

# The BHC Company synthesis of ibuprofen (1990's): the green synthesis

```
CC(C)Cc1ccccc1.CC(=O)OC(C)=O>F>CC(=O)c1ccc(CC(C)C)cc1  
CC(=O)c1ccc(CC(C)C)cc1.[HH]>Ni-Raney>CC(C)Cc1ccc(C(C)O)cc1  
CC(C)Cc1ccc(C(C)O)cc1.[C-]#[O+]>Pd>CC(C)Cc1ccc(C(C)C(=O)O)cc1
```

```
from rxnSMILES4AtomEco import atom_economy  
  
#use triple quotes (""" ) to define a multiline string  
reactions_smiles = """CC(C)Cc1ccccc1.CC(=O)OC(C)=O>F>CC(=O)c1ccc(CC(C)C)cc1  
CC(=O)c1ccc(CC(C)C)cc1.[HH]>Ni-Raney>CC(C)Cc1ccc(C(C)O)cc1  
CC(C)Cc1ccc(C(C)O)cc1.[C-]#[O+]>Pd>CC(C)Cc1ccc(C(C)C(=O)O)cc1"""  
atom_economy(reactions_smiles)
```

## Calculate atom economy for individual synthesis steps

```
from rxnSMILES4AtomEco import get_atom_economy  
# value = get_atom_economy(reactions_smiles)  
# print(value)  
  
# Split reactions_smiles into lines  
lines = reactions_smiles.splitlines()  
  
# Create a dictionary to store the results  
results_individual = {}  
  
# Loop through each line and call get_atom_economy for each one  
for i, line in enumerate(lines):  
    # Create Step 1, Step 2, ..., Step n  
    step_key = f"Step {i+1}"  
    # Call the function and store the result
```

```

    results_individual[step_key] = get_atom_economy(line)

# Now, 'results' contains the results for each line, e.g., \
# results["Step 1"], results["Step 2"], etc.

# Example: Print all results
for step, result_individual in results_individual.items():
    print(f"{step}: {result_individual:.1f}%")

```

### Calculate atom economy for cumulative synthesis steps

```

# Split reactions_smiles into lines
lines = reactions_smiles.splitlines()

# Create a dictionary to store the results
results_cumulative = {}

# Loop through each incremental combination of lines and call get_atom_economy
# Start from 1 to n
for i in range(1, len(lines) + 1):
    # Get the first i lines
    combined_reactions = "\n".join(lines[:i])

    # Call get_atom_economy with the combined lines up to the current step
    step_key = f"Step {i}"
    # Store the result
    results_cumulative[step_key] = get_atom_economy(combined_reactions)

    # Example: Print the current step's result
    print(f"{step_key}: {results_cumulative[step_key]:.1f}%")

```

### Multiplot of individual and cumulative atom economy

```

import matplotlib.pyplot as plt

# Extract the steps (x-axis) and Atom Economy values (y-axis) for \
# both individual and cumulative

# Step names: ['step_1', 'step_2', ...]
steps = list(results_individual.keys())

```

```

# Atom Economy values for individual reactions
individual_values = list(results_individual.values())
# Atom Economy values for cumulative reactions
cumulative_values = list(results_cumulative.values())

# Calculate the Byproduct(s) as the difference between 100% \
# and the desired product
byproduct_values = [100 - value for value in individual_values]

# Create a single plot

# Single axis for both plots
fig, ax = plt.subplots(figsize=(10, 7))
plt.rcParams.update({'font.size': 16})

# Plot the stem plot for cumulative Atom Economy values in black
ax.stem(steps, cumulative_values, linefmt='k:', markerfmt='k>:', basefmt=" ", \
        label="Cumulative Atom Economy").markerline.set_markersize(10)

# Bar plot for individual Atom Economy values
bars = ax.bar(steps, individual_values, color='#009E73', \
              label="Desired product", alpha=0.8) # Green bars
ax.bar(steps, byproduct_values, bottom=individual_values, color='#E69F00', \
        label="Byproduct(s)", alpha=0.8) # Orange stacked bars

# Add the text (value of desired product) in white in the middle of each bar
for i, bar in enumerate(bars):
    height = bar.get_height()
    ax.text(bar.get_x() + bar.get_width() / 2, height / 2, f'{height:.1f}%', \
            ha='center', va='center', color='white', fontweight='bold')

# Add labels and titles
ax.set_title('BHC Atom Economy: Individual- and Cumulative Steps\n\n\n')
ax.set_xlabel('\nSteps')
ax.set_ylabel('Atom Economy (%)')
# Set Y-axis from 0 to 100%
ax.set_ylim(0, 100)

# Add the legend
ax.legend(loc='upper center', bbox_to_anchor=(0.5, 1.2), ncol=3, reverse=True)

# Improve layout to avoid label overlap

```

```
plt.tight_layout()

# Show the plot
plt.show()
# To save the plot, if used, comment line above and uncomment lines below
#save_path = '/tmp/BHC_histogram.png' # Writable on many systems
#plt.draw() # Force render
#print(f"Saving to: {save_path}")
#plt.savefig(save_path, dpi=300, bbox_inches='tight')
#plt.close()
#print("Save completed (check directory).")
```