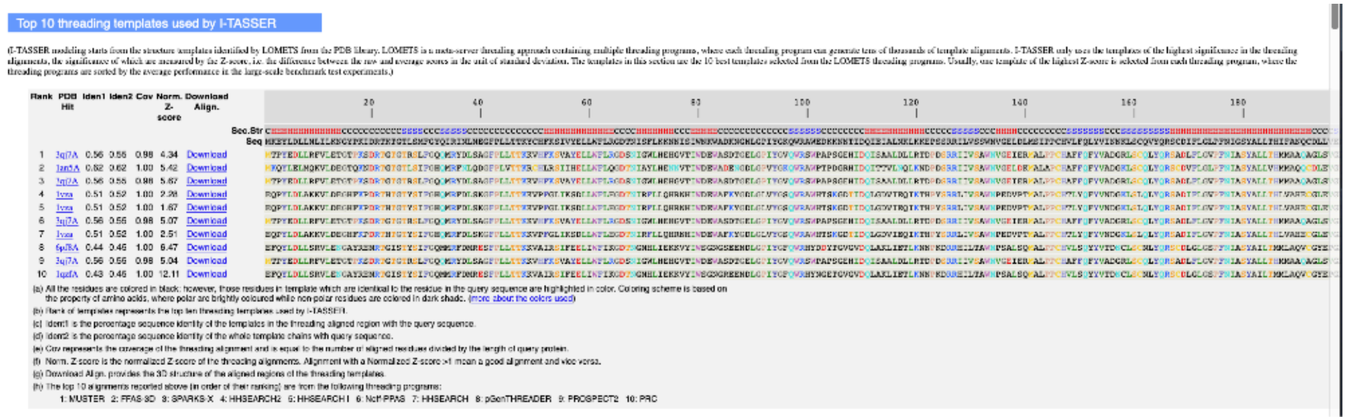
- Here are the Top 10 threading templates. Based on the sequence identity, coverage, and Normalized Z-score, is thymidylate synthase from W.g.b. an easy or hard target?



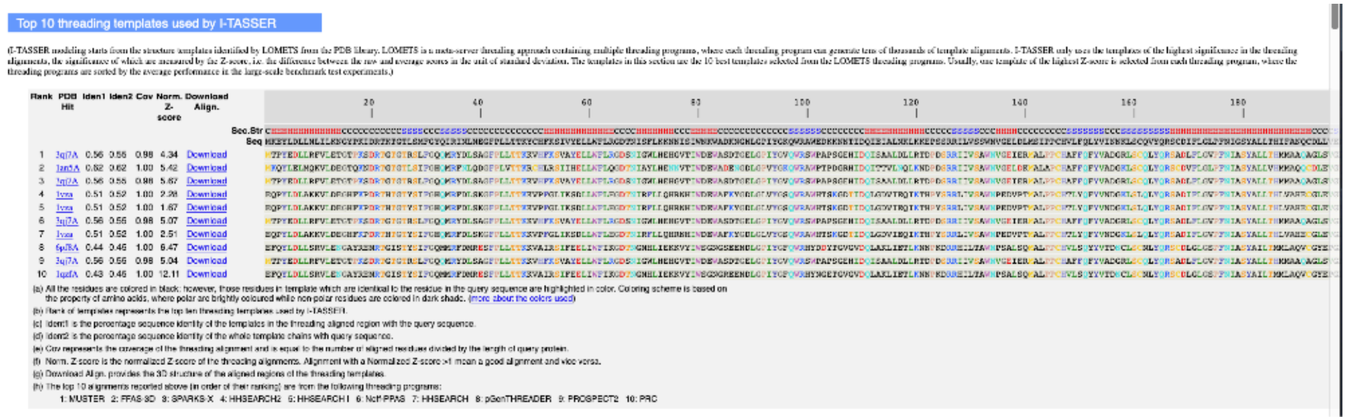
Top 10 threading templates used by I-TASSER

(I-TASSER modeling starts from the structure templates identified by LOMETS from the PDB library. LOMETS is a meta-server threading approach containing multiple threading programs, where each threading program can generate tens of thousands of template alignments. I-TASSER only uses the templates of the highest significance in the threading alignments, the significance of which are measured by the Z-score, i.e. the difference between the raw and average scores in the unit of standard deviation. The templates in this section are the 10 best templates selected from the LOMETS threading programs. Usually, one template of the highest Z-score is selected from each threading program, where the threading programs are sorted by the average performance in the large-scale benchmark test experiments.)

Rank	PDB Hit	Iden1	Iden2	Cov	Norm. Z-score	Download Align.
1	3qj7A	0.56	0.55	0.98	4.34	Download
2	1an5A	0.62	0.62	1.00	5.42	Download
3	3qj7A	0.56	0.55	0.98	5.67	Download
4	1vza	0.51	0.52	1.00	2.28	Download
5	1vza	0.51	0.52	1.00	1.67	Download
6	3qj7A	0.56	0.55	0.98	5.07	Download
7	1vza	0.51	0.52	1.00	2.51	Download
8	6pf8A	0.44	0.45	1.00	6.47	Download
9	3qj7A	0.56	0.55	0.98	5.04	Download
10	1qzfA	0.43	0.45	1.00	12.11	Download

(a) All the residues are colored in black; however, those residues in template which are identical to the residue in the query sequence are highlighted in color. Coloring scheme is based on the property of amino acids, where polar are brightly coloured while non-polar residues are colored in dark shade. (more about the colors used)
(b) Rank of templates represents the top ten threading templates used by I-TASSER.
(c) Ident1 is the percentage sequence identity of the templates in the threading aligned region with the query sequence.
(d) Ident2 is the percentage sequence identity of the whole template chains with query sequence.
(e) Cov represents the coverage of the threading alignment and is equal to the number of aligned residues divided by the length of query protein.
(f) Norm. Z-score is the normalized Z-score of the threading alignments. Alignment with a Normalized Z-score >1 mean a good alignment and vice versa.
(g) Download Align. provides the 3D structure of the aligned regions of the threading templates.
(h) The top 10 alignments reported above (in order of their ranking) are from the following threading programs:
1: MUSTER 2: FFAS-3D 3: SPARKS-X 4: HHSEARCH2 5: HHSEARCH I 6: Neff-PPAS 7: HHSEARCH 8: pGenTHREADER 9: PROSPECT2 10: PRC

- Here are the Top 10 threading templates. Based on the sequence identity, coverage, and Normalized Z-score, is thymidylate synthase from W.g.b. an easy or hard target?
- The sequence identity is not very high but in a reasonable range for homology modeling. The coverage is very high and Normalized Z-score is also high, so this not a hard target for I-TASSER.



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