

Any 2

Parameters

Case sensitive (modified residues sensitive search): 3

☐

Strand shift operation: 3

☐

Loop strand

Length: 4

Sequence (optional):

Define another sequence: 3

☐

☐

Include all models of the structure:

☐

2:18

Multiplet

SEARCH 1

Associated residues

Residue of the 1st strand: Any 2

Residue of the 2nd strand: Any

Residue of the 3rd strand: Any

Experimental method

Any 2

Include all models of the structure: ☐ 3

2:18

Stem

SEARCH 1

Experimental method

Any 2

Case sensitive (modified residues sensitive search): ☐ 3

Stem length

Exact length 4

length: _____

Sequence

First strand: _____

Second strand (optional): _____

Include all models of the structure: ☐ 3

2:18

DinuclStep

SEARCH 1

First basepair

Residue of the 1st strand: Any 2

Residue of the 2nd strand: Any

Second base pair

Residue of the 1st strand: Any

Residue of the 2nd strand: Any

Experimental method

Any

Inter base pair parameters

Shift (Dx): Any 2

Slide (Dy): Any

Rise (Dz): Any

Tilt (τ): Any

Roll (ρ): Any

Twist (Ω): Any

Include all models of the structure: ☐ 3

On pictures (top to bottom, left to right):
Residue, Base Pair, Loop, Multiplet,
Dinuclear Step and Stem screens