

Figure 1. TM-Aligner Homepage.

The screenshot shows the TM-Aligner homepage with several key elements highlighted by red arrows and letters:

- A**: Points to the 'Aligner' button in the top navigation bar.
- B**: Points to the large text area for pasting or uploading sequences.
- C**: Points to the 'Choose File' button for uploading a FASTA file.
- D**: Points to the dropdown menu for selecting an exchange weights matrix (currently set to Gonnet250).
- E**: Points to the input field for the gap open penalty (set to 8).
- F**: Points to the input field for the gap extension penalty (set to 1).
- G**: Points to the input field for an optional email ID.
- H**: Points to the 'RUN TM-ALIGNER' button.
- I**: Points to the 'RESET' button.
- J**: Points to the 'RUN WITH SAMPLE DATA' button.
- K**: Points to the 'Other MSA tools' section, which lists alternative tools like PralineTM, TM-Coffee, PROMALS, TM-align, Kalign, ClustalW, Muscle, and Mafft.

At the bottom of the page, there is a footer with the text: 'TM-Aligner Server is hosted by the Department of Natural Sciences, Shiv Nadar University' and 'If you are experiencing problems with the site, please contact the webmaster.'

TM-Aligner homepage consists of several section each performs a specific set of functions:

- 1). Common header (A) helps user to navigate through web server.
- 2). Input sequences are either pasted in the text-area provided at (B), or can be uploaded using 'Choose file' option at (C). Remember input sequences should be in fasta format without special characters, numbers and non-amino acid characters. Input file/sequences are checked for number of sequences (5000) and size (2MB) before submitting to server (for aligning more than 5000 sequences please contact webmaster). TM-Aligner accepts .fa/.fasta/.txt/.afasta file formats only.
- 3). TM-Aligner offers selection of the available Residue Exchange Matrices for scoring the alignments, including Dayhoff's PAM250 log odds matrix, BLOSUM62, PHAT (Default) a transmembrane-specific substitution matrix and GONNET250, user can select Exchange weights matrix using drop-down box provided in section (D).
- 4). User can also change Gap opening penalty (default:8) and Gap Extension (default:1) penalties from section (E) and (F).
- 5). User can specify email id at section (G) which will be used for forwarding result after job

completion.

6). 'RUN TM-Aligner' button is being provided at (H) for submitting sequences to server. User can clear form using 'RESET' button at (I).

7). Section (J) contain button to run TM-Aligner with sample data and default parameters (Exchange matrix : PHAT, Gap Open penalty 8 & Gap Extension penalty 1).

8). Links to other alignment tools are provided in section (K).

Figure 2. TM-Aligner Result-page

The screenshot shows the TM-Aligner result page. At the top, there is a link 'Click here to download alignment and TM-info' with a red arrow pointing to it labeled 'A'. Below this, the text 'Sequences are:' is followed by a list of sequences with checkboxes. A red arrow labeled 'B' points to these checkboxes. The sequences are displayed in a multi-colored alignment format. Below the sequences, there is a 'Sort Region' slider set to 'Sort from 1 to 524'. A red arrow labeled 'C' points to the slider. Below the slider, there are buttons for 'Sort', 'Delete Selected', and 'Export Selected'. A red arrow labeled 'D' points to the 'Sort' button, 'E' to 'Delete Selected', and 'F' to 'Export Selected'. Below these buttons, there are checkboxes for 'Zappo', 'Dotify', and 'Do not colour dots'. A red arrow labeled 'G' points to the 'Export Selected' button. At the bottom of the page, there is a footer with a 'TM-Aligner' logo and a 'RESET' button. A red arrow labeled 'H' points to the logo, and 'I' to the 'RESET' button. To the right, there is a link to the webmaster. A red arrow labeled 'J' points to the footer text, and 'K' to the webmaster link.

TM-Aligner Output-page

1). Link is provided at section (A) to download result and visualization transmembranes using TM-Info link.

2). Check-boxes are provided at (B) to select/de-select sequences either to download, delete or export sequences to other server(s) using (F) and (G).

3). Sequence portion or complete sequence is selected using slider provided at (C) to sort sequences, residues selected for sorting are shown at (E) and sorting is being performed using (D).

4). Alignment visualization schema can be changed with the help of drop-down box available at section (H). For better visualization check-boxes at (I) and (J) are provided to replace repeated residues with dots and to change coloring schema.

5). Direct link to webmaster is given in section (K).

Figure 3. TM-Info page

TM-Aligner

Sequence Visualization

The screenshot shows the TM-Aligner interface. At the top, there is a 'DOWNLOAD TM-INFO' button. Below it, the sequence '>5HT2B_HUMAN' is displayed. A table lists 14 regions with their residue ranges and corresponding amino acid sequences. The regions are categorized as 'outside', 'TMhelix', or 'inside'. The sequences are shown in a box with a wavy line representing the TM region. A red arrow labeled 'A' points to the '>5HT1B_HUMAN' label, another red arrow labeled 'B' points to the '>5HT2B_HUMAN' label, and a third red arrow labeled 'C' points to the 'DOWNLOAD TM-INFO' button.

Region	Residue	Seq
outside	1 to 58	MALSYRVSELQSTIPEHIQ
TMhelix	59 to 81	LLILMVIIPTIGGNTLVILAVSL
inside	82 to 92	EKKLQYATNYF
TMhelix	93 to 115	LMSLAVADLLVGLFVMPIALI
outside	116 to 129	MFEAMWPLPLVLCF
TMhelix	130 to 149	AWLFLDVLFFSTASIMHLCAI
inside	150 to 169	SVDRYIAIKKPIQANQYNSR
TMhelix	170 to 192	ATAFIKITVVWLISIGIAPVPI
outside	193 to 216	KGIETDVDNPNNITCVLTKE
TMhelix	217 to 239	FMLFGSLAAFFTPLAIMIVTY
inside	240 to 326	TIHALQKKAYLVKNKPPQRI
TMhelix	327 to 349	GIVFFLLMLMWC PFFITNITL
outside	350 to 363	CDSCNQTTLQMLLE
TMhelix	364 to 383	IFVWIGYVSSGVNPLVYTLF
inside	384 to 481	NKTFRDAFGRYITCNYRATI

- 1). Input sequences goes at section (A).
- 2). Section (B) provides meta info about input sequence (s) like location of TM regions, TM sequences etc.
- 3). User can download TM-Info in MS-Excel from section (C).