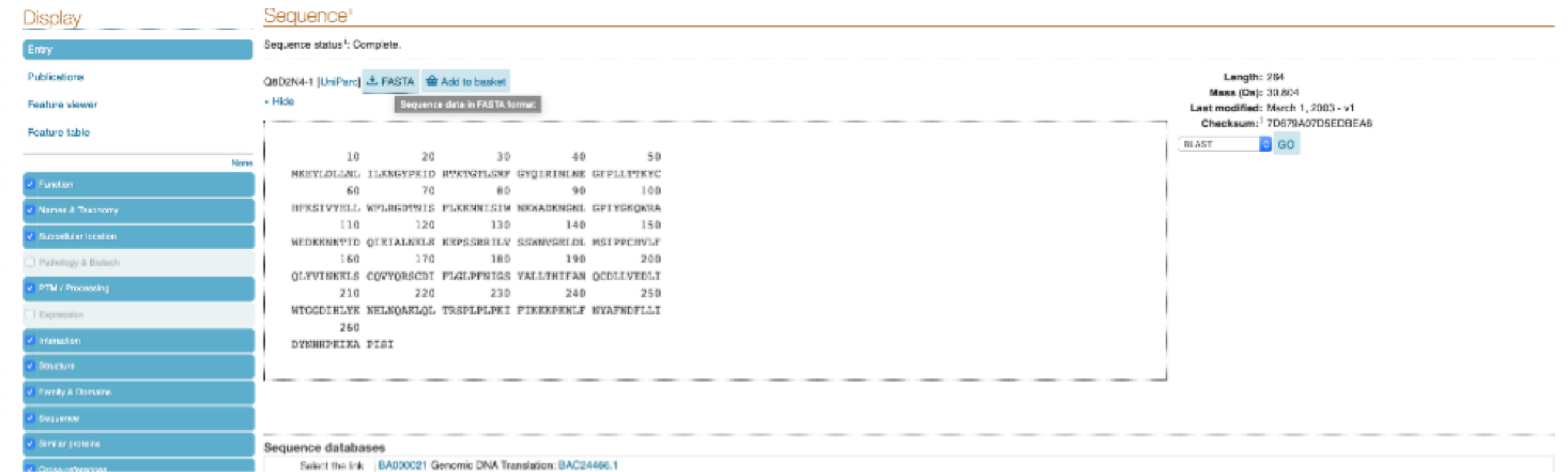
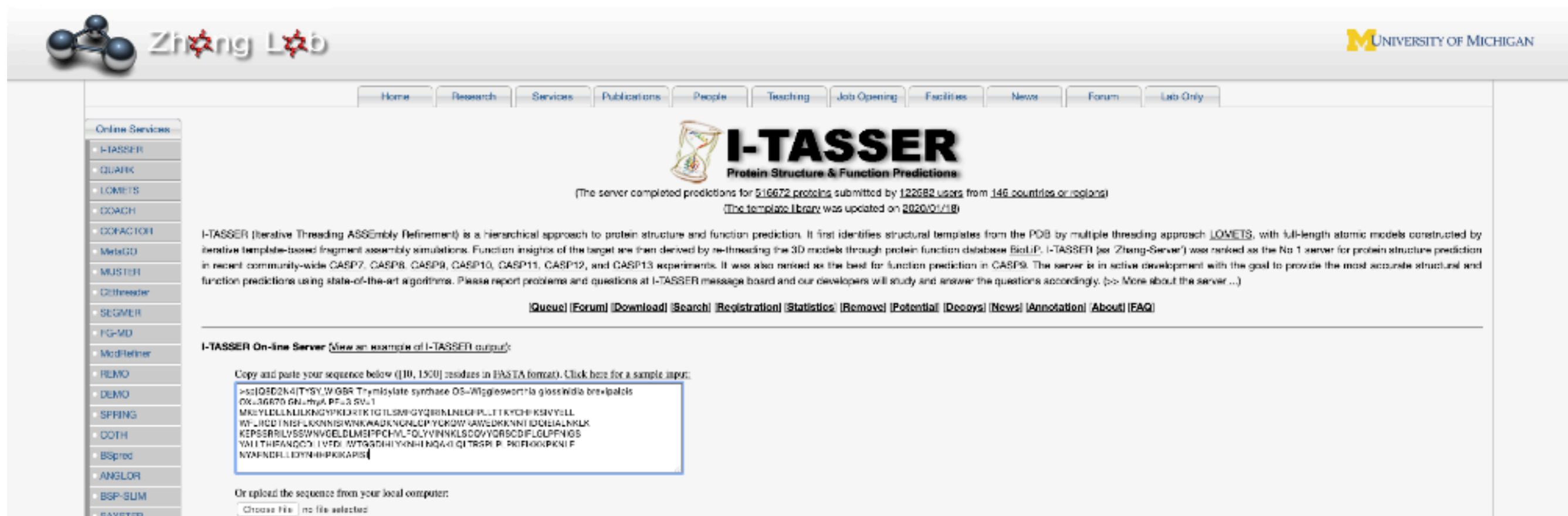


- To get the actual amino acid sequence, click on “Sequence” or scroll down and then click on FASTA. FASTA is a simple format for amino acid sequences based on one-letter codes.
- To run I-TASSER, you can visit the server interface at <https://zhanglab.ccmb.med.umich.edu/I-TASSER/>, register, paste the sequence into the appropriate field, and press “Run I-TASSER”.
- *But* let’s spare their servers and avoid the wait by not all submitting the same job.



The screenshot shows the 'Sequence' tab of the I-TASSER web interface. On the left, there is a sidebar with various tabs: 'Display', 'Entry', 'Publications', 'Feature viewer', and 'Feature table'. The 'Feature table' is currently selected, showing a list of features with checkboxes. The main content area displays the protein sequence in FASTA format, with a 'FASTA' button and an 'Add to basket' button. The sequence is shown in a grid format with columns for positions 10, 20, 30, 40, and 50. The sequence is:
 10 20 30 40 50
 NKEYLGLLGL ILKNGYKID RYKNTLSMF GYQIRINLE GFPLATKYC
 60 70 80 90 100
 HPSIVYELL WYLRGPTIS PLKKNSTIM NKAADENGRI GPIYEGKRA
 110 120 130 140 150
 MEDKKNYID QRTALAKL KPSRRILV SSANVGRIDL MSIPPRVLF
 160 170 180 190 200
 QLVTHNKLQ CQVYVSCDI PLGLPPTGS YALLTHIFAN QCOLIVEDLI
 210 220 230 240 250
 WTGDDHLYK NELNQAQGL TRSLPLPKI PIKKPKNLF NYAPNDFLLI
 260
 DYSHPRKA PISI

On the right, there is a summary box with the following information:
 Length: 264
 Mass (Da): 30,804
 Last modified: March 1, 2003 - v1
 Checksum: 7D679A07D5EDBEA6
 There is a 'BLAST' button and a 'GO' button.



The screenshot shows the 'Online Services' section of the I-TASSER web interface. The header includes the 'Zhang Lab' logo and the 'UNIVERSITY OF MICHIGAN' logo. The navigation bar includes links for 'Home', 'Research', 'Services', 'Publications', 'People', 'Teaching', 'Job Opening', 'Facilities', 'News', 'Forum', and 'Lab Only'. The 'Online Services' section lists various tools: I-TASSER, QUARK, LOMETS, DOATCH, DOFACON, MetaGO, MUSTER, COTHeater, SEGMENT, PG-MD, ModRefiner, PRED, DEMO, SPHING, COTH, BSpred, ANGLOR, BSP-SUM, and SAXTER. The 'I-TASSER' section is highlighted, showing the 'Protein Structure & Function Predictions' logo and a description of the server. The description states:
 I-TASSER (Iterative Threading ASSEMBly Refinement) is a hierarchical approach to protein structure and function prediction. It first identifies structural templates from the PDB by multiple threading approach LOMETS, with full-length atomic models constructed by iterative template-based fragment assembly simulations. Function insights of the target are then derived by re-threading the 3D models through protein function database BioLiP. I-TASSER (or Zhang-Server) was ranked as the No.1 server for protein structure prediction in recent community-wide CASP7, CASP8, CASP9, CASP10, CASP11, CASP12, and CASP13 experiments. It was also ranked as the best for function prediction in CASP9. The server is in active development with the goal to provide the most accurate structural and function predictions using state-of-the-art algorithms. Please report problems and questions at I-TASSER message board and our developers will study and answer the questions accordingly. (>> More about the server ...)

Below the description, there are links for 'Queue', 'Forum', 'Download', 'Search', 'Registration', 'Statistics', 'Remove', 'Potential', 'Decays', 'News', 'Annotation', 'About', and 'FAQ'. The 'I-TASSER On-line Server' section shows a text input field for pasting a sequence in FASTA format. The input field contains the following sequence:
 >=1042241TYSYWGSA Thymidylate synthase OS=Higginsonia glenniae brv-batals
 OK_36670 Glutathyl PL3 SV1
 MASYLDLNLKNGYKID RYKNTLSMF GYQIRINLE GFPLATKYC
 HPSIVYELL WYLRGPTIS PLKKNSTIM NKAADENGRI GPIYEGKRA
 MEDKKNYID QRTALAKL KPSRRILV SSANVGRIDL MSIPPRVLF
 QLVTHNKLQ CQVYVSCDI PLGLPPTGS YALLTHIFAN QCOLIVEDLI
 WTGDDHLYK NELNQAQGL TRSLPLPKI PIKKPKNLF NYAPNDFLLI
 DYSHPRKA PISI

Below the input field, there is a button for 'Run I-TASSER' and a link for 'Or upload the sequence from your local computer'.

- <http://zhanglab.ccmb.med.umich.edu/I-TASSER/output/S516679/>

