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**atomicdataMB**

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atomicdataMB provides support for the Neutral Cloud and Exospheres Model (nexoclom) and can be used as a standalone package.



## ATOMICMASS

`atomicmass` - Return the atomic mass of an atom or molecule.

This is really just a wrapper for `periodictable` (<https://periodictable.readthedocs.io/en/latest/index.html>) but returns the mass as an `astropy quantity` (<http://docs.astropy.org/en/stable/units/index.html>).

`atomicdataMB.atomicmass.atomicmass(species)`  
Return the atomic mass of an atom or molecule.

### Parameters

**species** Chemical formula requested species. See `periodictable` (<https://periodictable.readthedocs.io/en/latest/index.html>) for formatting options.

### Returns

The atomicmass of *species* as an astropy quantity with units = AMU ( $1 \text{ AMU} = 1.660539 \times 10^{-27} \text{ kg}$ ). If `periodictable` returns a `ValueError`, *None* is returned.

### Examples

```
>>> from atomicdataMB import atomicmass
>>> print(atomicmass('Na'))
22.98977 u
>>> print(atomicmass('H2O'))
18.01528 u
>>> print(atomicmass('X'))
WARNING: mathMB.atomicmass: X not found
None
```





## G\_VALUES

`g_values` - Routines related to g-values and radiation pressure The g-value is the the product of the solar flux at the dopler-shifted emission wavelength and the scattering probability per atom. See Killen, R.M. et al., *Icarus* 209, 75–87, 2009. (<http://dx.doi.org/10.1016/j.icarus.2010.02.018>.) for details on calculating g-values for important species in Mercury's atmosphere.

The radiation acceleration is given by  $a_{rad} = hg/m\lambda$ , where  $h$  is Plank's constant,  $g$  is the g-value as a function of radial velocity,  $m$  is the mass of the accelerated species, and  $\lambda$  is the wavelength of the absorbed photon.

**class** `atomicdataMB.g_values.RadPresConst` (*sp, aplanet*)  
Class containing radial acceleration vs. velocity for a specified atom.

**Parameters**

**sp** atomic species

**aplanet** Distance from the Sun. Can be given as an astropy quantity with distance units or as a float assumed to be in AU. Default = 1 AU

**database** Database containing solar system information. Default = `thesolarsystem` which probably shouldn't be overridden.

**Class Attributes**

**species** The input species

**aplanet** The input distance from the Sun

**velocity** Radial velocity deviation relative to the Sun in km/s. Positive values indicate motion away from the Sun. Given as a numpy array of astropy quantities

**accel** Radial acceleration vs. velocity with units  $\text{km/s}^2$ .

**class** `atomicdataMB.g_values.gValue` (*sp, wavelength=None, aplanet=<Quantity 1. AU>*)  
Class containing g-value vs. velocity for a specified atom and transition.

**Parameters**

**sp** atomic species

**wavelength** Wavelength of the transition. Default=None.

**aplanet** Distance from the Sun. Can be given as an astropy quantity with distance units or as a float assumed to be in AU. Default = 1 AU

**Class Attributes**

**species** The input species

**wavelength** The input wavelength

**aplanet** The input aplanet

**velocity** Radial velocity deviation relative to the Sun in km/s. Positive values indicate motion away from the Sun. Given as a numpy array of astropy quantities

**g** g-value as function of velocity in units 1/s.

`atomicdataMB.g_values.make_gvalue_table()`

Creates and populates gvalues database table. Creates a database table called gvalues. Fields in the table:

**filename** Filename in project tree containing the data; used only for populating the database

**reference** Source of the g-values

**species** Atomic species

**refpt** Distance from Sun in AU for which the g-values were calculated.

**wavelength** At-rest wavelength for the g-values in Å.

**velocity**  $\Delta v$  from rest in km/s.

**g** g-values in photons/s as a function of velocity.

**Parameters**

None

**Returns**

No Output

## PHOTOLOSSRATES

photolossrates - Determine photoionization and photodissociation rates

**class** atomicdataMB.photolossrates.**PhotoRate** (*species, aplanet\_=<Quantity 1. AU>*)  
Determine photoreactions and photorates for a species.

### Parameters

**species** Species to compute rates for.

**aplanet** Distance from the Sun. Default is 1 AU. Given as either a numeric type or an astropy quantity with length units.

### Class Attributes

**species** Species

**aplanet** Distance from the Sun; astropy quantity with units AU

**rate** Reaction rate; astropy quantity with units  $\text{s}^{-1}$ . Rate is the sum of all possible reactions for the species.

**reactions** Pandas dataframe with columns for reaction and rate (in  $\text{s}^{-1}$ ) for each reaction for the species.  
This can be used to determine the products produced by photolysis and photoionization.

### Example

```
>>> from atomicdataMB import PhotoRate
>>> kappa = PhotoRate('Na', 0.33)
>>> print(kappa)
Species = Na
Distance = 0.33 AU
Rate = 6.666666666666666e-05 1 / s
>>> print(kappa.rate)
6.666666666666666e-05 1 / s
>>> print(kappa.reactions)
      reaction                                kappa
0  Na, photon -> Na+, e  6.666666666666666e-05
>>> kappa = PhotoRate('H_2O')
>>> print(kappa)
Species = H_2O
Distance = 1.0 AU
Rate = 1.2056349999999999e-05 1 / s
>>> print(kappa.reactions)
      reaction                                kappa
0  H_2O, photon -> H_2, O  5.97e-07
1  H_2O, photon -> OH, H  1.03e-05
2  H_2O, photon -> H, H, O  7.54e-07
3  H_2O, photon -> H, OH+, e  5.54e-08
```

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4	H_2O, photon -> OH, H+, e	1.31e-08
5	H_2O, photon -> H_2O+, e	3.31e-07
6	H_2O, photon -> H_2, O+, e	5.85e-09

`atomicdataMB.photolossrates.make_photo_table()`

Creates and populates photorates database table. Creates a database table called photorates. Fields in the table:

**filename** Filename in project tree containing the data; used only for populating the database

**reference** Source of the photoionization or photodissociation rate

**species** Atomic or molecular species

**reaction** Photoionization or photodissociation reaction

If multiple reaction rates are found for a reaction, user is prompted to choose the best one. Most of the reactions are in: Huebner & Mukherjee (2015), *Astrophys. Space Sci.*, 195, 1-294.

#### Parameters

None

#### Returns

No output

## INITIALIZE\_ATOMICDATA

Populate the database with the available atomic data. Currently populates g-values and photoionization rates. If the database does not exist, it will be created. By default, the tables will only be created if

```
atomicdataMB.initialize_atomicdata.initialize_atomicdata (force=False)
```

Populate the database with available atomic data if necessary.

### Parameters

**force** By default, the database tables are only created if they do not already exist. Set force to True to force the tables to be remade. This would be necessary if there are updates to the atomic data.

### Output

No output.



## DATABASE\_CONNECT

`database_connect` - Return a database connection to saved atomic data

`atomicdataMB.database_connect.database_connect` (*database=None, port=None, return\_con=True*)

Return a database connection to saved atomic data Wrapper for `psycpg2.connect()` that determines database and port to use.

### Parameters

**database** Database to connect to. If not given, it must be supplied in the \$HOME/.nexoclom configuration file.

**port** Port the database server uses. If not given, it must be supplied in the \$HOME/.nexoclom configuration file.

**return\_con** False to return database name and port instead of connection. Default = True

### Returns

Database connection with `autocommit = True` unless `return_con = False`

### Examples

```
>>> from atomicdataMB import database_connect
>>> database, port = database_connect(return_con=False)
>>> print(f'database = {database}; port = {port}')
database = thesolarsystemmb; port = 5432
>>> with database_connect() as con:
...     cur = con.cursor()
...     cur.execute('SELECT DISTINCT species from gvalues')
...     species = cur.fetchall()
>>> species = [s[0] for s in species]
>>> print(species)
['Ca', 'OH', 'O', 'Ti', 'C', 'Mg+', 'Na', 'Mg', 'H', 'Mn', 'He',
 'Ca+', 'K', 'S']
```





## INSTALLATION

atomicdataMB can be installed with pip:

```
$ pip install atomicdataMB
```



## REPORTING ISSUES

This project is hosted on github at [atomicdataMB](https://github.com/mburger-stsci/atomicdataMB) (<https://github.com/mburger-stsci/atomicdataMB>). Please report bugs or make comments there.



## CONTRIBUTING

Please let me know if you would like to make contributions.

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**License** LICENSE



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