A Appendix

A.1 Additional results

Table 5: Mean absolute error (MAE $\pm$ σ; lower is better) of different predictors on the Caco-2 benchmark with varying numbers of test samples included in fine-tuning (n). Best results in bold; next-best is underlined.

	size	$n = 0$	$n = 7$	$n = 10$	$n = 25$	$n = 50$	$n = 100$
dummy	0	0.57±0.00	0.60±0.00	0.59±0.00	0.58±0.00	0.57±0.00	0.57±0.00
z	128	0.58±0.04	0.55±0.01	0.52±0.01	0.45±0.01	0.41±0.01	0.37±0.01
all attributes	208	0.60±0.09	**0.53**±0.01	0.51±0.01	0.42±0.01	0.37±0.01	0.32±0.01
all attributes+z	336	0.70±0.07	0.54±0.01	**0.50**±0.01	**0.41**±0.01	**0.36**±0.01	**0.31**±0.01
GES blanket	170	0.58±0.06	**0.53**±0.01	**0.50**±0.01	0.42±0.01	**0.36**±0.01	0.32±0.01
LiNGAM blanket	199	0.61±0.07	**0.53**±0.01	**0.50**±0.01	**0.41**±0.01	**0.36**±0.01	**0.31**±0.01
Group Lasso blanket	62	0.68±0.05	0.54±0.01	0.52±0.01	0.45±0.01	0.40±0.01	0.34±0.01
PPFS blanket	107	0.71±0.06	0.54±0.01	0.52±0.01	0.43±0.02	0.38±0.02	0.32±0.01
PL blanket	176	0.56±0.08	**0.53**±0.01	**0.50**±0.01	**0.41**±0.01	**0.36**±0.01	0.32±0.01
PL blanket (FS)	174	**0.53**±0.04	**0.53**±0.01	**0.50**±0.01	**0.41**±0.01	**0.36**±0.01	**0.31**±0.01

Table 6: Spearman correlation (ρ $\pm$ σ; higher is better) of different predictors on the Hepatocyte clearance benchmark with varying numbers of test samples included in fine-tuning (n). Best results in bold; next-best is underlined.

	size	$n = 0$	$n = 7$	$n = 10$	$n = 25$	$n = 50$	$n = 100$
dummy	0	—	—	—	—	—	—
z	128	0.27±0.01	0.09±0.02	0.11±0.02	0.15±0.03	0.20±0.03	0.24±0.03
all attributes	208	**0.37**±0.01	**0.13**±0.01	**0.16**±0.01	**0.22**±0.02	**0.27**±0.02	0.30±0.02
all attributes+z	336	0.35±0.01	**0.13**±0.02	0.14±0.01	0.21±0.01	0.25±0.02	0.29±0.02
GES blanket	163	0.35±0.01	0.11±0.02	0.15±0.02	0.20±0.02	0.25±0.02	0.30±0.02
LiNGAM blanket	194	**0.37**±0.01	**0.13**±0.02	**0.16**±0.01	0.21±0.02	0.26±0.02	0.31±0.02
Group Lasso blanket	168	0.35±0.01	0.11±0.02	0.12±0.02	0.18±0.01	0.23±0.02	0.29±0.02
PPFS blanket	107	0.36±0.01	**0.13**±0.02	**0.16**±0.01	0.21±0.01	**0.27**±0.01	**0.34**±0.01
PL blanket	151	0.36±0.01	0.11±0.02	0.14±0.01	0.19±0.01	0.23±0.01	0.27±0.02
PL blanket (FS)	174	0.35±0.00	0.11±0.02	0.14±0.01	0.20±0.02	0.24±0.02	0.28±0.01

Table 7: Spearman correlation ($\rho \pm \sigma$; higher is better) of different predictors on the Microsome clearance benchmark with varying numbers of test samples included in fine-tuning (n). Best results in bold; next-best is underlined.

	size	$n = 0$	$n = 7$	$n = 10$	$n = 25$	$n = 50$	$n = 100$
dummy	0	—	—	—	—	—	—
z	128	0.43±0.02	0.16±0.02	0.17±0.03	0.23±0.03	0.28±0.03	0.33±0.03
all attributes	208	0.65±0.01	0.39±0.04	0.43±0.02	0.47±0.02	0.50±0.02	0.53±0.02
all attributes+z	336	**0.66**±0.01	0.39±0.03	0.42±0.02	0.47±0.01	0.51±0.02	0.54±0.01
GES blanket	154	0.64±0.01	0.37±0.02	0.41±0.03	0.45±0.01	0.49±0.02	0.51±0.03
LiNGAM blanket	191	**0.66**±0.01	**0.41**±0.02	0.43±0.02	**0.49**±0.01	**0.53**±0.01	**0.55**±0.02
Group Lasso blanket	172	**0.66**±0.01	0.39±0.03	**0.44**±0.02	**0.49**±0.02	0.52±0.02	**0.55**±0.03
PPFS blanket	101	0.62±0.02	0.35±0.02	0.40±0.01	0.45±0.02	0.49±0.02	0.52±0.02
PL blanket	121	0.65±0.01	0.40±0.02	**0.44**±0.01	0.47±0.01	0.50±0.01	0.53±0.02
PL blanket (FS)	174	**0.66**±0.01	0.40±0.02	0.43±0.02	0.48±0.01	0.51±0.02	0.53±0.02

Table 8: Spearman correlation ($\rho \pm \sigma$; higher is better) of different predictors on the VDss benchmark with varying numbers of test samples included in fine-tuning (n). Best results in bold; next-best is underlined.

	size	$n = 0$	$n = 7$	$n = 10$	$n = 25$	$n = 50$	$n = 100$
dummy	0	—	—	—	—	—	—
z	128	0.49±0.02	0.16±0.02	0.21±0.04	0.32±0.04	0.41±0.02	0.47±0.01
all attributes	208	0.68±0.01	0.37±0.03	0.45±0.03	0.60±0.02	0.65±0.02	0.66±0.01
all attributes+z	336	0.64±0.01	0.32±0.03	0.39±0.03	0.55±0.02	0.60±0.01	0.62±0.01
GES blanket	170	0.68±0.01	0.40±0.03	0.48±0.03	0.60±0.02	0.64±0.01	0.66±0.01
LiNGAM blanket	196	0.68±0.01	0.38±0.03	0.45±0.03	0.60±0.01	0.64±0.01	0.65±0.01
Group Lasso blanket	145	0.65±0.01	0.36±0.02	0.42±0.03	0.57±0.02	0.62±0.01	0.63±0.02
PPFS blanket	83	0.68±0.01	0.40±0.01	0.46±0.02	0.60±0.01	0.64±0.01	0.66±0.01
PL blanket	109	0.67±0.01	0.39±0.03	0.46±0.04	0.59±0.02	0.64±0.01	0.65±0.01
PL blanket (FS)	174	**0.70**±0.01	**0.41**±0.02	**0.49**±0.03	**0.62**±0.01	**0.66**±0.00	**0.67**±0.01

Table 9: Mean absolute error (MAE $\pm \sigma$; lower is better) of different predictors on the PPBR benchmark with varying numbers of test samples included in fine-tuning (n). Best results in bold; next-best is underlined.

	size	$n = 0$	$n = 7$	$n = 10$	$n = 25$	$n = 50$	$n = 100$
dummy	0	**11.40**±0.00	11.45±0.25	11.31±0.20	11.03±0.09	10.89±0.07	10.84±0.03
z	128	15.26±0.26	11.64±0.28	11.46±0.27	10.98±0.13	10.78±0.05	10.51±0.10
all attributes	208	15.55±0.46	11.23±0.22	**10.92**±0.23	10.27±0.12	9.83±0.10	9.43±0.12
all attributes+z	336	14.27±0.33	**11.14**±0.21	10.96±0.17	10.26±0.14	9.76±0.10	9.30±0.08
GES blanket	12	17.44±0.39	11.64±0.31	11.33±0.25	10.88±0.12	10.51±0.12	10.02±0.17
LiNGAM blanket	192	15.39±0.30	11.25±0.11	11.07±0.20	10.28±0.11	9.79±0.14	9.41±0.15
Group Lasso blanket	136	16.17±0.43	11.39±0.19	11.03±0.29	10.45±0.19	9.91±0.12	9.47±0.12
PPFS blanket	97	15.73±0.63	11.31±0.24	11.04±0.14	10.56±0.17	10.08±0.10	9.72±0.14
PL blanket	173	15.39±0.61	11.17±0.18	10.99±0.21	10.36±0.17	9.87±0.19	9.55±0.21
PL blanket (FS)	174	14.55±0.67	11.20±0.15	**10.92**±0.31	**10.16**±0.16	**9.64**±0.14	**9.22**±0.19

Table 10: Mean absolute error (MAE $\pm$ σ; lower is better) of different predictors on the Lipophilicity benchmark with varying numbers of test samples included in fine-tuning (n). Best results in bold; next-best is underlined.

	size	$n = 0$	$n = 7$	$n = 10$	$n = 25$	$n = 50$	$n = 100$
dummy	0	0.99±0.00	1.02±0.01	1.00±0.01	0.98±0.00	0.97±0.00	0.97±0.00
z	128	0.79±0.01	0.97±0.01	0.94±0.01	0.86±0.01	0.81±0.01	0.78±0.01
all attributes	208	**0.62**±0.01	**0.85**±0.02	**0.79**±0.01	**0.67**±0.01	0.64±0.01	**0.61**±0.01
all attributes+z	336	**0.62**±0.01	**0.85**±0.02	**0.79**±0.01	0.68±0.01	0.64±0.01	**0.61**±0.01
GES blanket	188	**0.62**±0.01	**0.85**±0.01	0.80±0.01	0.68±0.01	0.64±0.01	**0.61**±0.01
LiNGAM blanket	197	**0.62**±0.01	**0.85**±0.02	**0.79**±0.01	0.68±0.01	**0.63**±0.01	**0.61**±0.00
Group Lasso blanket	66	0.72±0.01	0.93±0.02	0.89±0.02	0.78±0.02	0.73±0.01	0.70±0.01
PPFS blanket	102	0.65±0.01	0.89±0.02	0.83±0.01	0.72±0.01	0.67±0.01	0.64±0.01
PL blanket	174	0.63±0.01	0.86±0.01	0.81±0.01	0.68±0.01	0.64±0.01	0.62±0.01
PL blanket (FS)	174	**0.62**±0.01	0.87±0.02	0.80±0.01	0.69±0.01	0.65±0.01	0.62±0.00

Table 11: Mean absolute error (MAE $\pm$ σ; lower is better) of different predictors on the Solubility benchmark with varying numbers of test samples included in fine-tuning (n). Best results in bold; next-best is underlined.

	size	$n = 0$	$n = 7$	$n = 10$	$n = 25$	$n = 50$	$n = 100$
dummy	0	1.89±0.00	1.94±0.01	1.90±0.01	1.85±0.01	1.83±0.00	1.83±0.00
z	128	1.08±0.01	1.60±0.04	1.48±0.02	1.25±0.02	1.17±0.02	1.11±0.01
all attributes	208	**0.94**±0.01	**1.44**±0.03	1.31±0.03	1.09±0.02	**1.00**±0.01	0.96±0.01
all attributes+z	336	**0.94**±0.01	1.45±0.03	**1.30**±0.02	**1.07**±0.02	**1.00**±0.01	**0.95**±0.01
GES blanket	178	0.95±0.01	**1.44**±0.04	1.32±0.03	1.09±0.01	1.01±0.01	0.96±0.01
LiNGAM blanket	204	**0.94**±0.01	1.46±0.04	**1.30**±0.03	1.08±0.01	**1.00**±0.01	0.96±0.01
Group Lasso blanket	88	0.99±0.01	1.51±0.02	1.37±0.03	1.14±0.01	1.05±0.01	1.01±0.01
PPFS blanket	146	0.95±0.02	1.45±0.04	1.32±0.02	1.09±0.02	1.01±0.01	0.96±0.01
PL blanket	170	0.95±0.01	1.45±0.04	1.32±0.03	1.10±0.02	1.01±0.01	0.97±0.01
PL blanket (FS)	174	0.96±0.02	**1.44**±0.02	1.31±0.03	1.09±0.02	1.01±0.01	0.96±0.01

A.2 Molecular descriptors

Table 12: Descriptors used in small molecule experiments. All descriptors are calculated using RDKit.

Gasteiger/Marsili Partial Charges	NOCount	RingCount
BalabanJ	NumHAcceptors	FractionCSP3
BertzCT	NumHDonors	NumSpiroAtoms
HallKierAlpha	NumHeteroatoms	NumBridgeheadAtoms
Kappa1 - Kappa3	NumRotatableBonds	TPSA
Phi	NumValenceElectrons	LabuteASA
Chi0, Chi1	NumAmideBonds	PEOE_VSA1 – PEOE_VSA14
Chi0n – Chi4n	NumAromaticRings	SMR_VSA1 – SMR_VSA10
Chi0v – Chi4v	NumSaturatedRings	SlogP_VSA1 – SlogP_VSA12
MolLogP	NumAliphaticRings	EState_VSA1 – EState_VSA11
MolMR	NumAromaticHeterocycles	VSA_EState1 – VSA_EState10
MolWt	NumSaturatedHeterocycles	MQNs
ExactMolWt	NumAliphaticHeterocycles	Topliss fragments
HeavyAtomCount	NumAromaticCarbocycles	Autocorr2D
HeavyAtomMolWt	NumSaturatedCarbocycles	BCUT2D
NHOHCount	NumAliphaticCarbocycles	