Supporting Information:

The Development and Application of KinomePro-DL: A Deep Learning Based Online Small Molecule Kinome Selectivity Profiling Prediction Platform

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The Supporting Materials file includes ：

Figure S1: Kinome selectivity profile maps of 15 compound from internal collection obtained from Eurofin KINOMEscan (left column) and predicted by KinomeX (right column).

Figure S2: Kinome selectivity profile maps of 15 compound from internal collection obtained from Eurofin KINOMEscan (left column) and predicted by AMGU Model (right column).

Figure S3: Kinome selectivity profile maps of 15 compound from internal collection obtained from Eurofin KINOMEscan (left column) and predicted by KinScan Model (right column).

Table S1: Structural information for the eight test compounds

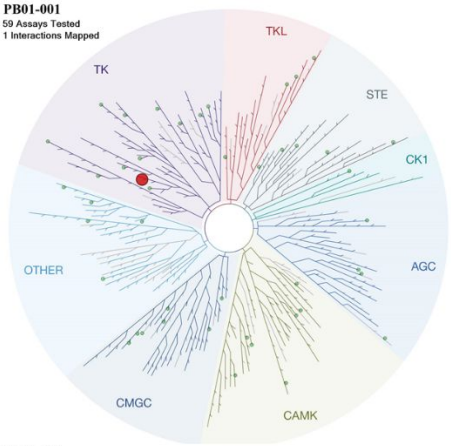
Table S2: Compound purity information

Figure S4: Comparison of the kinome selectivity profiles predicted by KinomePro-DL model and experimental results obtain from Eurofin KINOMEscan of Molecule 18.

Figure S5: Structures of known CDK2 inhibitors from ChemEMBL database with highest similarity compared to hit compounds 11 (a) and 18 (b). Numbers listed for each compound were similarity values obtained by molecular fingerprints using RDKit.

Figure S6: Screenshots of representative webpages of KinomePro-DL web server tool.

PB01-001
59 Assays Tested
1 Interactions Mapped



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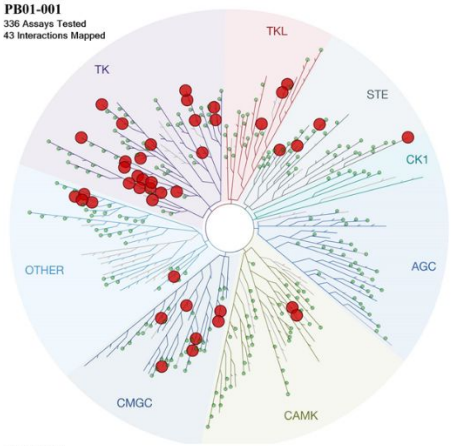
336 Assays Tested
43 Interactions Mapped



PB01-002
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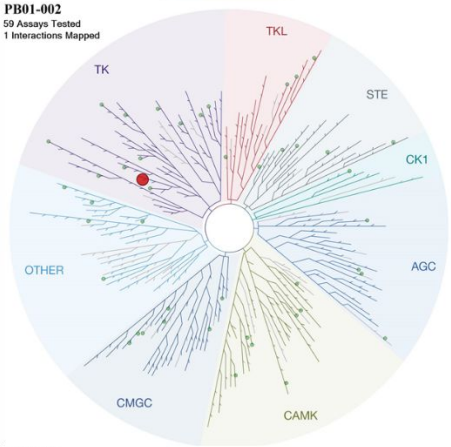

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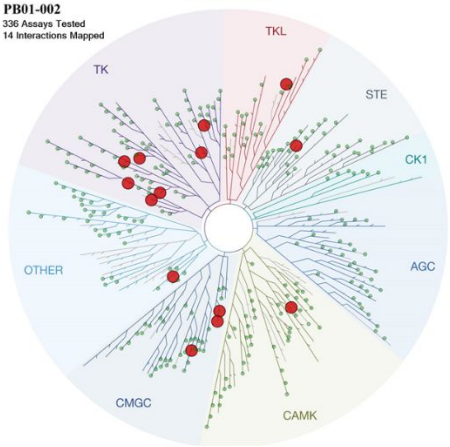
336 Assays Tested
14 Interactions Mapped



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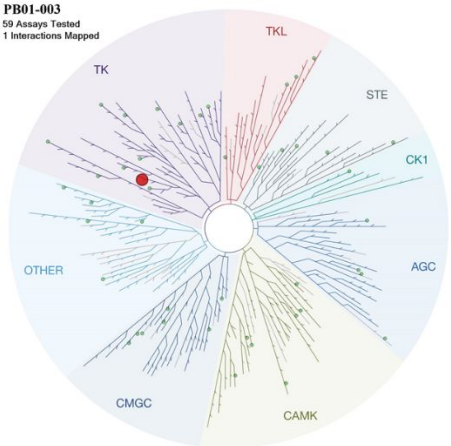

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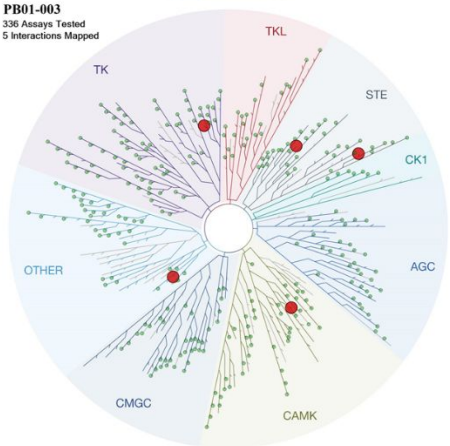
336 Assays Tested
5 Interactions Mapped



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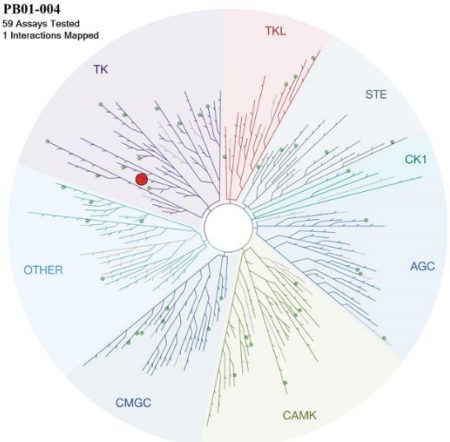

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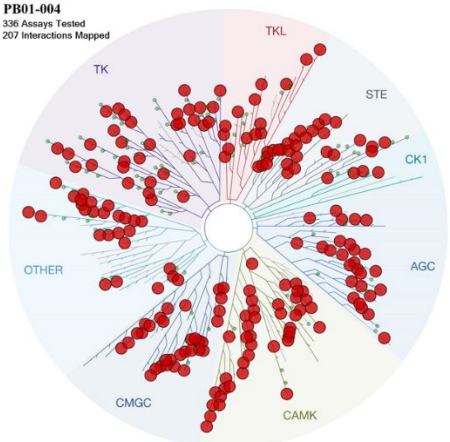
207 Interactions Mapped



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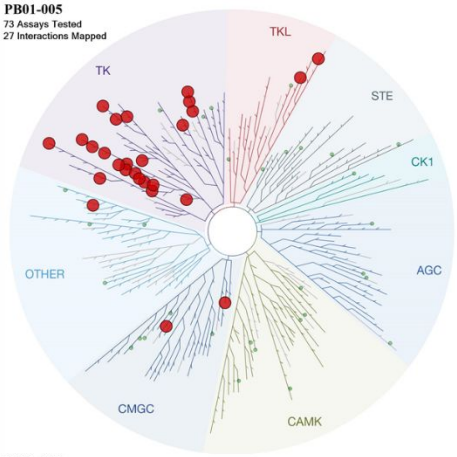
27 Interactions Mapped



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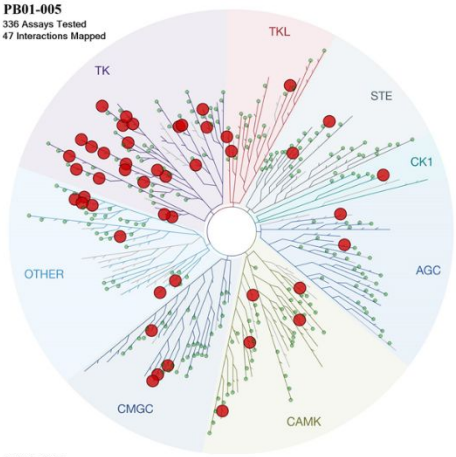

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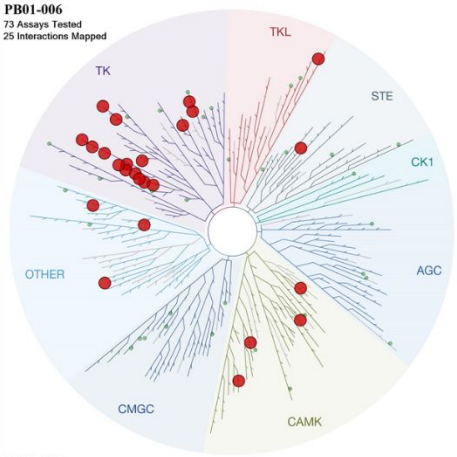

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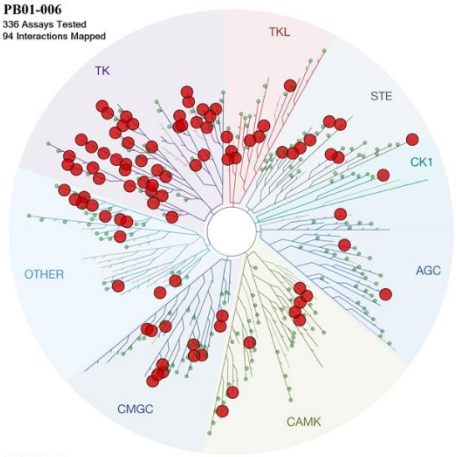
94 Interactions Mapped



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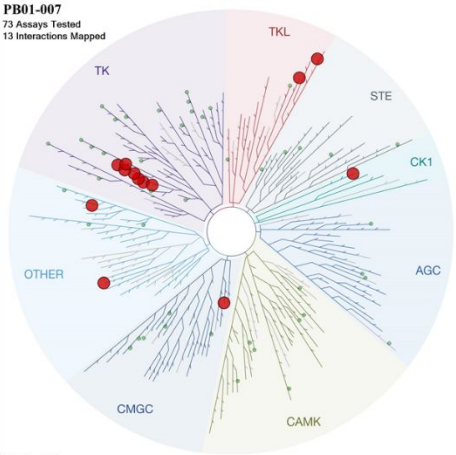
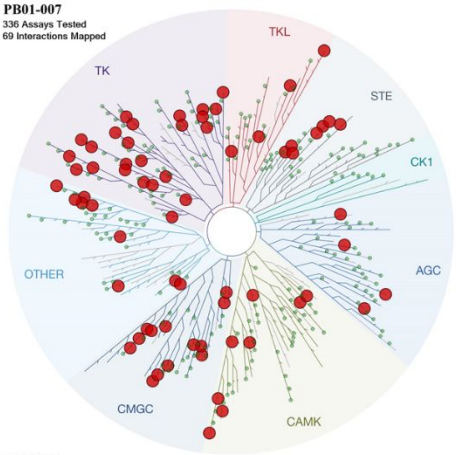
13 Interactions Mapped



PB01-007
336 Assays Tested
69 Interactions Mapped



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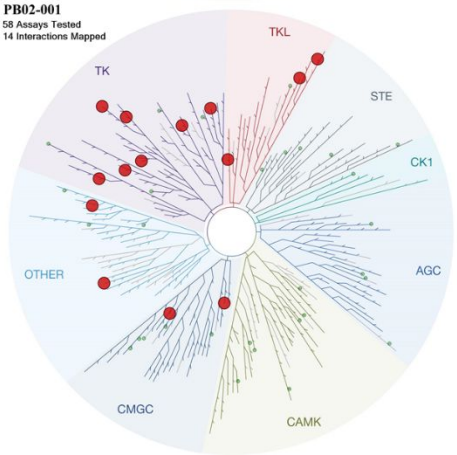
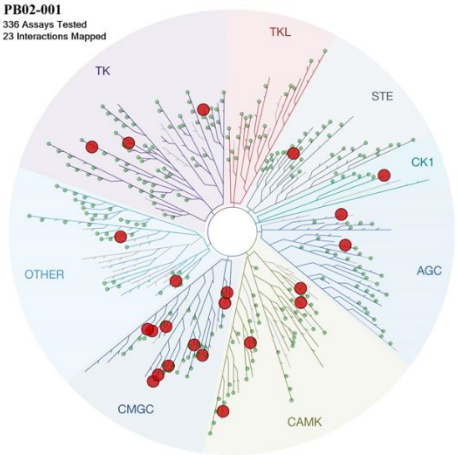


PB02-001
336 Assays Tested
23 Interactions Mapped



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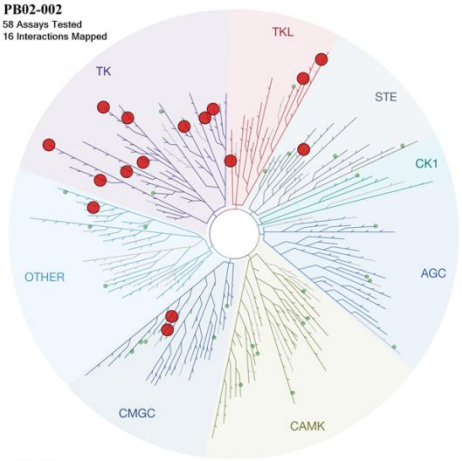
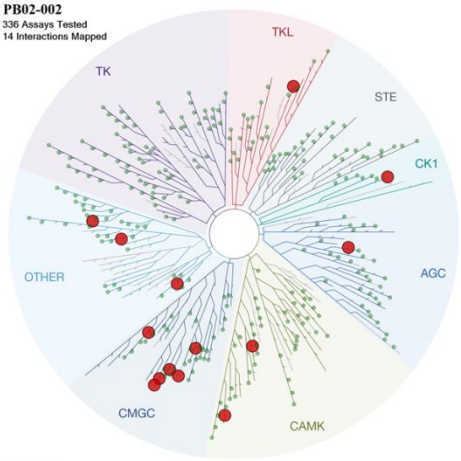
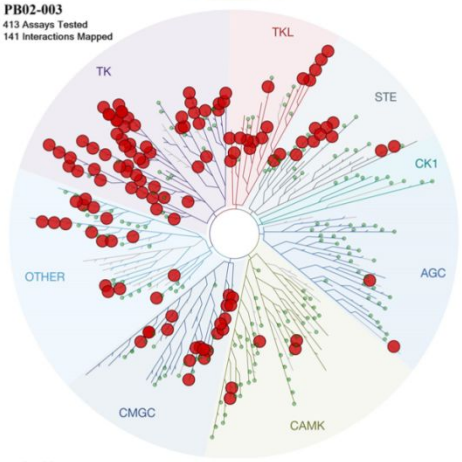
58 Assays Tested
16 Interactions Mapped



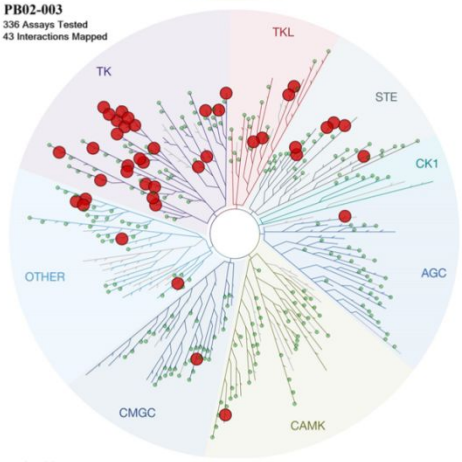
PB02-002
336 Assays Tested
14 Interactions Mapped



PB02-003
413 Assays Tested
141 Interactions Mapped



PB02-003
336 Assays Tested
43 Interactions Mapped



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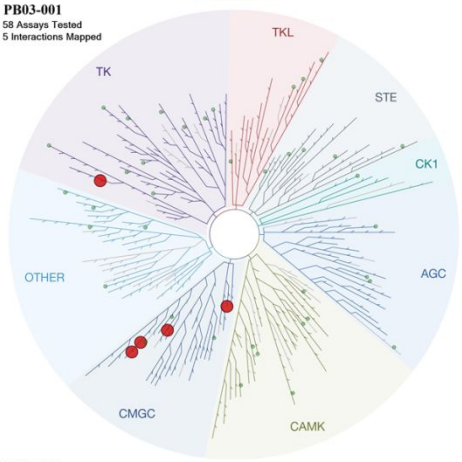

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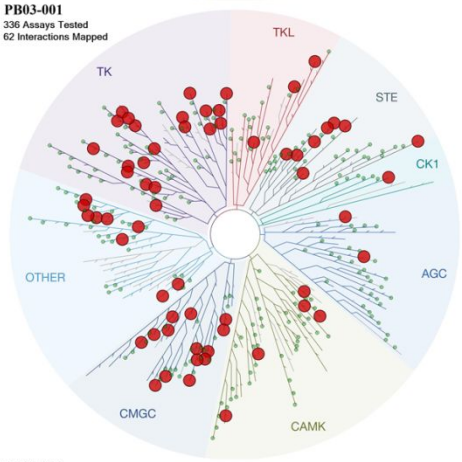
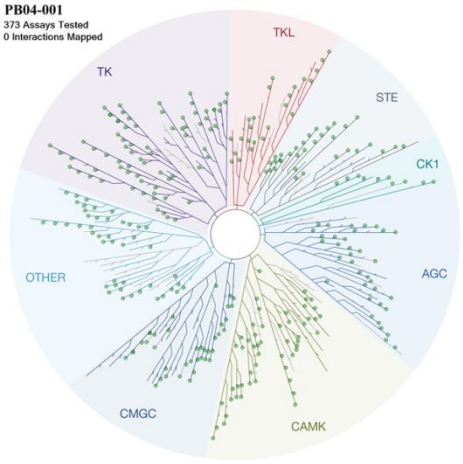
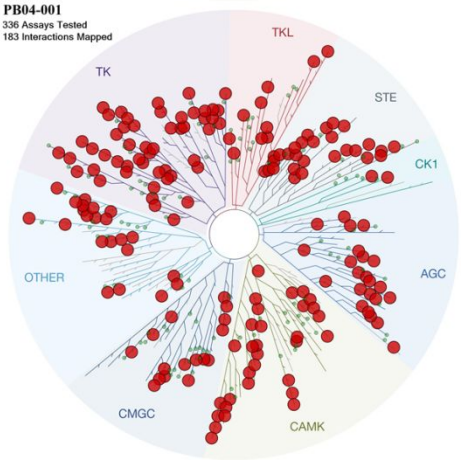
336 Assays Tested
62 Interactions Mapped



PB04-001
373 Assays Tested
0 Interactions Mapped



PB04-001
336 Assays Tested
183 Interactions Mapped



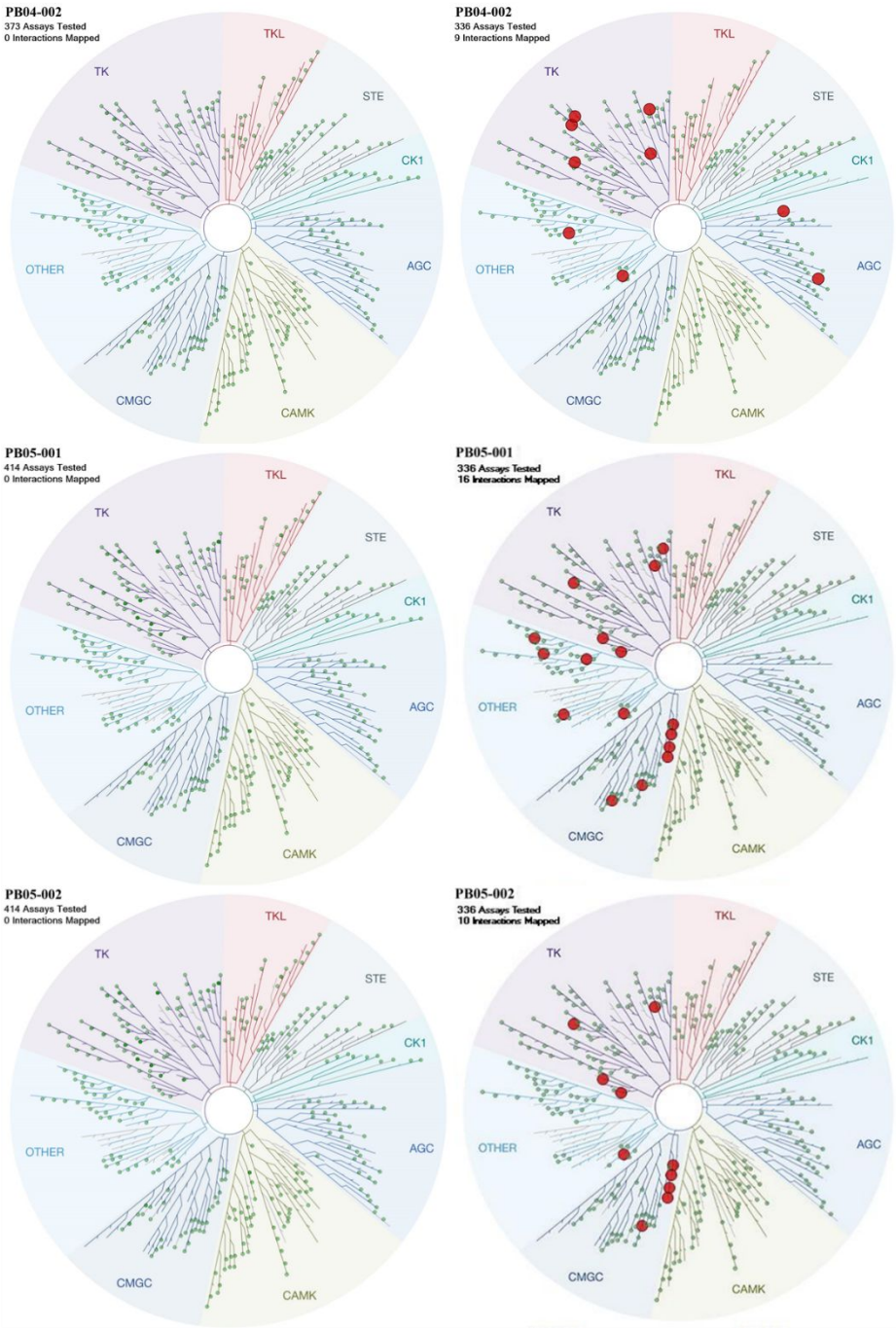
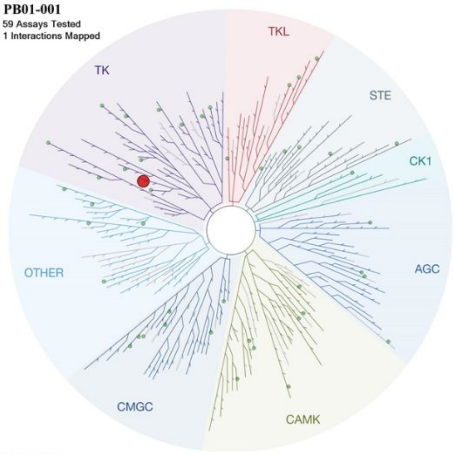


Figure S1: Kinome selectivity profile maps of 15 compound from internal collection obtained from Eurofin KINOMEscan (left column) and predicted by KinomeX (right column).

PB01-001
59 Assays Tested
1 Interactions Mapped



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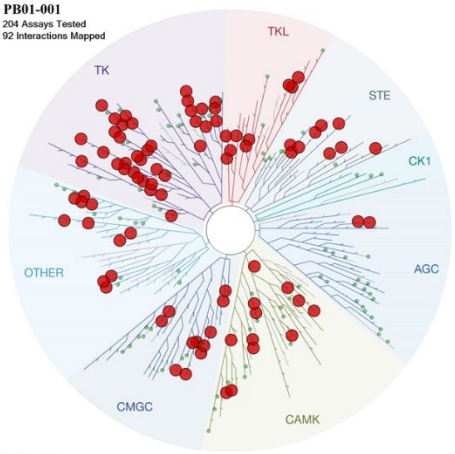
204 Assays Tested
92 Interactions Mapped



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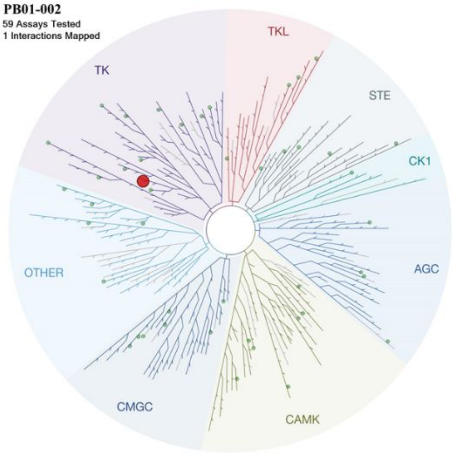
1 Interactions Mapped



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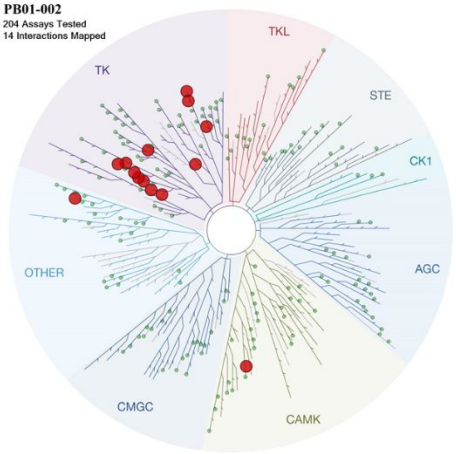
204 Assays Tested
14 Interactions Mapped



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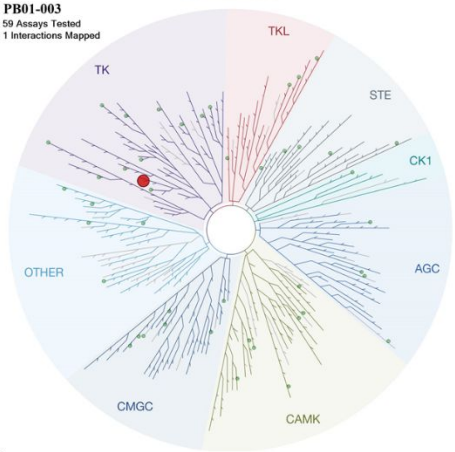

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204 Assays Tested
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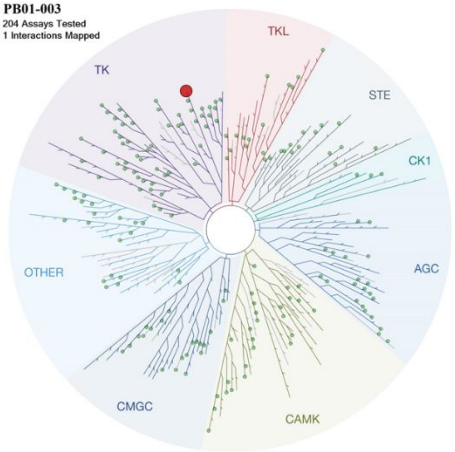

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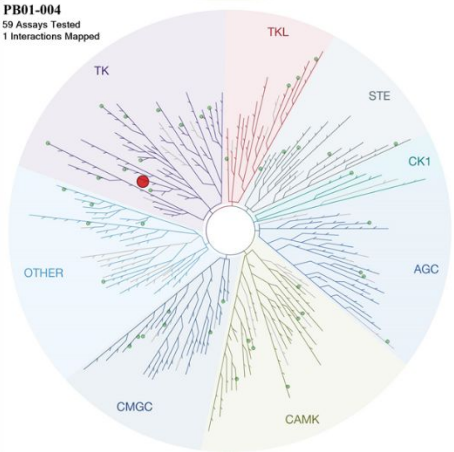

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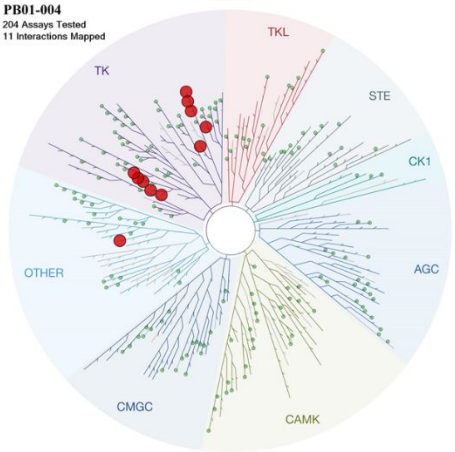
11 Interactions Mapped



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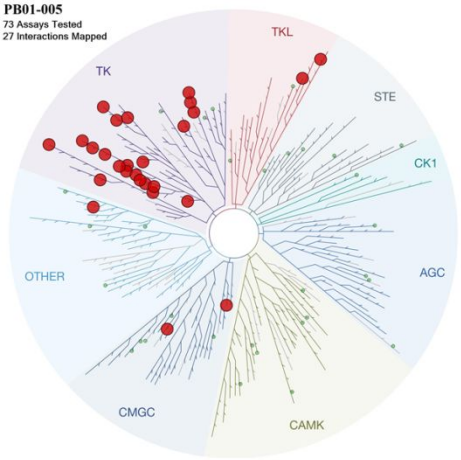
27 Interactions Mapped



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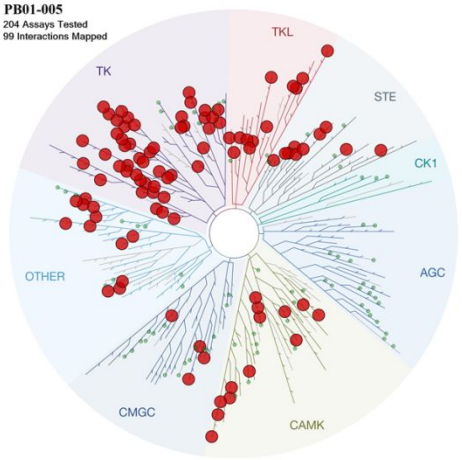
99 Interactions Mapped



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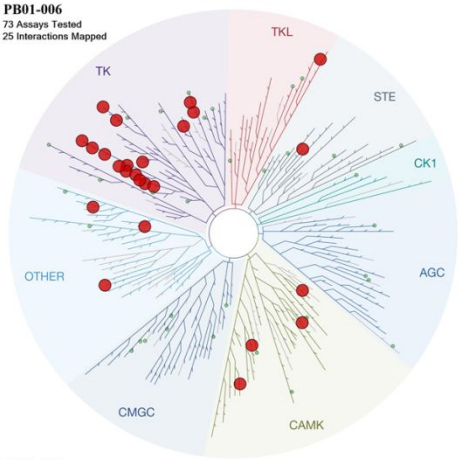

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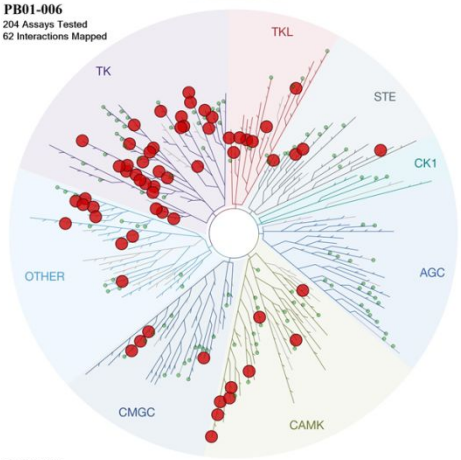
62 Interactions Mapped



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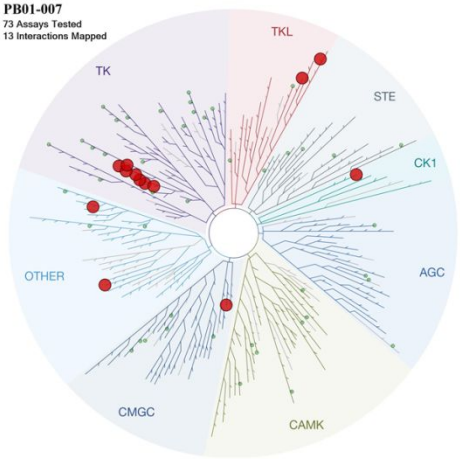

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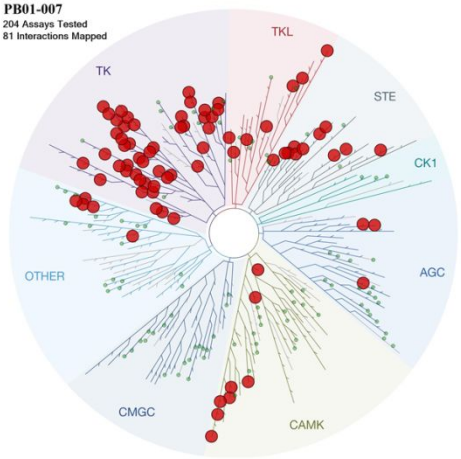

PB02-001
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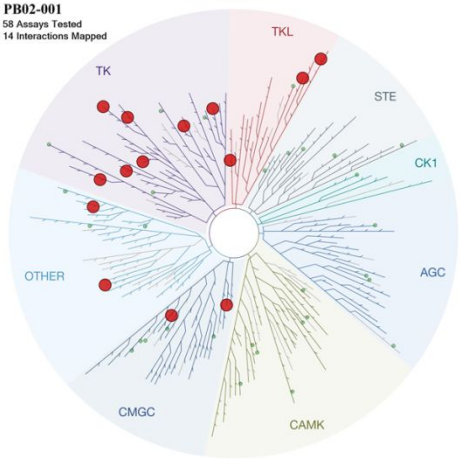

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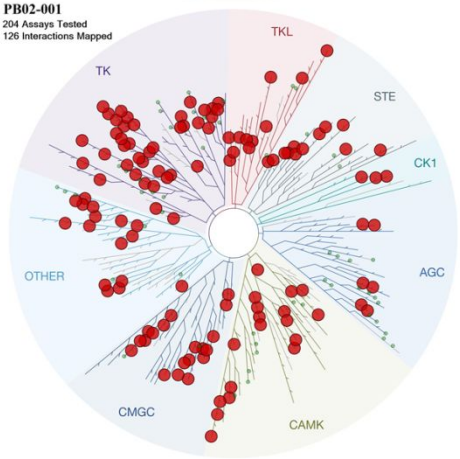
126 Interactions Mapped



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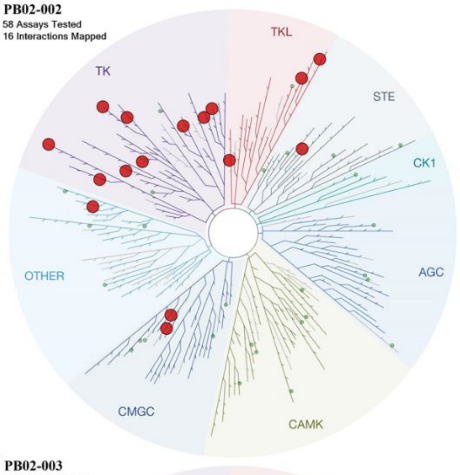

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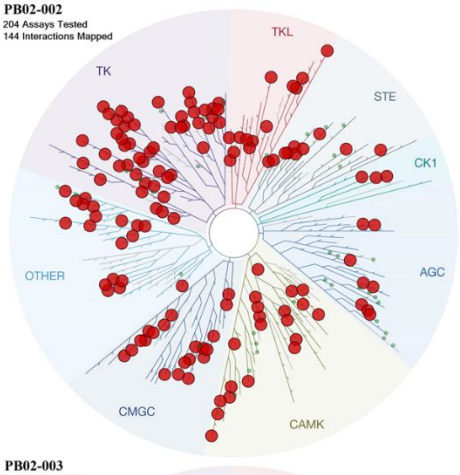
144 Interactions Mapped



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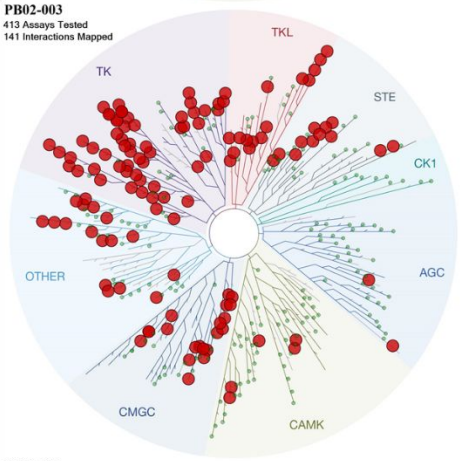

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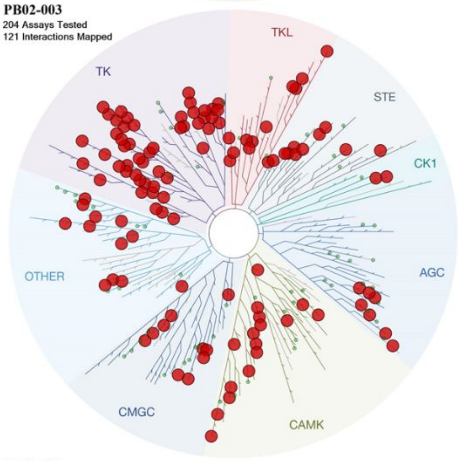

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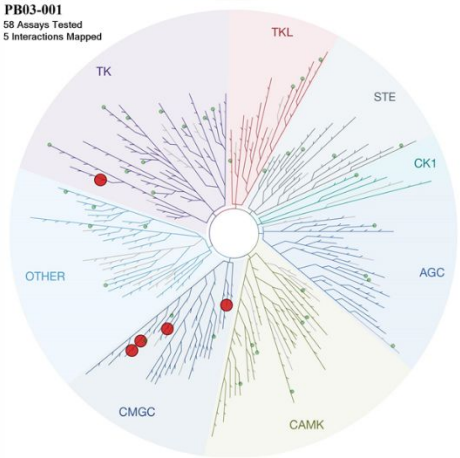

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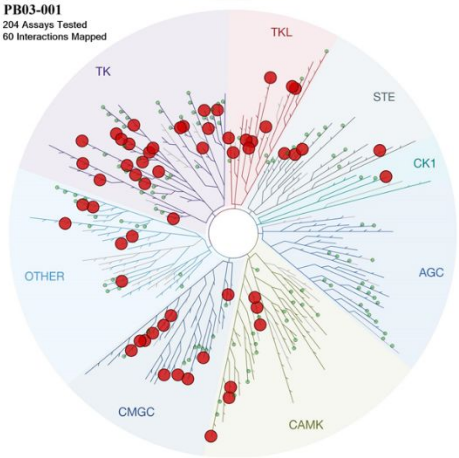
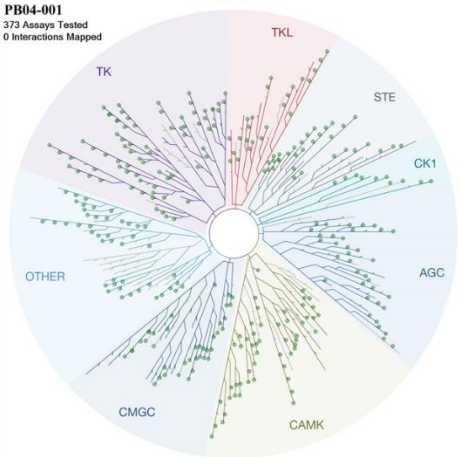
60 Interactions Mapped



PB04-001
373 Assays Tested
0 Interactions Mapped



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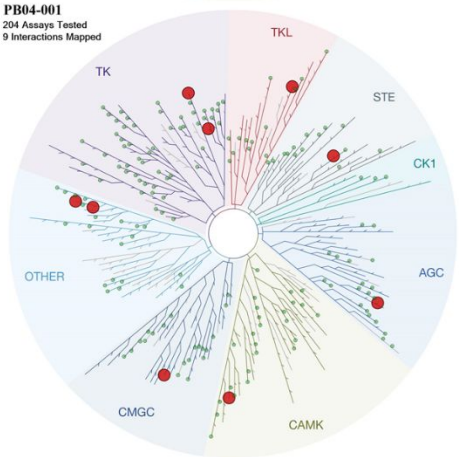
9 Interactions Mapped



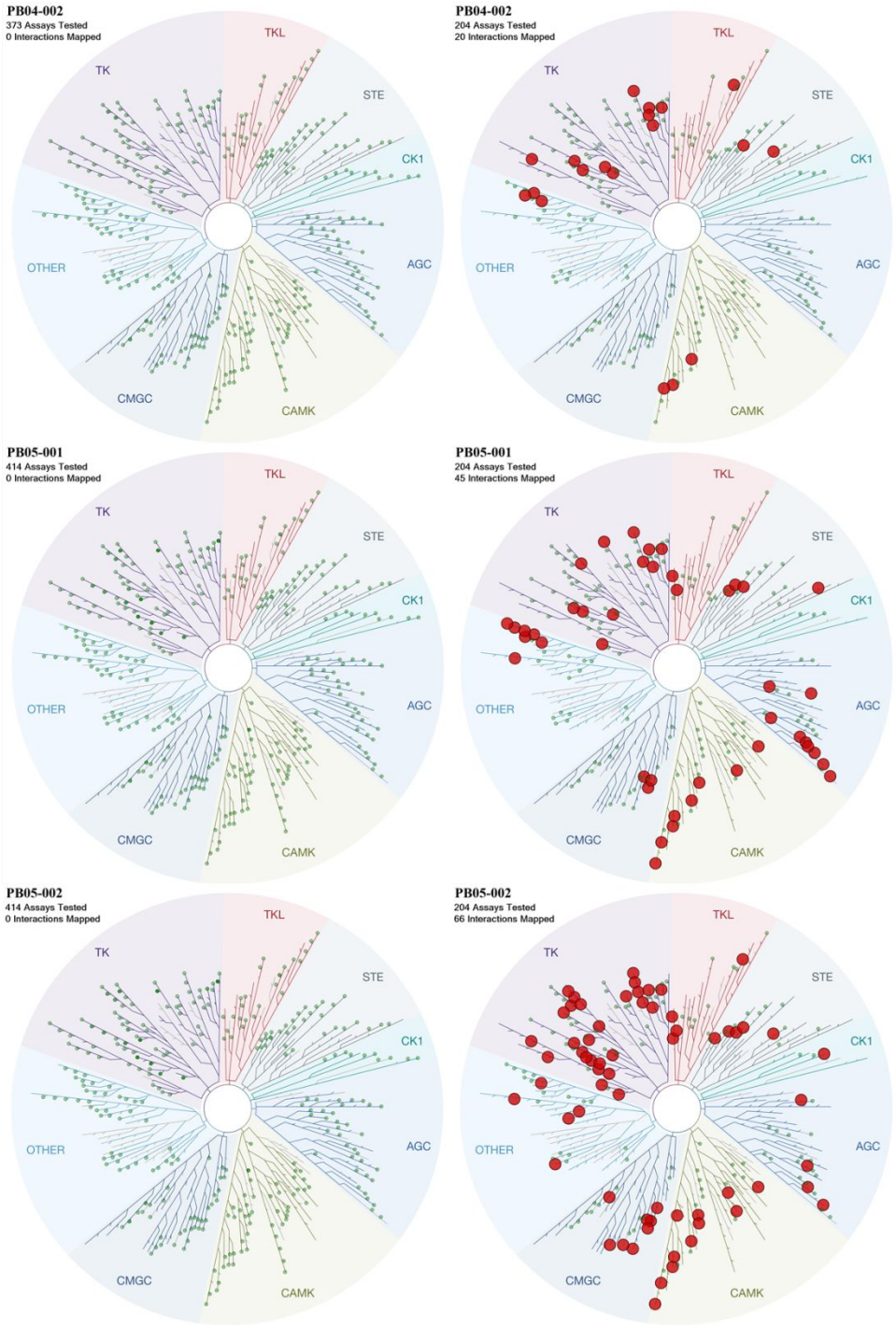
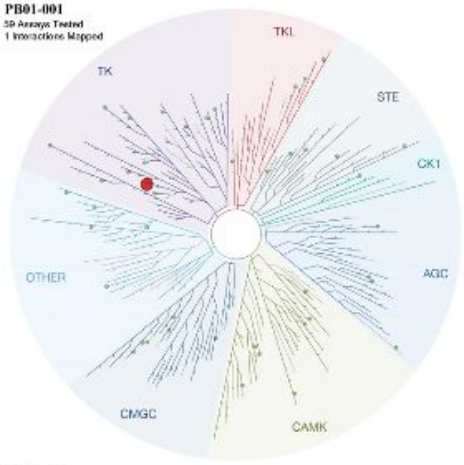
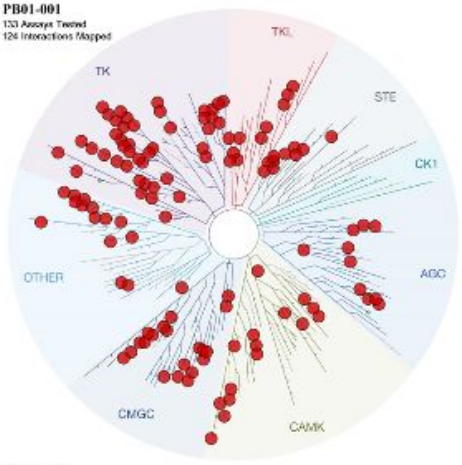


Figure S2: Kinome selectivity profile maps of 15 compound from internal collection obtained from Eurofin KINOMEscan (left column) and predicted by AMGU Model (right column).

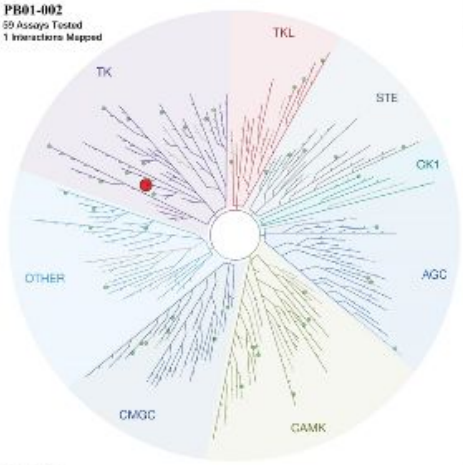
PB01-001
59 Assays Tested
1 Interactions Mapped



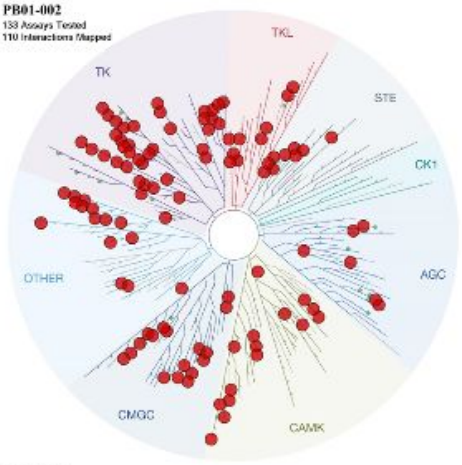
PB01-001
133 Assays Tested
124 Interactions Mapped



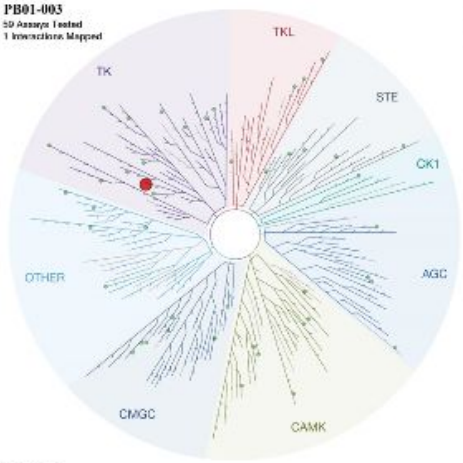
PB01-002
59 Assays Tested
1 Interactions Mapped



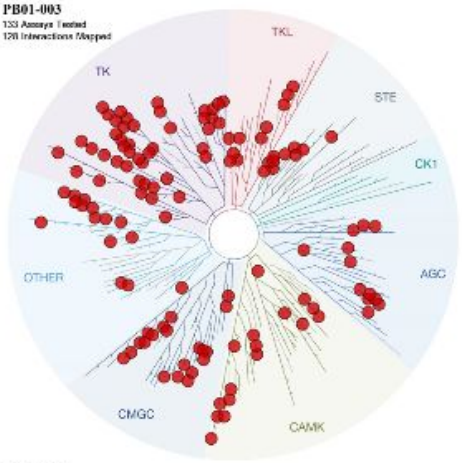
PB01-002
133 Assays Tested
110 Interactions Mapped



PB01-003
59 Assays Tested
1 Interactions Mapped



PB01-003
133 Assays Tested
126 Interactions Mapped



PB01-004
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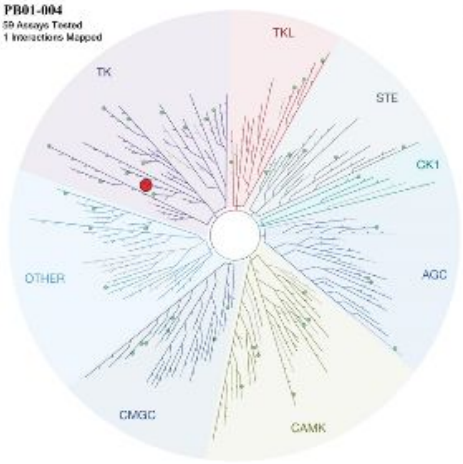
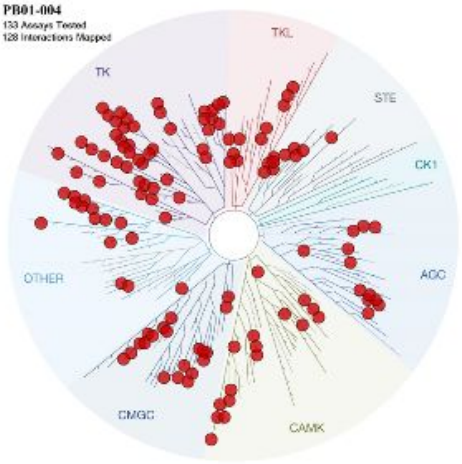
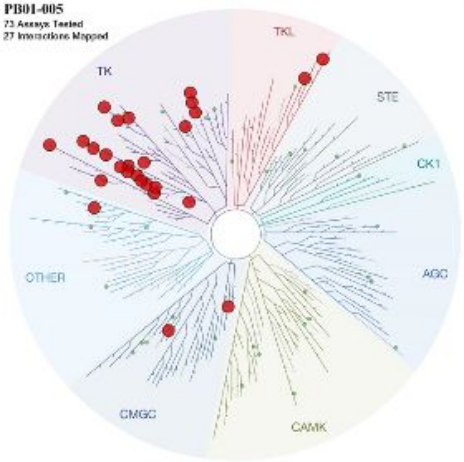


PB01-004
133 Assays Tested
128 Interactions Mapped



PB01-005
73 Assays Tested
27 Interactions Mapped



PB01-005
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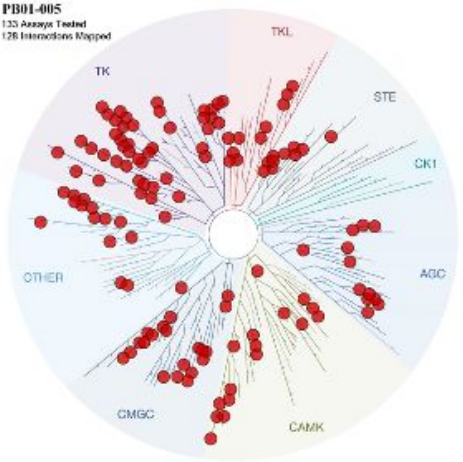
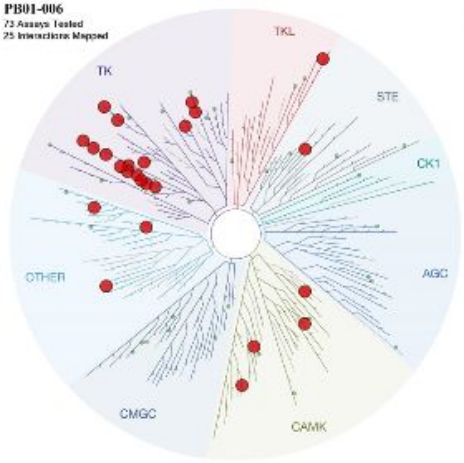
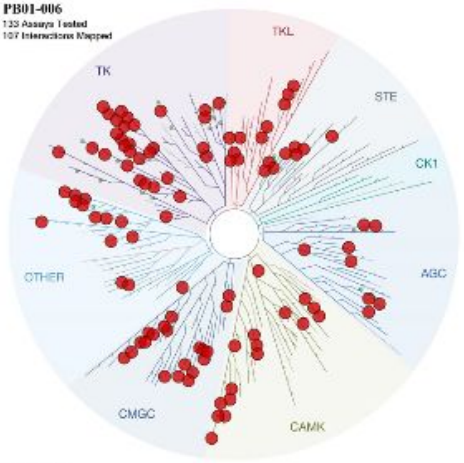


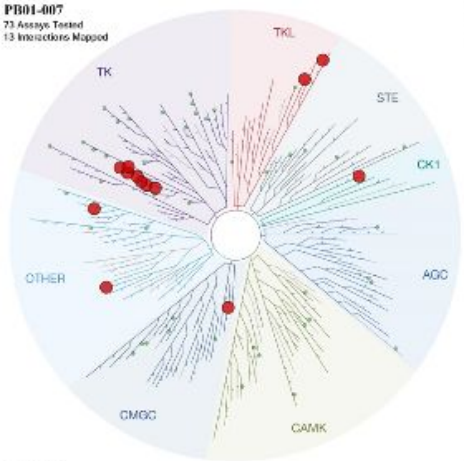
PB01-006
73 Assays Tested
25 Interactions Mapped



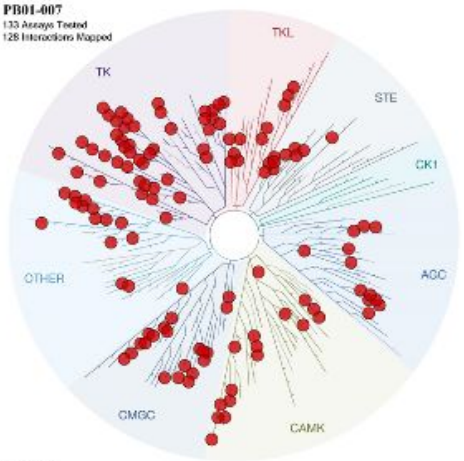
PB01-006
133 Assays Tested
107 Interactions Mapped



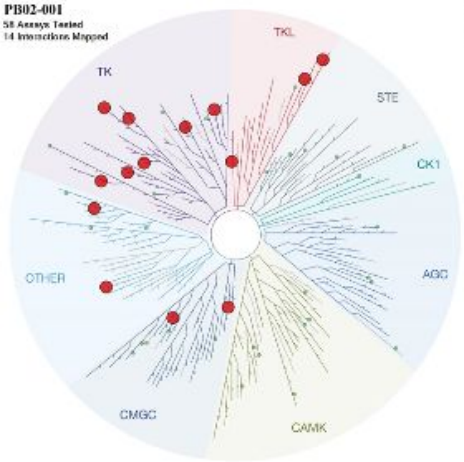
PB01-007
73 Assays Tested
13 Interactions Mapped



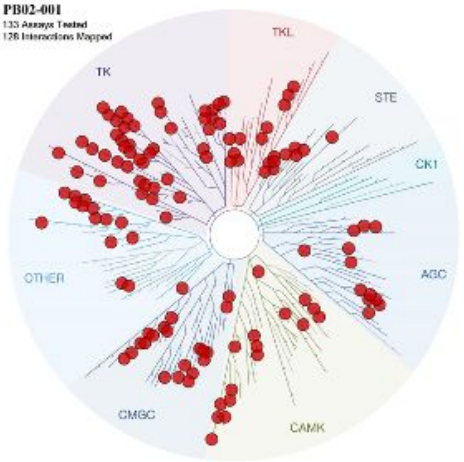
PB01-007
133 Assays Tested
126 Interactions Mapped



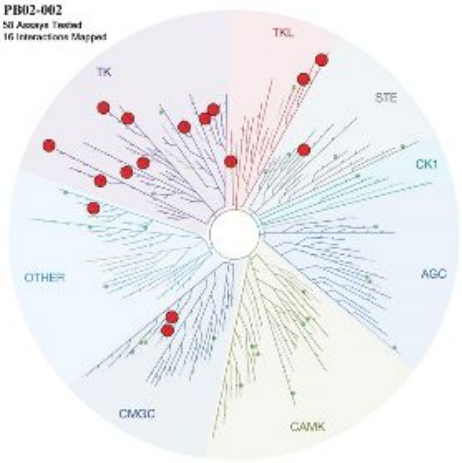
PB02-001
58 Assays Tested
14 Interactions Mapped



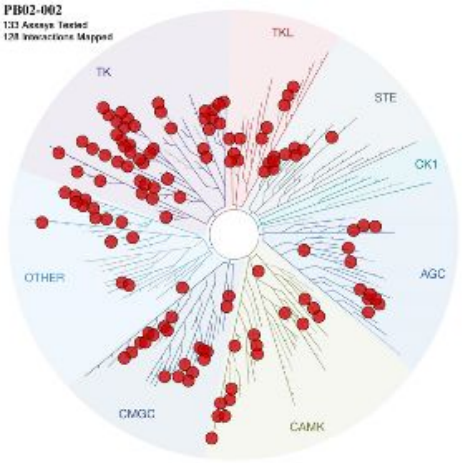
PB02-001
133 Assays Tested
126 Interactions Mapped



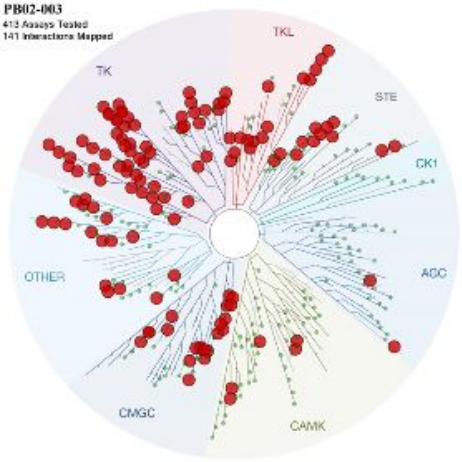
PB02-002
58 Assays Tested
16 Interactions Mapped



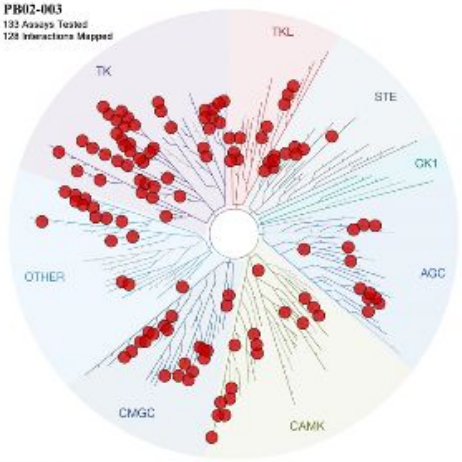
PB02-002
133 Assays Tested
128 Interactions Mapped



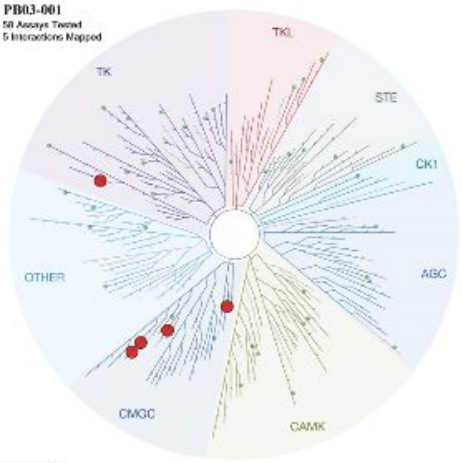
PB02-003
413 Assays Tested
141 Interactions Mapped



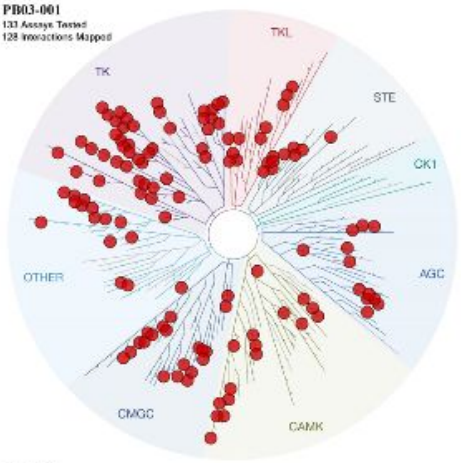
PB02-003
133 Assays Tested
128 Interactions Mapped



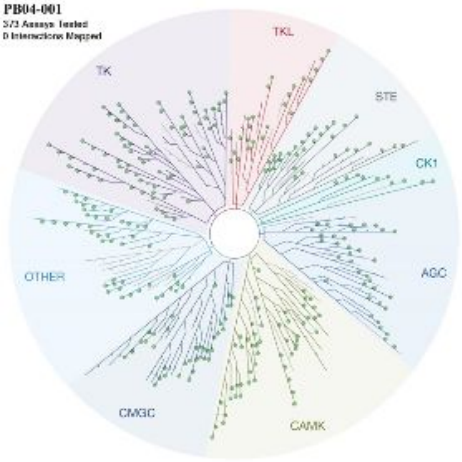
PB03-001
58 Assays Tested
5 Interactions Mapped



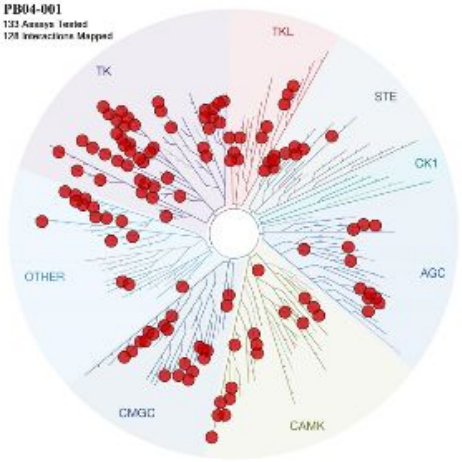
PB03-001
133 Assays Tested
128 Interactions Mapped



PB04-001
373 Assays Tested
0 Interactions Mapped



PB04-001
133 Assays Tested
128 Interactions Mapped



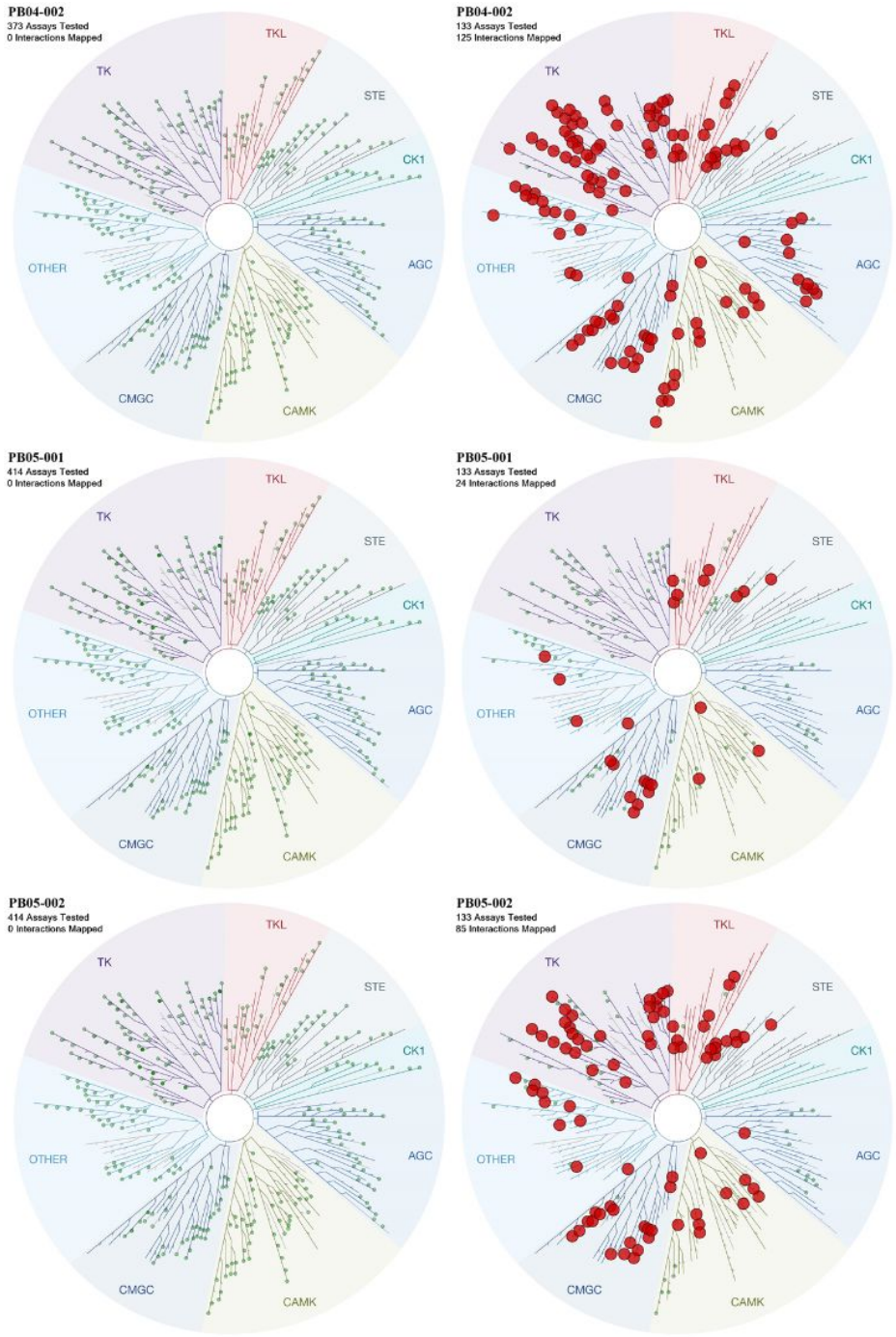


Figure S3: Kinome selectivity profile maps of 15 compound from internal collection obtained from Eurofin KINOMEscan (left column) and predicted by KinScan Model (right column).

Table S1: Structural information for the eight test compounds

Compound	**smiles**
Molecule-10	[H]N(C1=NC=C(CN2CCOCC2)C=C1)[C@]1([H])CCC2=C1C=CC=C2
Molecule-11	O=C(N1)C(C2=C(S3)CCCCC2)=C3N=C1CC4=CNN=C4
Molecule-17	FC1=CC=CC(C2=NC=NC(NC3C[C@@H]4CC[C@@H](N4S(C)(=O)=O)C3)=N2)=C1
Molecule-18	O=C(CC1=CC=C2C=NNC2=C1)NC3=NNC(C4CCOCC4)=C3
Molecule-20	O[C@@H]1C[C@H]2C[C@@H]1CC2CNC(NC3=NC=C(C4CCOCC4)S3)=O
Molecule-21	[H]N(C(=O)C[C@]1([H])CCC2=C(C1)C=CC=C2)C1=NN([H])C(=C1)C1([H])CCOCC1
Molecule-23	[H]N([H])S(=O)(=O)C1=CC=C(C=C1)C1=NC2=CC=C(C=C2C(=O)N1[H])C([H])(C)C
Molecule-25	[H]N(C[C@]1(C)CCOC1)C(=O)N([H])C1=NC=C(S1)C1([H])CCOCC1

Table S2: Compound purity information

Compound Name	IUPAC Name	HPLC analysis (retention time/min)	HPLC analysis (peak area)
Molecule 10	(R)-N-(2,3-dihydro-1H-inden-1-yl)-5-(morpholinomethyl)pyridin-2-amine	0.554	100%
Molecule11	2-((1H-pyrazol-4-yl)methyl)-3,5,6,7,8,9-hexahydro-4H-cyclohepta[4,5]thieno[2,3-d]pyrimidin-4-one	0.894	100%
Molecule17	(1R,3s,5S)-N-(4-(3-fluorophenyl)-1,3,5-triazin-2-yl)-8-(methylsulfonyl)-8-azabicyclo[3.2.1]octan-3-amine	1.239	100%
Molecule18	2-(1H-indazol-6-yl)-N-(5-(tetrahydro-2H-pyran-4-yl)-1H-pyrazol-3-yl)acetamide	0.958	97.4%
Molecule20	1-(((1R,2R,4R,5R)-5-hydroxybicyclo[2.2.1]heptan-2-yl)methyl)-3-(5-(tetrahydro-2H-pyran-4-yl)thiazol-2-yl)urea	1.066	100%
Molecule21	(R)-N-(5-(tetrahydro-2H-pyran-4-yl)-1H-pyrazol-3-yl)-2-(1,2,3,4-tetrahydronaphthalen-2-yl)acetamide	1.089	100%
Molecule23	4-(6-isopropyl-4-oxo-3,4-dihydroquinazolin-2-yl)benzenesulfonamide	1.193	95.33%
Molecule25	(S)-1-((3-methyltetrahydrofuran-3-yl)methyl)-3-(5-(tetrahydro-2H-pyran-4-yl)thiazol-2-yl)urea	0.924	100%
PB01-001	4-((2-(((1R,2R)-2-hydroxycyclohexyl)amino)benzo[d]thiazol-	——	99%

	6-yl)oxy)-N-methylpicolinamide		
PB01-002	4-(3-methoxy-4-((4-methoxybenzyl)oxy)phenoxy)-N-methylpicolinamide	——	95%
PB01-003	5-(3-methoxy-4-((4-methoxybenzyl)oxy)benzyl)pyrimidine-2,4-diamine	——	97%
PB01-004	4-((5-methoxy-6-((5-methoxypyridin-2-yl)methoxy)pyridin-3-yl)methyl)-2-(1-methyl-1H-pyrazol-4-yl)pyrimidine	——	97%
PB01-005	N-(4-((2-((1-ethyl-3,3-dimethyl-2-oxoindolin-5-yl)amino)-5-methylpyrimidin-4-yl)oxy)-2-methylphenyl)acetamide	——	97%
PB01-006	1-ethyl-5-((4-methoxy-5-methylpyrimidin-2-yl)amino)-3,3-dimethylindolin-2-one	——	99.67%
PB01-007	4-((2-acetyl-1,2,3,4-tetrahydroisoquinolin-6-yl)oxy)-2-((4-(tert-butyl)phenyl)amino)-7H-pyrrolo[2,3-d]pyrimidine-5-carbonitrile	——	90%
PB02-001	2-((6-(7-acetyl-2,7-diazaspiro[3.5]nonan-2-yl)-2-(pyridin-3-yl)pyrimidin-4-yl)amino)isonicotinonitrile	——	99.06%
PB02-002	1-(2-(6-((4-ethylpyridin-2-yl)amino)-2-(pyridin-3-yl)pyrimidin-4-yl)-2,7-diazaspiro[3.5]nonan-7-yl)ethan-1-one	——	99.22%
PB02-003	1-(2-(2-(1-(2-hydroxy-2-methylpropyl)-1H-pyrazol-4-yl)-6-((4-(trifluoromethoxy)pyridin-2-yl)amino)pyrimidin-4-yl)-2-azaspiro[3.4]octan-6-yl)ethan-1-one	——	97%
PB03-001	(R)-N-((5,5-difluoro-1-(3-methyl-6-((4-(trifluoromethyl)pyridin-2-yl)amino)picolinoyl)piperidin-2-yl)methyl)acetamide	——	94.71%
PB04-001	N-(4-bromo-2,5-difluorophenyl)-6-chloro-1H-pyrrolo[2,3-b]pyridine-3-sulfonamide	——	95%
PB04-002	N-(4-bromo-2,5-difluorophenyl)-6-methyl-7-oxo-6,7-dihydro-1H-pyrrolo[2,3-c]pyridine-3-sulfonamide	——	95%
PB05-001	2-((1R,5S,6R)-3-(2-((S)-2-methylazetidin-1-yl)-6-(trifluoromethyl)pyrimidin-4-yl)-3-azabicyclo[3.1.0]hexan-6-yl)acetic acid	——	97%
PB05-002	2-(3-(2-((S)-2-methylazetidin-1-yl)-6-(trifluoromethyl)pyrimidin-4-yl)-2-oxo-3-	——	97.61%

azabicyclo[3.1.0]hexan-6-yl)acetic acid

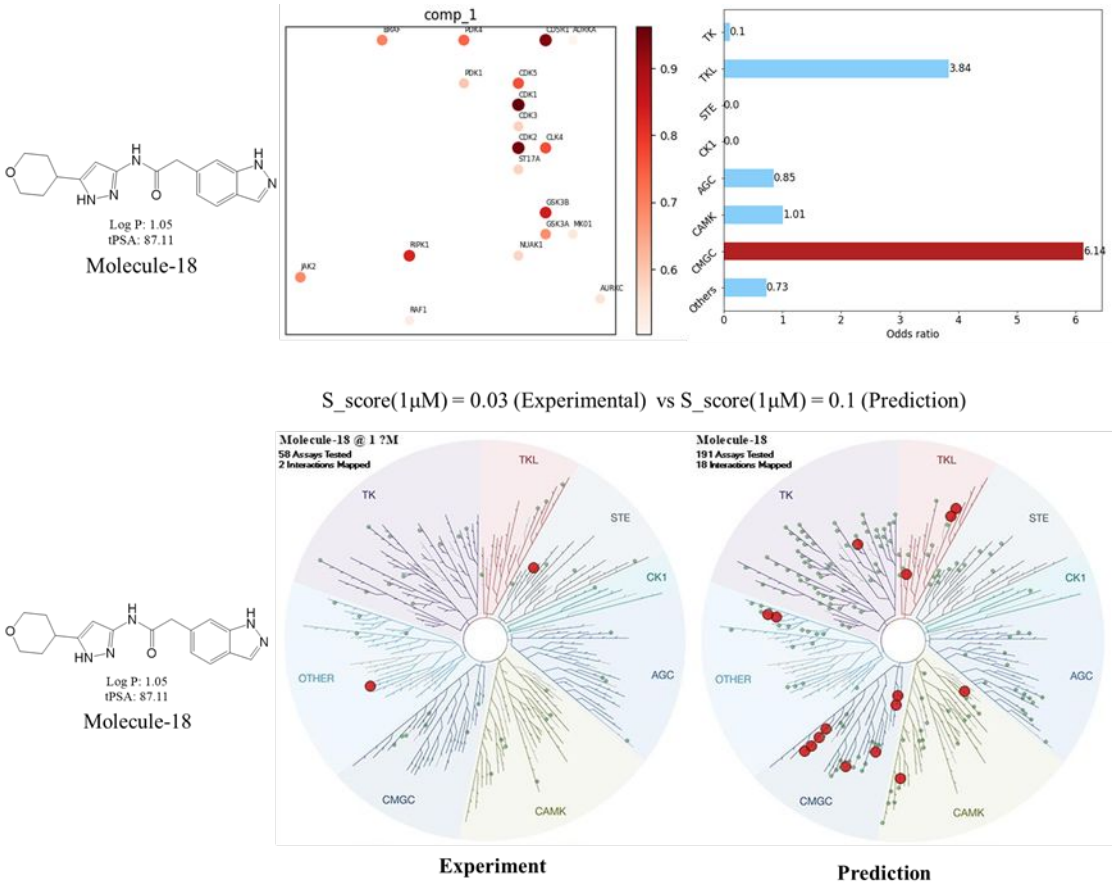


Figure S4. Comparison of the kinome selectivity profiles predicted by KinomePro-DL model and experimental results obtained from Eurofin KINOMEscan of Molecule 18.

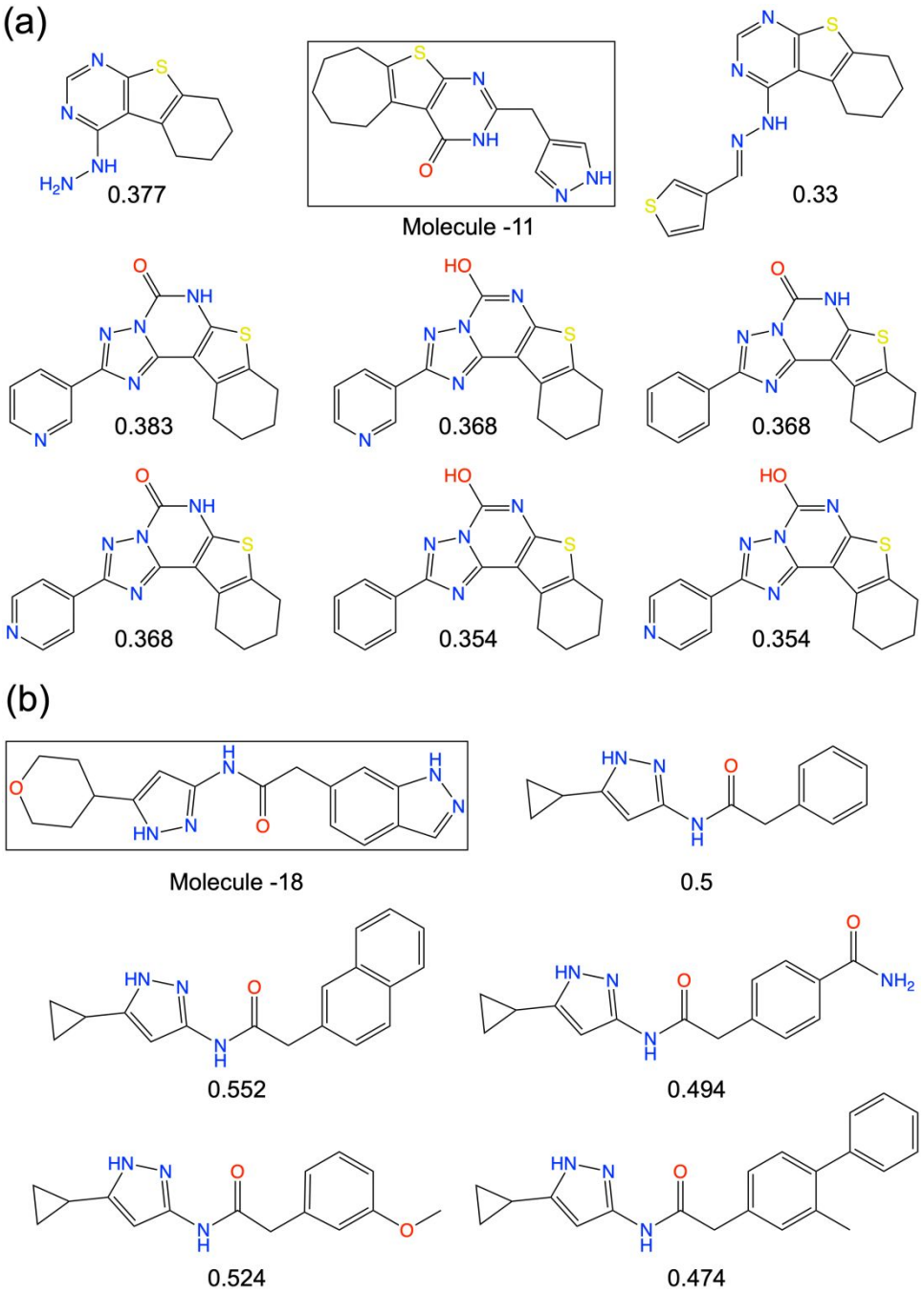


Figure S5: Structures of known CDK2 inhibitors from ChemEMBL database with highest similarity compared to hit compounds 11 (a) and 18 (b). Numbers listed for each compound were similarity values obtained by molecular fingerprints using RDKit.

KinomePro-DL

Home KinomePro-DL Batch_prediction Manual Contact

Descriptor

Description of the Model: Prediction the kinase activity profile of the compound

1.Kinase profile: the more red points in the map indicates that the compound potential selectivity may be worse; the less the map points indicates that the compound potential selectivity may be better.

2.Odds diagram: indicating that the compound may be a selective compound of a kinase group, the greater the odds value, the greater the selectivity of the kinase group, and vice versa.

3.Prediction result file: value range (0-1), the greater the value, the greater the potential activity of the target, and vice versa.

4.S_score: Value range (0-1), dividing the number of all targets predicted to be active by the total number of kinase profile targets (191), the greater the value, the worse the selectivity for the kinase profile, and vice versa.

KinomePro-DL

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Paste a single SMILES string | Draw a molecule using JMSE editor

SMILES

Example

Reset Submit

KinomePro-DL

Home KinomePro-DL Batch_prediction Manual Contact

Please select files for Batch_prediction and click "Submit"

Batch_prediction File

Select a csv file (csv format) Browse

S_score (Cut_off)

Default: 0.1

Example Here

Submit

Kinase Selectivity Score:

$$S(x) = \frac{N(kinases\ with\ \%Ctrl<x)}{N(number\ of\ kinases\ tested)} \in (0, 1)$$

Running time
(Don't close the web page!)
00 : 00 : 00

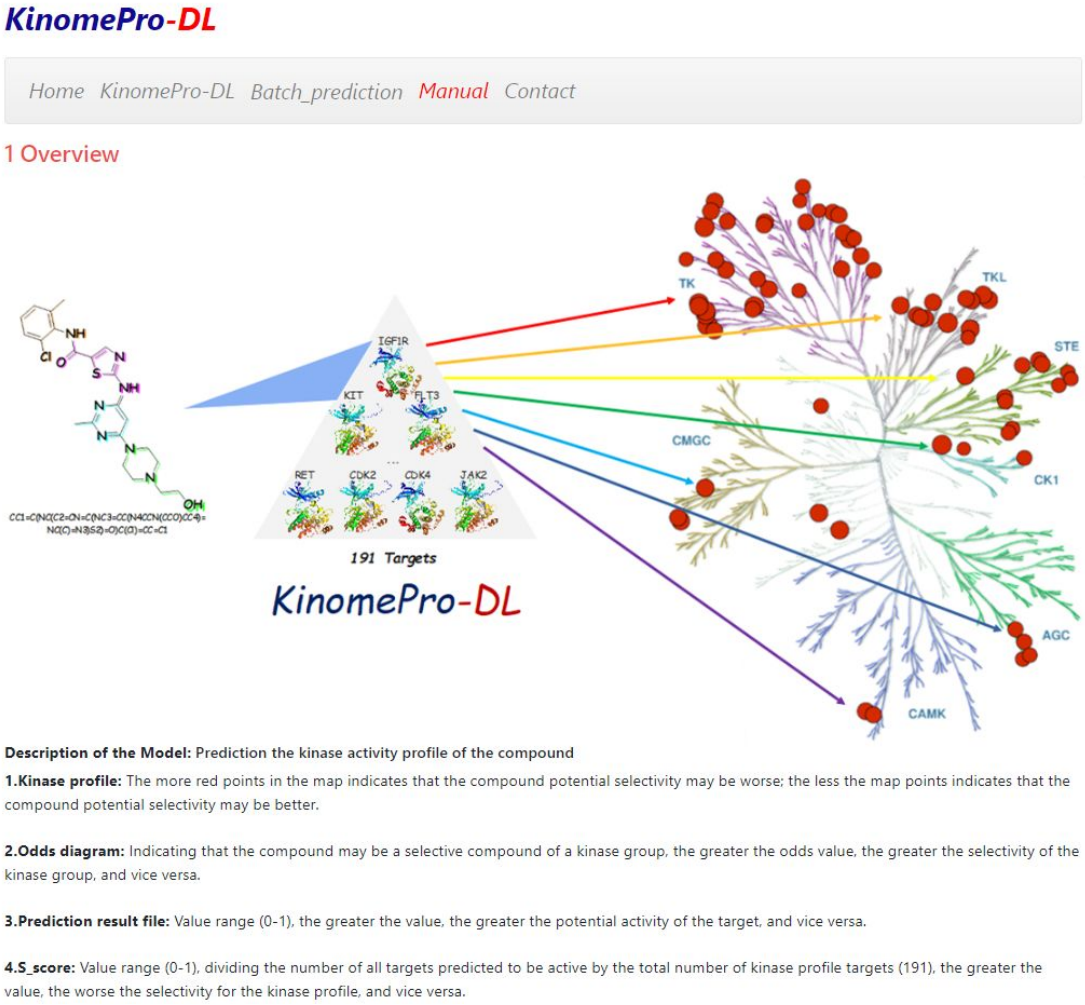

Figure S6: Screenshots of representative webpages of KinomePro-DL web server tool, including: Homepage, Single molecule prediction by submitting SMILES, Batch prediction by uploading summary file, and prediction by manually drawing compound structures.