

# Supporting Information

## Improving Scoring-Docking-Screening Powers of Protein-Ligand Scoring Functions using Random Forest

*Cheng Wang<sup>1</sup> and Yingkai Zhang<sup>1,2,\*</sup>*

<sup>1</sup>Department of Chemistry, New York University, New York, New York 10003

<sup>2</sup>NYU-ECNU Center for Computational Chemistry at NYU Shanghai, Shanghai 200062, China

\*To whom correspondence should be addressed.

E-mail: [yingkai.zhang@nyu.edu](mailto:yingkai.zhang@nyu.edu)

## Table of Contents

**Figure S1:** Performance comparison between scoring functions developed with different training sets using the  $\Delta_{\text{vina}}\text{RF}$  approach.

**Figure S2:** Performance comparison between scoring functions developed with different Vina feature sets using the  $\Delta_{\text{vina}}\text{RF}$  approach.

**Figure S3:** Performance comparison between scoring functions developed with Vina10, bSASA and Vina10 + bSASA features using the  $\Delta_{\text{vina}}\text{RF}$  approach.

**Figure S4** Importance of features measured by percentage of increased mean squared error (%IncMSE) for 20 features in  $\Delta_{\text{vina}}\text{RF}_{20}$ .

**Table S1:** Training Set Description.

**Table S2:** AutoDock Vina Features in Source Code.

**Table S3:** Pharmacophore Type Definition.

**Table S4:** Summary of the Scoring Functions Evaluated in CASF-2007 Benchmark.

**Table S5:** Summary of the Scoring Functions Evaluated in CASF-2013 Benchmark.

**Table S6:** Performance of 18 Scoring Functions in the Scoring Power Test in CASF-2007.

**Table S7:** Performance of 18 Scoring Functions in Ranking Power Test in CASF-2007.

**Table S8:** Success rates of 18 Scoring Functions in the Docking Power Test in CASF-2007.

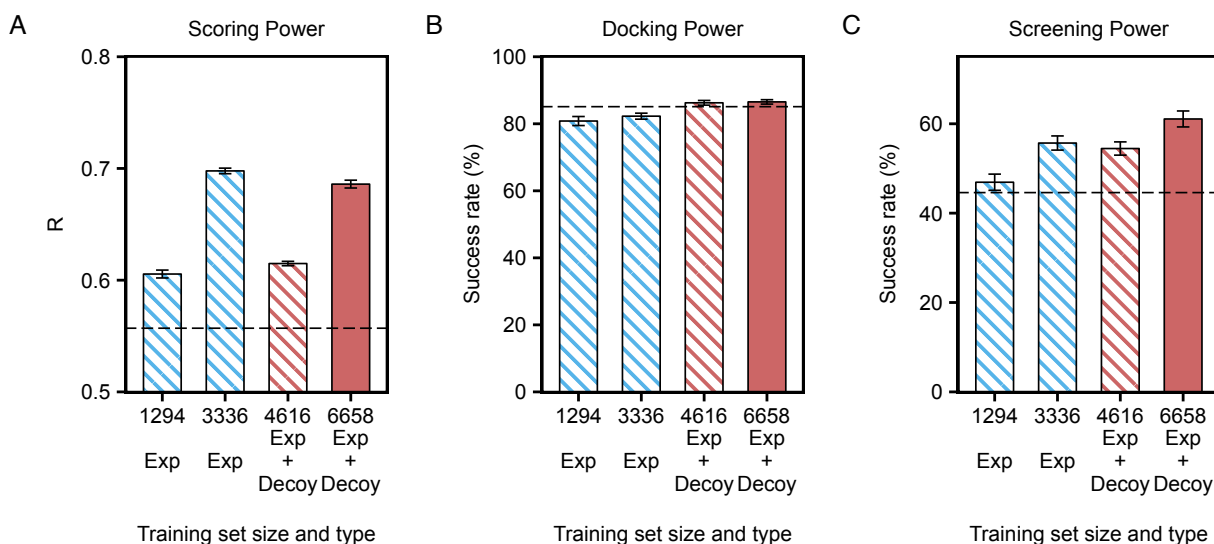
**Table S9:** Performance of 22 Scoring Functions in the Scoring Power Test in CASF-2013.

**Table S10:** Performance of 22 Scoring Functions in Ranking Power Test in CASF-2013.

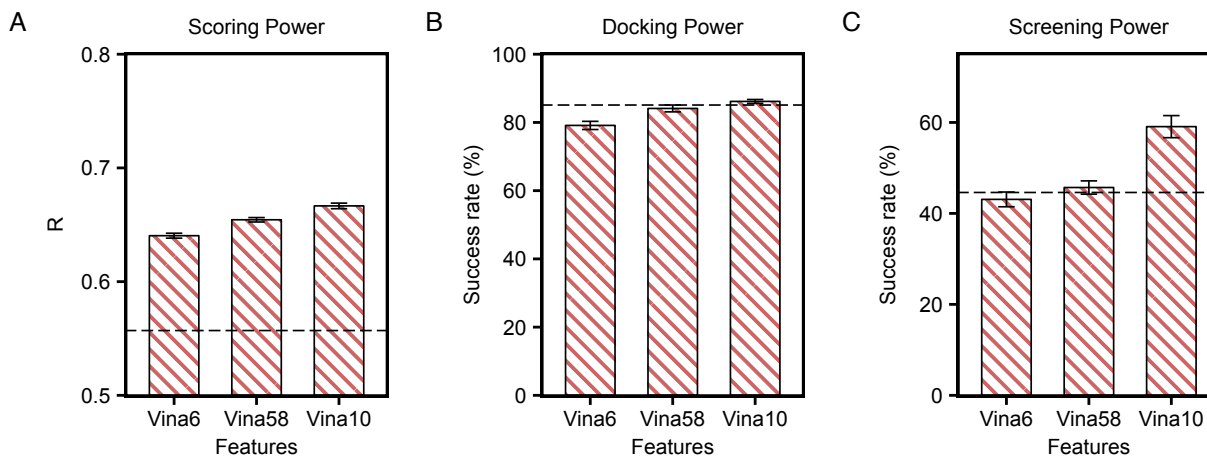
**Table S11:** Success rates of 22 Scoring Functions in the Docking Power Test in CASF-2013.

**Table S12:** Enrichment Factors of 22 Scoring Functions in the Screening Power Test in CASF-2013.

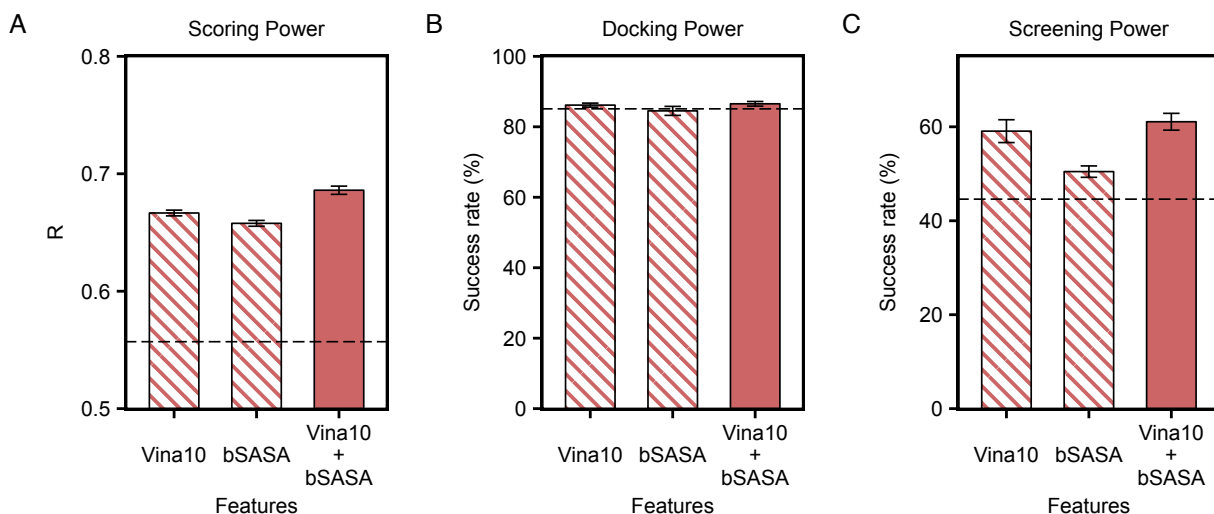
**Table S13:** Success Rates of Finding the Best Ligand Molecule of 22 Scoring Functions in the Screening Power Test in CASF-2013.



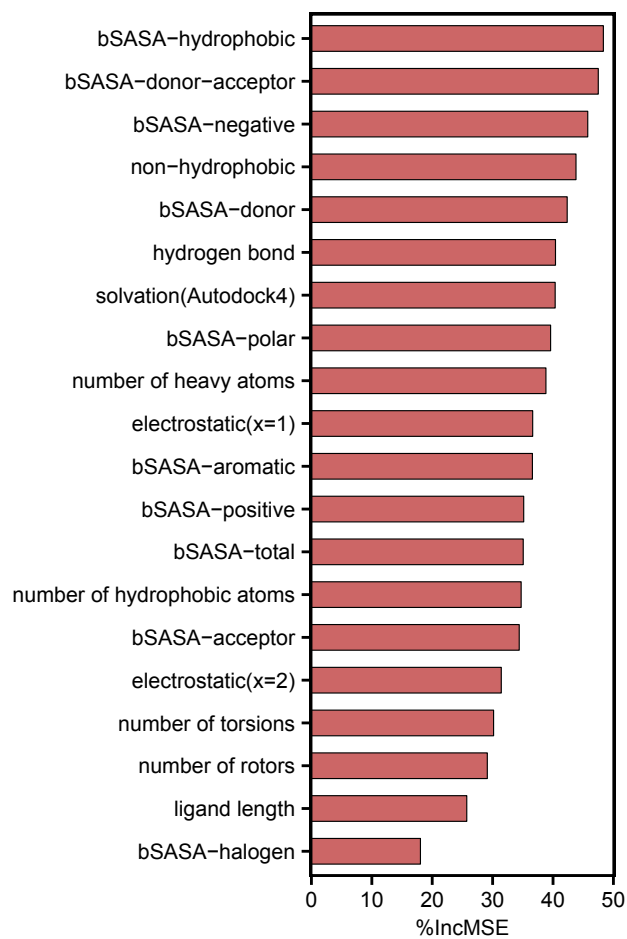
**Figure S1.** CASF-2013 benchmark test performance of scoring functions developed with the  $\Delta_{\text{vina}}\text{RF}$  approach using the same feature set (20 features as in  $\Delta_{\text{vina}}\text{RF}_{20}$ ) but **different training sets**. (A) Scoring power. (B) Docking power; (C) Screening power. For each training set, parameterization is run 10 times with different random seed for random forest and calculated by averaging over 10 performances. Experimental only training set is colored in blue and mixed training set is colored in red. 1294 structures are from PDBbind Refined 2007 + Weak + Decoy Crystal – Test. 3336 structures are PDBbind Refined 2014 + Weak + Decoy Crystal – Test. 4616 structures are combined by 1294 crystal structures and 3322 decoys structures. 6658 structures are combined by 3336 crystal structures and 3322 decoys structures. The AutoDock Vina performance is indicated by dashed line.



**Figure S2.** CASF-2013 benchmark test performance of scoring functions developed with the  $\Delta_{\text{vina}}$ RF approach using the combined experimental and decoy training set (6658) but with **different feature sets:** Vina6 refers the use of 6 features in the original Vina scoring function as the feature set, Vina58 means the use of all 58 features in the Vina source code as the feature set, and Vina 10 refers the use of top 10 features from the selection process as the feature set. (A) Scoring power. (B) Docking power; (C) Screening power. For each feature set, parameterization has been run 10 times with different random seed for random forest and calculated by averaging over 10 performances. The AutoDock Vina performance is indicated by dashed line.



**Figure S3.** CASF-2013 benchmark test performance of scoring functions developed with the  $\Delta_{\text{vina}}$ RF approach using the combined experimental and decoy training set (6658) but with **different feature sets:** Vina10, bSASA, and Vina10 + bSASA features. (A) Scoring power. (B) Docking power; (C) Screening power. For each feature set, parameterization is run 10 times with different random seed for random forest and calculated by averaging over 10 performances. The AutoDock Vina performance is indicated by dashed line.



**Figure S4.** Importance of features measured by percentage of increased mean squared error (%IncMSE) for 20 features in  $\Delta_{\text{vina}}\text{RF}_{20}$

**Table S1.** Training Set Description

	number of structures	source
Experimental	3336	PDBbind v2014 refined set <sup>[1]</sup> Selected structures from PDBbind v2014 general set <sup>[1]</sup> Crystal structures from CSAR-NRC HiQ <sup>[2,3]</sup>
Decoy	3322	Selected decoy structures from CSAR-NRC HiQ <sup>[2,3]</sup>

**Table S2.** AutoDock Vina Features in Source Code<sup>a</sup>

type	terms	parameters	number of terms
Intermolecular Interaction <sup>b</sup>	ad4_desolvation	$q$	2
	electrostatic	$x$	2
	gauss	$o, w$	31
	repulsion	$o$	8
	hydrophobic	$b$	4
	non_hydrophobic		1
Conformation Independent	vdW		1
	hydrogen bond	$b$	3
	num_tors		1
	num_rotors		1
	num_heavy_atoms		1
	num_hydrophobic_atoms		1
	ligand_max_num_h_bonds		1
	ligand_lengths_sum		1

<sup>a</sup>All terms are already defined with the AutoDock Vina source code. <sup>b</sup>The intermolecular interaction terms are the same as in smina.<sup>[4]</sup>



**Table S3.** Pharmacophore Type Definition

pharmacophore type name	definition <sup>a</sup>
Positive	N.4 (4 *) N.2 (3 *)
Negative	N.pl3 (C.cat) O (C (2 O or S [*])) O (P (2 O or S [*])) O (S (3 O [*])) S (C (4 *) [*]) S (C (2 (O or S [*])))
Donor-Acceptor	O (H) N.3 (H) N.2 (H) N.pl3 (H) S (H)
Donor	N.ar (H) N.am (H)
Acceptor	O Default N.3 N.1 N.ar (2 *) N.pl3 S [3 *]
Aromatic	N.ar C.ar
Hydrophobic	C [N] [O] [F] [P] [S]
Polar	N.am S (3 *) C (N) (O) (F) (P) (S)
Halogen	P F Cl Br I
Null	*

<sup>a</sup>The syntax is the same as in DOCK.<sup>[5]</sup> The parentheses ( ) specify “atoms that must be bonded to the parent atom”, while square brackets [ ] specify “atom that must not be bonded to the parent atom”. The integer in the definition represents the number of atoms associated to the parent atom. For example, oxygen in carboxylate or thioacetate is denoted as O (C (2 O or S [\*])). The syntax

means oxygen bonded to the carbon connected with at least 2 oxygen or sulfur atoms, which are not connected to other atoms. Pharmacophore types are only assigned to nine elements (C, N, O, F, S, P, Cl, Br, I), which is different from the pharmacophore types in DOCK. Only one pharmacophore type is assigned to each atom by the order of pharmacophore types in the table.

**Table S4.** Summary of the Scoring Functions Evaluated in CASF-2007 Benchmark

score function	number of descriptors	reference
LigScore1/LigScore2@DS	3/3	6
PLP1/PLP2@DS	2/3	7,8
PMF/PMF04@DS	1/1	9-12
Jain@DS	5	13
LUDI1/LUDI2/LUDI3@DS	4/4/4	14,15
GoldScore@GOLD	4	16
ChemScore@GOLD	6	17,18
ASP@GOLD	3	19
G-Score@SYBYL	6	16
PMF@SYBYL	1	9-12
D-Score@SYBYL	2	20
ChemScore@SYBYL	4	17,18
F-Score@SYBYL	5	
GlideScore-SP/XP@Schrödinger	10/10	21-23
DrugScore <sup>PDB</sup> /DrugScore <sup>CSD</sup>	2/2	24,25
X-Score	4	26
AutoDock Vina	6	27
$\Delta_{\text{vina}}\text{RF}_{20}$	20	

**Table S5.** Summary of the Scoring Functions Evaluated in CASF-2013 Benchmark

score function	number of descriptors	reference
LigScore1/LigScore2@DS	3/3	6
PLP1/PLP2@DS	2/3	7,8
PMF/PMF04@DS	1/1	9-12
Jain@DS	5	13
LUDI1/LUDI2/LUDI3@DS	4/4/4	14,15
GoldScore@GOLD	4	16
ChemScore@GOLD	6	17,18
ChemPLP@GOLD	9	28
ASP@GOLD	3	19
G-Score@SYBYL	6	16
PMF@SYBYL	1	9-12
D-Score@SYBYL	2	20
ChemScore@SYBYL	4	17,18
GlideScore-SP/XP@Schrödinger	10/10	21-23
London-dG@MOE	4	
ASE@MOE	1	29
Affinity@MOE	6	
Alpha-HB@MOE	2	
X-Score	4	26
AutoDock Vina	6	27
$\Delta_{\text{vina}} \text{RF}_{20}$	20	

**Table S6.** Performance of 18 Scoring Functions in the Scoring Power Test in CASF-2007<sup>a</sup>

score function <sup>b</sup>	<i>N</i>	<i>R</i>	<i>SD</i>
$\Delta_{\text{vina}}\text{RF}_{20}$	195	0.732	1.62
X-Score::HMScore	195	0.644	1.83
DrugScore <sup>CSD</sup>	195	0.569	1.96
AutoDock Vina	195	0.566	1.96
SYBYL::ChemScore	195	0.555	1.98
DS::PLP1	195	0.545	2.00
GOLD::ASP	193	0.534	2.02
SYBYL::G-Score	195	0.492	2.08
DS::LUDI3	195	0.487	2.09
DS::LigScore2	193	0.464	2.12
GlideScore-XP	178	0.457	2.14
DS::PMF	193	0.445	2.14
GOLD::ChemScore	178	0.441	2.15
SYBYL::D-Score	195	0.392	2.19
DS::Jain	189	0.316	2.24
GOLD::GoldScore	169	0.295	2.29
SYBYL::PMF-Score	190	0.268	2.29
SYBYL::F-Score	185	0.216	2.35

<sup>a</sup>The results except  $\Delta_{\text{vina}}\text{RF}_{20}$  and AutoDock Vina are obtained from literature.<sup>[30]</sup> <sup>b</sup>Scoring

functions are ranked by the Pearson correlation coefficients.

**Table S7.** Performance of 18 Scoring Functions in Ranking Power Test in CASF-2007<sup>a</sup>

score function <sup>b</sup>	success rates (%)
X-Score::HSScore	58.5
$\Delta_{\text{vina}}\text{RF}_{20}$	56.9
AutoDock Vina	53.8
DS::PLP2	53.8
DrugScore <sup>CSD</sup>	52.3
SYBYL::ChemScore	47.7
SYBYL::D-Score	46.2
SYBYL::G-Score	46.2
GOLD::ASP	43.1
DS::LUDI3	43.1
DS::Jain	41.5
DS::PMF	41.5
SYBYL::PMF-Score	38.5
GOLD::ChemScore	36.9
DS::LigScore2	35.4
GlideScore-XP	33.8
SYBYL::F-Score	29.2
GOLD::GoldScore	23.1

<sup>a</sup>The results except  $\Delta_{\text{vina}}\text{RF}_{20}$  and AutoDock Vina are obtained from literature.<sup>[30]</sup> <sup>b</sup>Scoring

functions are ranked by their success rates.

**Table S8.** Success rates of 18 Scoring Functions in the Docking Power Test in CASF-2007<sup>a</sup>

scoring function <sup>b</sup>	Docking (%)		
	The top pose	Top two poses	Top three poses
GOLD::ASP	82.5	90.2	92.3
$\Delta_{\text{vina}}\text{RF}_{20}$	80.5	87.7	89.2
AutoDock Vina	77.9	86.2	88.2
DS::PLP1	75.4	86.9	90.2
DrugScorePDB::PairSurf	74.3	89.1	91.8
GlideScore::SP	73.2	83.1	86.9
DS::LigScore2	71.6	85.8	88.0
GOLD::ChemScore	70.5	78.7	82.0
GOLD::GoldScore	68.9	79.8	85.2
X-Score1.2::HMScore	68.3	82.0	84.2
SYBYL::F-Score	64.5	74.3	82.0
SYBYL::ChemScore	60.1	72.1	78.7
DS::LUDI2	57.4	70.5	75.4
SYBYL::PMF-Score	48.1	61.7	63.4
DS::Jain	44.8	63.9	70.5
DS::PMF	43.7	53.0	56.8
SYBYL::G-Score	41.5	55.7	67.2
SYBYL::D-Score	30.6	50.3	59.0

<sup>a</sup>The results except  $\Delta_{\text{vina}}\text{RF}_{20}$  and AutoDock Vina are obtained from literature.<sup>[30]</sup> <sup>b</sup>Scoring

functions are ranked by success rates when the top one poses are considered.

**Table S9.** Performance of 22 Scoring Functions in the Scoring Power Test in CASF-2013<sup>a</sup>

score function <sup>b</sup>	<i>N</i>	<i>R</i>	SD
$\Delta_{\text{vina}}\text{RF}_{20}$	195	0.686	1.64
X-Score <sup>HM</sup>	195	0.614	1.78
ChemScore@SYBYL	195	0.592	1.82
ChemPLP@GOLD	195	0.579	1.84
PLP1@DS	195	0.568	1.86
G-Score@SYBYL	195	0.558	1.87
AutoDock Vina	195	0.557	1.85
ASP@GOLD	195	0.556	1.88
ASE@MOE	195	0.544	1.89
ChemScore@GOLD	189	0.536	1.90
D-Score@SYBYL	195	0.526	1.92
Alpha-HB@MOE	195	0.511	1.94
LUDI3@DS	195	0.487	1.97
GoldScore@GOLD	189	0.483	1.97
Affinity-dG@MOE	195	0.482	1.98
LigScore2@DS	190	0.456	2.02
GlideScore-SP	169	0.452	2.03
Jain@DS	191	0.408	2.05
PMF@DS	194	0.364	2.11
GlideScore-XP	164	0.277	2.18
London-dG@MOE	195	0.242	2.19
PMF@SYBYL	191	0.221	2.20

<sup>a</sup>The results except  $\Delta_{\text{vina}}\text{RF}_{20}$  and AutoDock Vina are obtained from literature. <sup>b</sup>Scoring functions are ranked by the Pearson correlation coefficients.



**Table S10.** Performance of 22 Scoring Functions in Ranking Power Test in CASF-2013<sup>a</sup>

score function <sup>b</sup>	Ranking success rates (%)	
	high-level	low-level
X-Score <sup>HM</sup>	58.5	72.3
ChemPLP@GOLD	58.5	72.3
$\Delta_{\text{vina}}\text{RF}_{20}$	55.4	73.8
PLP2@DS	55.4	72.3
GoldScore@GOLD	55.4	76.9
ChemScore@SYBYL	53.8	67.7
Affinity-dG@MOE	53.8	66.2
LigScore1@DS	52.3	61.5
Alpha-HB@MOE	52.3	66.2
G-Score@SYBYL	52.3	72.3
LUDI1@DS	52.3	69.2
AutoDock Vina	49.2	72.3
D-Score@SYBYL	49.2	63.1
PMF@DS	49.2	66.2
ASP@GOLD	47.7	72.3
ChemScore@GOLD	46.2	63.1
London-dG@MOE	43.1	60.0
PMF@SYBYL	43.1	61.5
GlideScore-SP	43.1	56.9
Jain@DS	41.5	58.5
ASE@MOE	40.0	64.6
GlideScore-XP	35.4	47.7

<sup>a</sup>The results except  $\Delta_{\text{vina}}\text{RF}_{20}$  and AutoDock Vina are obtained from literature.<sup>[31]</sup> <sup>b</sup>Scoring

functions are ranked by high-level success rates.

**Table S11.** Success rates of 22 Scoring Functions in the Docking Power Test in CASF-2013<sup>a</sup>

score function <sup>b</sup>	docking (%)		
	The top pose	Top two poses	Top three poses
$\Delta_{\text{vina}}\text{RF}_{20}$	86.7	93.3	94.4
AutoDock Vina	85.1	89.7	92.3
ChemPLP@GOLD	81.0	86.7	89.7
ChemScore@GOLD	77.9	83.1	88.2
GlideScore-SP	78.5	85.6	87.7
LigScore2@DS	76.9	84.1	86.7
PLP1@DS	76.9	84.1	86.2
Alpha-HB@MOE	75.4	82.6	86.2
GlideScore-XP	74.4	82.6	85.6
ASP@GOLD	71.8	81.5	87.2
GoldScore@GOLD	71.3	81.0	85.6
LUDI1@DS	59.0	75.4	83.1
Affinity-dG@MOE	63.1	74.9	81.0
ChemScore@SYBYL	59.5	69.2	75.4
London-dG@MOE	59.5	73.8	78.5
X-Score <sup>HM</sup>	61.0	73.3	77.9
G-Score@SYBYL	45.1	61.5	72.3
Jain@DS	48.2	62.1	70.8
PMF@SYBYL	51.8	60.0	66.7
PMF04@DS	51.8	62.6	66.2
ASE@MOE	51.3	60.0	63.6
D-Score@SYBYL	18.5	29.7	42.6

<sup>a</sup>The results except  $\Delta_{\text{vina}}\text{RF}_{20}$  and AutoDock Vina are obtained from literature.<sup>[31]</sup> <sup>b</sup>Scoring

functions are ranked by success rates when the top one poses are considered.

**Table S12.** Enrichment Factors of 22 Scoring Functions in the Screening Power Test in CASF-2013<sup>a</sup>

score function <sup>b</sup>	enrichment factor		
	top 1%	top 5%	top 10%
$\Delta_{\text{vina}}\text{RF}_{20}$	20.95	6.44	3.89
GlideScore-SP	19.54	6.27	4.14
ChemScore@GOLD	18.90	6.83	4.08
GlideScore-XP	16.81	6.02	4.07
LigScore2@DS	15.90	6.23	3.51
AutoDock Vina	15.57	5.55	3.62
ChemPLP@GOLD	14.28	5.88	4.31
LUDI1@DS	12.53	4.28	2.80
ASP@GOLD	12.36	6.23	3.79
Affinity-dG@MOE	8.21	4.15	3.19
London-dG@MOE	8.08	3.36	2.51
GoldScore@GOLD	7.95	4.52	3.16
PLP1@DS	6.92	4.28	3.04
Jain@DS	5.90	2.51	1.80
PMF@SYBYL	5.38	2.21	1.90
ChemScore@SYBYL	5.26	2.38	2.18
Alpha-HB@MOE	4.87	3.23	1.32
PMF04@DS	4.87	2.87	2.63
ASE@MOE	4.36	2.35	1.59
X-Score <sup>HM</sup>	2.31	2.14	1.41
D-Score@SYBYL	2.31	1.79	1.46
G-Score@SYBYL	1.92	1.26	1.44

<sup>a</sup>The results except  $\Delta_{\text{vina}}\text{RF}_{20}$  and AutoDock Vina are obtained from literature.<sup>[31]</sup> <sup>b</sup>Scoring functions are ranked by their average enrichment factor obtained at the top 1% level.

**Table S13.** Success Rates of Finding the Best Ligand Molecule of 22 Scoring Functions in the Screening Power Test in CASF-2013<sup>a</sup>

score function <sup>b</sup>	success rates of finding the best ligand molecule among (%) <sup>c</sup>		
	top 1%	top 5%	top 10%
$\Delta_{\text{vina}}\text{RF}_{20}$	60.0 (39)	80.0 (52)	86.2 (56)
GlideScore-SP	60.0 (39)	72.3 (47)	76.9 (50)
GlideScore-XP	52.3 (34)	69.2 (45)	73.8 (48)
ChemScore@GOLD	49.2 (32)	78.5 (51)	83.1 (54)
LigScore2@DS	47.7 (31)	75.4 (49)	83.1 (54)
AutoDock Vina	44.6 (29)	60.0 (39)	69.2 (45)
ChemPLP@GOLD	41.5 (27)	70.8 (46)	84.6 (55)
LUDI2@DS	38.5 (25)	53.8 (35)	66.2 (43)
ASP@GOLD	36.9 (24)	75.4 (49)	81.5 (53)
Affinity-dG@MOE	23.1 (15)	50.8 (33)	66.2 (43)
PLP1@DS	21.5 (14)	52.3 (34)	70.8 (46)
GoldScore@GOLD	21.5 (14)	52.3 (34)	66.2 (43)
London-dG@MOE	21.5 (14)	36.9 (24)	49.2 (32)
Jain@DS	16.9 (11)	29.2 (19)	40.0 (26)
ChemScore@SYBYL	15.4 (10)	33.8 (22)	50.8 (33)
Alpha-HB@MOE	13.8 (9)	36.9 (24)	63.1 (41)
PMF@SYBYL	13.8 (9)	23.1 (15)	38.5 (25)
PMF04@DS	12.3 (8)	30.8 (20)	47.7 (31)
ASE@MOE	12.3 (8)	30.8 (20)	38.5 (25)
X-Score <sup>HM</sup>	9.23 (6)	21.5 (14)	32.3 (21)
D-Score@SYBYL	6.15 (4)	20.0 (13)	24.6 (16)
G-Score@SYBYL	4.62 (3)	16.9 (11)	30.8 (20)

<sup>a</sup>The results except  $\Delta_{\text{vina}}\text{RF}_{20}$  and AutoDock Vina are obtained from literature.<sup>[31]</sup> <sup>b</sup>Scoring functions are ranked by their success rates obtained at the top 1% level. <sup>c</sup>Numbers in brackets are the number of successful cases over total 65 cases.

## References

- [1] Y. Li, Z. H. Liu, J. Li, L. Han, J. Liu, Z. X. Zhao, R. X. Wang, *J. Chem. Inf. Model.* **2014**, *54*, 1700.
- [2] J. B. Dunbar, Jr., R. D. Smith, C. Y. Yang, P. M. Ung, K. W. Lexa, N. A. Khazanov, J. A. Stuckey, S. Wang, H. A. Carlson, *J. Chem. Inf. Model.* **2011**, *51*, 2036.
- [3] S. Y. Huang, X. Q. Zou, *J. Chem. Inf. Model.* **2011**, *51*, 2107.
- [4] D. R. Koes, M. P. Baumgartner, C. J. Camacho, *J. Chem. Inf. Model.* **2013**, *53*, 1893.
- [5] L. L. Jiang, R. C. Rizzo, *J. Phys. Chem. B* **2015**, *119*, 1083.
- [6] A. Krammer, P. D. Kirchhoff, X. Jiang, C. M. Venkatachalam, M. Waldman, *J. Mol. Graphics Modell.* **2005**, *23*, 395.
- [7] G. Verkhivker, K. Appelt, S. T. Freer, J. E. Villafranca, *Protein Eng.* **1995**, *8*, 677.
- [8] G. M. Verkhivker, D. Bouzida, D. K. Gehlhaar, P. A. Rejto, S. Arthurs, A. B. Colson, S. T. Freer, V. Larson, B. A. Luty, T. Marrone, P. W. Rose, *J. Comput.-Aided Mol. Des.* **2000**, *14*, 731.
- [9] I. Muegge, Y. C. Martin, *J. Med. Chem.* **1999**, *42*, 791.
- [10] I. Muegge, *Perspect. Drug Discovery Des.* **2000**, *20*, 99.
- [11] I. Muegge, *J. Comput. Chem.* **2001**, *22*, 418.
- [12] I. Muegge, *J. Med. Chem.* **2006**, *49*, 5895.
- [13] A. N. Jain, *J. Comput.-Aided Mol. Des.* **1996**, *10*, 427.
- [14] H. J. Bohm, *J. Comput.-Aided Mol. Des.* **1994**, *8*, 243.
- [15] H. J. Bohm, *J. Comput.-Aided Mol. Des.* **1998**, *12*, 309.
- [16] G. Jones, P. Willett, R. C. Glen, A. R. Leach, R. Taylor, *J. Mol. Biol.* **1997**, *267*, 727.
- [17] M. D. Eldridge, C. W. Murray, T. R. Auton, G. V. Paolini, R. P. Mee, *J. Comput.-Aided Mol. Des.* **1997**, *11*, 425.
- [18] C. A. Baxter, C. W. Murray, D. E. Clark, D. R. Westhead, M. D. Eldridge, *Proteins: Struct., Funct., Genet.* **1998**, *33*, 367.
- [19] W. T. M. Mooij, M. L. Verdonk, *Proteins: Struct., Funct., Bioinf.* **2005**, *61*, 272.
- [20] T. J. A. Ewing, S. Makino, A. G. Skillman, I. D. Kuntz, *J. Comput.-Aided Mol. Des.* **2001**, *15*, 411.

- [21] R. A. Friesner, J. L. Banks, R. B. Murphy, T. A. Halgren, J. J. Klicic, D. T. Mainz, M. P. Repasky, E. H. Knoll, M. Shelley, J. K. Perry, D. E. Shaw, P. Francis, P. S. Shenkin, *J. Med. Chem.* **2004**, *47*, 1739.
- [22] T. A. Halgren, R. B. Murphy, R. A. Friesner, H. S. Beard, L. L. Frye, W. T. Pollard, J. L. Banks, *J. Med. Chem.* **2004**, *47*, 1750.
- [23] R. A. Friesner, R. B. Murphy, M. P. Repasky, L. L. Frye, J. R. Greenwood, T. A. Halgren, P. C. Sanschagrin, D. T. Mainz, *J. Med. Chem.* **2006**, *49*, 6177.
- [24] H. Gohlke, M. Hendlich, G. Klebe, *J. Mol. Biol.* **2000**, *295*, 337.
- [25] H. F. G. Velec, H. Gohlke, G. Klebe, *J. Med. Chem.* **2005**, *48*, 6296.
- [26] R. X. Wang, L. H. Lai, S. M. Wang, *J. Comput.-Aided Mol. Des.* **2002**, *16*, 11.
- [27] O. Trott, A. J. Olson, *J. Comput. Chem.* **2010**, *31*, 455.
- [28] O. Korb, T. Stutzle, T. E. Exner, *J. Chem. Inf. Model.* **2009**, *49*, 84.
- [29] J. Goto, R. Kataoka, H. Muta, N. Hirayama, *J. Chem. Inf. Model.* **2008**, *48*, 583.
- [30] T. J. Cheng, X. Li, Y. Li, Z. H. Liu, R. X. Wang, *J. Chem. Inf. Model.* **2009**, *49*, 1079.
- [31] Y. Li, L. Han, Z. H. Liu, R. X. Wang, *J. Chem. Inf. Model.* **2014**, *54*, 1717.