The ModelSEED database welcomes user contributions. The following directions summarize the protocol for contributing thermodynamic reactions to the database.

1. Clone the [ModelSEED repository](https://github.com/ModelSEED/ModelSEEDDatabase)
2. Identify the reaction compounds in the ModelSEED system
   1. Use the compound names and ModelSEED scripts
      1. The TSV column headers should follow the [example file](https://github.com/ModelSEED/ModelSEEDDatabase/blob/chemistry_staging/Biochemistry/Curation/janakagithub/Iron_oxidation-sulfur_metabolism_newCompounds.tsv)
         1. The ‘NAMES’ header is the compound name
         2. The ‘ID’ header is an arbitrary identifier from the contributor
      2. Execute the “Add\_new\_curated\_compounds” python script via a command-line
         1. Open the code\_staging branch of the repository
         2. Pass the composed TSV file as an argument of the python script
   2. Alternatively, parse the [compound names](https://raw.githubusercontent.com/ModelSEED/ModelSEEDDatabase/master/Biochemistry/Aliases/Unique_ModelSEED_Compound_Names.txt) and [compound aliases](https://raw.githubusercontent.com/ModelSEED/ModelSEEDDatabase/master/Biochemistry/Aliases/Unique_ModelSEED_Compound_Aliases.txt) for the sought reaction compound.
      1. Exchange the compound names in the reaction strings with ModelSEED IDs
3. Synchronize the contributed reactions with the ModelSEED reactions
   1. Determine the reactions for which all compounds are described in ModelSEED
   2. Execute the “Add\_new\_curated\_reactions” python script via a command-line
      1. Pass a TSV file with the completely defined reactions as the argument
         1. The 2.a method only requires a TSV file with the compound names
         2. The 2.b method requires a TSV file with the ModelSEED IDs in lieu of the compound names in the reaction strings.