Description of All Site Features for Website Viewer and Download Files of STarMir

Site ID	Predicted sites are sequentially numbered along the target sequence
Target	Accession number of the target mRNA
miRNA	Name of the microRNA (miRNA)
Target_Len	Length of the target
Site_Position	Start and end position of the target region (site) predicted to be bound by miRNA
Seed_Position	Start and end position of the target sub-region complementary to the miRNA seed (i.e. positions 2-7/8 of the miRNA)
Seed_Type	6mer, offset 6mer, 7mer-A1, 7mer-m8, and 8mer seed sites (Bartel 2009, *Cell*, **136**, 215-33)
Site_Access	A measure of structural accessibility as computed by the average probability of a nucleotide being single-stranded (i.e., unpaired) for the nucleotides in the predicted binding site
Seed_Access	A measure of structural accessibility as computed by the average of single-stranded probabilities of the nucleotides in the target sub-region complementary to the miRNA seed
Upstream_Access (# nt)	A measure of structural accessibility as computed by the average of single-stranded probabilities for the block of nucleotides upstream of the predicted binding site (# is the block size)
Dwstream_Access (# nt)	A measure of structural accessibility as computed by the average of single-stranded probabilities for the block of nucleotides downstream of the predicted binding site (# is the block size)
Upstream_AU (# nt)	Percentage of AU for the block of nucleotides upstream of the binding site (# is the block size)
Dwstream_AU (# nt)	Percentage of AU for the block of nucleotides downstream of the binding site (# is the block size)
Site_Location	Relative starting location of the predicted binding site along the length of the sequence (e.g., for 3′ UTR, 0 indicates the 5′ end of the UTR, and 1 corresponds to the 3′ end)
3′_bp	Presence of contiguous Watson Crick base pairing for miRNA nucleotide positions 12-17 (sites with 3′_bp are also called 3′ compensatory/supplementary sites)
Site_Consv	Conservation score by the PhastCons program for the binding site
Seed_Consv	Conservation score by the PhastCons program for the target sub-region complementary to the miRNA seed
Offseed_Consv	Conservation score by the PhastCons program for nucleotides within the target site, but outside the seed complementary region
dG_hybrid = ΔG_{hybrid}	A measure of stability for miRNA:target hybrid as computed by RNAhybrid (Rehmsmeier et al. 2004, *RNA* **10**, 1507-1517)
dG_nucl = ΔG_{nucl}	A measure of the potential of nucleation for miRNA:target hybridization (Long et al 2007, *Nat. Struct. Mol. Biol.* **14**, 287-294)
dG_total = ΔG_{total}	A measure of the total energy change of the hybridization (Long et al 2007, *Nat. Struct. Mol. Biol.* **14**, 287-294)
LogitProb	Probability of the site being an miRNA binding site as predicted by our nonlinear logistic model
Target_Mismatch	Nucleotides in the target binding site that are not base paired with the miRNA
Target_Match	Nucleotides in the target binding site that are base paired with the miRNA
Mir_Match	Nucleotides in the miRNA that are base paired with the target mRNA
Mir_Mismatch	Nucleotides in the miRNA that are not base paired with the target mRNA
Hybrid Conformation	The last four fields above present information for the miRNA:target hybrid conformation predicted by RNAhybrid. In each of the fields, spaces are included so the fields can be easily aligned to produce a simple diagram of the hybrid conformation as illustrated below:

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Target_Mismatch: U    UUUCC     U              A
Target_Match:     GACU     AUGUA      CUACCUC
Mir_Match:        UUGA     UACGU      GAUGGAG
Mir_Mismatch:                    UGGAU         A
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