

PAPER

# A New Paradigm for Applying Deep Learning to Protein-Ligand Interaction Prediction

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## Abstract

Protein-ligand interaction prediction poses a significant challenge in the field of drug design. Numerous machine learning and deep learning models have been developed to identify the most accurate docking poses of ligands and active compounds against specific targets. However, the current models often suffer from inadequate accuracy and lack practical physical significance in their scoring systems. In this research paper, we introduce IGModel, a novel approach that leverages the geometric information of protein-ligand complexes as input for predicting the root mean square deviation (RMSD) of docking poses and the binding strength (the negative value of the logarithm of binding affinity, pKd) with the same prediction framework. By incorporating the geometric information, IGModel ensures that its scores carry intuitive meaning. The performance of IGModel has been extensively evaluated on various docking power test sets, including the CASF-2016 benchmark, PDBbind-CrossDocked-Core, and DISCO set, consistently achieving state-of-the-art accuracies. Furthermore, we assess IGModel's generalization ability and robustness by evaluating it on unbiased test sets and sets containing target structures generated by AlphaFold2. The exceptional performance of IGModel on these sets demonstrates its efficacy. Additionally, we visualize the latent space of protein-ligand interactions encoded by IGModel and conduct interpretability analysis, providing valuable insights. This study presents a novel framework for deep learning-based prediction of protein-ligand interactions, contributing to the advancement of this field.

**Key words:** protein-ligand interaction, scoring function, deep learning, graph neural network

### Key Messages

- We introduce the first framework for simultaneously predicting the RMSD of the ligand docking pose and its binding strength to the target.
- IGModel can effectively improve the accuracy of identifying the near-native binding poses of the ligands, and can still outperform most baseline models in scoring power, ranking power and screening power tasks.
- IGModel is still ahead of other state-of-the-art models in the unbiased data set and the target structure predicted by AlphaFold2, proving its excellent generalization ability.
- Latent space provided by IGModel learns the physical interactions, thus indicating the robustness of the model.

## Introduction

Understanding the precise binding poses of ligands within protein receptor structures holds immense significance in the field of drug design[1, 2, 3, 4]. By accurately predicting ligand binding poses, researchers gain valuable insights into the intricate mechanisms underlying drug-target interactions. This knowledge empowers them to optimize binding affinity,

selectivity, and pharmacological properties, ultimately leading to the development of more potent and efficient therapeutic agents[5, 6].

Although experimental methods can be employed to determine the binding mode of small molecules within proteins, their efficiency tends to be relatively low, and their accuracy is not always guaranteed[7, 8]. Experimental technique such

as X-ray diffraction offers atomic insights into protein-ligand interactions, is often time-consuming, resource-intensive, and may encounter challenges in obtaining high-resolution structures or capturing dynamic aspects of the binding process[9, 10]. Additionally, experimental approaches may be limited by the availability of suitable protein samples and the complexity of the system under investigation. Consequently, relying solely on experimental techniques for ligand binding pose determination may not always meet the demands of high-throughput drug discovery and design[11].

Computational methods, such as molecular docking, play a pivotal role in this endeavor, offering efficient and accurate tools to explore the vast chemical space and guide rational drug design efforts[12, 13, 14, 15]. To guide fast and accurate protein-ligand complex structure prediction, especially the ligand binding pattern (given that the protein structure is already known or determined), the scoring functions (SFs) are developed[16, 17]. SFs are used to calculate the binding energy or score associated with each pose, allowing for the ranking and selection of the most favorable binding configurations[17, 9]. During ligand pose prediction, SFs consider various factors, such as the complementarity of molecular shapes, electrostatic interactions, van der Waals forces, hydrogen bonding, and solvation effects[11]. By evaluating these energy terms, SFs estimate the overall binding affinity or likelihood of a ligand pose being biologically relevant. SFs help guide the exploration of ligand conformational space, identifying potential binding modes and providing insights into the binding strength and specificity of ligand-receptor interactions[18]. They enable researchers to prioritize ligand poses for further analysis or optimization, facilitating the rational design of drug candidates with improved binding affinity and selectivity[9, 19].

In the 1980s, people began to design rules for evaluating ligand binding mode based on physical knowledge and expert experience, or using the force field parameters from biomolecule simulation systems, which was the early SF[20]. The traditional SF is usually a polynomial with few parameters and atom type definitions, thus is not accurate enough to describe the conformational space of the protein-ligand complex[21]. Another category of SF involves machine learning (ML)-based approaches, which have been traced back to 2004[22]. This kind of SF predicts the ligand binding affinity by extracting interaction features using various machine learning techniques[23, 24]. Over the years, numerous notable SFs have been proposed, including RF-Score[25] (as well its virtual screen version, RF-score-VS), NN-Score[26], AGL-Score[27], etc. These SFs have achieved excellent performance ("scoring power"[28]) under the PDBbind related benchmarks. The growing availability of public experimental data and advancements in DL algorithms have led to a rising trend of utilizing DL models for predicting protein-ligand interactions[29, 30, 31]. Since 2017, numerous DL-based models have been introduced for predicting protein-ligand affinity. For example, AtomNet[32],  $K_{deep}$ [33] and Pafnucy[34] employed 3D convolutional neural networks (CNN) to establish a connection between the 3D mesh representation of the complex and its affinity. Additionally, our group has contributed two 2D convolution-based models, namely OnionNet and OnionNet-2, which assess protein-ligand affinity by counting the number of contacts between ligand atoms and protein atoms/residues in different distance intervals[35, 36]. However, recent studies have revealed that ML or DL models trained with only native structures exhibit limited performance when applied to docking power and screening power tasks, despite their

strong performance in scoring power[37]. In order to make the model applicable to practical scenarios, researchers began to design predictors that can be directly applied to identify near-native poses of the ligand or screening active compounds. For instance, DeepBSP employed 3D CNN to predict the RMSD of ligand docking poses[38]. The DeepRMSD+Vina, previously proposed by our group, adopts the modified formats of van der Waals and columbic terms used in many traditional force fields in molecular mechanics as features and has been demonstrated to be effective in docking power and docking pose optimization[39]. In addition, DeepDock utilized a graph neural network to learn the distance probability distribution between protein-ligand atoms, rather than directly predicting the protein-ligand binding affinity or the ligand pose RMSD[40]. However, it turns out that many DL scoring functions could not perform well for all evaluation metrics[28]. Building upon the idea of DeepDock, RTMScore introduced a novel graph representation and employed a graph transformer model to learn distance probability distributions, achieving state-of-the-art results across multiple virtual screening test sets and docking poses prediction tasks[41]. More researches now realized the importance to have balanced performance for both docking and screening tasks[42, 43, 44].

Among the numerous deep learning methods mentioned above, they either provide affinity prediction or ligand pose prediction, with few being able to simultaneously offer directly interpretable indicators with physical meanings, which is more intuitive for computational drug developers[45, 28]. Other methods lack robustness, especially when using predicted structures or cross-docked structures as protein templates, there are few approaches that can accurately predict the optimal ligand binding poses[46, 47].

To these ends, we proposed a SF based on the geometric graph neural network, named IGModel, to further elevate the upper limit of protein-ligand interaction prediction, especially the docking poses prediction. The input of IGModel includes two graphs: one is the protein binding pocket graph, and the other is the protein-ligand atomic interaction graph. Unlike previous graph representations[48, 49], IGModel integrates the distance and orientation between interacting atoms as geometric features of the complex to provide a more comprehensive description of the relative positions of the ligand within the binding pocket. We employ EdgeGAT layers proposed by Kamiński et al.[50] to encode the protein-ligand interaction to obtain a latent vector which is further decoded into the RMSD of the pose and the binding strength to the protein through two decoding modules. Therefore, IGModel can be subdivided into two sub-branches, namely IGModel<sub>RMSD</sub> and IGModel<sub>pkd</sub>. In the CASF-2016[28] docking power test, IGModel<sub>RMSD</sub> achieved the highest Top1 docking success rate (97.5% and 95.1% when including and excluding the native poses, respectively). On cross-docking datasets like PDBbind-CrossDocked-Core set[51] and DISCO set[52], IGModel still performs well, which is comparable or even better than other baseline models. In addition, IGModel can also show excellent performance on the unbiased test set and the datasets containing target structures generated by AlphaFold2[53], proving that IGModel has outstanding generalization ability and are practical for drug discovery. The model captures key charge-charge or hydrogen bond interactions indicating potential robustness for protein-ligand interaction prediction and the model thus could also be used for lead optimization. Overall, we present a highly accurate ligand pose and binding

affinity prediction model which would be an useful tool for drug design.

## Methods

### Datasets

In this study, the native protein-ligand complexes from the PDBbind database (v.2019)[54] along with their corresponding docking poses are utilized for training. In order to increase the diversity of ligand binding conformations, an average of 15 docking poses are generated by AutoDock Vina[55] and ledock[56] for each native protein-ligand complex. Samples from CASF-2016 and those with peptide ligands were excluded, as well as any samples that failed to be parsed by certain programs, such as rdkit[57]. The actual root mean square deviation (RMSD) of docking poses are calculated using the spyrmsd package[58]. The binding affinity (pKd) of the native protein-ligand complex is represented as the negative logarithm of the dissociation constant ( $K_d$ ), inhibition constant ( $K_i$ ), and half-inhibitory concentration (IC50). The parameters for molecular docking and the distributions of RMSD and pKd of docking poses are shown in Supplementary part 1.

### Graphical representation of protein-ligand complexes

Physically, ligand binding within the pocket is influenced by non-bonding interactions, and the potential energy surfaces of protein-ligand binding reveal geometric preferences among atoms. Therefore, accurately describing the relative positions of atoms in the protein-ligand system is crucial for characterizing the protein-ligand interactions. In this study, we construct a heterogeneous graph  $G^{RR,LL,RL}$  to encode protein-ligand interactions. This graph comprises two node types: protein atom nodes ( $V^R$ ) and ligand atom nodes ( $V^L$ ). To conserve computational resources, only protein atoms within 8 Å of the ligand co-crystal structure are used for interaction modeling, without considering all atoms. There are four message-passing channels in  $G^{RR,LL,RL}$ , namely  $E^{RR}$  ( $V^R$  to  $V^R$ ),  $E^{LL}$  ( $V^L$  to  $V^L$ ),  $E^{RL}$  ( $V^R$  to  $V^L$ ), and  $E^{LR}$  ( $V^L$  to  $V^R$ ).

Within the ligand subgraph  $G^L=(V^L, E^{LL})$ , we define seven types of ligand atoms: C, N, O, P, S, Hal (representing halogen elements F, Cl, Br, and I), and DU (representing other element types). If a covalent bond exists between atoms  $i$  and  $j$ , an edge  $e_{ij}^L$  is defined between nodes  $v_i^L$  and  $v_j^L$ . The rdkit package enables the extraction of physical and chemical information related to the chemical bond, which is used as the edge feature in conjunction with the bond length. For the protein subgraph  $G^R=(V^R, E^{RR})$ , we redefined atom types based on the element type, the residue type it belongs to, and whether it is located in the main chain or the side chain. For example, "LYS-MC" and "LYS-SC" represent the C atom on the main chain and side chain of LYS, respectively. The one-hot encoding of atom types, along with aromaticity, charge, and the distance to the  $\alpha$ -C atom, are collectively used as node features for  $G^R$ . When the distance between two nodes  $v_i^R$  and  $v_j^R$  is less than 5 Å, an edge  $e_{ij}^R$  is established, and the edge length serves as the edge feature. If the distance between a protein node  $v_i^R$  and a ligand node  $v_i^L$  is less than 8 Å, directed edges  $e_{i,i}^{RL}$  and  $e_{i,i}^{LR}$  are created, where  $e_{i,i}^{RL}$  denotes the direction from  $v_i^R$  to  $v_i^L$ , and  $e_{i,i}^{LR}$  represents the direction from  $v_i^L$  to  $v_i^R$ . This multilateral architecture facilitates the integration of node and edge information within the protein-ligand graph. To provide a more comprehensive description of the relative positions between protein-ligand atoms, in addition

to considering the interatomic distance, we introduce a novel orientation feature. Specifically, we introduce a dihedral angle  $\varphi$  (formed by the geometric center of the pose,  $v_i^L$ ,  $v_i^R$ , and  $\alpha$ -C), as well as two angles  $\theta_1$  and  $\theta_2$ , as shown in Figure 1B. In Figure 1B,  $C_\alpha$ , R, L and P represent the  $C_\alpha$  of the residue, a certain atom within the residue, a certain atom within the ligand and the geometric center of the ligand, respectively.  $\theta_1$  and  $\theta_2$  are the angles formed between the  $C_\alpha$ -R edge and the L-R edge, as well as P-L edge and R-L edge, respectively. Finally,  $\sin(\varphi/2)$ ,  $\cos(\theta_1/2)$ ,  $\cos(\theta_2/2)$ , and distance are utilized as features for the interaction edge. Table 1 summarizes all the node and edge features within this heterogeneous graph.

As we all know, the physicochemical environment of the binding pocket is critical for ligand binding[59, 60]. However, macroscopic descriptions of binding pockets cannot be effectively conveyed solely through atomic-level interaction graphs. To address this limitation, we construct an undirected graph  $G^P=(V^P, E^P)$  to describe the residue states at the binding pocket. Similar to RTMScore, we defined the binding pocket as the residues within 8 Å around the co-crystallized ligand. Each node  $v_i^P \in V^P$  represents a residue within the binding pocket, and an edge  $e_{ij}^P$  is established when the minimum distance between two residues is less than 10 Å. Node features primarily encompass the residue type, distance distribution between internal atoms, and position relative to the pocket center, while edge features represent the distances between nodes in the main chain atoms. Table 2 summarizes the detailed node and edge features of the binding pocket graph.

### Architecture

IGModel mainly contains three parts: the interaction feature encoding module, the RMSD decoding module and the pKd decoding module.

The encoding part of IGModel comprises two branches, dedicated to handling the binding pocket graph and the protein-ligand interaction graph, with each branch containing two EdgeGAT layers. When the binding pocket graph is input into the encoder, its node features  $h_{pock}$  and edge features  $f_{pock}$  are updated as shown in Eq.1. The updated node features  $h'_{pock}$  is converted into a vector of length 1024 to represent the binding pocket embedding.

$$h'_{pock}, f'_{pock} = EGATConv(EGATConv(h_{pock}, f_{pock})) \quad (1)$$

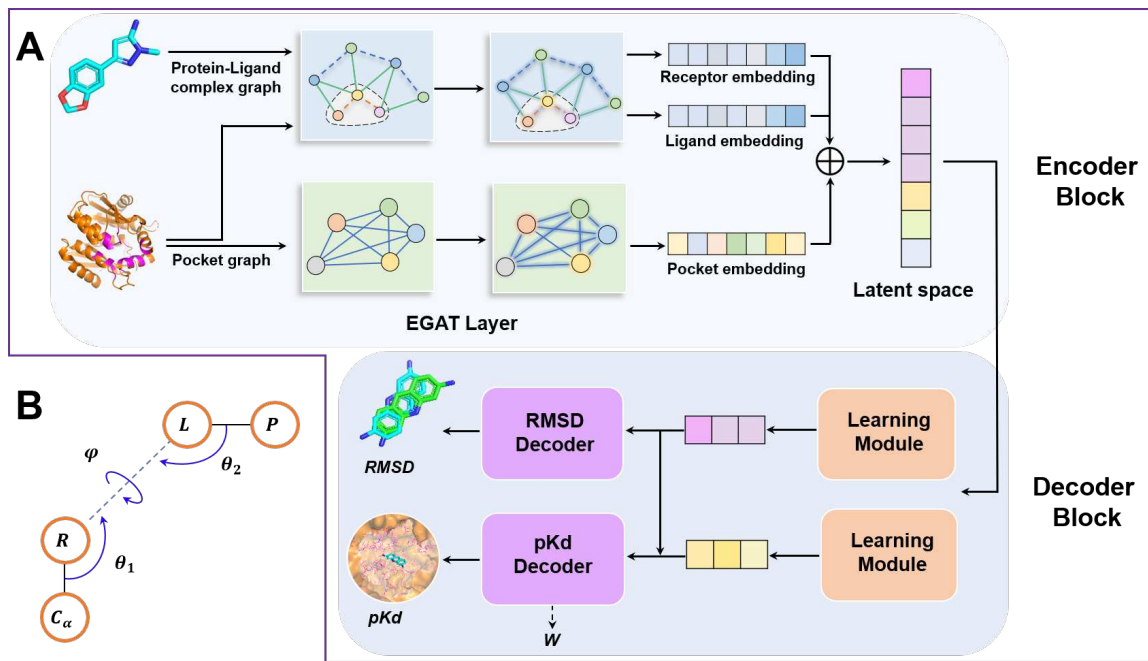
For the protein-ligand interaction graph, the first round of message passing is shown in Eq.2-5. After the first round of message passing, the nodes of protein and ligand atoms have been updated. The updated nodes of the protein and the ligand subgraphs,  $h'_{rec}$  and  $h'_{lig}$ , are as shown in Eq.6-7. After two rounds of updates, the node features of the protein and the ligand are transformed into 1024-dimensional vectors, which serves as embeddings containing information about the protein and ligand atoms. Combining these two embeddings with the binding pocket embedding yields the final latent space describing the protein-ligand interaction.

$$h'_{rec1}, f'_{rec1} = EGATConv(h_{rec}, f_{rec}) \quad (2)$$

$$h'_{rec2}, f'_{lig-rec} = EGATConv((h_{lig}, h_{rec}), f_{lig-rec}) \quad (3)$$

$$h'_{lig1}, f'_{lig1} = EGATConv(h_{lig}, f_{lig}) \quad (4)$$

$$h'_{lig2}, f'_{rec-lig} = EGATConv((h_{rec}, h_{lig}), f_{rec-lig}) \quad (5)$$



**Fig. 1.** Overview of IGModel. A, Illustration of predicting RMSD and pKd from the protein-ligand complex structure. B, The orientation information on the relative positions of protein-ligand atoms.  $C_\alpha$ , R, L and P represent the  $C_\alpha$  of the residue, a certain atom within the residue, a certain atom within the ligand, and the geometric center of the ligand, respectively. The  $\theta_1$  and  $\theta_2$  are the angles between  $C_\alpha$ -R and L-R, and between P-L and R-L, respectively. The  $\psi$  denotes the dihedral angle formed by  $C_\alpha$ , R, L and P.

$$h'_{rec} = \text{BatchNorm}(h'_{rec1}) + \text{BatchNorm}(\text{Linear}(h'_{rec2})) \quad (6)$$

$$h'_{lig} = \text{BatchNorm}(h'_{lig1}) + \text{BatchNorm}(\text{Linear}(h'_{lig2})) \quad (7)$$

The two learning modules in the decoding part consist of a gMLP[61] layer and two linear layers. After passing through these two learning modules, the latent space is converted into two 128-dimensional vectors, namely  $V_{RMSD}$  and  $V_{pKd}$ . In order to make the predicted pKd perceive the change of the RMSD of the ligand pose, we map  $V_{RMSD}$  to a new vector  $V'_{pKd}$  on the space of  $V_{pKd}$ , which is integrated with  $V_{pKd}$  for decoding the pKd.

The training data consists of experimentally determined structures and virtual conformations generated by molecular docking. However, only the binding affinity of native complexes are available. Here, we assume that the binding strength of the binding pose against the target is inversely proportional to its RMSD relative to the native conformation, while the native protein-ligand conformation has the greatest binding affinity. In this work, we aim to learn the relationship between the RMSD of the docking pose and the binding strength through DL. In detail, the model also predicted a decay factor  $W$  (as shown in Figure 1A and Eq.8) with a value range of 0-1 in the pKd decoding part to describe the magnitude of the reduction of pKd with RMSD. Through  $W$  and the previous assumptions, the binding strength ( $pKd_{label}$ ) of the docking pose to the receptor can be deduced, this will serve as the label for pKd (Eq.9).

$$W = \text{Sigmoid}(\text{Linear}(V'_{pKd} + V_{pKd})) \quad (8)$$

$$pKd_{label} = pKd_{nat} - W * RMSD_{real} \quad (9)$$

In Eq.8,  $pKd_{nat}$  is binding affinity between the native conformation of the ligand and the receptor, and  $RMSD_{real}$  is the real RMSD of the docking pose. When  $RMSD_{real}$  is close to 0,  $pKd_{label}$  will be close to  $pKd_{nat}$ .

The loss function during training is defined as follows:

$$\mathcal{L} = \alpha * mse(RMSD_{real}, RMSD_{pred}) + \beta * mse(pKd_{label}, pKd_{pred}) + \gamma * \frac{1}{N} \sum pKd_{pred} \quad (10)$$

where  $\alpha$ ,  $\beta$  and  $\gamma$  are the weights when summing up the components within the loss function. The last term in the loss function is used to constrain the convergence direction of pKd, thus improving the stability of pKd prediction.

## Results

### Evaluation on CASF-2016 benchmark

Distance information between protein and ligand atoms is crucial for describing protein-ligand interaction[25, 35, 21]. However, in this work, we have also incorporated relative positional information between protein and ligand atoms to enhance the characterization of interaction. As illustrated in Figure 2, we introduced two angles,  $\theta_1$  and  $\theta_2$ , as well as a dihedral angle  $\phi$ , which are obviously rotation invariant. Graph representation based on distance and direction will more comprehensively restore the geometric information of protein-ligand atoms.

The performance of the SF is generally evaluated from four aspects: scoring power, ranking power, docking power and screening power as defined in CASF-2016 benchmark[28]. Previous research has shown that some SFs with strong docking power or screening power often have poor scoring power and ranking power, such as DeepRMSD+Vina[39] and RTMScore[41]. In other words, training a model that can be applicable to various tasks with balanced performance is quite challenging[43]. Despite our model primarily focusing on identifying near-native conformation of the ligand (docking

**Table 1.** Node and Edge Features employed for protein-ligand interaction graph.

Features	Size
Nodes (Ligand atoms)	
One hot encoding for the element of the atom ("C", "N", "O", "P", "S", "Hal", "DU")	7
Edges (Ligand-Ligand nodes)	
One hot encoding for the bond type ("SINGLE", "DOUBLE", "TRIPLE", "AROMATIC")	4
Whether the bond is conjugated	1
Whether the bond is in ring	1
One hot encoding for the stereo configuration the bond ("STEREONONE", "STEREOANY", "STEREOZ", "STEREOE")	4
The edge length	1
Nodes (Protein atoms)	
One hot encoding for residue type ("GLY", "ALA", "VAL", "LEU", "ILE", "PRO", "PHE", "TYR", "TRP", "SER", "THR", "CYS", "MET", "ASN", "GLN", "ASP", "GLU", "LYS", "ARG", "HIS", "OTH")	21
One hot encoding for the element of the atom ("C", "N", "O", "S", "DU")	5
Whether the atom is located in the main chain ([1, 0] or [0, 1])	2
Whether the atom is aromatic ([1, 0] or [0, 1])	2
One hot encoding for charge (-1, 0, 1) of the atom	3
Distance between the atom and the $\alpha$ -C atom	1
Edges (Protein-Protein nodes)	
The edge length	1
Edges (Protein-Ligand nodes)	
The edge length	1
$\sin(\varphi/2)$ , $\varphi$ is the dihedral angle formed by the ligand center, the ligand atom, the protein atom and the $\alpha$ -C atom of the residue where the protein atom is located	1
$\cos(\theta_1)$ , $\theta_1$ is the angle formed by the ligand atom, the protein atom and the $\alpha$ -C atom of the residue where the protein atom is located	1
$\cos(\theta_2)$ , $\theta_2$ is the angle formed by the protein atom, the ligand atom and the ligand center	1

power), what is surprising is that it also has a relatively balanced performance in other tasks (Figure 2 and Table 3). Firstly, for docking power, the top 1 success rate of IGModel<sub>rmsd</sub> with native poses included in the test set is 97.5%, and the value remains as high as 95.3% when the native poses are excluded. At the same time, IGModel<sub>pkd</sub> can also achieve the higher top 1 success rates compared to most models, which are 93.0% and 90.0% when crystal structures are included and excluded in the test set, respectively. In addition, screening power refers to the ability of the SFs to identify the true binders to a specific receptor among a large library of compounds, which is measured by two indicators: the first one is the success rate of identifying the highest-affinity binder among the 1%, 5% or 10% top-ranked ligands over all 57 target proteins in the test set; the second indicator is enrichment factor (EF) that is calculated by the average percentage of the true binders among the 1%, 5% or 10% top-ranked candidates across all 57 targets. IGModel achieved a Top 1% success rate of 66.7%, which is comparable to RTMScore[41] but slightly lower than GT\_ft\_1.0[43]. However, the EF achieved by IGModel<sub>pkd</sub> is only 19.8, which is significantly lower than RTMScore and GT\_ft\_1.0, but still higher than most predictors, such as DeepDock[40]. In general, IGModel exhibits a relatively balanced performance across various metrics based on CASF-2016 benchmark. The ablation experiments of IGModel on the validation set and CASF-2016 docking power are shown in Support Information

part 3. Interestingly, for scoring power, IGModel<sub>pkd</sub> achieved a Person correlation coefficient (PCC) of 0.831, which is very close to the 0.834 and 0.824 achieved by GatedCGN\_ft\_1.0[43] and PLANET[42] respectively. The scatter plots of IGModel<sub>pkd</sub> on the validation set and CASF-2016 core set are shown in Support Information part 2. Lastly, for ranking power test, IGModel<sub>pkd</sub> achieved a Spearman correlation coefficient (SCC) of 0.723, which is higher than the 0.686 achieved by GatedCGN\_ft\_1.0.

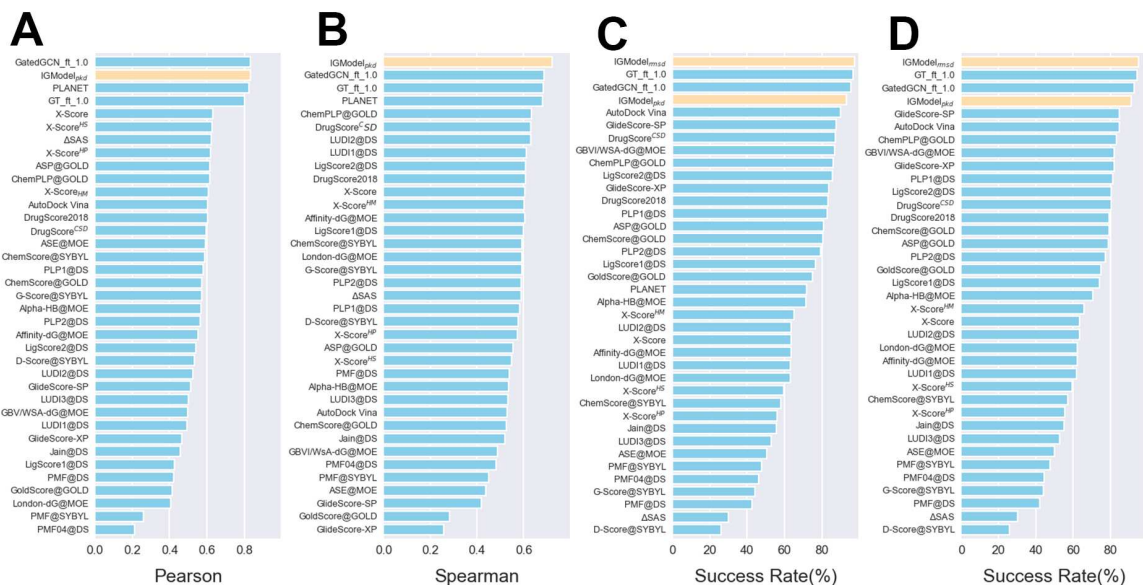
### Evaluation on the redocking and cross-docking test sets

Currently, in most molecular docking applications, the protein is treated as a rigid molecule, which deviated from the actual protein-ligand binding behavior observed in the real world, since the binding pocket could accommodate different compounds with flexible side-chains and sometimes also adjusted backbones[63]. Cross-docking refers to redocking a certain ligand to a non-cognate receptor[52]. Redocking and cross-docking are two ways for evaluating molecular docking, which refers to redocking a certain ligand to a cognate receptor and docking a ligand to a non-cognate receptor in the original pocket, respectively. To comprehensively assess the docking power of IGModel, various redocking and cross-docking benchmarks were adopted.



**Table 2.** Node and Edge Features Employed for protein pocket graph

Features	Size
<b>Nodes</b>	
One hot encoding for residue type (“GLY”, “ALA”, “VAL”, “LEU”, “ILE”, “PRO”, “PHE”, “TYR”, “TRP”, “SER”, “THR”, “CYS”, “MET”, “ASN”, “GLN”, “ASP”, “GLU”, “LYS”, “ARG”, “HIS”, “OTH”)	21
Max distance between any atom and $\alpha$ -C atom	1
Distance between atoms named C and N	1
Distance between $\alpha$ -C atom and the pocket center	1
Max and Min distance between any atom and the pocket center	2
$\sin(\phi/2)$ and $\sin(\psi/2)$ , where $\phi$ and $\psi$ are main chain dihedral angles	2
$\sin(\chi_i/2)$ , where $\chi_i$ ( $i = 1, 2, 3, 4$ and $5$ ) is the side chain dihedral angle. If a dihedral angle does not exist in the residue, it is set to -2.	5
<b>Edges</b>	
Distance between the $\alpha$ -C atoms of two residues	1
Distance between the main-chain carboxyl O atoms of two residues	1
Distance between the main-chain N atoms of two residues	1
Distance between the main-chain carboxyl C atoms of two residues	1
Distance between the centers of two residues	1
Max and min distance between two residues	2



**Fig. 2.** Comparison of the scoring power, ranking power and docking power in the CASF-2016 benchmark with other SFs. The CASF-2016 benchmark is compared with other traditional SFs reported in refxx, as well as some recently reported DL-based models. **A.** Scoring power measures the correlation between the scores of the model and experimental affinity, and the evaluation metric is the Pearson correlation coefficient. **B.** Ranking power evaluates the ability of a SF to rank the known ligands for a certain target, and its evaluation metric is the Spearman correlation coefficient. **C** and **D** show the top 1 success rate when the crystal structures are included and excluded from the test set, respectively.

The first test set we assessed is PDBbind-CrossDocked-Core, with all receptors and ligands derived from the PDBbind v2016 core set. Each ligand was extracted from 285 protein-ligand crystal structures, and then was redocked into the original protein or other four proteins belonging to the same target cluster by three docking softwares: Surflex-Dock, Glide SP and AutoDock Vina. IGModel was tested in these three groups of poses and compared with other SFs, and the results are shown in Table 4 and Figure 3. For cross-docking, the top 1 success rates on poses generated by IGModel<sub>rmsd</sub> with Surflex, Glide and Vina are 0.662, 0.595 and 0.594

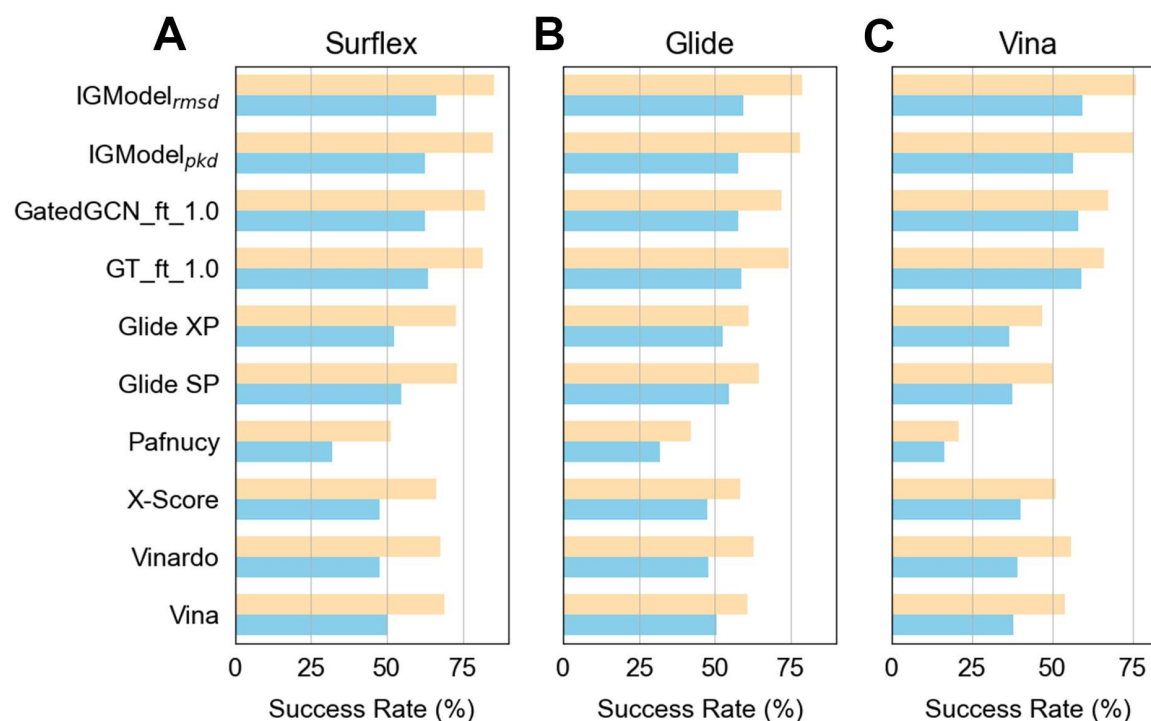
respectively, which is slightly better than GT\_ft\_1.0 and GatedGCN\_ft\_1.0, and significantly ahead of most predictors. Meanwhile, IGModel<sub>pkd</sub> is still able to perform well that is comparable with GatedGCN\_ft\_1.0, though it is slight worse than IGModel<sub>rmsd</sub>. For redocking tasks, the top 1 success rates of IGModel<sub>rmsd</sub> and IGModel<sub>pkd</sub> on poses generated by Surflex, Glide and Vina are 0.854 and 0.850, 0.786 and 0.779 as well as 0.761 and 0.754 respectively, which demonstrate a significant advantage over other SFs.

Another cross-docking test set used in this study is DISCO, which contains 4399 crystal protein-ligand complexes across 95

**Table 3.** The docking power and screening power of several representative SFs on the CASF-2016 benchmark.

Scoring function	docking power		screening power	
	top 1 success rate (w/o native poses)	top 1 success rate (with native poses)	top 1% success rate	enrichment factor
AutoDock Vina[28]	0.846	0.902	0.298	7.70
ChemPLP@GOLD[28]	0.832	0.860	0.351	11.91
GlideScore-SP[28]	0.846	0.877	0.368	11.44
$\Delta_{Vina}RF_{20}$ [28]	0.849	0.891	0.421 (0.456)	11.73 (12.36)
$\Delta_{Vina}XGB$ [62]		0.920	0.368	13.14
$\Delta_{LinE9}XGB$ [45]		0.867	0.404	12.61
OnionNet-SFCT+Vina[44]		0.937	0.421	15.50
DeepBSP[38]	0.872	0.885		
DeepDock[40]		0.870	0.439	16.41
RTMScore[41]	0.934	0.973	0.667	28.0
GT_ft_1.0[43]	0.940	0.966	0.719	28.12
GatedGCN_ft_1.0[43]	0.926	0.954	0.661	23.54
IGModel <sub>pkd</sub>	0.909	0.933	0.667	19.40
IGModel <sub>rmsd</sub>	0.951	0.975		

Note: The results of SFs other than IGModel are cited from the reference.



**Fig. 3.** Docking power of IGModel and other SFs on PDBbind-CrossDocked-Core set. **A**, **B** and **C** show the top 1 success rate of SFs on poses generated by Surflex, GLide and AutoDock Vina, respectively.

protein targets[52]. These targets are sourced from DUD-E[64], thus covering a wide range of protein families. The poses of ligands are generated by AutoDock Vina[55], with 20 poses generated for each protein-ligand pair by default. In order to be consistent with our previous research, each specific target-ligand was treated as a single case when calculating the top1 success rate, which is different from the integrated idea when

tested on PDBbind-CrossDocked-Core set. The performance of IGModel compared to several representative SFs on DISCO set is shown in Figure 4. It can be clearly seen that IGModel<sub>rmsd</sub> is ahead of other baseline SFs, while IGModel<sub>pkd</sub> performs comparably to GatedGCN\_ft\_1.0. The excellent performance of IGModel in redocking and cross-docking tasks proves its significant practical application value.

**Table 4.** Docking power (Top 1 success rate) of IGModel and other SFs on the PDBbind-CrossDocked-Core set.

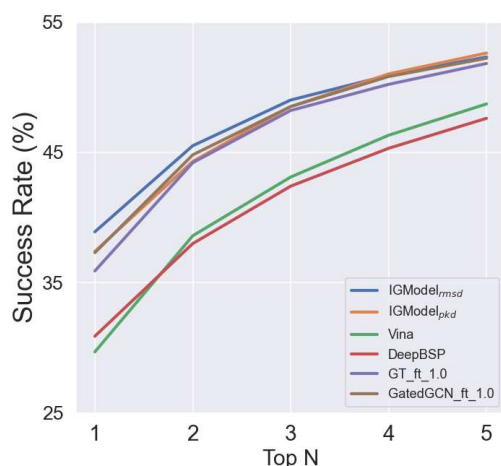
SFs	Surflex		Glide SP		Vina	
	Redocking	Cross-docking	Redocking	Cross-docking	Redocking	Cross-docking
AD4	0.702	0.498	0.603	0.498	0.551	0.437
Vina	0.691	0.505	0.606	0.505	0.540	0.380
Vinardo	0.677	0.477	0.628	0.477	0.558	0.391
X-Score	0.663	0.475	0.582	0.475	0.512	0.401
Pafnucy	0.512	0.319	0.422	0.319	0.211	0.165
Glide SP	0.730	0.547	0.645	0.547	0.502	0.376
Glide XP	0.726	0.525	0.610	0.525	0.470	0.366
GT_ft_1.0	0.815	0.636	0.743	0.585	0.660	0.590
GatedGCN_ft_1.0	0.822	0.627	0.719	0.575	0.674	0.581
IGModel <sub>pkd</sub>	0.850	0.626	0.779	0.577	0.754	0.565
IGModel <sub>rmsd</sub>	0.854	0.662	0.786	0.595	0.761	0.594

Note: The results of SFs other than IGModel are cited from reference[43].

**Table 5.** Pearson and Spearman correlation coefficient of IGModel and other SFs tested on the CASF2016-AF2, unbiased-v2019 and unbiased-v2019-AF2 datasets.

SFs	CASF2016-AF2		unbias-v2019		unbias-v2019-AF2	
	PCC	SCC	PCC	SCC	PCC	SCC
Vina	0.035	0.071	0.364	0.356	0.209	0.192
DeepBSP	0.401	0.375	0.543	0.507	0.451	0.418
DeepRMSD	0.463	0.430	0.285	0.246	0.261	0.247
DeepRMSD+Vina	0.248	0.290	0.405	0.362	0.299	0.287
GT_ft_1.0	0.503	0.455				
GatedGCN_ft_1.0	0.560	0.524				
zPoseScore	0.659	0.593	0.604	0.535	0.554	0.507
IGModel <sub>pkd</sub>	0.736	0.649	0.611	0.522	0.580	0.519
IGModel <sub>rmsd</sub>	0.751	0.669	0.633	0.542	0.609	0.552

Note: The results of SFs other than IGModel are cited from reference[46].



**Fig. 4.** The top N success rate of IGModel and other baseline models on DISCO set.

## Generalization Assessment of IGModel

In this paper, we assessed the generalization ability of the IGModel from two additional perspectives. Firstly, most of SFs do not rigorously eliminate redundancy in the training set, which may lead to the results of SFs on the test set being much better than in actual scenarios. Therefore, we introduced a unbiased test set (called unbiased-v2019 set in this work) that we previously proposed, which contains the protein-ligand pairs with low similarity to those in PDBbind database v2019, and the native conformation of the ligands were excluded[46]. The similarity is defined as the product of protein sequence similarity (calculated by NW-align) and the Tanimoto similarity of the ligand Morgan fingerprints calculated by rdkit[57]. Secondly, when the native conformation of the target is unknown, predicting the binding pose of the ligand becomes even more challenging. Computation methods such as AlphaFold2[53] provide solutions rapidly obtaining high-precision protein structures. Then, on the basis of these predicted protein structures, molecular docking was applied to generate poses of the ligands. In our previously study, CASF-2016 and the unbiased-v2019 were used to construct the test



**Table 6.** Top1 success rate of IGModel and other SFs tested on the CASF2016-AF2, unbiased-v2019 and unbiased-v2019-AF2 datasets.

SFs	CASF2016-AF2		unbias-v2019		unbias-v2019-AF2	
	2Å	3Å	2Å	3Å	2Å	3Å
Vina	0.127	0.208	0.453	0.526	0.130	0.219
DeepBSP	0.180	0.324	0.453	0.584	0.169	0.254
DeepRMSD	0.269	0.425	0.210	0.324	0.089	0.185
DeepRMSD+Vina	0.261	0.416	0.441	0.534	0.144	0.253
GT_ft_1.0	0.273	0.448				
GatedGCN_ft_1.0	0.292	0.465				
zPoseScore	0.339	0.506	0.599	0.700	0.185	0.274
IGModel <sub>pKd</sub>	0.338	0.558	0.562	0.690	0.227	0.318
IGModel <sub>rmsd</sub>	0.364	0.571	0.587	0.690	0.227	0.296

Note: The results of SFs other than IGModel are cited from reference[46].

sets for the AlphaFold2 version, namely CASF-2016-AF2 and unbiased-2019-AF2, respectively[46].

We assessed the docking power of SFs on the three datasets mentioned above. Table 5 shows the Pearson correlation coefficient (PCC) and Spearman correlation coefficient (SCC) between the scores of SFs and the true RMSD. It can be clearly seen that, compared to other baseline SFs, IGModel exhibits remarkably high accuracy. Especially on the unbiased-v2019-AF2 set, IGModel can still perform robustly. The Top1 success rate achieved by SFs with 2Å and 3Å as cutoffs is shown in Table 6, and what is exciting is that IGModel still significantly outperforms other SFs. This effectively verifies the generalization ability and robustness of IGModel in different situations. For CASF2016-AF2 and unbiased-v2019-AF2, two datasets based on the structures predicted by AlphaFold2, since the poses generated by molecular docking have larger RMSDs relative to the native poses, the overall top1 success rate is lower.

## Discussion

Different SFs were developed with various training data for either pKd or RMSD predictions, and a single score (either a traditional SF or a ML/DL-based SF) may perfectly address the docking pose quality[44] regarding the pose selection and virtual screening[28]. For pose selection, RMSD reflects the difference between the docking pose and the native conformation (thus solving the "how it binds" problem), but cannot represent the binding strength with the target protein; while for virtual screening, pKd represents the binding strength between the molecule and the target (regarding the "how strong it binds" problem), but cannot reflect the difference between the docking pose and the native pose [65].

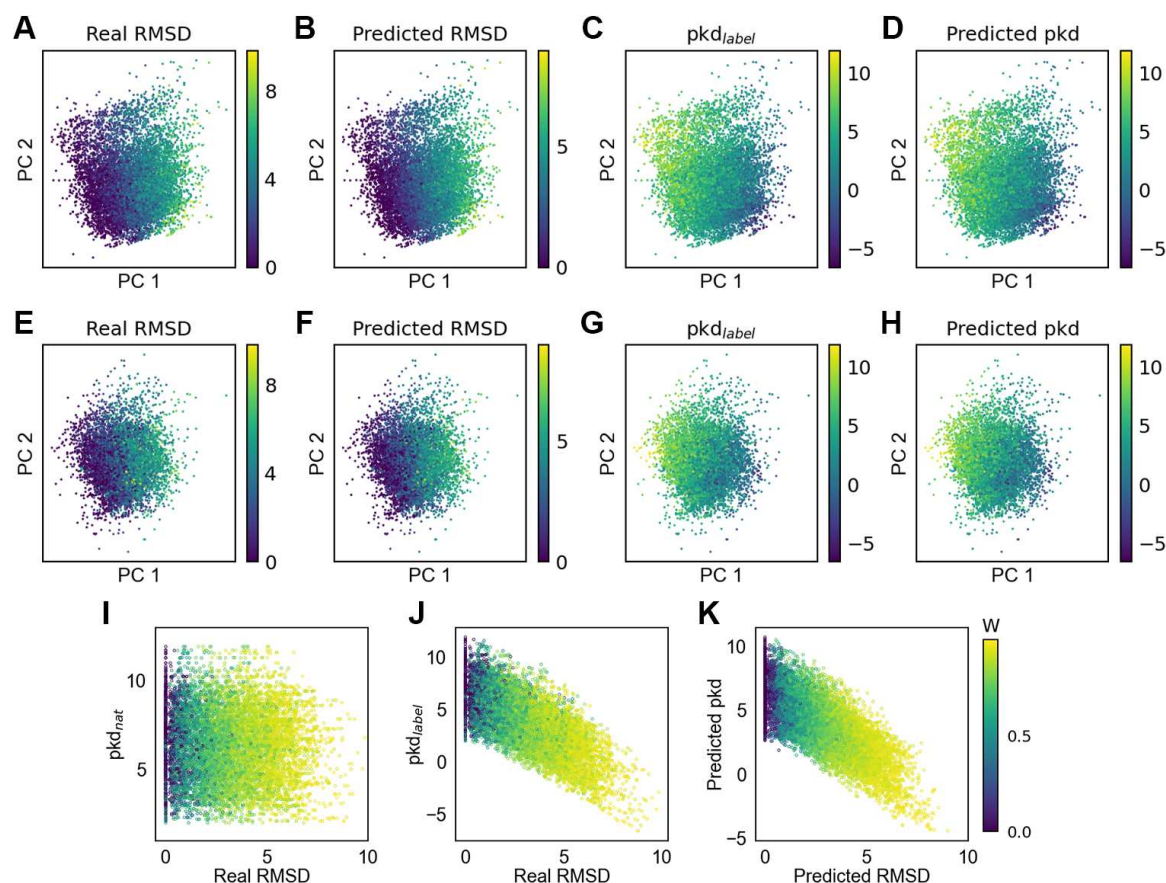
Early ML-based or DL-based SFs usually directly predict protein-ligand binding affinity (pKd) given the native protein-ligand complex structures [25, 34, 35, 36]. However, testing shows that the scores of such models are difficult to distinguish correct binding poses generated by docking tools [28], and their accuracies on screening tasks are neither satisfied[37]. Later, researchers began to directly predict the RMSD of the docking poses (such as Gnina [66], DeepRMSD[39] and DeepBSP[38]), or use scores from other mathematical spaces (such as DeepDock[40], RTMScore[41] and GenScore[43]) but trained with docking poses. The distance likelihood potential

generated by DeepDock, RTMScore and Genscore is difficult to intuitively describe RMSD and the binding strength and could not provide an explicit and physical meaningful predictions for computational chemists. Whereas, RMSD corrected pKd is also used as training target to construct ML models, it could provide direct estimate for both pose binding pattern and molecule binding strength with a single score[62, 45].

To this end, we try to answer the two questions (RMSD prediction for "how it binds" and pKd prediction for "how strong it binds") within one integrated framework, where we characterize the protein-ligand interaction through two geometric graph modules: the pocket graph module and the protein-ligand atomic graph module, and then apply EdgeGAT layers[50] to encode the interaction features. Tests under different scenarios have shown that IGModel is good at predicting the RMSD of the docking poses for both redocking, cross-docking and AF2-based docking tasks, indicating that it has a excellent generalization ability and robustness for pose selection (Tables 3, 4 and 5).

In order to more clearly display the protein-ligand interaction potential energy surface encoded by the graph neural network, we visualized the ligand embedding output by the last EdgeGAT layer in the protein-ligand graph branch and the overall complex embedding. First, we cluster the latent space and the ligand embedding of the samples in the validation set through principal component analysis (PCA), and then color them according to real RMSD, predicted RMSD, pKd<sub>label</sub> and predicted pKd respectively. The distributions of RMSD and pKd on the latent space are shown in Figure 5 A-D. It can be clearly found that as the RMSD and pKd change, obvious layering appears on the pattern. Similar trends can also be observed in ligand embedding pattern (Figure 5 E-H). However, there is a significant phenomenon that the latent space image has a larger coverage area compared to the ligand embedding, which means that the latent space is better able to distinguish the differences between different clusters. This may be attributed to the integration of protein pocket information within the latent space, thus enhancing the representation of protein-ligand interactions.

IGModel, as the first deep learning model capable of simultaneously predicting the RMSD of ligand docking poses relative to the native conformation and the binding strength to the target, is founded on the assumption of the negative correlation between binding strength and RMSDs of docking



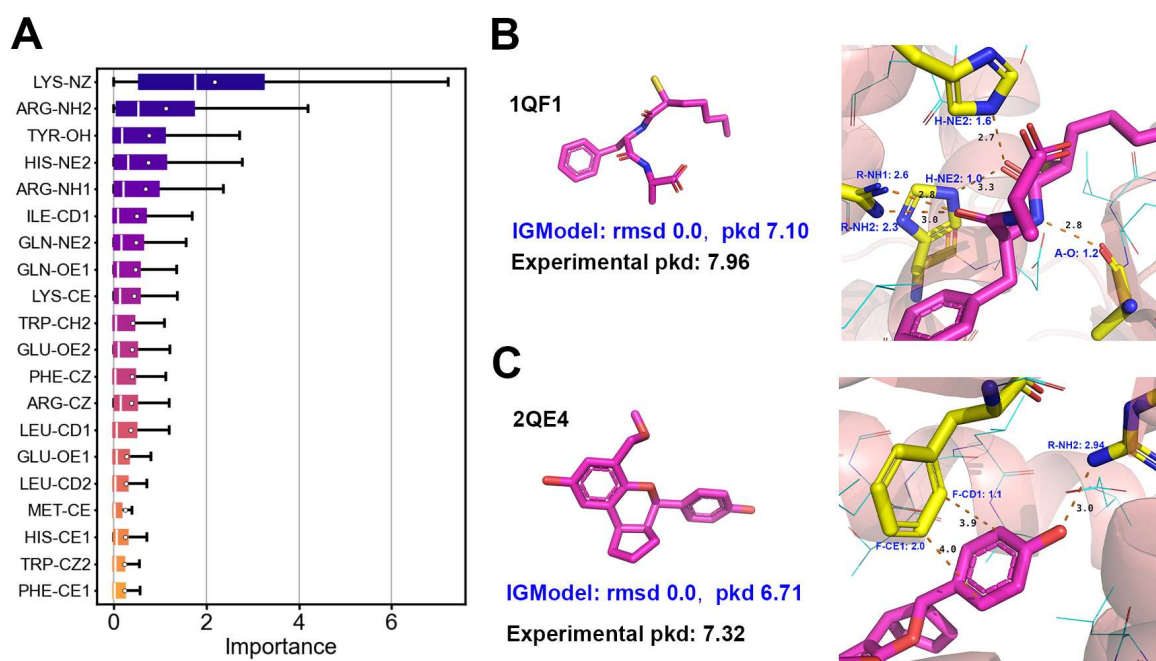
**Fig. 5.** Visualization of the complex embedding, ligand embedding and the decay factor  $W$ . A-D (E-H) show the visualization of the complex embedding (ligand embedding) of samples in the validation set after PCA clustering, colored according to real RMSD, predicted RMSD,  $pKd_{label}$  and predicted  $pKd$ , respectively. I-K present visualization of the decay weight of binding strength with respect to RMSD variations, organized according to  $pKd_{nat}$ -real RMSD,  $pKd_{label}$ -real RMSD and predicted  $pKd$ -Predicted RMSD, respectively. Where  $pKd_{nat}$  refers to the binding affinity of the native protein-ligand complex.

poses. However, the decay weight of binding strength with respect to the RMSDs of docking poses is unknown. Previously, researchers have empirically set functions for the variation of binding strength with RMSD [62, 45], but such manual interventions may introduce systematic errors. Therefore, we hope that the model can obtain the corresponding decay weights based on different protein-ligand complexes (as shown in Figure 1). We display the decay weights according to  $pKd_{nat}$ -real RMSD (Figure 5I),  $pKd_{label}$ -real RMSD (Figure 5J) and predicted  $pKd$ -predicted RMSD (Figure 5K) respectively. One clear trend is that as the RMSD increases, the decay weight  $W$  also increases. This aligns with the initial assumption that poses closer to the native conformation have the stronger binding strength.

Next we also explore the ability of the model to learning physical protein-ligand interactions. It is assumed that protein-ligand binding is majorly driven by non-bonded interactions [67], solvation effects [68] and entropic effects [69]. For non-bonded interactions, in particular, short-range interactions such as hydrophobic interactions, cation- $\pi$  interactions, salt bridges, hydrogen bonds and  $\pi$ - $\pi$  stacking usually provide favorable binding free energies for the protein-ligand complex [70, 71, 67]. However, most current ML/DL-based SFs fail

to explicitly or implicitly emphasize or highlight the direct non-bonded interactions between the protein and the ligand.

Atoms located in different residue side chains, and even those at different positions within the same residue, often exhibit distinct physicochemical properties. Therefore, comprehensively considering multiple features such as residue type, element type, main chain/side chain, polar/non-polar and aromaticity, effectively assigns physiologically relevant identifiers to protein atoms. This makes it possible for IGModel to capture key non-bonded interactions such as hydrogen bonding (Figure 6). We extracted the attention values generated by IGModel for each protein-ligand atom pair in the protein-ligand complexes from CASF-2016 docking poses to examine whether the physical interactions are highlighted or have been paid enough "attentions". The importance of a protein atom is defined as the sum of attention values of the protein-ligand interaction edges in which this protein atom participates. For example, if a protein atom forms edges with five ligand atoms, the importance of the protein atom is represented by the sum of these five attention values. Subsequently, the importance of all protein atom types was counted, with top 20 ranked types displayed in Figure 6 A. We can clearly find that seven of top eight most important protein atoms are polar atoms, which implies the significant role



**Fig. 6.** Explainability and case study. A. Ranking of importance of protein atoms at the binding pocket (only the top 20 protein atom types are shown). B and C show two cases (1QF1 and 2QE4) where IGModel identifies key interactions, including hydrogen bonding and  $\pi$ - $\pi$  stacking. In the two pictures located on the right, the distances between key atoms are shown (black), and the names and importance values of key atoms in the protein are colored in blue.

of polar interactions in protein-ligand binding[70] for binding strength and binding specificity. In addition, certain non-polar atoms, such as ILE-CD1 and PHE-CZ, also play a crucial role. This is because alpha carbon atoms and aromatic rings typically participate in the hydrophobic interactions, while it is the most frequently occurring interaction type in protein-ligand binding. Figure 6B shows that the protein atoms involved in hydrogen bonding have higher importance values, which shows that IGModel is capable of recognizing hydrogen bonds and assigning them greater attention. In Figure 6C, the periphery of the benzene ring in phenylalanine that is close to the benzene ring of the small molecule also has a high importance value, which indicates that IGModel has the ability to detect  $\pi$ - $\pi$  stacking.

## Conclusion

In this work, we propose a new scoring framework called IGModel for protein-ligand interaction prediction, which can simultaneously predicts the RMSD of the ligand binding pose and the binding strength with the target. IGModel applies EdgeGAT layer to encode the two input graphs into the latent space characterizing the protein-ligand interaction, and then decodes the latent space into RMSD and pKd through two decoders respectively. The results show that it achieves SOTA performance in almost all docking power test sets. Although IGModel aims to provide a more comprehensive quality assessment for docking poses, it still performs well on the CASF-2016 scoring power and ranking power test, which is comparable or even better to the other models. For screening power, our model is also ahead of most baseline SFs. Furthermore, IGModel is also evaluated on the more challenging unbiased set unbiased-v2019 and data set containing

target structure predicted by AlphaFold2, proving its strong generalization capabilities. We also visualized the latent space encoded by IGModel, providing an intuitive representation of the energy space describing the RMSD and binding strength of the docking pose. Through case studies, it was observed that IGModel is capable of identifying critical interactions, such as hydrogen bonding and  $\pi$ - $\pi$  stacking.

It is undeniable that one SF is difficult to perform perfectly in all tasks, but IGModel can achieve a relatively balanced performance. The most importance is that IGModel is a new framework for predicting protein-ligand interactions, which breaks the tradition that the SFs only output a single score, and ensures that the output values have intuitive physical meanings. We believe that this framework is valuable for molecular docking and even the modification and optimization of lead compounds in drug design. In summary, our research proposes a new paradigm for the design of SFs in the future, along with new challenges.

## Competing interests

No competing interest is declared.

## Author contributions statement

Z.W. designed research, performed research, analyzed data and wrote the paper; S.W., Y.L., J.G. and Y.W. analyzed data; Y.M. analyzed data and wrote the paper; L.Z. and W.L. designed research, analyzed data and wrote the paper.

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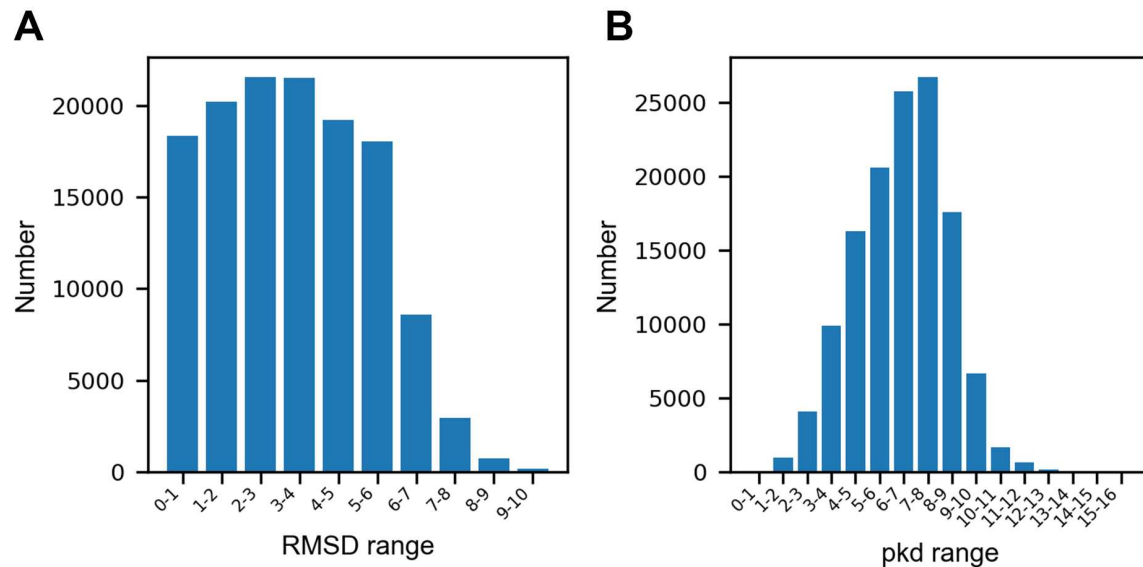


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## Supporting Materials

### Part 1. Details of docking poses in the training set

In this work, docking poses were generated by AutoDock Vina and ledock, where the search space is a 15Å\*15Å\*15Å cubic, the maximum number generated is set to 10, and other parameters are used by default. The RMSD distribution of docking poses and the pKd distribution of the native conformations corresponding to these docking poses are shown in Figure S1.



**Fig. S1.** The RMSD (A) and pKd (B) distributions of docking poses in the training set.

### Part 2. Performance of IGModel and some representative scoring functions in CASF-2016 benchmark

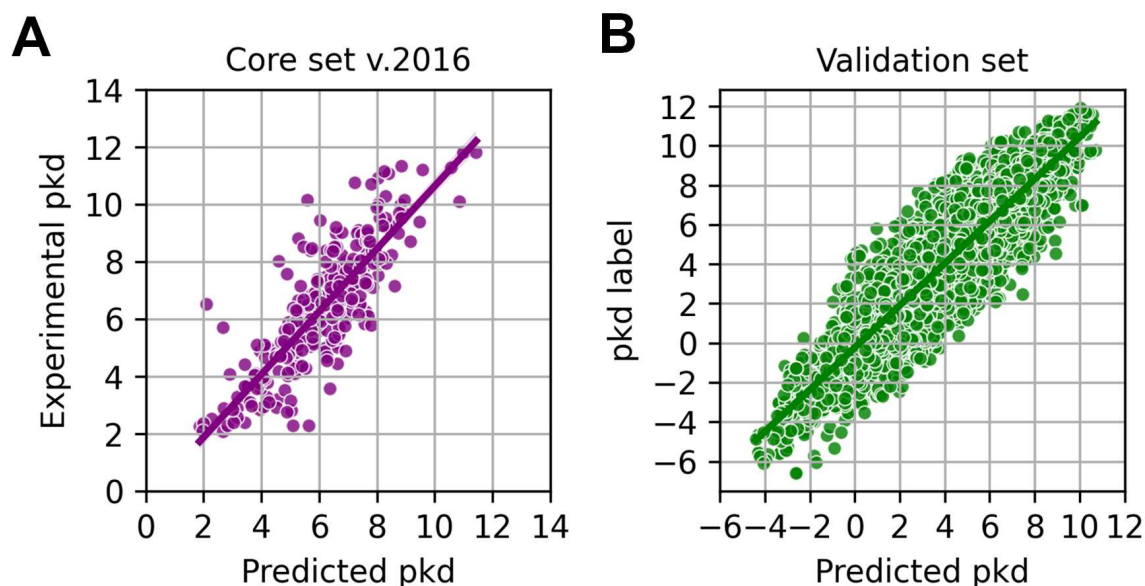
The Pearson correlation coefficient (PCC) and root-mean-squared error (RMSE) achieved by IGModel<sub>pkd</sub> on CASF-2016 core set are 0.831 and 1.254, respectively, as shown in Figure S2A. Figure S2B shows the results of IGModel<sub>pkd</sub> on the validation set, including crystal structures and decoys. The performance of IGModel<sub>pkd</sub> and several recently published representative models on CASF-2016 scoring power in Table S1.

**Table S1.** The scoring power of IGModel<sub>pkd</sub> and other representative scoring functions in CASF-2016 benchmark

Year	SFs	PCC	RMSE	Training set
2023	IGModel <sub>pkd</sub>	0.831	1.254	PDBbind v2019 (general set)
2023	GatedGCN_ft_1.0	0.834		PDBbind v2020 (general set)
2023	GT_ft_1.0	0.802		PDBbind v2020 (general set)
2023	PLANET	0.824	1.247	PDBbind v2020 (general set)
2022	RTMScore	0.455		PDBbind v2020 (general set)
2022	MPNN	0.813	1.511	PDBbind v2016 (general set)

### Part 3. The ablation study of IGModel

As shown in Table S2, when removing Angle 1, Angle 2, dihedral angle formed between the protein atoms and the ligand atoms in the protein-ligand interaction graph, or removing the pocket graph, the performance of IGModel shows varying degrees of decrease.



**Fig. S2.** A. The correlation between the pKd predicted by  $IGModel_{pKd}$  and the experimental pKd for 285 native protein-ligand complexes in the CASF-2016 core set. B. The scatter plot of pKd predicted by  $IGModel_{pKd}$  against the pKd labels on the validation set.

**Table S2.** The ablation experiment of  $IGModel$  on the validation set and CASF-2016 docking power

	Validation set				CASF-2016			
	RMSD		pKd		RMSD (Top 1 success rate)		pKd (Top 1 success rate)	
	PCC	RMSE	PCC	RMSE	including crystal poses	excluding crystal poses	including crystal poses	excluding crystal poses
$IGModel$ W/O Angle 1	0.917	0.815	0.896	1.216	96.1%	94.0%	92.3%	88.4%
$IGModel$ W/O Angle 2	0.923	0.787	0.902	1.247	97.9%	94.4%	93.7%	90.5%
$IGModel$ W/O dihedral angle	0.923	0.792	0.898	1.276	95.1%	91.9%	92.3%	87.4%
$IGModel$ W/O pocket graph	0.894	0.914	0.895	1.281	94.7%	91.2%	86.3%	84.4%
$IGModel$	0.927	0.768	0.905	1.220	97.5%	95.1%	93.3%	90.9%