Build DIAMOND Database

Build a DIAMOND formatted database from a FASTA input file.

Parameters in GUI

Parameter	Description	Default value
Database	A name of the binary DIAMOND database file that should be created.	
Genomic library	Genomes that should be used to build the database.	

Parameters in Workflow File

Type: diamond-build

Parameter	Parameter in the GUI	Type
database	**Database**	*string*
genomic-library	**Genomic library**	*url-datasets*

Input/Output Ports

The element has 1 *output port*:

Name in GUI: Output DIAMOND database

Name in Workflow File: out

Slots:

SlotInGUI	Slot in Workflow File	Type
Output URL	**url**	*string*