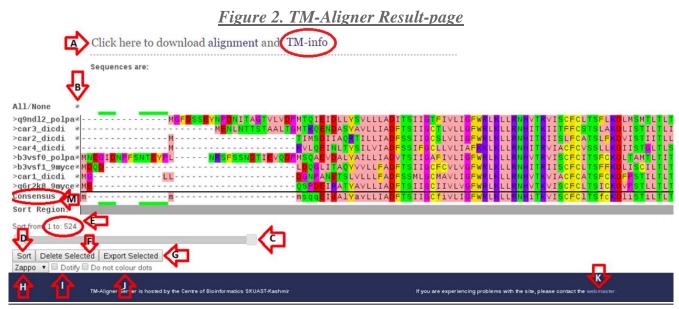*Figure 1. TM-Aligner Homepage.*



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).

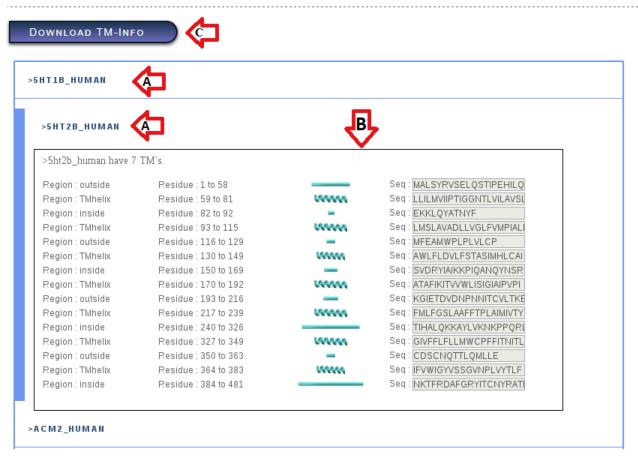8). Links to other alignment tools are provided in section (**K**).

*Figure 2. TM-Aligner Result-page*



*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



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**).