## Kelsy C Cotto

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7607715/publications.pdf

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|          |                | 1478505      | 1372567        |  |
|----------|----------------|--------------|----------------|--|
| 10       | 1,425          | 6            | 10             |  |
| papers   | citations      | h-index      | g-index        |  |
|          |                |              |                |  |
|          |                |              |                |  |
| 16       | 16             | 16           | 3627           |  |
| 10       | 10             | 10           | 3027           |  |
| all docs | docs citations | times ranked | citing authors |  |
|          |                |              |                |  |
|          |                |              |                |  |

| #  | Article                                                                                                                                                                                         | IF   | CITATIONS |
|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 1  | DGIdb 3.0: a redesign and expansion of the drug–gene interaction database. Nucleic Acids Research, 2018, 46, D1068-D1073.                                                                       | 14.5 | 686       |
| 2  | Integration of the Drug–Gene Interaction Database (DGIdb 4.0) with open crowdsource efforts. Nucleic Acids Research, 2021, 49, D1144-D1151.                                                     | 14.5 | 439       |
| 3  | ORegAnno 3.0: a community-driven resource for curated regulatory annotation. Nucleic Acids Research, 2016, 44, D126-D132.                                                                       | 14.5 | 142       |
| 4  | Standard operating procedure for somatic variant refinement of sequencing data with paired tumor andÂnormal samples. Genetics in Medicine, 2019, 21, 972-981.                                   | 2.4  | 67        |
| 5  | CIViCpy: A Python Software Development and Analysis Toolkit for the CIViC Knowledgebase. JCO Clinical Cancer Informatics, 2020, 4, 245-253.                                                     | 2.1  | 10        |
| 6  | Exploring the Genomic Landscape of Cancer Patient Cohorts with GenVisR. Current Protocols, 2021, 1, e252.                                                                                       | 2.9  | 7         |
| 7  | Open-Sourced CIViC Annotation Pipeline to Identify and Annotate Clinically Relevant Variants Using Single-Molecule Molecular Inversion Probes. JCO Clinical Cancer Informatics, 2019, 3, 1-12.  | 2.1  | 6         |
| 8  | Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. Cancer Genetics, 2022, 264-265, 90-99.                                                      | 0.4  | 3         |
| 9  | A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.                                                                                          | 13.2 | 3         |
| 10 | <i>In Silico</i> Epitope Prediction Analyses Highlight the Potential for Distracting Antigen Immunodominance with Allogeneic Cancer Vaccines. Cancer Research Communications, 2021, 1, 115-126. | 1.7  | 1         |