TABLE 1. Parameters of Molecules and Molecular Interactions

(a) Information about molecules

	Types of Molecules					
	Prot	DNA	RNA	Lipid	Carb	Met
Concentration	x		x	x	x	x
Localization	x		?	x	x	x
Covalent modifications						
phosphorylation	x		?	x	?	
acetylation	x	?	?	?	?	?
methylation	x	x	?	?	?	?
other modifications	x	?	x	x	?	
Cleavage (proteolysis)	x		x	?	x	
Non-covalent modification, e.g., conformation	x		x			
Binding sites	x	x	x	?	?	?

(b) Information about interactions

	Types of Interactions				
	Prot-Prot	Prot-DNA	Prot-RNA	Prot-Small molecule	Genetic
Binding probability/confidence	x	x	x	x	x
Binding affinity	x	x	x	x	
Consequence of interaction					
modification (see above)	x	x	x	x	?
transcription/translation		x	x		?
anabolism/catabolism of molecules	x	x	x	x	?
cleavage (see above)	x	x	x	x	?

An "x" indicates that the parameter is relevant for the given molecule (*a*) or molecular interaction (*b*), and a "?" indicates that relevance is likely but not yet well established. Information about molecules and their actions can be found to various degrees in the databases listed in Table 2. Note that many modification states or molecular activities are dependent on inputs from other molecules, e.g., when phosphorylation activates a protein. Such actions and their conditions are not yet recorded systematically, or using a standardized nomenclature, and thus are difficult to represent in automated map generation. Protein interaction maps are therefore most powerful when associated with free-text annotation that can be accessed from the graphical output. (Carb) Carbohydrate; (Met) metabolite.