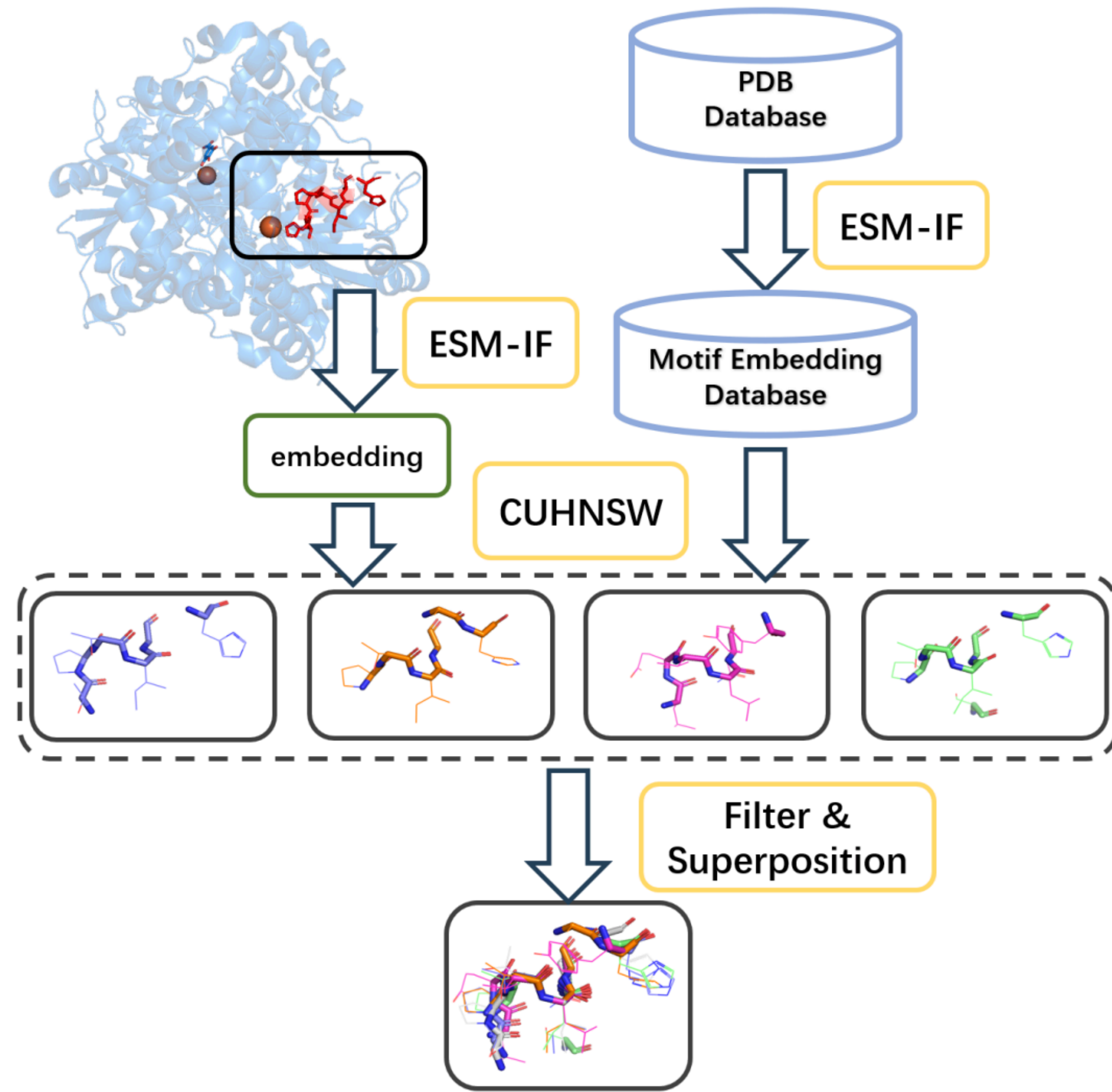

Enhancing Protein Mutation Effect Prediction through a Retrieval-Augmented Framework

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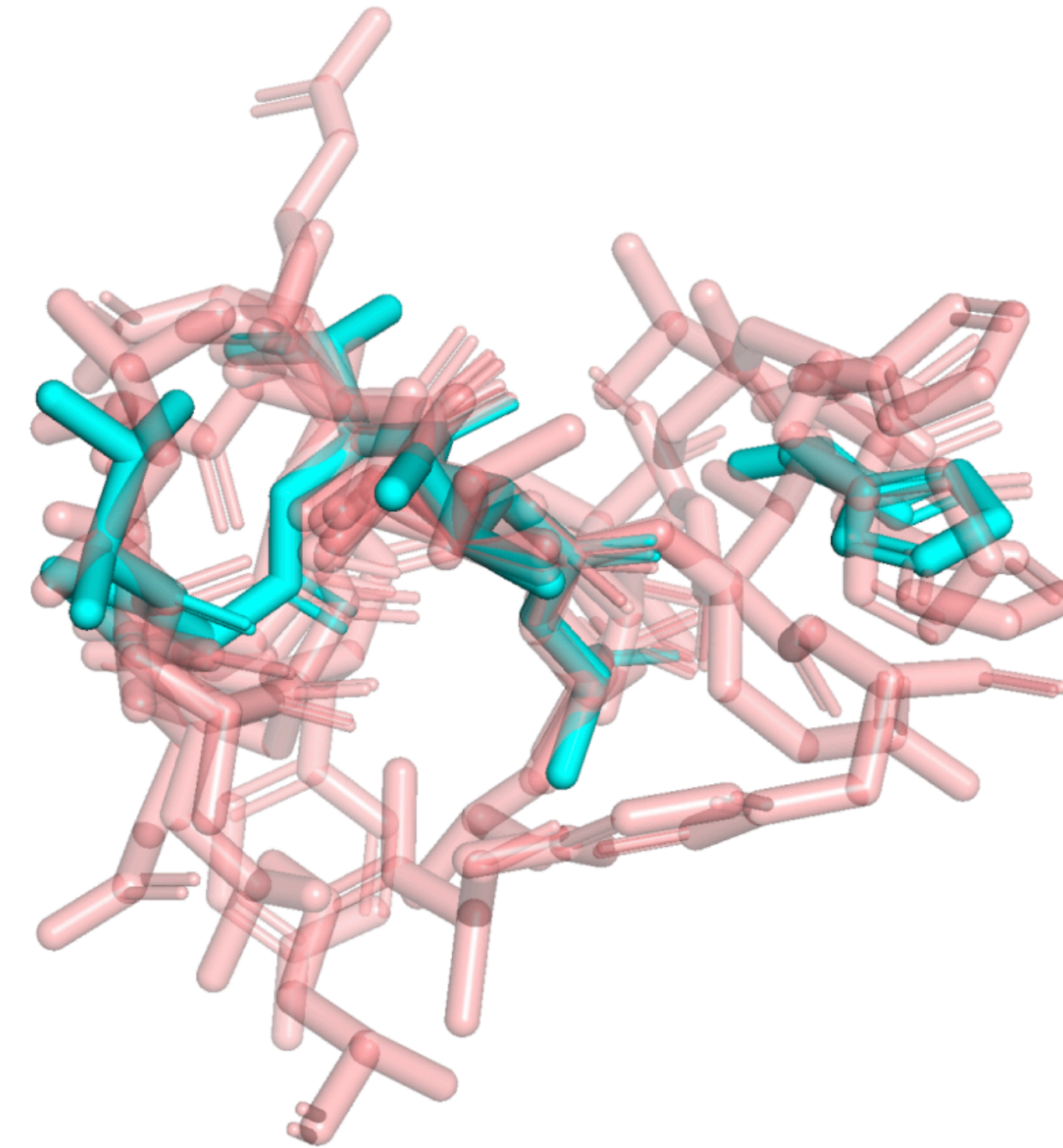
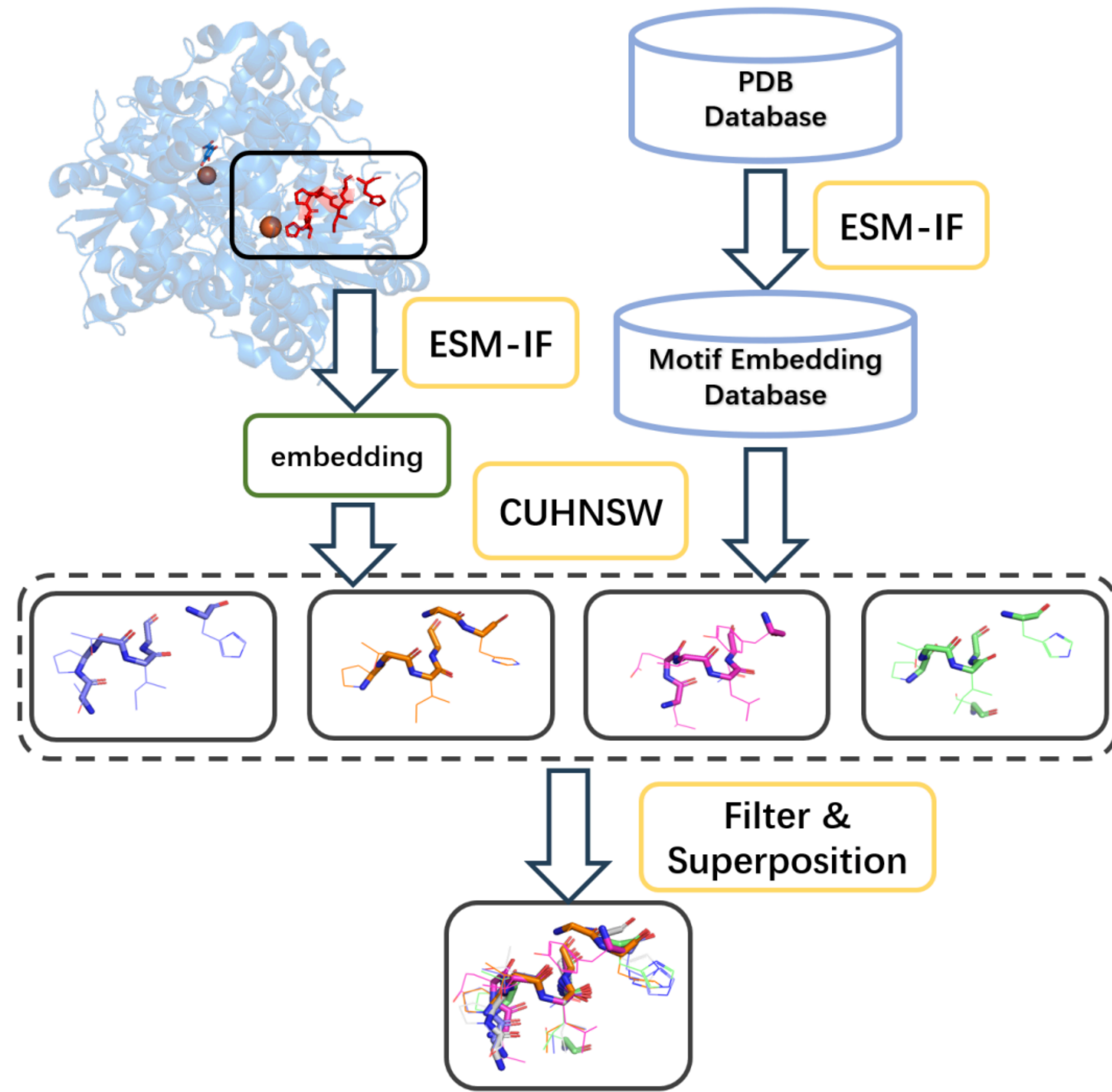
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Structure Motif Embedding Database



Structure Motif Embedding Database



MSM-Profile

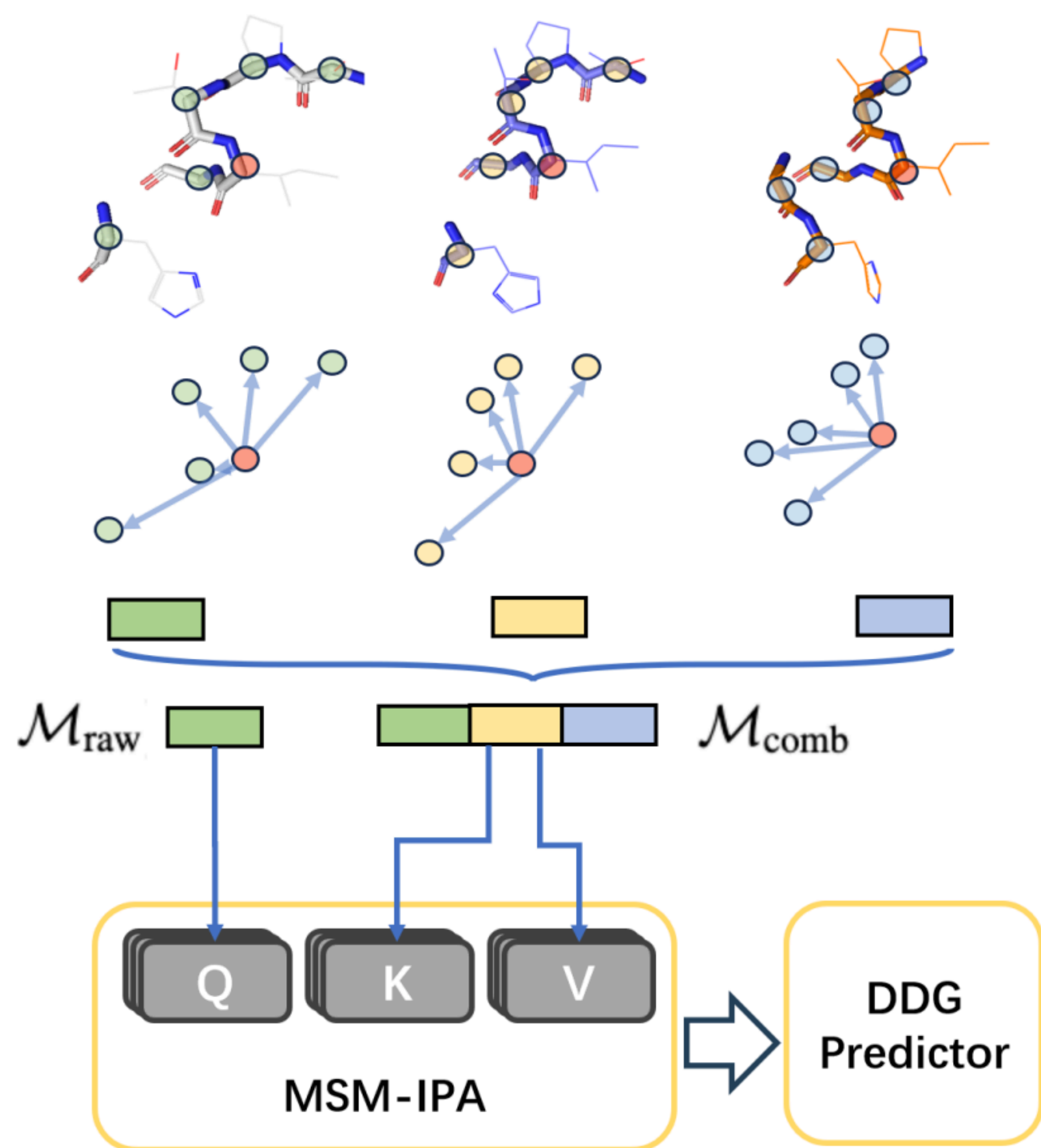
Table 4: Performance comparison between MSA-Profile and MSM-Profile on the SKEMPI2.0 dataset.

Category	Method	Pearson (P.S.)	Spearman (P.S.)	Pearson	Spearman
Profile	MSA-Profile	0.0826	0.0822	0.0159	0.0666
	MSM-Profile	0.1551	0.1766	0.1433	0.1739
	MSM-Profile (Filtered)	0.1905	0.1886	0.1653	0.2063

Table 5: Performance of MSA-Profile, MSM-Profile, and their combination on the s669 dataset.

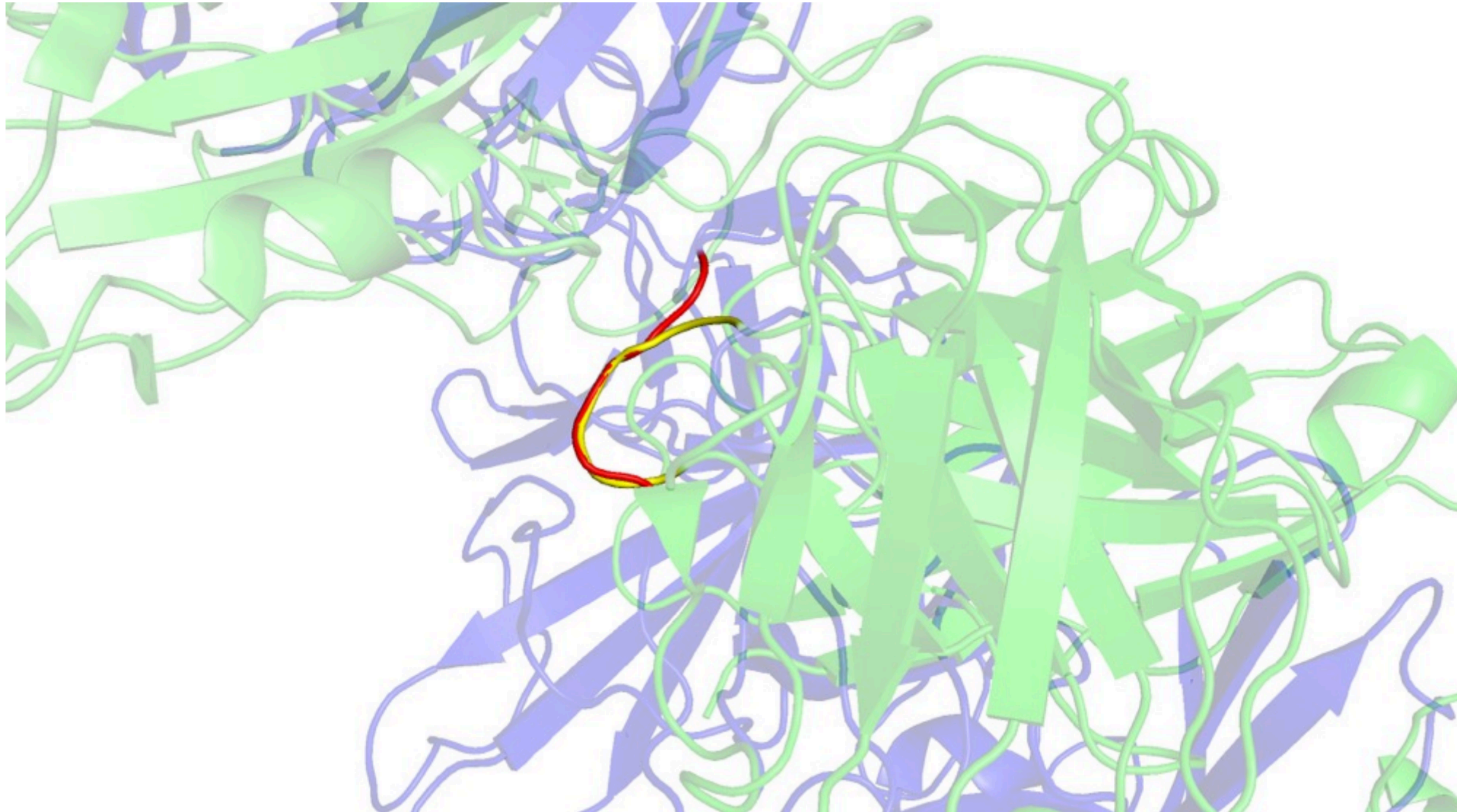
Method	Pearson
MSA-Profile	0.17
MSM-Profile	0.19
MSA-Profile + MSM-Profile	0.23

MSM-IPA

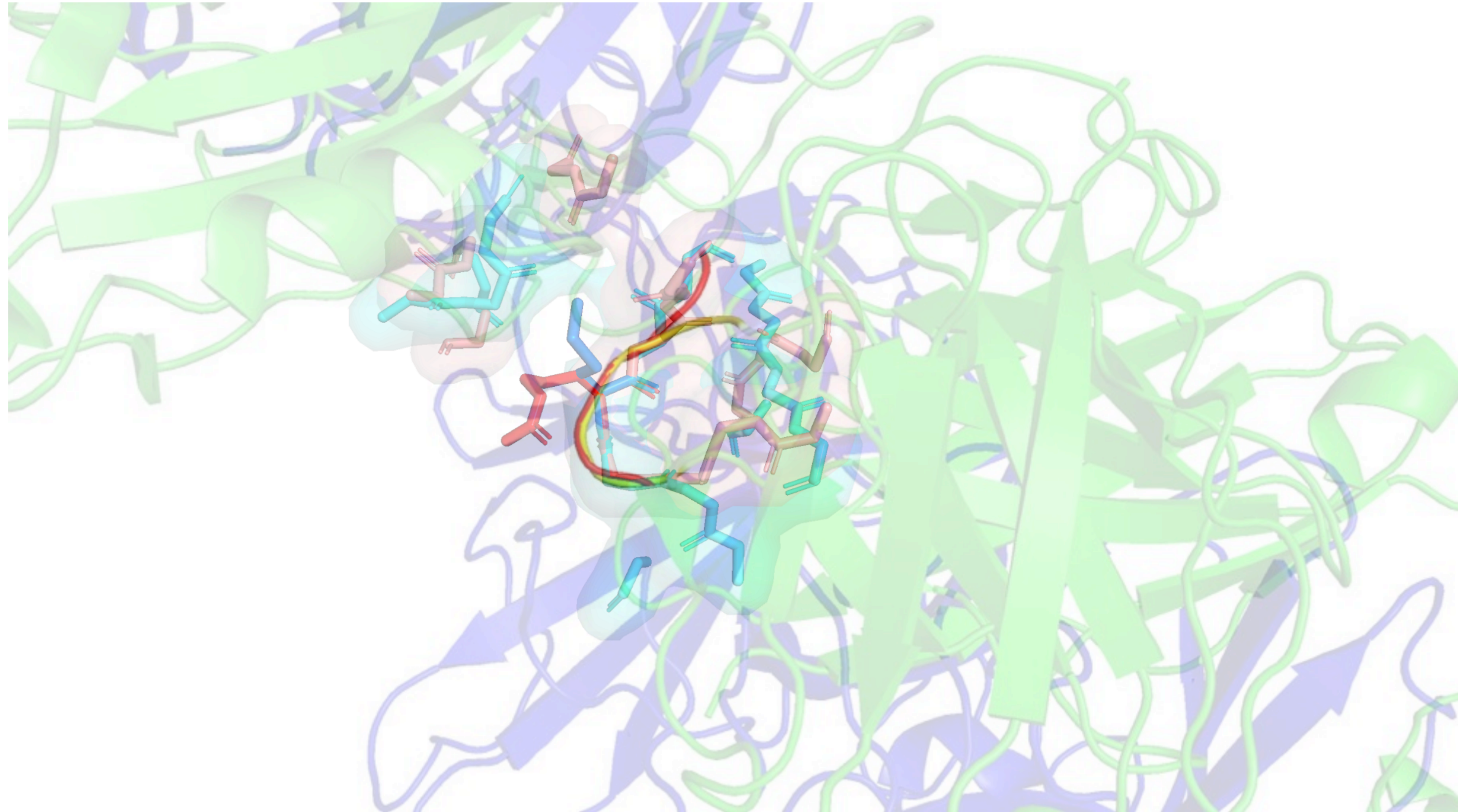


	w/o retrieval	w retrieval
SKEMPI2.0	0.62	0.68
S669	0.45	0.54
Novozymes	0.32	0.48

Comparison of Local Structures via Multiple Structure Motif Alignment



Comparison of Local Structures via Multiple Structure Motif Alignment



Comparison of Local Structures via Multiple Structure Motif Alignment

