Algorithm 1: BRICS Algorithm for Fragmentation

Input : Molecule
Output : Set of final fragments

1 BRICS_Algorithm(*molecule*)
2   bonds_to_break ← Find_Bonds(*molecule*)
3   fragments ← Break_Bond(*predefined_bonds*)
4   filtered_fragments ← Apply_Substructure_Filters(*fragments*)
5   stabilized_fragments ← Stabilize_Fragments(*filtered_fragments*)
6   **return** *stabilized_fragments*
7

8 Find_Bonds(*molecule*)
   Data: molecule
   Result: List of bonds to break
9   bonds_to_break ← empty list
10   **for** *each bond in the molecule* **do**
11   **if** *the bond and its chemical environment match one of the 16 predefined bond types* **then**
12   Add it to the list of bonds to break
13   **end**
14   **end**
15   **return** *bonds_to_break*
16

17 Break_Bond(*bonds_to_break*)
   Data: bonds_to_break
   Result: fragments
18   fragments ← empty list
19   **for** *each bond in the bonds_to_break* **do**
20   break the bond and add resulting fragment to the fragment list
21   **end**
22   **return** *fragments*
23

24 Apply_Substructure_Filters(*fragments*)
   Data: list of fragments
   Result: Filtered list of fragments
25   filtered_fragments ← empty list
26   **for** *each fragment in fragments* **do**
27   **if** *fragment size is reasonable and not a duplicate or overlapping with other fragments*
       then
28   Add it to the list of filtered fragments
29   **end**
30   **end**
31   **return** *filtered_fragments*
32

33 Stabilize_Fragments(*fragments*)
   Data: list of fragments
   Result: List of stabilized fragments
34   stabilized_fragments ← empty list
35   **for** *each fragment in filtered_fragments* **do**
36   Add supplementary atoms (e.g., hydrogen atoms) to make the fragment chemically stable
37   Add the stabilized fragment to the list of stabilized fragments
38   **end**
39   **return** *stabilized_fragments*
40