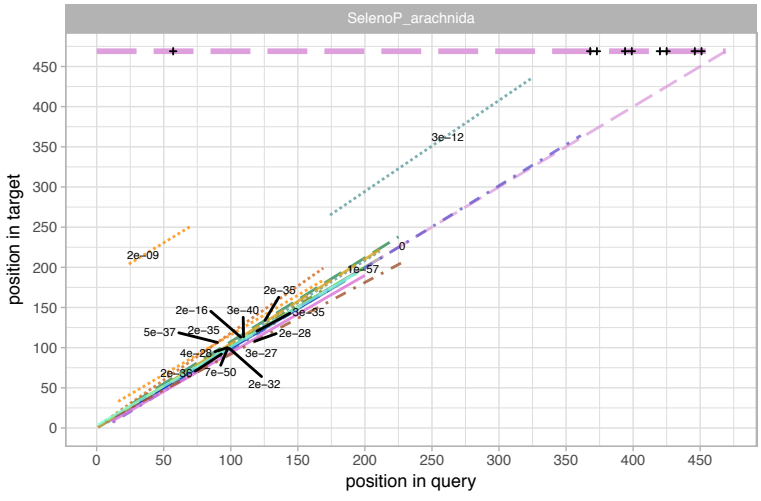
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Title	Processive recoding and metazoan evolution of selenoprotein P: Up to 132 UGAs in molluscs
Authors	Baclaocos, Janinah;Santesmasses, Didac;Mariotti, Marco;Bierła, Katarzyna;Vetick, Michael B.;Lynch, Sharon;McAllen, Rob;Mackrill, John J.;Loughran, Gary;Guigó, Roderic;Szpunar, Joanna;Copeland, Paul R.;Gladyshev, Vadim N.;Atkins, John F.
Publication date	2019-08-20
Original Citation	Baclaocos, J., Santesmasses, D., Mariotti, M., Bierła, K., Vetick, M. B., Lynch, S., McAllen, R., Mackrill, J. J., Loughran, G., Guigó, R., Szpunar, J., Copeland, P. R., Gladyshev, V. N. and Atkins, J. F. (2019) 'Processive recoding and metazoan evolution of selenoprotein P: up to 132 UGAs in molluscs', Journal of Molecular Biology, 431(22), pp.4381-4407. https://doi.org/10.1016/j.jmb.2019.08.007
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Link to publisher's version	https://www.sciencedirect.com/science/article/pii/S0022283619305133?via%3Dihub - 10.1016/j.jmb.2019.08.007
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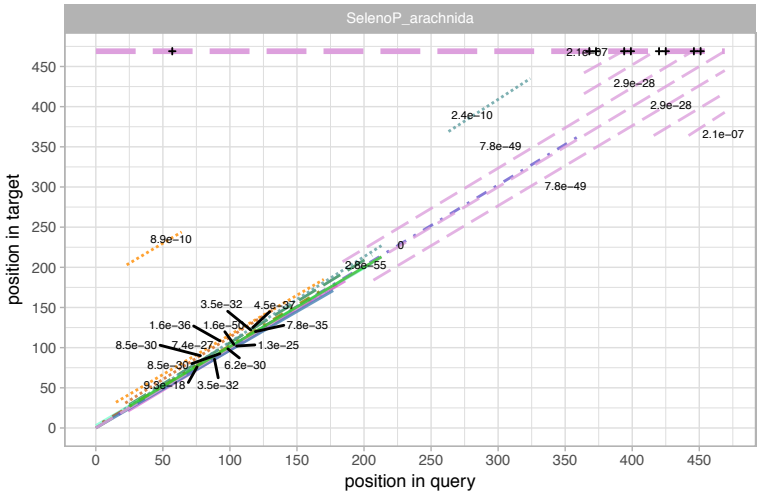
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University College Cork, Ireland
Coláiste na hOllscoile Corcaigh

Figure S3

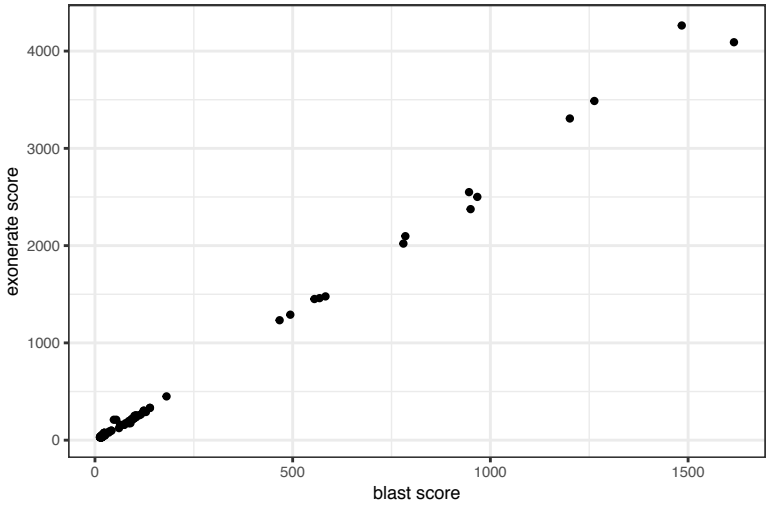
A. Protein alignments from blast



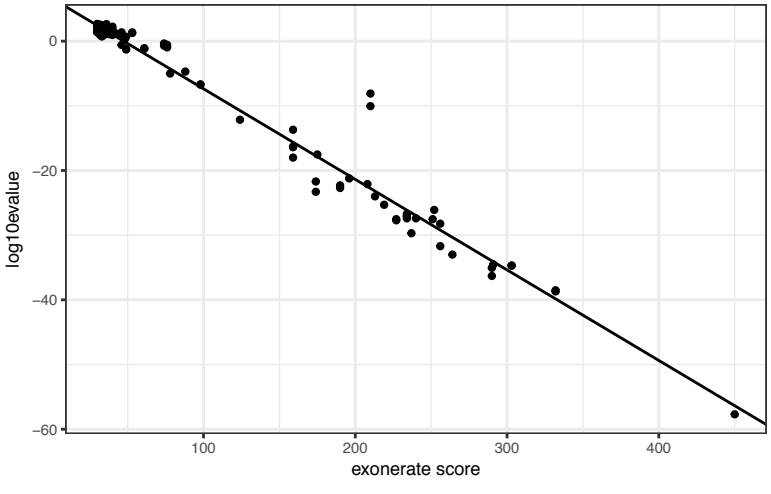
Protein alignments from exonerate



B. Comparing scores of identical blast and exonerate hits



Log(evalue) is inversely proportional to exonerate score
[removing hits with saturated evalue =0.0]



C.

