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P2	Pal Arumay, Chakrabarti Pinak, Hubbard Simon	Coevolution of residues at the interface vis-à-vis the rest of the protein surface in homodimers
P3	Khandelwal Garima, Jayaram B	Energy based signatures of different genomic components
P4	Richa T, Sivaraman Thirunavukkarasu	A heuristic algorithm for reconciling the discrepancies between ΔG_{HX} and ΔG_U of proteins
P5	Khurana Renu, Dongre PM, Nagare BJ	Identification of lead antimalarial agents using pharmacophore modeling and virtual screening
P6	Shandilya Manish, Kapoor Abhijeet, Kundu Suman	Structural insight of human dopamine β -hydroxylase, a drug target for complex traits and functional significance of exonic SNPs
P7	Das Uddipan, Kumar Manoj, Kaur Punit, Srinivasan A, Singh TP, Hariprasad Gururao	Group III phospholipase A2 from the scorpion, <i>Mesobuthus tamulus</i> : targeting and reversible inhibition with native peptides
P8	Ghosh Ambarnil, Chattopadhyay Shiladitya, Mamta Chawla-Sarkar, Nandy Papiya, Nandy Ashesh	Characterization of conserved regions in rotaviral VP7 proteins: a graphical representation approach towards epitope prediction
P9	Sengupta Arjun, Basant A, Rege MM, Sharma S Sonawat HM	Metabonomics of host response to malarial parasite
P10	Prayaga Phani Deep, Sankararamakrishnan R	Existence of a stable structure surrounding the start codon: a comparison between mRNAs having start codons with weak and strong Kozak contact
P11	Singh Poonam, Khan Sajjad, Azhar Asim, Rasheed Q, Naseem Asma, Jairajpuri Md Aman	Serine protease inhibitors: targeting surface cavities for hindering polymerization in serpins
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