1,799,191 document results

View secondary documents | View 744848 patent results | Analyze search results | Sort on: Date Cited by Relevance

Search within results...

Limit to Exclude

Year
- 2017 (903)
- 2016 (229,537)
- 2015 (321,660)
- 2014 (317,236)
- 2013 (309,805)

Author Name
- Baroli, L. (495)
- Alouini, M.S. (448)
- Zhang, H. (439)
- Wang, B. (436)
- Li, B. (418)

Subject Area
- Computer Science (1,799,191)
- Engineering (675,083)
- Mathematics (479,056)
- Physics and Astronomy (133,059)
- Social Sciences (126,303)

Document Type
- Conference Paper (1,062,033)
- Article (593,952)
- Editorial (31,924)
- Article in Press (26,736)
- Book Chapter (21,418)

Source Title
- Journal of Machine Learning Research
- IEEE Transactions on Evolutionary Computation
- Bioinformatics
- Evolutionary Computation
- Wiley Interdisciplinary Reviews: Computational Molecular Science

Keyword
- Artificial Intelligence
- Computer Science
- Document analysis
- Machine Learning
- Pattern Recognition

Affiliation
- University of California, Berkeley, CA, USA
- University of California, Los Angeles, CA, USA
- University of California, Santa Barbara, CA, USA
- University of California, San Diego, CA, USA
- University of California, Davis, CA, USA

Country/Territory
- United States

Source Type
- Book
- Journal
- Conference Proceeding
- Patent
- Website

Language
- English

Limit to Exclude

Export refined search results

Specific results:
1. LIBSVM: A Library for Support Vector Machines
   - Chang, C.-C., Lin, C.-J.
   - ACM Transactions on Intelligent Systems and Technology, 2011
   - 8835

2. Scikit-learn: Machine Learning in Python
   - Pedregosa, F., Varoquaux, G., Gramfort, A., (…), Pretot, M., Duchesnay, É.
   - Open Access

3. UCHiME improves sensitivity and speed of chimera detection
   - Edgar, R.C., Haas, B.J., Clemente, J.C., Quince, C., Knight, R.
   - Bioinformatics, 2011
   - 1892

4. Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega
   - Sievers, F., Wilm, A., Dineen, D., (…), Thompson, J.D., Higgins, D.G.
   - Molecular Systems Biology, 2011
   - Open Access

5. ImageNet classification with deep convolutional neural networks
   - Krizhevsky, A., Sutskever, I., Hinton, G.E.
   - 1684

   - Peakall, R., Smouse, P.E.
   - Bioinformatics, 2012
   - 1671

7. Cytoscape 2.8: New features for data integration and network visualization
   - Smoot, M.E., Ono, K., Ruscheinski, J., Wang, P.-L., Ideker, T.
   - Bioinformatics, 2011
   - 1620

8. The ORCA program system
   - Neeve, F.
   - Wiley Interdisciplinary Reviews: Computational Molecular Science, 2012
   - 1400

9. GROMACS 4.5: A high-throughput and highly parallel open source molecular simulation toolkit
   - Pronk, S., Päll, S., Schulz, R., (…), Hess, B., Lindahl, E.
   - Bioinformatics, 2013
   - 1331

10. Differential evolution: A survey of the state-of-the-art
    - Das, S., Suganthan, P.N.
    - IEEE Transactions on Evolutionary Computation, 2011
    - 1319

11. Data Mining: Concepts and Techniques
    - Han, J., Kamber, M., Pei, J.
    - Data Mining: Concepts and Techniques, 2012
    - 1284

12. RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies
    - Stamatakis, A.
    - Bioinformatics, 2014
    - 1262

13. Robust principal component analysis?
    - Candès, E.J., Li, X., Ma, Y., Wright, J.
    - Journal of the ACM, 2011
    - 1198

14. Scaling up MIMO: Opportunities and challenges with very large arrays
    - Rusek, F., Persson, D., Lau, B.K., (…), Edfors, O., Tufvesson, F.
    - 1162

15. SLIC superpixels compared to state-of-the-art superpixel methods
    - Achanta, R., Shaji, A., Smith, K., (…), Fua, P., Süsstrunk, S.
    - IEEE Transactions on Pattern Analysis and Machine Intelligence, 2012
    - 1160
<table>
<thead>
<tr>
<th>Title</th>
<th>Authors</th>
<th>Year</th>
<th>Journal</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>RSEM: Accurate transcript quantification from RNA-Seq data with or</td>
<td>Li, B., Dewey, C.N.</td>
<td>2011</td>
<td>BMC Bioinformatics</td>
<td>1144</td>
</tr>
<tr>
<td>without a reference genome</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Geneious Basic: An integrated and extendable desktop software</td>
<td>Kearse, M., Moir, R.</td>
<td>2012</td>
<td>Bioinformatics</td>
<td>1054</td>
</tr>
<tr>
<td>platform for the organization and analysis of sequence data</td>
<td>Wilson, A. (..),</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Meintjes, P., Drummond, A.</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Integrative Genomics Viewer (IGV): High-performance genomics data</td>
<td>Thorvaldsdóttir, H.</td>
<td>2013</td>
<td>Briefings in Bioinformatics</td>
<td>1045</td>
</tr>
<tr>
<td>visualization and exploration</td>
<td>Robinson, J.T.,</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mesirov, J.P.</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CloudSim: A toolkit for modeling and simulation of cloud computing</td>
<td>Calheiros, R.N.,</td>
<td>2011</td>
<td>Software - Practice and Experience</td>
<td>993</td>
</tr>
<tr>
<td>environments and evaluation of resource provisioning algorithms</td>
<td>Ranjan, R., Beloglazov, A., De Rose, C.A.F., Buyya, R.</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>