Pimer-BLAST-DX Documentation

Release 0.1

Takao Shibamoto and Kokulapalan Wimalanathan

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1.1.1 Subpackages

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Module contents

primer_blast_dx.specCheck package

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primer_blast_dx.specCheck.specCheck module

Module contents

result: primer3 result

Returns: better result

primer_blast_dx.**findPrimers**(*inputData*, *resultFormat='better'*)
return primer3 result with given format Args:

inputData: input data resultFormat: result format (raw/better)

Returns: result

primer_blast_dx.**findPrimersFile**(*taskPath*, *taskResultPath*)
find primers from the task file and store the result to a task result file Args:

taskPath: location of the task file taskResultPath: location of the task result file to store

primer_blast_dx.**findPrimersFromTask**(*task*)
return primer3 result from task. Checks exception Args:

inputData: input data

Returns: task result

primer_blast_dx.**get_masked_seq**(*primer_seq*, *genome_seq*)

primer_blast_dx.**get_offtarget_attrs**(*off_target*, *side*, *idx*, *data*, *side_cols*, *target_cols*, *pysam_fasta*)

primer_blast_dx.**get_target_attrs**(*target*, *side*, *idx*, *data*, *side_cols*, *target_cols*, *pysam_fasta*)

primer_blast_dx.**run**(*task*)
run findPrimers and specCheck Args:

task (dic): task data saveTmp (bool): true if user wants to save temporary files

Returns: dic: result dictionary

primer_blast_dx.**specCheck**(*task*, *taskResult*)
Dealing with input files both task and task results

primer_blast_dx.**transformInput**(*data*)
separate input to seq_args and global_args Args:

data: input data

Returns: separated input data

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