Sources

GMDHreg: Regression using GMDH Algorithms

<https://rdrr.io/cran/GMDHreg/>

GMDHreg: an R Package for GMDH Regression

<https://cran.r-project.org/web/packages/GMDHreg/vignettes/GMDHreg.html>

Package ‘GMDHreg’

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<https://archive.ics.uci.edu/ml/datasets/Protein+Data>

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<https://www.rcsb.org/docs/tools/pairwise-structure-alignment>

CASP5 Website

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<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6748739/>

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<https://chemistrytalk.org/protein-folding/>

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Kabsch, W. (1976). A solution for the best rotation to relate two sets of vectors. Acta Cryst. A32, 922–923.