

# Test results for the CDK 1.0.x branch

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## Keywords

Cdk

## Abstract

The Chemistry Development Kit has never really been without any bugs, which is reflected in the number of failing JUnit tests. For trunk/ this is today 106 failing tests (live stats). The stable cdk-1.0.x/ branch, however, the number of failing tests is not much lower: 64 failing tests today (live stats).

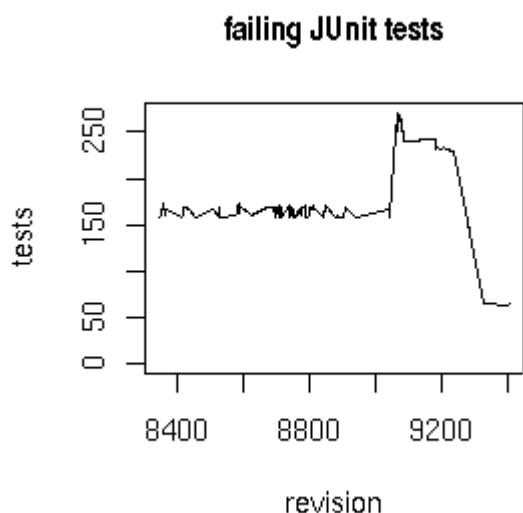
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The [Chemistry Development Kit](#) has never really been without any bugs, which is reflected in the number of failing JUnit tests. For [trunk/](#) this is today 106 failing tests ([live stats](#)). The stable [cdk-1.0.x/](#) branch, however, the number of failing tests is not much lower: 64 failing tests today ([live stats](#)).

Overall, only a low percentage of the tests fails (<2% for cdk-1.0.x/ and <3% for trunk/), and, more importantly, it is particular algorithms that are typically broken. For example, in the structgen module 8 tests fail, for both CDK versions. In the **cdk-1.0.x/** branch it is the valency checker code that causes quite a few fails, which I discussed in [Atom typing in the CDK](#) and which is the reason for the atom type perception refactoring in progress in trunk/ (see [Evidence of Aromaticity](#)). Not all code in trunk/ has yet been updated yet, and this causes quite a few failing tests for trunk/ in the **reaction**, **qsarAtomic** and **qsarBond** modules.

Back to the **cdk-1.0.x/** branch. Previous CDK releases tended to have around 40 failing tests, so I was worried about the number of tests failing now. Maybe backported patches causes additional fails? To study that I had my machine run the JUnit tests for all revisions of the **cdk-1.0.x/** branch since the branch was made in commit [8343](#). The result looks like:



Indeed, it is a number of backports that cause the clear increase in bugs between commit 9044 and 9058. Nothing particular I can see, and worse, the intermediate revisions do not compile and do not have test results:

104	9044	3731	84	73	979.709	0
105	9045	0	0	0	0.000	0
106	9046	0	0	0	0.000	0
107	9047	0	0	0	0.000	0
108	9048	0	0	0	0.000	0
109	9049	0	0	0	0.000	0
110	9050	0	0	0	0.000	0
111	9051	0	0	0	0.000	0

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112	9052	0	0	0	0.000	0
113	9053	0	0	0	0.000	0
114	9054	0	0	0	0.000	0
115	9055	0	0	0	0.000	0
116	9056	0	0	0	0.000	0
117	9057	0	0	0	0.000	0
118	9058	3740	104	146	989.566	0

I should have taken more care when merging in these patches, even though they are supposed to fix issues:

Merged r8697: Add a method to the query atom container creator which creates an

queryatomcontainer. This replaces each pseudoatom to an anyatom.

Merged r8699 and r8700: Added test file by Volker (see cdk-user) for the shortest path problem;

JUnit test provided by Volker Haehnke (haehnke - bioinformatik uni-frankfurt de), somewhat rewritten.

Merged r8701: Renamed a variable to comply with [http://en.wikipedia.org/wiki/Dijkstra's\\_algorithm](http://en.wikipedia.org/wiki/Dijkstra's_algorithm)

Merged r8751: Bug fixes for bugs #1783367 'SmilesParser incorrectly assigns double bonds' and

#1783381 'SmilesParser uses Molecule instead of IMolecule'. Test case for bug #1783367.

Merged r8754 and r8773: Fix and test case for bug #1783547 and #1783546 'Lost aromaticity in

SmilesParser with Biphenyl and Benzene'

Merged r8774: Add a MDL RXN reader which uses the MDLV2000Reader instead of the MDLReader

Merged r8775, r8776, r8777: bug fixes for #150354 #1783774 #1778479 in the SmilesParser,

SmilesGenerator and MDLWriter/PseudoAtom.

Merged r8791: Code for v,mass atom two digits mass atom and exception handling

Merged r8800: Fixed reading of MDL molfiles with exactly 12 columns (==valid) in the bond block

Merged r8802: Made a little more memory efficient by removing unnesscary cloning operations

Merged r8803: Fixed it so that we make a deep copy of the input molecule

Merged r8809: Added code to work on a local copy of theinput molecule

Merged r8811: Updated Javadocs

Merged 8824 8821 8820 8819 8817 8816: Added code to properly work on a local copy

## chem-bla-ics

I'm quite sure it must be the deep-cloning fix ported from the commits 8800-8824. I already fixed a number of bugs in the IP calculation code which is still a good deal of the failing tests in the cdk-1.0.x/ branch (and affects trunk/ too), as can be seen by the drop in bugs just after the big increase:

r9079 | egonw | 2007-10-15 13:24:10 +0200 (Mon, 15 Oct 2007) | 1 line

Renamed container to localClone to clear up code. Fixed a bug where the uncloned atoms was searched in the cloned atomcontainer. More bugs like this are in the code. Miguel is contacted about this problem.

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r9082 | egonw | 2007-10-15 13:48:15 +0200 (Mon, 15 Oct 2007) | 1 line

Renamed container to localClone to clear up code. Fixed a bug where the uncloned atoms was searched in the cloned atomcontainer.

The big drop in number of fails is caused by the removal of the SMARTS code from the branch, which has been present since the start of the branch (see [this page](#)).

From this analysis I conclude that CDK 1.0.2 can soon be released. With the note that the ionization potential calculation is not safe to use.