



On the inconsistent treatment of gene-protein-reaction rules in context-specific metabolic models

URL: <https://academic.oup.com/bioinformatics/advance-article-abstract/doi/10.1093/bioinformatics/btz832/5625152?redirectedFrom=fulltext>

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Publication: Bioinformatics

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Source URL (retrieved on 26 abr 2024 - 16:36): <https://www.bsc.es/ca/research-and-development/publications/the-inconsistent-treatment-gene-protein-reaction-rules-context>