

Supplemental Information

Table S1: The performance (Pearson) of finetune_pearson, finetune_mse and LumiNet on the CASF-2016 and FEP datasets.

Model	CASF-2016	FEP2	FEP1
finetune_pearson	0.818	0.517	0.543
finetune_mse	0.809	0.445	0.486
LumiNet	0.848	0.463	0.646

Table S2: The performance of the LumiNet model versus baseline model on the FEP1 dataset.^a

Model		BACE	CDK2	JNK1	MCL	p38	PTP1B	Thrombin	TYK	Averag
	No.	36	16	21	42	34	23	11	16	25
LumiNet	R	0.44	0.53	0.45	0.81	0.6	0.79	0.91	0.6	0.65
	ρ	0.42	0.57	0.50	0.80	0.6	0.70	0.89	0.5	0.64
	RMS	1.7	1.39	0.75	0.83	1.0	1.16	1.05	1.1	1.13
PIGNET2 ¹	R	0.42	0.77	0.36	0.78	0.6	0.76	0.83	0.6	0.64
	ρ	0.42	0.67	0.43	0.75	0.6	0.77	0.78	0.5	0.63
	RMS	0.83	1.45	1.14	0.82	1.1	1.03	0.44	2.4	1.16
PBCNET ²	R	0.61	0.66	0.41	0.72	0.56	0.75	0.84	0.64	0.65
	ρ	0.52	0.66	0.47	0.73	0.56	0.71	0.82	0.61	0.64
	RMS	0.91	1.35	1.21	1.11	1.15	1.23	0.42	1.54	1.11
FEP+	R	0.78	0.48	0.85	0.77	0.65	0.8	0.71	0.89	0.74
	ρ	0.74	0.41	0.9	0.78	0.64	0.82	0.62	0.87	0.72
	RMSE	1.03	1.11	1	1.41	1.03	1.22	0.93	0.93	1.08
Glide-SP	R	0	-0.56	0.24	0.59	0.14	0.55	0.53	0.79	0.29
	ρ	0.11	-0.36	0.27	0.5	-0.24	0.23	0.49	0.79	0.23
	RMSE	1.4	2.63	2.16	1.54	3.24	2.8	0.92	2.06	2.09
MM-GB/SA	R	-0.4	-0.53	0.65	0.42	0.66	0.67	0.93	0.79	0.4
	ρ	-	-	-	-	-	-	-	-	-
	RMSE	-	-	-	-	-	-	-	-	-
DeltaDelta ³	R	0.13	0.24	0.55	0.4	0.37	0.47	0.05	0.31	0.32
	ρ	-	-	-	-	-	-	-	-	-
	RMSE	-	-	-	-	-	-	-	-	-
Default2018 ⁴	R	0.14	0.95	0.31	0.29	0.34	0.38	0.27	0.33	0.38
	ρ	-	-	-	-	-	-	-	-	-
	RMSE	-	-	-	-	-	-	-	-	-
Dense ⁴	R	0.37	0.96	-0.1	0.22	0.14	0.63	0.01	0.25	0.31
	ρ	-	-	-	-	-	-	-	-	-
	RMSE	-	-	-	-	-	-	-	-	-

^a RMSEs are reported in kcal·mol⁻¹.

Table S3: The performance of the LumiNet model versus baseline model on the FEP2 dataset.^a

Model		CDK 8	c-Met	Eg 5	HIF-2 α	PFKFB3	SHP- 2	SYK	TNKS2	Averag e
	No.	33	24	28	42	40	26	44	27	33
LumiNet	R	0.32	0.75	0.5	0.39	0.47	0.39	0.35	0.52	0.46
	ρ	0.26	0.73	0.2	0.43	0.50	0.46	0.42	0.41	0.43
	RM	1.74	1.43	2.0	1.12	0.96	1.09	1.10	1.08	1.32
Glide SP	R	0	0	0	0.4	0.47	0.44	0.24	0.37	0.24
	ρ	0.13	0.13	-	0.42	0.51	0.44	0.21	0.32	0.26
	RM	2.49	3.01	1.9	1.51	1.57	1.52	1.27	1.35	1.83
PBCNET	R	0.55	0.7	0.64	0.19	0.43	0.4	0.47	0.36	0.47
	ρ	0.63	0.76	0.58	0.3	0.47	0.56	0.48	0.32	0.51
	RM	1.61	1.88	1.11	1.57	1.4	1.57	1.08	1.71	1.49
FEP+	R	0.62	0.9	0.71	0.61	0.79	0.71	0.5	0.4	0.66
	ρ	0.74	0.88	0.72	0.59	0.79	0.78	0.42	0.41	0.67
	RMSE	2.09	1.43	1.23	1.6	1.78	1.39	1.61	2.2	1.67
MM-GB/SA	R	0.77	0.6	0.14	0.54	0.5	0.6	0	0.26	0.43
	ρ	0.82	0.64	0.1	0.48	0.54	0.5	-0.12	0.22	0.4
	RMSE	7.03	5.96	10.09	11.69	6.99	8.76	15.81	7.9	9.28

^a RMSEs are reported in kcal·mol⁻¹.

Table S4: The performance of LumiNet on the PDE10A dataset based on four

partitioning methods of time splits and random splits.^a

Method	Random split		Temporal split 201 1		Temporal split 201 2		Temporal split 201 3	
	ρ	RMSE	ρ	RMSE	ρ	RMSE	ρ	RMSE
Mean of train. and val	–	1.19	–	1.03	–	1.18	–	1.22
Vanilla GOLD.PLP ⁶	0.31	–	0.20	–	0.29	–	0.54	–
Template GOLD.PLP ⁶	0.45	–	0.31	–	0.56	–	0.66	–
RF-PLP ⁷	0.56	1.10	0.40	1.05	0.62	0.97	0.61	0.99
AttentiveFP ⁸	0.70	0.86	0.40	1.07	0.32	1.74	0.44	1.16
2D3D hybrid	0.72	0.85	0.57	0.81	0.56	1.25	0.61	0.95
ACNN ⁹	0.65	1.00	0.37	1.45	0.08	1.60	0.54	1.02
PotentialNet ¹⁰	0.55	1.68	0.34	2.53	0.45	2.22	0.67	1.90
AttentiveFP extended	–	–	0.41	1.12	0.51	1.08	0.60	1.07
2D3D hybrid extended	–	–	0.57	0.82	0.68	0.90	0.66	0.90
LumiNet	0.80	0.76	0.55	0.91	0.74	0.82	0.68	1.14

^a RMSEs are reported in kcal·mol⁻¹.

Table S5: The performance of LumiNet on the PDE10A dataset based on three partitioning methods of structural binding models.^a

Method	aminohetaryl_c1_a		c1_hetaryl_alkyl_c2_		aryl_c1_amide_c2_	
	ρ	RMSE	ρ	RMSE	ρ	RMSE
Mean of train. and val	–	1.18	–	1.14	–	1.24
Vanilla GOLD.PLP	0.20	–	0.38	–	0.25	–
Template GOLD.PLP	0.33	–	0.49	–	0.59	–
RF-PLP	0.40	1.48	0.42	1.09	0.52	1.18
AttentiveFP	0.40	1.28	0.11	2.04	0.24	1.25
2D3D hybrid	0.47	1.04	0.31	1.36	0.50	1.05
LumiNet	0.56	-	0.64	-	0.49	-

^a RMSEs are reported in kcal·mol⁻¹.

Table S6: Semi-supervised learning for the best effect of the first strategy optimization on the FEP1 dataset.^a

No. iter		BAC E	CDK 2	JNK1	MCL1	p38	PTP1 B	Thrombin	TYK2	Average
		No.	36	16	21	42	34	23	11	16
LumiNet	R	0.44	0.53	0.45	0.81	0.6	0.79	0.91	0.60	0.65
	ρ	0.42	0.57	0.50	0.80	0.6	0.70	0.89	0.59	0.64
	RMSE	1.7	1.39	0.75	0.83	1.0	1.16	1.05	1.16	1.13
iteration 1	R	0.48	0.66	0.61	0.62	0.65	0.75	0.86	0.72	0.67
	ρ	0.50	0.72	0.64	0.63	0.68	0.75	0.85	0.73	0.69
	RMSE	-	-	-	-	-	-	-	-	-
iteration 2	R	0.47	0.67	0.68	0.75	0.65	0.73	0.92	0.69	0.70
	ρ	0.48	0.73	0.73	0.76	0.67	0.71	0.87	0.68	0.70
	RMSE	-	-	-	-	-	-	-	-	-

^a MAEs and RMSEs are reported in kcal·mol⁻¹.

Table S7: Semi-supervised learning for the best effect of the first strategy optimization on the FEP2 dataset.^a

No. iter		CDK8	c-Met	Eg5	HIF-2 α	PFKF B3	SHP-2	SYK	TNKS 2	Average
	No.	33	24	28	42	40	26	44	27	33
LumiNet	R	0.32	0.7	0.50	0.39	0.47	0.39	0.35	0.52	0.46
	ρ	0.26	0.7	0.22	0.43	0.50	0.46	0.42	0.41	0.43
	RMS	1.74	1.4	2.05	1.12	0.96	1.09	1.1	1.08	1.32
iteration 1	R	0.34	0.89	0.60	0.40	0.38	0.50	0.40	0.51	0.50
	ρ	0.27	0.85	0.38	0.48	0.44	0.55	0.41	0.47	0.48
	RMSE	-	-	-	-	-	-	-	-	1.23
iteration 2	R	0.44	0.81	0.70	0.41	0.36	0.57	0.45	0.49	0.53
	ρ	0.44	0.77	0.51	0.50	0.45	0.59	0.43	0.40	0.51
	RMSE	-	-	-	-	-	-	-	-	1.21

^a RMSEs are reported in kcal·mol⁻¹.

Table S8: Semi-supervised learning for the average effect of the second strategy optimization on the FEP1 dataset.^a

Repeat	No. 2			No. 6		
	R	ρ	RMSE	R	ρ	RMSE
1	0.67	0.64	0.89	0.75	0.75	0.81
2	0.69	0.71	0.95	0.71	0.72	0.81
3	0.67	0.66	1.05	0.74	0.75	0.81
4	0.66	0.65	1.00	0.72	0.73	0.87
5	0.70	0.69	0.93	0.74	0.71	0.81
Average	0.68	0.67	0.96	0.73	0.73	0.82

^a RMSEs are reported in kcal·mol⁻¹.

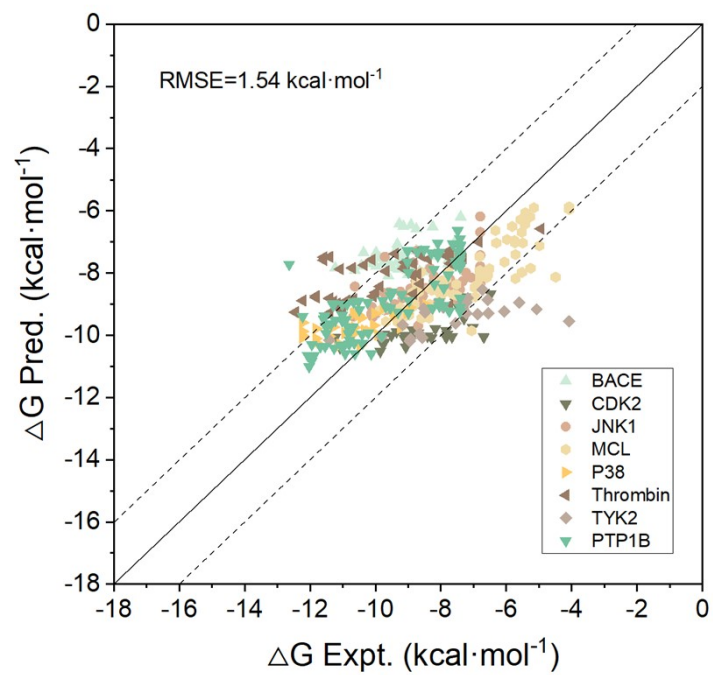


Figure S1: The performance of LumiNet on the extended FEP1 dataset⁵, which includes 8 targets and 407 ligands.

References

1. S. Moon, S.-Y. Hwang, J. Lim and W. Y. Kim, PIGNet2: a versatile deep learning-based protein–ligand interaction prediction model for binding affinity scoring and virtual screening, *Digital Discovery*, 2024, **3**, 287-299.
2. J. Yu, Z. Li, G. Chen, X. Kong, J. Hu, D. Wang, D. Cao, Y. Li, R. Huo, G. Wang, X. Liu, H. Jiang, X. Li, X. Luo and M. Zheng, Computing the relative binding affinity of ligands based on a pairwise binding comparison network, *Nature Computational Science*, 2023, **3**, 860-872.
3. J. Jiménez-Luna, L. Pérez-Benito, G. Martínez-Rosell, S. Sciabola, R. Torella, G. Tresadern and G. De Fabritiis, DeltaDelta neural networks for lead optimization of small molecule potency, *Chemical Science*, 2019, **10**, 10911-10918.
4. A. T. McNutt and D. R. Koes, Improving $\Delta\Delta G$ Predictions with a Multitask Convolutional Siamese Network, *Journal of Chemical Information and Modeling*, 2022, **62**, 1819-1829.
5. H. Goel, A. Hazel, V. D. Ustach, S. Jo, W. Yu and A. D. MacKerell, Rapid and accurate estimation of protein–ligand relative binding affinities using site-identification by ligand competitive saturation, *Chemical Science*, 2021, **12**, 8844-8858.
6. A. Tosstorff, J. C. Cole, R. Taylor, S. F. Harris and B. Kuhn, Identification of Noncompetitive Protein–Ligand Interactions for Structural Optimization, *Journal of Chemical Information and Modeling*, 2020, **60**, 6595-6611.
7. A. Tosstorff, J. C. Cole, R. Bartelt and B. Kuhn, Augmenting Structure-Based Design with Experimental Protein-Ligand Interaction Data: Molecular Recognition, Interactive Visualization, and Rescoring, *ChemMedChem*, 2021, **16**, 3428-3438.
8. Z. Xiong, D. Wang, X. Liu, F. Zhong, X. Wan, X. Li, Z. Li, X. Luo, K. Chen, H. Jiang and M. Zheng, Pushing the Boundaries of Molecular Representation for Drug Discovery with the Graph Attention Mechanism, *Journal of Medicinal*

Chemistry, 2020, **63**, 8749-8760.

9. J. Gomes, B. Ramsundar, E. N. Feinberg and V. S. Pande, Atomic convolutional networks for predicting protein-ligand binding affinity, *arXiv preprint arXiv:1703.10603*, 2017.
10. E. N. Feinberg, D. Sur, Z. Wu, B. E. Husic, H. Mai, Y. Li, S. Sun, J. Yang, B. Ramsundar and V. S. Pande, PotentialNet for Molecular Property Prediction, *ACS Central Science*, 2018, **4**, 1520-1530.