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Note on: Graph Theory-Based Sequence Descriptors as Remote Homology Predictors

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Fragment

Alignment-free (AF) methodologies have increased in popularity in the last decades as alternative tools to alignment-based (AB) algorithms for performing comparative sequence analyses. They have been especially useful to detect remote homologs within the twilight zone of highly diverse gene/protein families and superfamilies. **[...] Read more.**

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References

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