Electronic Supplementary Information for

Diversity-Oriented Synthesis for Novel, Selective and Drug-like Inhibitors for a Virulent Phosphatase from Mycobacterium Tuberculosis

Rongjun He, Yunpeng Bai, Zhi-Hong Yu, Li Wu, Andrea Michelle Gunawan, Zhong-Yin Zhang^{*}

Department of Biochemistry and Molecular Biology and Chemical Genomics Core Facility Indiana University School of Medicine 635 Barnhill Drive, Indianapolis, IN, USA, 46202

E-mail:zyzhang@iu.edu

Index

1.	Fig. S1 Lineweaver-burk plot for 11h mediated mPTPB inhibition	Page 2
2.	Fig. S2 Proposed binding mode of 11h in complex with mPTPB	Page 3
3.	Fig. S3 Sequence alignment and structure comparison analysis between mPTPB	Page 4
	and mammalian PTPs	
4.	Fig. S4 Cellular studies of compound 11h in mPTPB transfected Raw264.7	Page 5
	cells	
5.	Characterizations of compounds 1-11	Page 6
6.	Copies of ¹ H and ¹³ C NMR Spectra of compounds 1-11	Page 12
7.	Copies of LC-MS Spectra of compounds 5-11	Page 36
8.	mPTPB inhibition studies for compounds 5-11, expression and purification of	Page 55
	recombinant mPTPB, and mPTPB inhibition studies for compounds 5-11,	
	expression and purification of recombinant mPTPB, and cellular studies of 11h	
9.	Procedures for molecular modeling studies of 11h in complex with mPTPB	Page 57
10.	References	Page 57

Kinetic studies were carried out to probe the mechanism of inhibition of **11h**, and Lineweaver-Burk plot indicates that **11h** is a noncompetitive inhibitor against mPTPB with a K_i of 1.5 μ M.



Fig. S1 Lineweaver-Burk plot for **11h** mediated mPTPB inhibition. **11h** concentrations were 0 (•), 1.25 (\circ), 2.5 (∇) μ M, respectively.

To get an insight of **11h**'s good activity and specificity against mPTPB, the binding mode of **11h** with mPTPB was built using AutoDock 4.2.5^[1] based on the mPTPB•OMTS complex structure (PDB ID: $2OZ5^{[2]}$). As shown in Fig. S2 A, **11h** locates in the deep and broad active site pocket of mPTPB, 5-salicylic acid head group interacts with the catalytic P-loop, while benzthiazole and 3-bromo benzene structure motifs interact with three helices α 3A, α 7, α 8. In detail, the carboxylic acid group of **11h** forms H-bonds with backbone amide of F161, A162, and side chain of R166; the hydroxyl group forms H-bonds with K164 and D165 (Fig. S2 B). These polar interactions provide essential binding affinity between **11h** and mPTPB. In addition, benzothiazole is sandwiched by F161 and F98 and forms π - π interactions with them; and bromobenzene moiety resides in a hydrophobic pocket constituted by F98, L199, I203, M206, I207, F211 and L227. These hydrophobic and Van der Waals force strengthen the binding between **11h** and mPTPB.



Fig. S2 Proposed binding mode of **11h** with mPTPB. (**A**) A global view of **11h** binding into the deep and broad active site of mPTPB. (**B**) A detailed view of **11h**•mPTPB complex. **11h** (in cyan) and protein residues (in gray) within 5Å distance are shown in stick, polar interactions are highlighted in dotted yellow line. P-loop of PTP1B (PDBID: 2HNQ)^[3] (in green, side chain residues written in blue) was superimposed into **11h**•mPTPB complex, which shows that **11h** has weaker interactions with P-loop of PTP1B than that of mPTPB.

11h has at least 20-fold selectivity against a panel of mammalian PTPs. To understand the molecular basis of its excellent specificity, we carried out sequence alignment and structure comparison analysis. As shown in Fig. S3 A, three of the seven P-loop residues (CFAGKDR) (three residues highlighted in blue) that interact with compound **11h** are unique to mPTPB when compared with over 50 human PTPs. These three residues significantly contribute to the binding affinity in our binding mode (Fig S1 B), specifically, K164 and D165 make strong polar interactions with the hydroxyl group of **11h**, and F161 interacts with the benzothiazole ring through π - π interaction. In contrast, the cognate residues in human PTPs can only provide limited Van der Waals interaction with **11h**. The structure superimposition indicates that three helices of α 3A, α 7 and α 8 are also unique to mPTPB (Fig. S3 B and C), which provides hydrophobic interactions with the 3-bromobenzene group, and these interactions would be absent in PTP1B and VHR. Collectively, these unique features of mPTPB likely contribute to the observed specificity of compound **11h** against mPTPB.



Fig. S3 Sequence alignment and structure comparison analysis between mPTPB and mammalian PTPs. (**A**) Sequence alignment of the catalytic P-loop of mPTPB with classical PTPs and DSPs. (**B**) Structure superimposition of mPTPB (PDB ID: 2OZ5, represented in gray ribbon) and PTP1B (PDBID: 2HNQ^[3], represented in blue ribbon). (**C**) Structure superimposition of mPTPB (PDB ID: 2OZ5, represented in gray ribbon) with VHR (PDB ID: 1VHR^[4], represented in green ribbon). The structures were superimposed based on the nine residues used for alignment in panel **A**.

mPTPB secreted by *Mtb* down-regulates Erk1/2 activation in macrophage cells to block IL-6 production, while up-regulates Akt to promote survival, and mPTPB inhibitors can rescue these processes.^[5] In our studies, **11h** was able to increase Erk1/2 phosphorylation and decrease Akt phosphorylation induced by IFN- γ in mPTPB transfected Raw264.7 cells at 5 μ M, 10 μ M, in a dose dependent manner. In contrast, compound **11a** with an IC₅₀ of 25 μ M has no such effects at 10 μ M, indicating **11h**'s excellent cellular activity in targeting mPTPB.



Fig. S4 Cellular studies of compound 11h in mPTPB transfected Raw264.7 cells

Characterizations of compounds 1-11



⁶ 1 **1.** ¹H NMR (500 MHz, DMSO-*d*₆) δ 7.12 (s, 1H), 6.38 (s, 1H), 1.66 (s, 6H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 160.2, 155.1, 151.8, 126.3, 116.8, 105.9, 103.9, 102.5, 25.2. ESI-MS Cacld. for $C_{10}H_{12}NO_4$ (M+H⁺): m/z 210.0761; found 210.0760.

² **2.** ¹H NMR (500 MHz, CDCl₃) δ 7.14 (s, 1H), 6.20 (s, 1H), 3.84 (s, 3H). ¹³C NMR (125 MHz, CDCl₃) δ 170.4, 158.5, 145.6, 124.8, 118.4, 102.1, 101.6, 51.6. ESI-MS Cacld. for C₈H₁₁N₂O₃ (M+H⁺): m/z 183.0764; found 183.0766.



3 3. ¹H NMR (500 MHz, CDCl₃) δ 10.77 (s, 1H), 8.07 (s, 1H), 6.25 (s, 1H), 4.53 (br, 2H), 3.84 (s, 3H). ¹³C NMR (125 MHz, CDCl₃) δ 169.2, 163.1, 152.6, 140.5, 105.4, 100.3, 71.6, 51.9. ESI-MS Cacld. for C₈H₉INO₃ (M+H⁺): m/z 293.9622; found 293.9622.



4 4. ¹H NMR (500 MHz, CDCl₃) δ 12.00 (s, 1H), 7.60 (d, J = 8.6 Hz, 1H), 6.26 (d, J = 8.6 Hz, 1H), 4.72 (brs, 2H), 3.89 (s, 3H). ¹³C NMR (125 MHz, CDCl₃) δ 170.1, 162.2, 153.3, 130.8, 105.7, 102.5, 72.4, 52.1. ESI-MS Cacld. for C₈H₉INO₃ (M+H⁺): m/z 293.9622; found 293.9627.



^{5a} **5a.** ¹H NMR (500 MHz, DMSO-*d*₆) δ 11.47 (s, 1H), 7.95 (t, *J* = 5.5 Hz, 1H), 7.54 (s, 1H), 6.96 (s, 1H), 3.32-3.27 (m, 2H), 1.17 (t, *J* = 7.2 Hz, 3H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 172.6, 162.3, 157.7, 153.2, 136.0, 114.8, 107.9, 97.6, 37.2, 14.6. ESI-MS Cacld. for $C_{10}H_{11}N_2O_4$ (M+H⁺): m/z 223.0713; found 223.0711.



5b 5b. ¹H NMR (500 MHz, DMSO-*d*₆) δ 11.50 (s, 1H), 8.56 (t, *J* = 6.0 Hz, 1H), 7.55 (s, 1H), 7.55-7.32 (m, 5H), 7.00 (s, 1H), 4.50 (d, *J* = 5.9 Hz, 2H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 172.48, 162.4, 157.7, 153.2, 138.7, 135.6, 128.4, 127.2, 115.0, 108.0, 99.5, 97.6, 45.7. ESI-MS Cacld. for C₁₅H₁₃N₂O₄ (M+H⁺): m/z 285.0870; found 285.0878.

6 6. ¹H NMR (500 MHz, DMSO-*d*₆) δ 11.63 (s, 1H), 7.37 (s, 1H), 6.91 (s, 1H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 172.1, 158.8, 154.5, 149.0, 123.2, 109.7, 108.0, 99.0. ESI-MS Cacld. for C₈H₄NO₅ (M-H⁺): m/z 194.0095; found 194.0087.



7 7. ¹H NMR (500 MHz, DMSO-*d*₆) δ 11.16 (s, 1H), 10.67 (s, 1H), 7.31 (s, 1H), 6.52 (s, 1H), 4.63 (s, 2H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 171.35, 163.4, 158.2, 149.4, 119.7, 116.0, 106.3, 104.0, 66.6. ESI-MS Cacld. for C₉H₆NO₅ (M-H⁺): m/z 208.0251; found 208.0243.



8. ¹H NMR (500 MHz, DMSO- d_6) δ 7.29 (s, 1H), 6.62 (s, 1H), 4.78 (s, 2H), 4.63 (s, 2H). ¹³C NMR (125 MHz, DMSO- d_6) δ 169.2, 163.1, 158.6, 150.7, 121.3, 115.7, 106.8, 104.6, 99.5, 66.8, 42.4. ESI-MS Cacld. for C₁₁H₈NO₇ (M-H⁺): m/z 266.0306; found 266.0306.



9 9. ¹H NMR (500 MHz, DMSO- d_6) δ 8.16-8.12 (m, 3H), 7.63-7.58 (m, 3H), 7.32 (s, 1H). ¹³C NMR (125 MHz, DMSO- d_6) δ 172.1, 162.5, 160.2, 154.7, 134.2, 132.0, 129.3, 127.1, 126.0, 121.0, 110.7, 98.7. ESI-MS Cacld. for C₁₄H₈NO₄ (M-H⁺): m/z 254.0459; found 254.0457.



¹⁰ **10.** ¹H NMR (500 MHz, DMSO-*d*₆) δ 8.16 (d, J = 7.3 Hz, 2H), 8.07 (s, 1H), 7.59-7.54 (m, 3H), 7.02 (s, 1H). ESI-MS Cacld. for C₁₄H₁₁N₂O₃ (M+H⁺): m/z 255.0764; found 255.0760.



^{11a} **11a.** ¹H NMR (500 MHz, DMSO- d_6) δ 11.40 (s, 1H), 10.76 (s, 1H), 8.23 (s, 1H), 7.76 (d, J = 7.9 Hz, 2H), 7.38 (t, J = 7.8 Hz, 2H), 7.08-7.05 (m, 2H). ¹³C NMR (125 MHz, DMSO- d_6) δ 171.9, 166.1, 160.4, 158.3, 140.0, 129.1, 122.9, 122.9, 121.1, 118.5, 107.8, 105.8. ESI-MS Cacld. for C₁₄H₉N₂O₃S (M-H⁺): m/z 285.0339; found 285.0337.



^{OH} 11b. ¹H NMR (500 MHz, DMSO- d_6) δ 11.95 (s, 1H), 10.82 (s, 1H), 7.78-7.74 (m, 3H), 7.39 (t, J = 7.7 Hz, 2H), 7.18 (d, J = 8.5 Hz, 1H), 7.07 (t, J = 7.3 Hz, 1H). ¹³C NMR (125 MHz, DMSO- d_6) δ 172.1, 164.8, 158.2, 156.0, 140.1, 129.1, 128.0, 122.8, 118.2, 115.8, 111.1, 106.0. ESI-MS Cacld. for C₁₄H₁₁N₂O₃S (M+H⁺): m/z 287.0485; found 287.0491.



^{11c} **11c.** ¹H NMR (500 MHz, DMSO- d_6) δ 11.39 (s, 1H), 8.17-8.16 (m, 2H), 8.00-7.98 (m, 2H), 7.83 (d, J = 8.2 Hz, 1H), 7.59-7.56 (m, 3H), 6.94 (s, 1H). ESI-MS Cacld. for C₁₈H₁₃N₂O₃S (M+H⁺): m/z 337.0641; found 337.0644.



^{11d} **11d.** ¹H NMR (500 MHz, DMSO- d_6) δ 8.20 (s, 1H), 8.05 (d, J = 7.5 Hz, 1H), 7.54 (dd, J = 1.4, 8.0 Hz, 1H), 7.41 (m, 1H), 7.21 (m, 1H), 6.95 (s, 1H). ESI-MS Cacld. for C₁₄H₁₀ClN₂O₃S (M+H⁺): m/z 321.0095; found 321.0086.



^{11e} **11e.** ¹H NMR (500 MHz, DMSO-*d*₆) δ 8.15 (s, 1H), 7.68 (d, J = 6.4 Hz, 1H), 7.28-7.24 (m, 2H), 7.17-7.14 (m, 1H), 6.90 (s, 1H), 2.27 (s, 3H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 171.8, 169.2, 160.4, 158.3, 138.2, 131.7, 130.8, 126.6, 125.7, 124.3, 122.8, 121.3, 107.2, 105.0, 17.8, ESI-MS Cacld. for C₁₅H₁₃N₂O₃S (M+H⁺): m/z 301.0641; found 301.0638.



^{11f} **11f.** ¹H NMR (500 MHz, DMSO-*d*₆) δ 11.46 (s, 1H), 10.93 (s, 1H), 8.27 (s, 1H), 7.99 (s, 1H), 7.62 (d, *J* = 8.4 Hz, 1H), 7.40 (t, *J* = 8.1 Hz, 1H), 7.12-7.10 (m, 2H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 171.8, 165.7, 160.4, 157.9, 141.4, 133.4, 130.7, 123.1, 122.1, 121.0, 117.6, 116.7, 106.2, 99.5. ESI-MS Cacld. for C₁₄H₁₀ClN₂O₃S (M+H⁺): m/z 321.0095; found 321.0102.



^{11g} **11g.** ¹H NMR (500 MHz, DMSO-*d*₆) δ 8.22 (s, 1H), 7.60 (d, J = 9.0 Hz, 1H), 7.51 (s, 1H), 7.26 (t, J = 7.8 Hz, 1H), 7.03 (s, 1H), 6.89 (d, J = 7.5 Hz, 1H), 2.30 (s, 3H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 171.8, 166.1, 160.4, 158.3, 140.0, 138.3, 128.9, 123.7, 122.9, 121.1, 119.0, 115.8, 107.7, 105.7, 21.2. ESI-MS Cacld. for C₁₅H₁₃N₂O₃S (M+H⁺): m/z 301.0641; found 301.0639.



^{11h} **11h.** ¹H NMR (500 MHz, DMSO- d_6) δ 11.45 (br, 1H), 10.91 (br, 1H), 8.27 (s, 1H), 8.10 (s, 1H), 7.68 (d, J = 7.8 Hz, 1H), 7.34 (t, J = 8.0 Hz, 1H), 7.24 (d, J = 7.8 Hz, 1H), 7.09 (s, 1H). ¹³C NMR (125 MHz, DMSO- d_6) δ 171.7, 165.6, 160.4, 157.9, 141.5, 131.0, 125.2, 123.1, 121.8, 121.0, 120.5, 117.1, 108.3, 106.1. ESI-MS Cacld. for C₁₄H₁₀BrN₂O₃S (M+H⁺): m/z 364.9590; found 364.9594.



¹¹ⁱ **11i.** ¹H NMR (500 MHz, DMSO-*d*₆) δ ¹H NMR (500 MHz, DMSO-*d*₆) 9.42 (s, 1H), 8.69 (s, 1H), 8.14 (s, 1H), 8.02 (d, *J* = 9.0 Hz, 1H), 7.65 (d, *J* = 2.5 Hz, 1H), 7.56 (s, 1H), 7.42-7.40 (m, 1H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 170.1, 166.4, 161.3, 157.9, 151.9, 145.4, 140.3, 134.6, 128.7, 127.6, 124.3, 124.2, 109.5, 99.5. ESI-MS Cacld. for C₁₄H₇Cl₂N₂O₃S (M-H⁺): m/z 352.9560; found 352.9562.



¹¹*j* **11***j*. ¹H NMR (500 MHz, DMSO-*d*₆) δ 10.78 (s, 1H), 8.21 (s, 1H), 7.77-7.75 (m, 2H), 7.22 (t, *J* = 8.9 Hz, 2H), 7.02 (s, 1H). ESI-MS Cacld. for C₁₄H₁₀FN₂O₃S (M+H⁺): m/z 305.0391; found 305.0396.



^{11k} **11k.** ¹H NMR (500 MHz, DMSO- d_6) δ 8.25 (s, 1H), 7.80 (d, J = 8.9 Hz, 2H), 7.43 (d, J = 8.9 Hz, 2H), 7.06 (s, 1H). ¹³C NMR (125 MHz, DMSO- d_6) δ 171.8, 165.7, 160.4, 158.1, 139.0, 128.9, 126.2, 123.0, 121.0, 119.8, 108.1, 106.0. ESI-MS Cacld. for C₁₄H₁₀ClN₂O₃S (M+H⁺): m/z 321.0095; found 321.0095.



¹¹¹ **111.** ¹H NMR (500 MHz, DMSO-*d*₆) δ 11.40 (s, 1H), 10.66 (s, 1H), 8.21 (s, 1H), 7.64 (d, *J* = 8.6 Hz, 2H), 7.40 (d, *J* = 8.6 Hz, 2H), 7.00 (s, 1H), 1.28 (s, 9H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 171.85, 166.29, 160.4, 158.5, 145.4, 137.5, 125.7, 122.8, 121.1, 118.5, 107.6, 105.6, 34.0, 31.2. ESI-MS Cacld. for C₁₈H₁₉N₂O₃S (M+H⁺): m/z 343.1111; found 343.1114.

^{11m} **11m.** ¹H NMR (500 MHz, DMSO-*d*₆) δ 11.40 (s, 1H), 8.30 (s, 1H), 8.25 (d, J = 9.3 Hz, 2H), 7.97 (d, J = 9.3 Hz, 2H), 7.13 (s, 1H). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 171.8, 165.3, 160.4, 157.5, 145.9, 141.5, 125.4, 123.5, 121.4, 117.8, 109.1, 106.7. ESI-MS Cacld. for C₁₄H₁₀N₃O₅S (M+H⁺): m/z 332.0336; found 332.0337.

Copies of ¹H and ¹³C NMR Spectra of compounds 1-11



















































































Copies of LC-MS Spectra of compounds 5-11



Exact Mass: 222.0641 Molecular Weight: 222.1974





5b Chemical Formula: C₁₅H₁₂N₂O₄ Exact Mass: 284.0797 Molecular Weight: 284.2668





Exact Mass: 195.0168 Molecular Weight: 195.1290



HO. HOOC H 7

Chemical Formula: C₉H₇NO₅ Exact Mass: 209.0324 Molecular Weight: 209.1556





Chemical Formula: C₁₁H₉NO₇ Exact Mass: 267.0379 Molecular Weight: 267.1917





Chemical Formula: C₁₄H₉NO₄ Exact Mass: 255.0532 Molecular Weight: 255.2256





Chemical Formula: C₁₄H₁₀N₂O₃ Exact Mass: 254.0691 Molecular Weight: 254.2408





Chemical Formula: C₁₄H₁₀N₂O₃S Exact Mass: 286.0412 Molecular Weight: 286.3058





Exast Mass: 286.0412 Melecular Weight: 286.3058





Molecular Weight: 336-3645





Chemical Formula: C₁₅H₁₂N₂O₃S Exact Mass: 300.0569 Molecular Weight: 300.3324

Current Chromatogram(s)





Chemical Formula: C₁₄H₉ClN₂O₃S Exact Mass: 320.0022 Molecular Weight: 320.7509





Chemical Formula: C₁₅H₁₂N₂O₃S Exact Mass: 300.0569 Molecular Weight: 300.3324





Chemical Formula: C₁₄H₉BrN₂O₃S Exact Mass: 363.9517 Molecular Weight: 365.2019





Chemical Formula: C₁₄H₈Cl₂N₂O₃S Exact Mass: 353.9633 Molecular Weight: 355.1959





Chemical Formula: C₁₄H₉FN₂O₃S Exact Mass: 304.0318 Molecular Weight: 304.2963





Chemical Formula: C₁₄H₉ClN₂O₃S Exact Mass: 320.0022 Molecular Weight: 320.7509





Chemical Formula: C₁₈H₁₈N₂O₃S Exact Mass: 342.1038 Molecular Weight: 342.4121





Chemical Formula: C₁₄H₉N₃O₅S Exact Mass: 331.0263 Molecular Weight: 331.3034



mPTPB inhibition studies for compounds **5-11**, expression and purification of recombinant mPTPB, and cellular studies of **11h**

The inhibition assays were performed on 96-well plates at 25°C in 50 mM 3,3-dimethylglutarate buffer, pH 7.0, containing 1 mM EDTA with an ionic strength of 0.15M adjusted by NaCl. The reaction was started by the addition of 50 µl of the enzyme to 150 µl of reaction mixture containing *p*-nitrophenyl phosphate (*p*NPP) and various concentrations of the inhibitor [final concentration of mPTPB: 20 nM, final concentration of *p*NPP: 3 mM (the K_m value)]. The reaction was quenched after 10 min by the addition of 50 µl of 5N NaOH. The absorbance at 405 nm was detected by a Spectra MAX340 microplate spectrophotometer (Molecular Devices). IC₅₀ values were calculated by fitting the absorbance at 405 nm *versus* inhibitor concentration to the following equation:

 $AI/A0=IC_{50}/(IC_{50}+[I])$, where AI is the absorbance at 405 nm of the sample in the presence of inhibitor; A0 is the absorbance at 405 nm in the absence of inhibitor; and [I] is the concentration of the inhibitor.

Expression and purification of recombinant mPTPB were described previously.^[5] Briefly, pET28b-mPTPB (a generous gift from Dr. Christoph Grunder, University of California, Berkeley) was used to transform into E.coli BL21/DE3 and grown in LB medium containing 50 µg/ml kanamycin at 37°C to an OD600 of 0.5. Following the addition of IPTG to a final concentration of 20 µM, the culture was incubated at 20°C with shaking for additional 16 hr. The cells were harvested by centrifugation at 5000 rpm for 5 min at 4°C. The bacterial cell pellets were resuspended in 20 mM Tris, pH 7.9, 500 mM NaCl, 5 mM imidazole, and were lysed by passage through a French press cell at 1,200 p.s.i. twice. Cellular debris was removed by centrifugation at 16,000 rpm for 30 min at 4°C. The protein was purified form the supernatant using standard procedures of Ni-nitrilotriacetic acid-agarose (Qiagen) affinity purification. The protein eluted from Ni-NTA column was concentrated with an Amicon Ultra centrifugal filter device (Millipore) and the buffer was changed to 20 mM Tris, pH 7.5, 150 mM NaCl, 1 mM EDTA and 1 mM DTT. Protein concentration was determined using the Bradford dye binding assay (Bio-Rad) diluted according to the manufacturer's recommendations with bovine serum albumin as standard. The purified mPTPB were made to 20% glycerol and stored at -20°C.

For cellular studies, mPTPB transfected Raw264.7 mouse macrophages were cultured in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% FBS (Invitrogen), penicillin (50 units/mL), and streptomycin (50 μ g/mL) under a humidified atmosphere containing 5% CO₂ at 37°C. Transfected Raw264.7 cells were seeded in a 12-well plate at a density of 4 x 10⁴ cells/well. The following day cells were treated with mPTPB inhibitor **11h** for 1 h, then stimulated with IFN- γ (200 U/ml) for 1 h. Subsequently, the cells were washed with ice-cold phosphate buffered saline, and lysed with lysis buffer on ice for 30 min. Cell lysate was then cleared by centrifuging at 13,000 rpm for 15 min. The phosphorylations of Erk1/2 and Akt were detected by Western blotting.

Procedures for molecular modeling studies of **11h** in complex with mPTPB

The 3D-structure of **11h** was built and energy-minimized in Chem3D, and the coordinates of mPTPB were taken from the mPTPB•OMTS complex structure (PDBID: 2OZ5). Both ligand and receptor were pre-docking processed in AutoDockTools 1.4.6, such as merge non-polar hydrogens, add Gasteiger charges, set rotatable bond for ligand, add solvation parameter for receptor, and so on. The docking space was visually set around the catalytic active site, the energy grid size was set to 46× 60 ×46 points with 0.375Å spacing on each axis, and the energy grid maps for each atom type (i.e. A, C, HD, N, NA, OA, SA, Br), as well as the electrostatics and de-solvation maps were calculated using the AutoGrid 4. The molecular dockings were carried out using AutoDock 4.2.5 program, the optimal binding conformation was determined by LGALS (Lamarckian Genetic Algorithm with Local Search) algorithm. 500 separate docking runs were performed; the binding conformations were clustered and ranked according to the calculated binding free energy. The binding mode analyses were performed in AutoDockTools 1.4.6 by visual inspections and energy comparisons.

References

1. G. M. Morris, D. S. Goodsell, R. S. Halliday, R. Huey, W. E. Hart, R. K. Belew, A. J. Olson, *J. Comput. Chem.* **1998**, *19*, 1639-1662.

2. C. Grundner, D. Perrin, R. H. van Huijsduijnen, D. Swinnen, J. Gonzalez, C. L. Gee, T. N. Wells, T. Alber, *Structure* **2007**, *15*, 499-509.

3. D. Barford, A. J. Flint, N. K. Tonks, Science 1994, 263, 1397-1404.

4. J. Yuvaniyama, J. M. Denu, J. E. Dixon, M. A. Saper, Science 1996, 272, 1328-1331.

5. B. Zhou, Y. He, X. Zhang, J. Xu, Y. Luo, Y. Wang, S. G. Franzblau, Z. Yang, R. J. Chan, Y. Liu, J. Zheng, Z.-Y. Zhang, *Proc. Natl. Acad. Sci. USA* **2010**, *107*, 4573-4578.