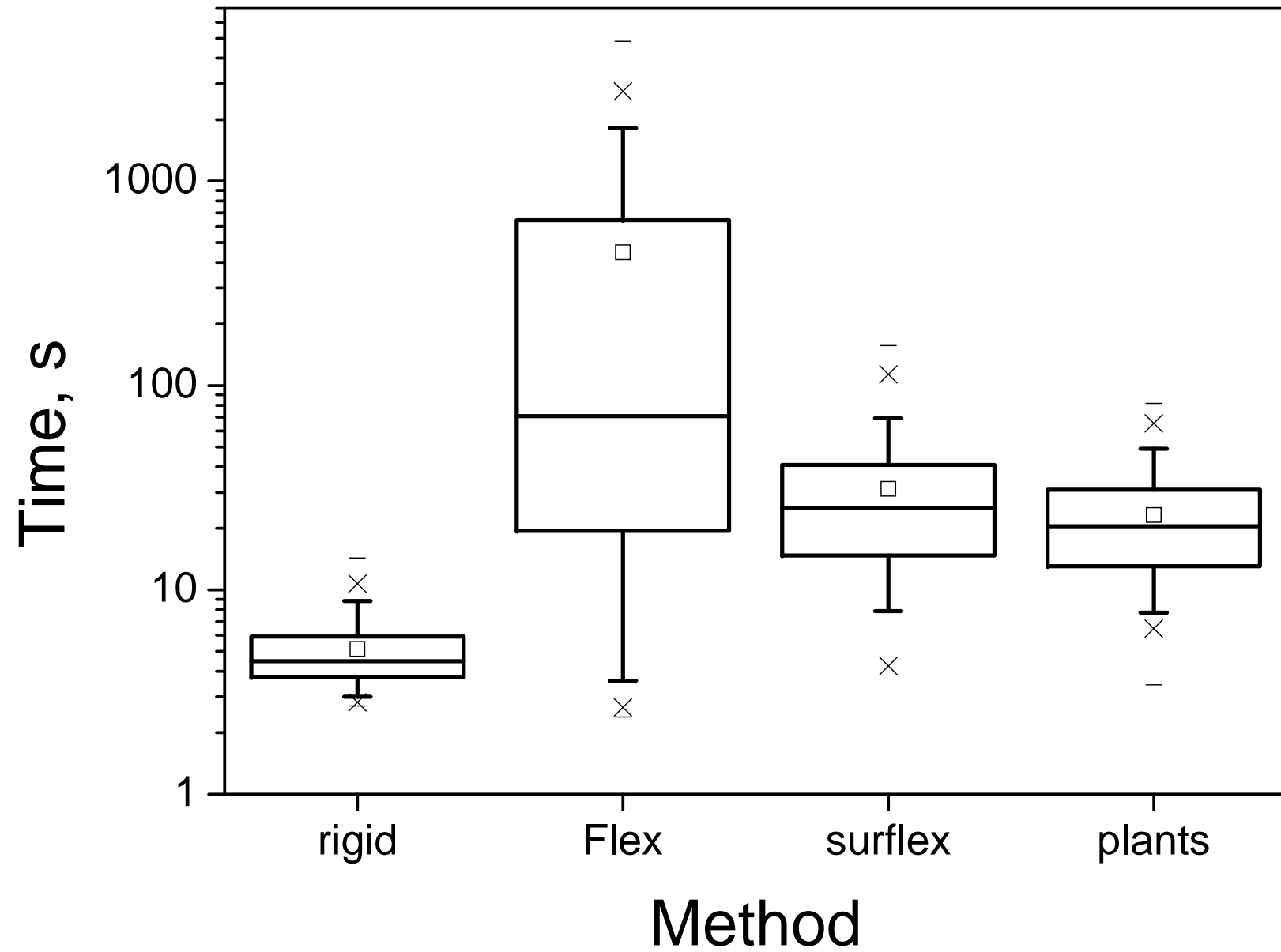


Supplementary Figure 1



Supplementary Figure 2

Supplementary Table 1: Pharmacophore descriptors used for training the GFA model to estimate selectivity

Descriptor Name	Descriptor Type
Desc1	Number of all features
Desc2	number of location features
Desc3	Has Shape (1) or not (0)
Desc4	Number of Excluded Volumes (EVs)
Desc5	Number of Hydrogen Bond Acceptors (HBAs)
Desc6	Number of Hydrogen Bond Donors (HBDs)
Desc7	Number of Positive Ionizables
Desc8	Number of Negative Ionizables
Desc9	Number of Aromatic Ring features
Desc10	Number of Hydrophobic features
Desc11-Desc20	HBA-HBA feature distance ^a
Desc21-Desc30	HBA-HBD feature distance
Desc31-Desc40	HBA-POS feature distance
Desc41-Desc50	HBA-NEG feature distance
Desc51-Desc60	HBA-RA feature distance
Desc61-Desc70	HBA-HYD feature distance
Desc71-Desc80	HBD-HBD feature distance
Desc81-Desc90	HBD-POS feature distance
Desc91-Desc100	HBD-NEG feature distance
Desc101-Desc110	HBD-RA feature distance
Desc111-Desc120	HBD-HYD feature distance
Desc121-Desc130	POS-POS feature distance
Desc131-Desc140	POS-NEG feature distance
Desc141-Desc150	POS-RA feature distance

Desc151-Desc160	POS-HYD feature distance
Desc161-Desc170	NEG-NEG feature distance
Desc171-Desc180	NEG-RA feature distance
Desc181-Desc190	NEG-HYD feature distance
Desc191-Desc200	RA-RA feature distance
Desc201-Desc210	RA-HYD feature distance
Desc211-Desc220	HYD-HYD feature distance

^a For each pair of feature types, the feature-feature distance is put into a distance bin (1-10), with a bin size of 2.0 Å. The distance bin count is used as the descriptor value. For instance, descriptors Desc11 to Desc20 are used for HBA-HBA distances. Desc11 is the number of HBA-HBA distances in the range 0-2.0 Å, Desc12 is the number of HBA-HBA distances in the range of 2.0-4.0 Å, and so on. Distances greater than 20.0 Å are counted in the last bin, i.e. Desc20. Similar descriptors are defined for the other types of feature-feature distances.

Supplementary Table 2. OpenEye Filter file used to select drug-like ligands

MIN_MOLWT	150	"Minimum molecular weight"
MAX_MOLWT	750	"Maximum molecular weight"
MIN_NUM_HVY	10	"Minimum number of heavy atoms"
MAX_NUM_HVY	55	"Maximum number of heavy atoms"
MIN_RING_SYS	0	"Minimum number of ring systems"
MAX_RING_SYS	7	"Maximum number of ring systems"
MIN_RING_SIZE	0	"Minimum atoms in any ring system"
MAX_RING_SIZE	20	"Maximum atoms in any ring system"
MIN_CON_NON_RING	0	"Minimum number of connected non-ring atoms"
MAX_CON_NON_RING	20	"Maximum number of connected non-ring atoms"
MIN_FCNGRP	0	"Minimum number of functional groups"
MAX_FCNGRP	20	"Maximum number of functional groups"
MIN_UNBRANCHED	0	"Minimum number of connected unbranched non-ring atoms"
MAX_UNBRANCHED	8	"Maximum number of connected unbranched non-ring atoms"
MIN_CARBONS	5	"Minimum number of carbons"
MAX_CARBONS	40	"Maximum number of carbons"
MIN_HETEROATOMS	2	"Minimum number of heteroatoms"
MAX_HETEROATOMS	20	"Maximum number of heteroatoms"
MIN_Het_C_Ratio	0.10	"Minimum heteroatom to carbon ratio"
MAX_Het_C_Ratio	1.0	"Maximum heteroatom to carbon ratio"
MIN_HALIDE_FRACTION	0.0	"Minimum Halide Fraction"
MAX_HALIDE_FRACTION	0.5	"Maximum Halide Fraction"
ADJUST_ROT_FOR_RING	true	"BOOLEAN for whether to estimate degrees of freedom in rings"
MIN_ROT_BONDS	0	"Minimum number of rotatable bonds"
MAX_ROT_BONDS	20	"Maximum number of rotatable bonds"
MIN_RIGID_BONDS	0	"Minimum number of rigid bonds"
MAX_RIGID_BONDS	50	"Maximum number of rigid bonds"
MIN_HBOND_DONORS	0	"Minimum number of hydrogen-bond donors"
MAX_HBOND_DONORS	6	"Maximum number of hydrogen-bond donors"
MIN_HBOND_ACCEPTORS	0	"Minimum number of hydrogen-bond acceptors"
MAX_HBOND_ACCEPTORS	10	"Maximum number of hydrogen-bond acceptors"
MIN_LIPINSKI_DONORS	0	"Minimum number of hydrogens on O & N atoms"
MAX_LIPINSKI_DONORS	5	"Maximum number of hydrogens on O & N atoms"
MIN_LIPINSKI_ACCEPTORS	0	"Minimum number of oxygen & nitrogen atoms"
MAX_LIPINSKI_ACCEPTORS	10	"Maximum number of oxygen & nitrogen atoms"
MIN_COUNT_FORMAL_CRG	0	"Minimum number formal charges"
MAX_COUNT_FORMAL_CRG	3	"Maximum number of formal charges"
MIN_SUM_FORMAL_CRG	-2	"Minimum sum of formal charges"
MAX_SUM_FORMAL_CRG	2	"Maximum sum of formal charges"
MIN_CHIRAL_CENTERS	0	"Minimum chiral centers"
MAX_CHIRAL_CENTERS	4	"Maximum chiral centers"
MIN_XLOGP	-2.0	"Minimum XLogP"
MAX_XLOGP	6.0	"Maximum XLogP"
MIN_SOLUBILITY	moderately	"Minimum solubility"
PSA_USE_SandP	true	"Count S and P as polar atoms"
MIN_2D_PSA	0.0	"Minimum 2-Dimensional (SMILES) Polar Surface Area"

MAX_2D_PSA 150.0 "Maximum 2-Dimensional (SMILES) Polar Surface Area"
 AGGREGATORS true "Eliminate known aggregators"
 PRED_AGG false "Eliminate predicted aggregators"
 GSK_VEBER true "PSA>140 or >10 rot bonds"
 MAX_LIPINSKI 2 "Maximum number of Lipinski violations"
 MIN_ABS 0.5 "Minimum probability F>10% in rats"
 PHARMACOPIA true "LogP > 5.88 or PSA > 131.6"
 ALLOWED_ELEMENTS H,C,N,O,F,S,Cl,Br,I,P
 ELIMINATE_METALS Sc,Ti,V,Cr,Mn,Fe,Co,Ni,Cu,Zn,Y,Zr,Nb,Mo,Tc,Ru,Rh,Pd,Ag,Cd
 #specific, undesirable functional groups
 RULE 0 quinone
 RULE 0 pentafluorophenyl_esters
 RULE 0 paranitrophenyl_esters
 RULE 0 HOBT_esters
 RULE 0 triflates
 RULE 0 lawesson_s_reagent
 RULE 0 phosphoramides
 RULE 0 beta_carbonyl_quat_nitrogen
 RULE 0 acylhydrazide
 RULE 0 cation_C_Cl_I_P_or_S
 RULE 0 phosphoryl
 RULE 0 alkyl_phosphate
 RULE 0 phosphinic_acid
 RULE 0 phosphanes
 RULE 0 phosphoranes
 RULE 0 imido_yl_chlorides
 RULE 0 nitroso
 RULE 0 N_P_S_Halides
 RULE 0 carbodiimide
 RULE 0 isonitrile
 RULE 0 triacyloxime
 RULE 0 cyanohydrins
 RULE 0 acyl_cyanides
 RULE 0 sulfonylnitrile
 RULE 0 phosphorylnitrile
 RULE 0 azocyanamides
 RULE 0 beta_azo_carbonyl
 RULE 0 polyenes
 RULE 0 saponin_derivatives
 RULE 1 cytochalasin_derivatives
 RULE 4 cycloheximide_derivatives
 RULE 1 monensin_derivatives
 RULE 1 squalestatin_derivatives
 #functional groups which often eliminate compounds from consideration
 RULE 0 acid_halide
 RULE 0 aldehyde
 RULE 0 alkyl_halide
 RULE 0 anhydride

RULE 0 azide
RULE 0 azo
RULE 0 di_peptide
RULE 0 michael_acceptor
RULE 0 beta_halo_carbonyl
RULE 0 nitro
RULE 0 oxygen_cation
RULE 0 peroxide
RULE 0 phosphonic_acid
RULE 0 phosphonic_ester
RULE 0 phosphoric_acid
RULE 0 phosphoric_ester
RULE 0 sulfonic_acid
RULE 0 sulfonic_ester
RULE 0 tricarbo_phosphene
RULE 0 epoxide
RULE 0 sulfonyl_halide
RULE 0 halopyrimidine
RULE 0 perhalo_ketone
RULE 0 aziridine
RULE 1 oxalyl
RULE 0 alphahalo_amine
RULE 0 halo_amine
RULE 0 halo_alkene
RULE 0 acyclic_NCN
RULE 0 acyclic_NS
RULE 0 SCN2
RULE 0 terminal_vinyl
RULE 0 hetero_hetero
RULE 0 hydrazine
RULE 0 N_methoyl
RULE 0 NS_beta_haloethyl
RULE 0 propiolactones
RULE 0 iodoso
RULE 0 iodoxy
RULE 0 noxide

#groups of molecules

RULE 0 dye

#functional groups which are allowed, but may not be wanted in high quantities

#common functional groups

RULE 6 alcohol
RULE 4 alkene
RULE 4 amide
RULE 4 amino_acid
RULE 2 amine
RULE 4 primary_amine
RULE 4 secondary_amine
RULE 4 tertiary_amine

RULE 2 carboxylic_acid
RULE 6 halide
RULE 0 iodine
RULE 2 ketone
RULE 4 phenol
RULE 1 imine
RULE 1 methyl_ketone
RULE 1 alkylaniline
RULE 4 sulfonamide
RULE 1 sulfonylurea
RULE 0 phosphonamide
RULE 0 alphahalo_ketone
RULE 0 oxaziridine
RULE 1 cyclopropyl
RULE 2 guanidine
RULE 0 sulfonimine
RULE 0 sulfinimine
RULE 1 hydroxamic_acid
RULE 0 sulfinylthio
RULE 0 disulfide
RULE 0 enol_ether
RULE 0 enamine
RULE 0 organometallic
RULE 0 dithioacetal
RULE 1 oxime
RULE 0 isothiocyanate
RULE 0 isocyanate
RULE 3 lactone
RULE 3 lactam
RULE 1 thioester
RULE 1 carbonate
RULE 0 carbamic_acid
RULE 1 thiocarbamate
RULE 0 triazine
RULE 1 malonic
#other functional groups
RULE 2 alkyne
RULE 4 aniline
RULE 4 aryl_halide
RULE 2 carbamate
RULE 3 ester
RULE 5 ether
RULE 1 hydrazone
RULE 0 nonacylhydrazone
RULE 1 hydroxylamine
RULE 2 nitrile
RULE 2 sulfide
RULE 2 sulfone

RULE 2 sulfoxide
RULE 0 thiourea
RULE 1 thioamide
RULE 1 thiol
RULE 2 urea
RULE 0 hemiketal
RULE 0 hemiacetal
RULE 0 ketal
RULE 1 acetal
RULE 0 aминаl
RULE 0 hemiaminal
#protecting groups
RULE 0 benzyloxycarbonyl_CBZ
RULE 0 t_butoxycarbonyl_tBOC
RULE 0 fluorenylmethoxycarbonyl_Fmoc
RULE 1 dioxolane_5MR
RULE 1 dioxane_6MR
RULE 1 tetrahydropyran_THP
RULE 1 methoxyethoxymethyl_MEM
RULE 2 benzyl_ether
RULE 2 t_butyl_ether
RULE 0 trimethylsilyl_TMS
RULE 0 t_butyldimethylsilyl_TBDMS
RULE 0 triisopropylsilyl_TIPS
RULE 0 t_butyldiphenylsilyl_TBDPS
RULE 1 phthalimides_PHT
RULE 2 arenesulfonyl

Supplementary Table 3. List of HET codes for the 157 ligands of the sc-PDB Diverse Set and their respective targets

HET_CODE	Targets
115	3-hydroxy-3-methylglutaryl-coenzyme a reductase
1CS	acetolactate synthase catalytic subunit
20A	camp-specific 3',5'-cyclic phosphodiesterase 4b
215	serine/threonine-protein kinase b-raf
2IG	Renin
356	dipeptidyl peptidase 4
3B9	dna ligase
3CC	carbonic anhydrase 2
3LP	glycylpeptide n-tetradecanoyltransferase
3QC	kinesin-like protein kif11
501	thrombin
521	tyrosine-protein phosphatase non-receptor type 1
55V	trimethoprim-sensitive dihydrofolate reductase
5RM	camp-specific 3',5'-cyclic phosphodiesterase 4b
61	metallo beta-lactamase
669	3-oxoacyl-[acyl-carrier-protein] synthase 3
675	urokinase-type plasminogen activator
6C3	macrophage colony-stimulating factor 1 receptor
760	acetylcholinesterase
783	trypsin
792	disintegrin and metalloproteinase domain-containing protein 17
839	wee1-like protein kinase
87Y	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
905	coagulation factor vii
915	lethal factor
961	retinoic acid receptor gamma
984	mitogen-activated protein kinase 10
A3M	dipeptidyl peptidase 4
A46	glycogen phosphorylase
A80	cellular retinoic acid-binding protein 1
AD3	Adenosylhomocysteinase iag-nucleoside hydrolase
AEE	epidermal growth factor receptor
AH1	protease
ALJ	chitinase
AO5	methionine aminopeptidase 2
AXX	probable serine/threonine-protein kinase pkng
AZM	carbonic anhydrase 9 carbonic anhydrase 12
AZZ	deoxynucleoside kinase

	glycogen phosphorylase serum albumin
BAU	uridine phosphorylase 1 uridine phosphorylase
BBT	neutrophil collagenase
BCZ	Neuraminidase sialidase-2
BDI	queuine trna-ribosyltransferase
BFS	scytalone dehydratase
BHY	glutamate receptor 2
BIG	5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase
BIT	myosin-2 heavy chain
BRZ	glyceraldehyde-3-phosphate dehydrogenase
C4C	focal adhesion kinase 1
CA2	3-dehydroquinase dehydratase
CBT	beta-lactamase tem
CEI	Obelin renilla-luciferin 2-monooxygenase
CEL	prostaglandin g/h synthase 1 carbonic anhydrase 2
CIA	cgmp-specific 3',5'-cyclic phosphodiesterase
CMB	coagulation factor x
CMF	RNA-directed RNA polymerase
CMU	thymidine phosphorylase
CRZ	fatty acid-binding protein
CT5	atp-dependent molecular chaperone hsp82 heat shock protein hsp 90-alpha
D1L	acetyl-coa carboxylase
DBQ	activated cdc42 kinase 1
DD2	scavenger mrna-decapping enzyme dcps
DEO	macrophage metalloelastase
DES	estrogen-related receptor gamma estrogen receptor alpha transthyretin
DEX	glucocorticoid receptor
DZG	pyruvate kinase isozymes m1/m2
DZP	serum albumin
E4D	estrogen receptor alpha
E89	queuine trna-ribosyltransferase
ED2	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha
EI1	estrogen receptor alpha
EQI	estradiol 17-beta-dehydrogenase 1
ET	bacterial regulatory protein, tetr family hth-type transcriptional regulator qacr
F13	beta-lactamase
FDI	neuraminidase
FLP	cytochrome p450 2c9

FR4	adenosine deaminase
FRG	interleukin-2
FSN	thrombin
GB7	alpha-mannosidase 2
GEO	deoxynucleoside kinase deoxycytidine kinase
GIO	chitinase
GNT	Acetylcholinesterase soluble acetylcholine receptor
GRR	peroxisome proliferator-activated receptor gamma
GVR	udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine deacetylase
H11	corticosteroid 11-beta-dehydrogenase isozyme 1
H24	beta-secretase 1
H7J	cathepsin s
HA3	histone deacetylase 4
HEF	reverse transcriptase/ribonuclease h
HM5	methionine aminopeptidase 1
HR2	3-hydroxy-3-methylglutaryl-coenzyme a reductase
HUP	acetylcholinesterase
I84	aldose reductase
IAD	tryptophan synthase alpha chain
IC1	casein kinase i homolog 1
IMN	prostaglandin reductase 2 aldo-keto reductase family 1 member c3 prostaglandin g/h synthase 2 phospholipase a2
IMQ	iag-nucleoside hydrolase
IXM	cell division protein kinase 5 cdc2-like cdk2/cdc28 like protein kinase glycogen synthase kinase-3 beta
KAI	glutamate receptor, ionotropic kainate 2 glutamate receptor 4
LG7	androgen receptor
LI9	mitogen-activated protein kinase 14
LQQ	cyclin homolog
LS1	cell division protein kinase 2
MC9	vitamin d3 receptor
MD7	dihydroorotate dehydrogenase
MTI	purine nucleotide phosphorylase
NDR	progesterone receptor
NGH	stromelysin-2 macrophage metalloelastase
OA1	biotin carboxylase
OEF	thyroid hormone receptor beta
P1S	sam dependent isoflavanone 4'-o-methyltransferase/(+)-6a-hydroxymaackiain-3-O-methyltransferase
P1Z	prostaglandin reductase 2

P21	bifunctional protein glmu//udp-n-acetylglucosamine pyrophosphorylase/glucosamine-1-phosphate n-acetyltransferase
P34	poly [adp-ribose] polymerase 15 hypothetical exotoxin a
P4A	[pyruvate dehydrogenase [lipoamide]] kinase isozyme 4
PAF	pantothenate synthetase
PAU	pantothenate kinase
PBF	tyrosyl-trna synthetase
PFP	serine/threonine-protein kinase chk1
PH7	rna-directed rna polymerase
PM2	tryptase beta-2
PVB	cell division control protein 2 homolog uncharacterized protein srp2
R6C	pyridoxal kinase
R78	serine/threonine-protein kinase plk1
R88	squalene--hopene cyclase
RNP	Lactotransferrin cellulase
ROF	camp-specific 3',5'-cyclic phosphodiesterase 4d camp-specific 3',5'-cyclic phosphodiesterase 4b
RQ3	hemoglobin subunit beta/hemoglobin subunit alpha
RRC	cell division protein kinase 2 pyridoxal kinase cell division protein kinase 5
RXC	caspase-3
S22	dual specificity protein kinase ttk
SAG	amine oxidase [flavin-containing] b
SB8	peptide deformylase
SCT	thymidine kinase
SHM	Streptavidin avidin
SLX	reticuline oxidase
STC	beta-lactamase
SWA	alpha-1,2-mannosidase alpha-mannosidase 2 putative alpha-1,2-mannosidase
T74	activated cdc42 kinase 1
TCD	retinoic acid receptor RXR-alpha
TDZ	fatty acid-binding protein
THM	thymidylate kinase glycogen phosphorylase
TIM	beta-2 adrenergic receptor
TNK	HIV-1 RT alpha-chain
TPR	thymidylate synthase
TSX	phosphoenolpyruvate carboxykinase
TTT	3c-like proteinase
TYR	prephenate dehydrogenase

	ribonucleoside-diphosphate reductase 1 subunit alpha chorismate mutase tyrosyl-trna synthetase cysteine synthase
VDN	camp-specific 3',5'-cyclic phosphodiesterase 4b cgmp-specific 3',5'-cyclic phosphodiesterase
VGA	glutamate racemase
VGB	o-glcnacase nagj
VGG	calmodulin-domain protein kinase 1
VIB	putative hmp/thiamine-binding protein ykof thiamine pyrophosphokinase thiamin pyrophosphokinase 1
XM5	ribosyldihydronicotinamide dehydrogenase [quinone]
XX5	angiotensin-converting enzyme 2
ZAM	enoyl-[acyl-carrier-protein] reductase [NADH]
ZMA	adenosine receptor alpha2a

Supplementary Table 4. Profiling accuracy of 29 ligands (Set 1) by 10 computational protocols: successful, target rank ≤ 25 , green; ambiguous, $25 < \text{target rank} \leq 50$, orange; failed, target rank > 50 , red. Numbers in cells indicate the rank of top-ranked true target entry.

Ligand	ECFP4	ROCS	Rigid1	Rigid2	Flex1	Flex2	Surflex1	Surflex2	Plants1	Plants2
3B9	40	267	53	17	56	17	19	27	236	442
55V	1	5	1	1	8	7	503	32	58	9
AD3	10	6	4	4	4	4	6	6	1	1
AZZ	3	5	96	28	181	40	128	27	14	19
BAU	1	2	2	1	1	1	125	6	28	3
BCZ	1	4	15	5	2	3	1	1	2	2
CEI	7	1	175	220	2	13	19	1	3	2
CEL	7	5	16	5	7	4	12	5	11	81
CT5	1	1	19	7	23	11	53	6	33	5
DES	1	2	2	2	2	2	7	2	24	3
ET	457	2	169	146	244	190	245	118	848	211
GEO	34	4	10	25	166	34	24	8	105	56
GNT	1	1	161	20	326	58	19	1	4	1
I84	151	47	635	238	282	103	81	309	49	80
IMN	6	6	56	95	20	17	336	49	218	41
IXM	1	4	3	2	3	2	186	26	554	56
NGH	1	7	27	5	25	5	44	8	554	70
P34	2480	2225	557	959	1122	1499	712	325	319	431
PAU	1	292	440	644	126	623	677	523	407	559
PVB	2420	410	29	19	29	15	1110	506	1353	305
RNP	286	974	1151	931	1496	1201	31	429	1034	224
ROF	1	1	4	3	5	8	43	5	25	4
RRC	1	1	1	1	2	2	5	2	261	30
SHM	2	2	100	26	2	1	2	1	9	3

SWA	6	44	57	12	59	12	171	25	329	10
THM	3	13	35	93	41	138	2	2	1	1
TYR	3	3	1	1	1	1	19	19	497	20
VDN	1	1	10	5	12	3	148	13	25	5
VIB	25	132	60	283	25	283	137	11	333	37

Supplementary Table 5. Profiling accuracy of 128 ligands (Set 2) by 8 computational protocols:

successful, target rank ≤ 25 , green; ambiguous, $25 < \text{target rank} \leq 50$, orange; failed, target rank > 50 , red. Numbers in cells indicate the rank of top-ranked true target entry.

HET	Rigid1	Rigid2	Flex1	Flex2	Surflex1	Surflex2	Plants1	Plants2
115	1	1	1	1	2	1	266	61
1CS	40	15	9	6	120	6	390	18
20A	50	21	29	11	188	19	484	37
215	1	1	1	1	189	12	177	9
2IG	1	1	7	4	2	1	248	15
356	9	10	48	22	180	28	310	118
3CC	1	1	1	1	314	153	916	89
3LP	605	803	670	735	1684	309	1100	361
3QC	1	1	1	1	55	3	52	4
501	18	12	1	1	14	149	98	26
521	20	10	2	1	6	1	54	6
5RM	1	1	1	1	110	10	17	3
61	47	10	118	25	593	449	173	194
669	98	36	494	139	1668	340	1121	245
675	1	1	1	1	107	7	46	6
6C3	13	18	15	20	118	15	44	4
760	387	291	360	141	54	73	12	210
783	3	5	6	3	23	3	10	3
792	16	7	31	11	223	28	370	68
839	1	1	1	1	44	5	85	13
87Y	1	1	1	1	1	1	1	1
905	2	2	5	4	27	2	5	1
915	2	2	1	1	21	5	289	20
961	1	1	1	1	1	1	1	1
984	4	2	6	2	6	1	94	8
A3M	28	9	48	16	1	1	125	9
A46	16	7	20	9	46	5	143	14
A80	9	4	3	3	70	7	169	23
AEE	1	1	1	1	9	1	302	19
AH1	1	3	1	1	6	3	1	1
ALJ	6	3	27	9	166	7	139	11
AO5	39	18	96	42	156	8	548	155
AXX	1	1	2	1	74	5	465	53
AZM	26	2	1	1	2283	228	1692	150
BBT	64	10	55	38	924	58	328	16
BDI	15	3	20	4	15	5	97	35
BFS	1	1	1	1	368	20	451	67
BHY	280	258	93	261	22	4	34	6
BIG	1	1	2	3	1	1	3	2

HET	Rigid1	Rigid2	Flex1	Flex2	Surflex1	Surflex2	Plants1	Plants2
BIT	3	1	1	1	1	1	9	1
BRZ	276	321	347	170	817	283	1398	338
C4C	59	20	85	28	743	34	1202	121
CA2	1	1	1	1	2	1	26	2
CBT	4	3	7	5	917	244	1554	262
CIA	42	17	9	42	58	11	22	3
CMB	45	17	43	24	49	7	125	10
CMF	2	2	1	1	40	2	158	18
CMU	1	1	1	1	72	7	214	21
CRZ	28	8	1	9	1767	183	1480	199
D1L	1	1	1	1	65	5	89	15
DBQ	1	1	1	1	533	58	376	256
DD2	12	5	337	110	16	1	5	3
DEO	79	17	1	1	43	3	105	17
DEX	1	1	1	1	2	1	3	2
DZG	619	135	120	24	407	438	18	534
DZP	1	1	1	1	298	123	319	229
E4D	1	1	1	1	46	3	292	16
E89	1	1	1	1	1	1	3	1
ED2	271	121	547	246	221	155	410	384
EI1	1	1	1	1	9	2	87	16
EQI	4	4	4	4	908	120	291	42
F13	272	50	256	45	410	187	1037	239
FDI	4	13	5	17	33	10	1249	133
FLP	1	1	3	1	462	69	831	183
FR4	4	2	11	2	54	96	504	76
FRG	95	84	87	28	833	56	884	73
FSN	1	2	1	2	19	4	12	3
GB7	1	1	1	1	255	134	872	69
GIO	23	7	23	7	2004	110	172	11
GRR	3	28	15	23	286	217	255	48
GVR	225	78	517	187	39	9	1963	301
H11	1	1	1	1	116	3	31	12
H24	27	101	45	29	59	2	641	48
H7J	46	17	177	62	1812	283	421	118
HA3	273	271	668	222	2	1	39	320
HEF	12	3	38	13	70	12	1	2
HM5	177	77	283	111	1256	242	335	29
HR2	1	1	1	1	2	1	18	2
HUP	508	299	535	295	29	61	1	157
IAD	54	12	49	15	7	2	198	40
IC1	3	2	3	2	407	138	245	33
IMQ	2	1	4	2	3	5	1	1
KAI	1	1	1	1	20	1	196	17
LG7	1	1	6	1	36	6	9	3

HET	Rigid1	Rigid2	Flex1	Flex2	Surflex1	Surflex2	Plants1	Plants2
LI9	1	1	1	1	7	2	96	13
LQQ	2	1	1	1	247	105	97	8
LS1	1	1	1	1	14	5	227	15
MC9	1	1	1	1	11	6	90	21
MD7	1	1	1	1	87	15	65	29
MTI	235	54	212	53	96	19	435	86
NDR	4	3	5	3	117	9	23	5
OA1	1	1	1	1	7	2	813	108
OEF	2	2	2	2	26	4	3	1
P1S	73	18	239	56	1799	322	1692	407
P1Z	81	28	26	9	1085	180	46	237
P21	1	1	6	1	677	106	1876	302
P4A	125	44	445	165	61	365	1238	467
PAF	433	205	3	170	166	72	518	135
PBF	147	30	225	42	391	54	746	109
PFP	4	4	7	4	795	88	98	29
PH7	7	1	57	16	141	109	352	224
PM2	385	110	406	154	269	21	1519	185
R6C	9	2	37	14	58	30	330	36
R78	42	51	1	4	69	5	75	9
R88	2	2	3	2	533	325	59	55
RQ3	66	26	96	40	2266	508	1835	641
RXC	97	445	292	402	1301	459	1738	536
S22	2	2	12	8	65	118	1160	102
SAG	985	316	847	244	71	335	14	26
SB8	2	8	13	20	27	3	1040	148
SCT	1	1	1	1	4	2	70	13
SLX	1	1	1	1	57	2	31	3
STC	8	6	1	1	365	90	276	186
T74	5	5	1	1	2	1	27	2
TCD	6	6	7	6	106	273	4	212
TDZ	35	16	21	18	464	46	963	218
TIM	1	1	1	5	11	1	6	1
TNK	2	2	3	2	3	1	1	1
TPR	10	6	2	1	86	255	113	225
TSX	1	1	1	1	1	11	7	6
TTT	15	7	2	1	1095	262	2	1
VGA	915	448	469	114	1518	152	1587	172
VGB	1	1	1	1	169	19	212	21
VGG	1	1	1	1	3	3	130	13
XM5	1019	1472	1522	1820	1004	232	845	357
XX5	76	19	20	5	394	33	1097	746
ZAM	89	34	79	31	187	150	12	4
ZMA	169	49	521	123	995	85	1379	174