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Output format

Short description:

Each identified Rossmann fold sequence domain is associated with three neural network scores, one for each of the three cofactors FAD, NAD and NADP. A score above 0.5 indicates that the domain is predicted to be specific for the particular cofactor. The prediction scores are followed by a summary of the predicted cofactor specificity. If multiple specificities are predicted the identifiers are separated with a slash e.g. NAD/NADP. The approximate Rossmann fold sequence boundaries are provided next to the summary and these are followed by the amino acid sequence. If no Rossmann fold sequence domains are identified the domain count is 0 and no scores or domain boundaries are reported.

Example:

#	SEQUENCE ID	Domain	FAD	NAD	NADP	Cofactor(s)	From	To	Sequence
Input_1	1	0.670	0.387	0.585	FAD/NADP	5	46	SQKRVVVLGSGVIGLSSALILARKGYSVHILARDLPEDVSSQ	
Input_2	1	0.765	0.258	0.073	FAD	1	48	MRVVVIGAGVIGLSTALCIHERYHSLQPLDVKVYADRFTPTTTDVA	
Input_3	1	0.939	0.228	0.169	FAD	1	43	MKVIVLGSSHGGYEAVEELLNLHPDAEIQWYEKGDFISFLSGM	
Input_3	2	0.502	0.837	0.063	FAD/NAD	147	185	EVNNVVVIGSGYIGIEAAEAFKAGKKVTVIDILDRPLG	
Input_4	0	-	-	-	-	-	-	-	

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