Supplementary Information

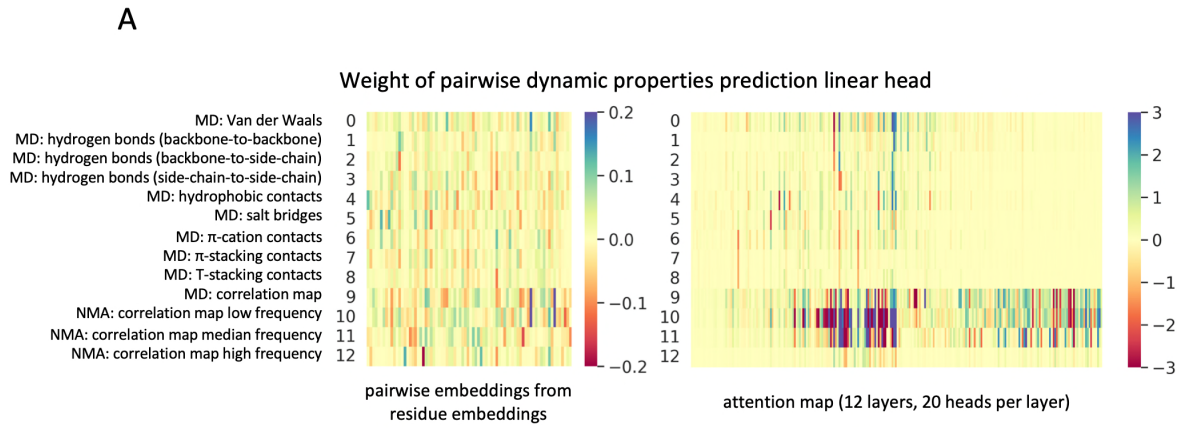
Supplementary Table 1

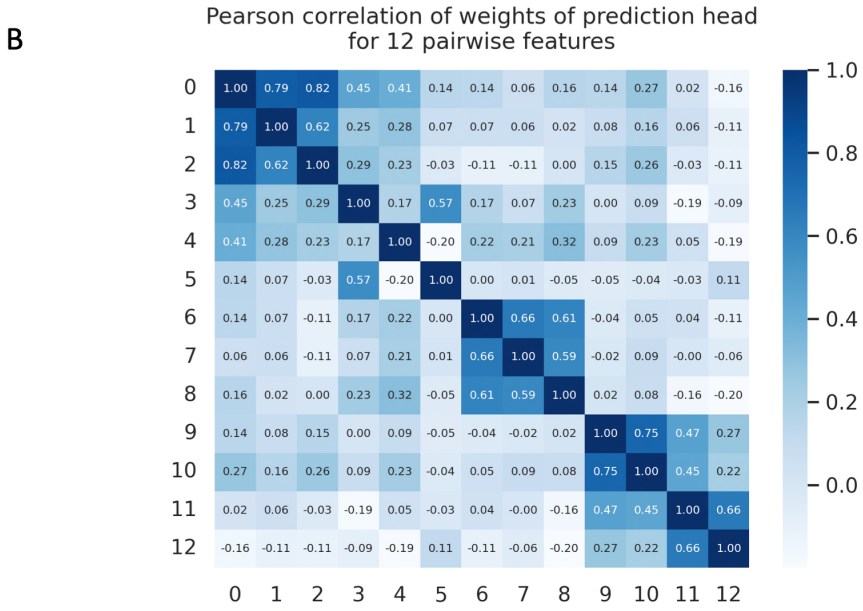
Supplementary Figure 1-6

Supplementary Table 1: residue-level and pairwise dynamic features

Method	Feature	Dimension	Description	Package
NMA	Correlation map	$L \times L \times 3$	Slowest N modes accounting for 33%, 66%, and 100% of overall dynamics in ANM (for correlation map) or GNM (for residue fluctuation)	ProDy
	Residue fluctuation	$L \times 3$		
MD	Correlation map	$L \times L \times 1$	Correlation of Cα movement	mdtraj
	Interaction map	$L \times L \times 9$	hydrogen bonds (side-chain-to-side-chain, backbone-to-backbone, backbone-to-side-chain), salt bridges, hydrophobic contacts, π-cation contacts, π-stacking contacts, T-stacking contacts, Van der Waals	GetContacts
	Residue fluctuation	$L \times 1$	Root mean squared fluctuation (RMSF)	mdtraj
	Surface Area	$L \times 2$	Mean and standard deviation	mdtraj
	Secondary Structure	$L \times 8$	Percentage of eight DSSP assignments	mdtraj
	Dihedral angles: phi, psi, chi1	$L \times 3 \times 12$	Percentages in 12 angle ranges	mdtraj

NMA: normal mode analysis
MD: molecular dynamics
L: protein length

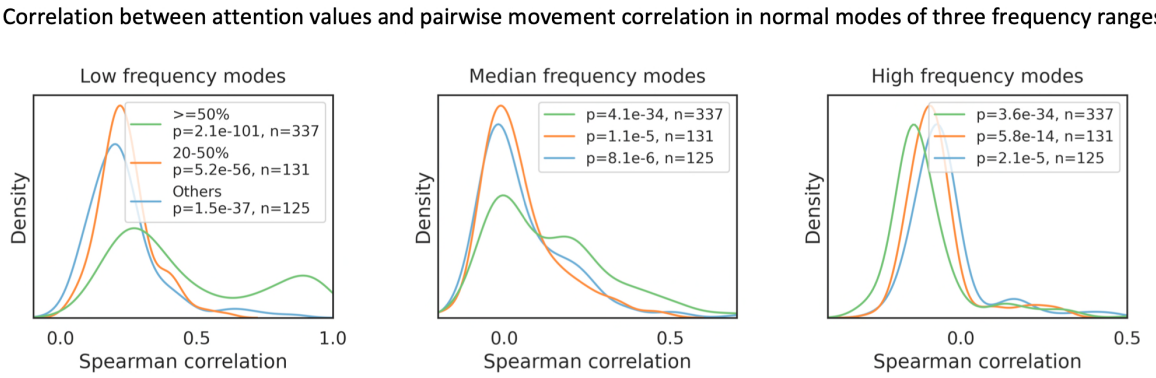




Supplementary Figure 1. Analysis of SeqDance's pairwise feature prediction head.

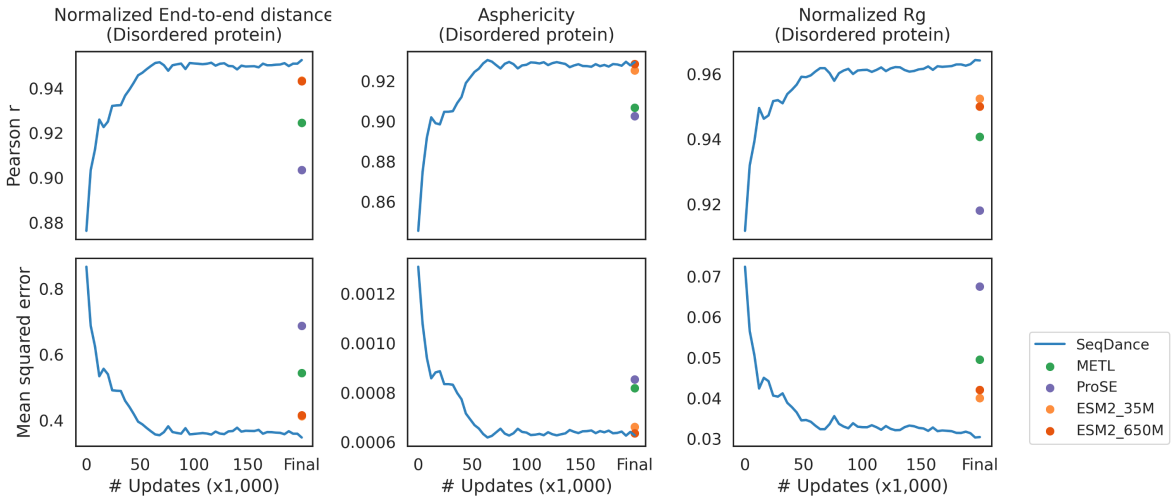
A. The weight of the pairwise feature prediction linear layer. For a protein of length *L*, the pairwise features' dimension is $L \times L \times 13$, comprising nine types of interactions, one movement correlation from molecular dynamics (MD) data and three movement correlations from normal mode analysis (NMA) data. The input for the pairwise feature prediction head consists of pairwise embeddings (dimension $L \times L \times 78$) derived from residue embeddings and attention maps (dimension $L \times L \times 240$). Given the different absolute values of pairwise embedding and attention map, we plotted them separately.

B. Pearson correlation between weights of prediction heads of different features, representing the row-wise correlation of the data shown in panel A.



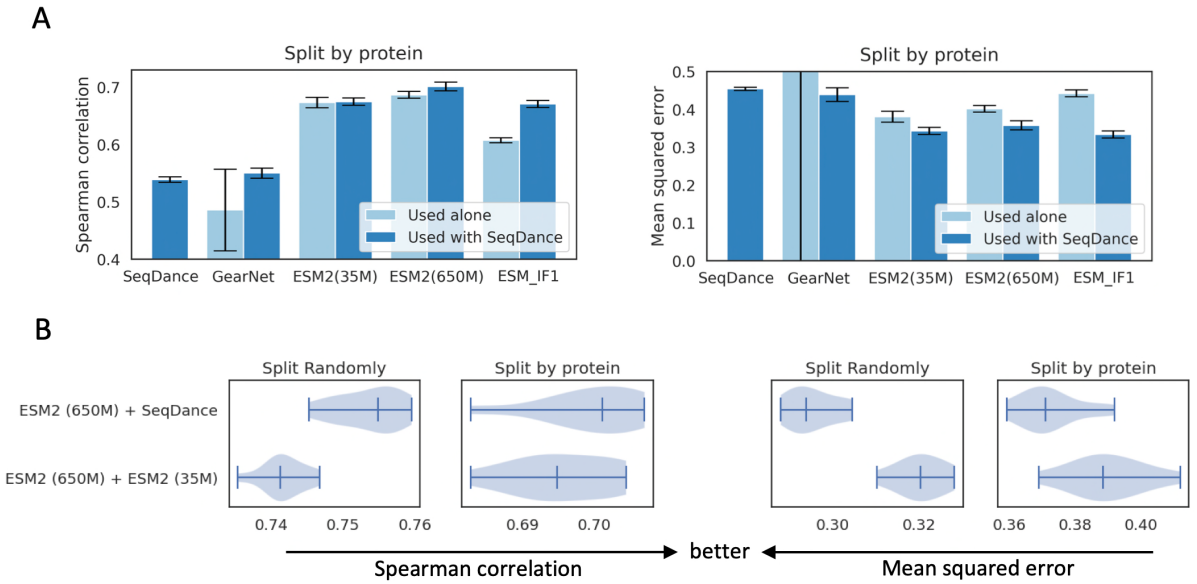
Supplementary Figure 2. Correlation between attention values and pairwise movement correlation in normal modes of three frequency ranges.

Held-out proteins were clustered into three clusters based on the sequence identity to training sequences. P-values were calculated using a one-sample t-test with the null hypothesis that the mean value is zero.



Supplementary Figure 3. SeqDance embeddings encode global conformational properties of disordered regions.

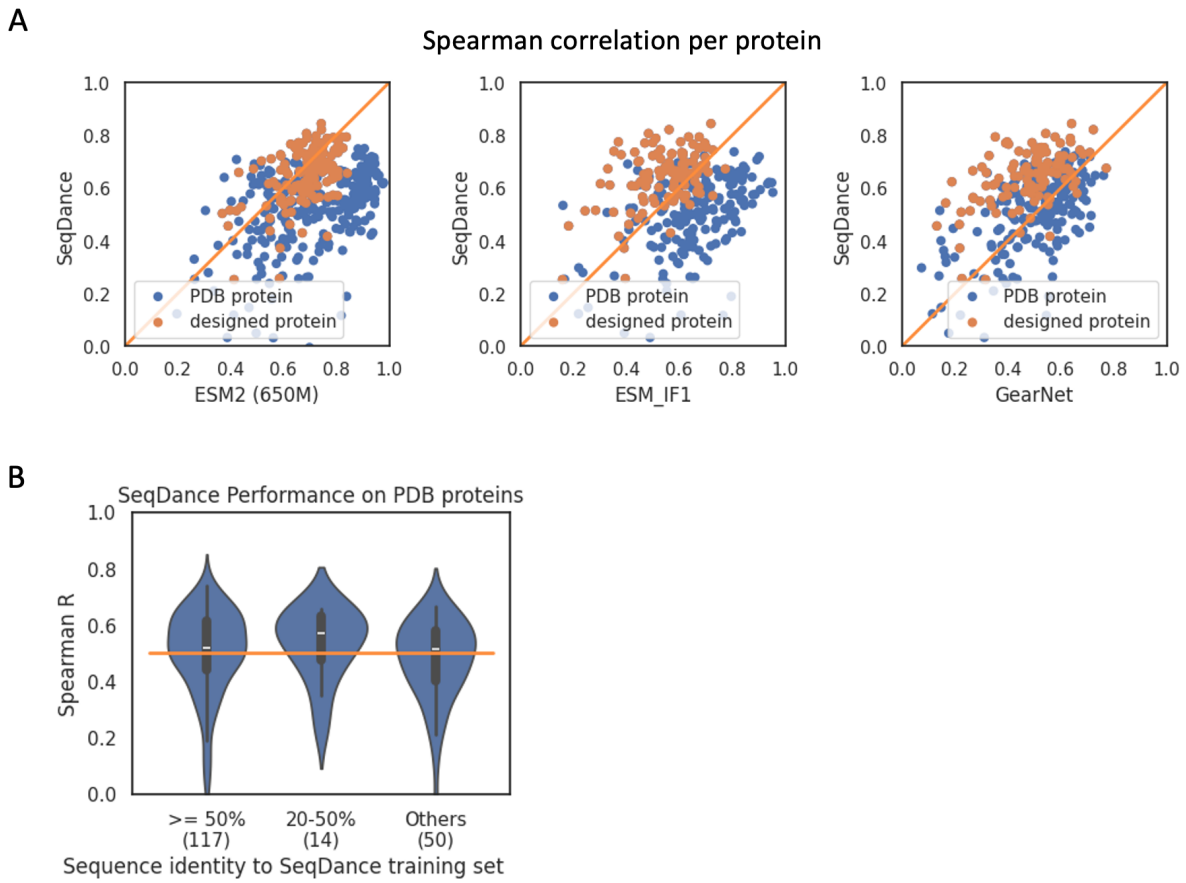
Performance comparison of embeddings from SeqDance, METL, ProSE, and ESM2 in predicting the normalized end-to-end distance (two ESM2 models overlapped), asphericity, normalized radius of gyration of disordered proteins. The training and test split was 6:4 with a 20% sequence identity cutoff. The results presented are the averages of ten repeats. Disordered proteins with over 20% sequence identity (with at least 60% coverage) to any SeqDance training sequences were removed from the analysis. The x-axis represents the number of pre-training steps for SeqDance, "Final" on the x-axis represents the evaluation of released codes of the other methods, and 200k steps for SeqDance.



Supplementary Figure 4. SeqDance's overall performance on the protein stability dataset.

A. Comparison of SeqDance, GearNet, ESM2, and ESM_IF1 embeddings in predicting mutation effects on protein folding stability. The training and test sets were divided by protein, and four-fold cross-validation was employed to determine Spearman correlation and mean squared error. The plots show the means and standard deviations of evaluation metrics across ten independent repeats.

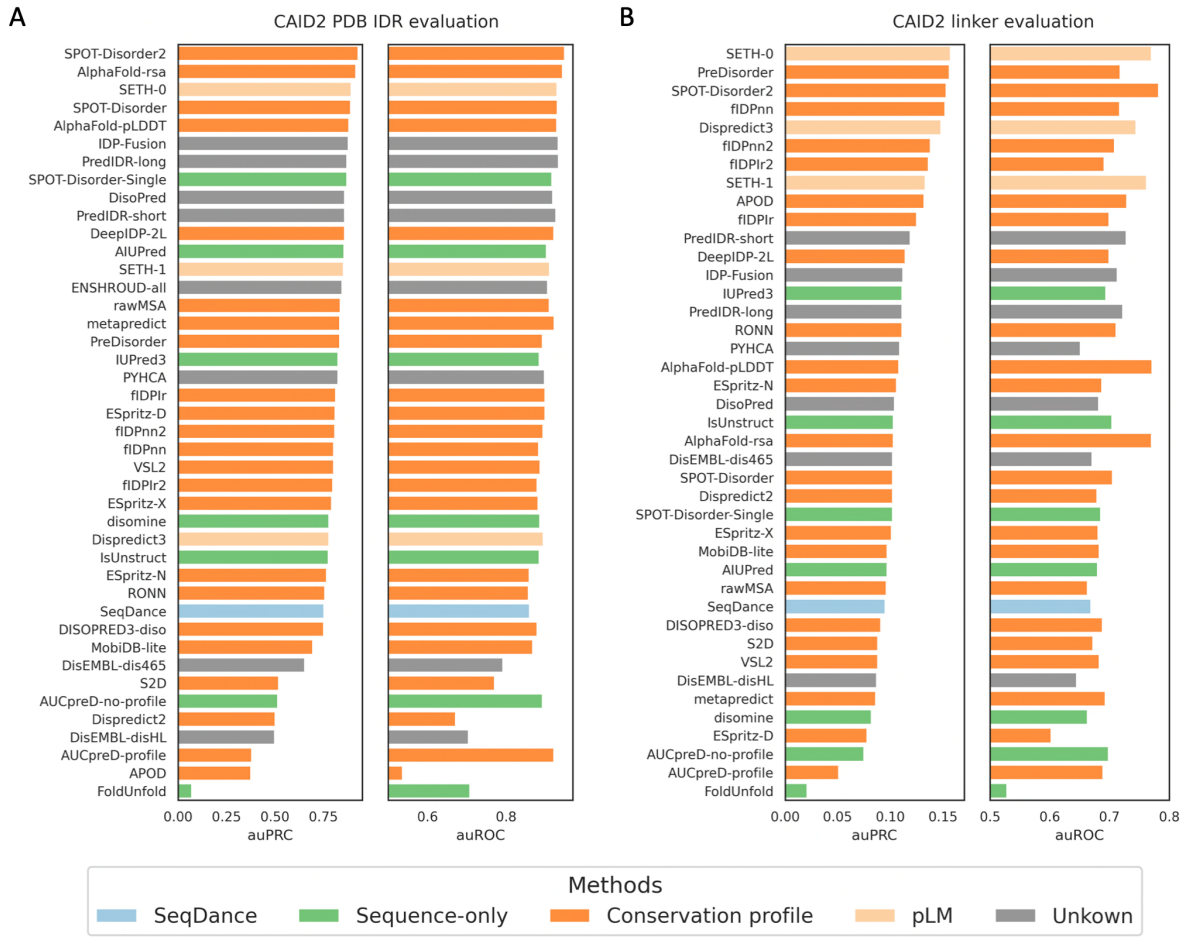
B. Comparison of the combination of SeqDance and ESM2 (650M) and the combination of ESM2 (35M) and ESM2 (650M) in predicting mutation effects. The training and test sets were divided either randomly or by protein, and four-fold cross-validation was employed to determine Spearman correlation and mean squared error (MSE). The violin plots show the distribution of evaluation metrics across ten independent repeats.



Supplementary Figure 5. SeqDance performance on individual proteins.

A. Performance comparison between designed proteins and PDB proteins across different methods.

B. Comparison of SeqDance's performance on PDB proteins categorized by sequence similarity to the pre-training dataset. Among the PDB proteins, 117 have at least 50% sequence identity (with at least 80% coverage) to at least one SeqDance training sequence, 14 have at least 20% sequence identity (with at least 60% coverage), and 50 are unrelated. The orange horizontal line represents a Spearman correlation of 0.5.



Supplementary Figure 6. Fine-tuning SeqDance for predicting intrinsically disordered regions (IDRs) related tasks.

Performance comparison for predicting PDB IDRs (disordered residues in PDB structures) (**A**) and linker regions (**B**) in Critical Assessment of Intrinsic Disorder (CAID2). Performance is evaluated using the area under the Receiver Operating Characteristic curve (auROC) and the area under the Precision-Recall curve (auPRC). The auROC and auPRC for other methods were obtained from the CAID2 website. Methods evaluated in CAID2 are classified into four categories: sequence-only methods using features from single sequences; conservation profile-based methods; protein language model (pLM)-based methods; and methods with unknown inputs.