**TargetScan predicts the following site types:**

* **8mer: an exact match to positions 2-8 of the mature miRNA (the seed + position 8) followed by an 'A'**
* **7mer-m8: an exact match to positions 2-8 of the mature miRNA (the seed + position 8)**
* **7mer-1A: an exact match to positions 2-7 of the mature miRNA (the seed) followed by an 'A'**
* **3' compensatory: an imperfect match to the seed, together with pairing to the 3' portion of the miRNA that can compensate for the single-nucleotide bulge or mismatch (**[**Friedman et al., 2009**](http://genome.cshlp.org/content/19/1/92.long)**).**

**Sites with PCT > 0.75 are highlighted with yellow.**

mirSVRScore:

http://cbio.mskcc.org/microrna\_data/manual.html