From drug screening to target deconvolution: A target-based drug discovery pipeline using Leishmania casein kinase 1 isoform 2 to identify compounds with anti-leishmanial activity

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From drug screening to target deconvolution: *A target-based drug discovery pipeline using* Leishmania *casein kinase 1 isoform 2 to identify compounds with anti-leishmanial activity*.

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Running Title: *Leishmania CK1.2 drug screening*

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Keyword: Casein kinase I, Leishmaniasis, Therapeutic target, drug screening

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ABSTRACT

Existing therapies for leishmaniases present significant limitations, such as toxic side effects, and are rendered inefficient by parasite resistance. It is of utmost importance to develop novel drugs targeting *Leishmania* that take these two limitations into consideration. We thus chose a target-based approach using an exo-protein kinase, *Leishmania* casein kinase 1.2 (LmCK1.2) that was recently shown to be essential for intracellular parasite survival and infectivity. We developed a four-step pipeline to identify novel selective anti-leishmanial compounds. In step 1, we screened 5018 compounds from kinase-biased libraries with *Leishmania* and mammalian casein kinase 1 in order to identify hit compounds and assess their specificity. For step 2, we selected 88 compounds among those with the lowest IC_{50} to test their biological activity on host-free parasites using a resazurin reduction assay and on intramacrophagic amastigotes using a high content phenotypic assay. Only seventy-five compounds showed anti-leishmanial

activity and were retained for step 3 to evaluate their toxicity against mouse macrophages and human cell lines. The four compounds that displayed a selectivity index above 10 were then assessed for their affinity to LmCK1.2 using a target deconvolution strategy in step 4. Finally, we retained two compounds, PP2 and compound 42, for which LmCK1.2 seems to be the primary target. Using this four-step pipeline, we identify from several thousand molecules, two lead compounds with a selective anti-leishmanial activity.

INTRODUCTION

The protozoan parasite *Leishmania* is the causative agent of leishmaniasis, a potentially fatal disease with worldwide distribution. Depending on the species, three clinical forms of the disease can be distinguished, cutaneous (CL, e.g. *L. major*), mucocutaneous (MCL, e.g. *L. braziliensis*) and fatal visceral leishmaniasis (VL, e.g. *L. donovani*) (1). Several treatment options are available, which either show important side effects or are unaffordable. In all endemic regions, the first line of treatment is pentavalent antimonials, despite their important side effects and the appearance of parasite resistance. Although their target has not been identified, one member, sodium stibogluconate was shown to inhibit the energy metabolism and macromolecule biosynthesis (2) (3). The second line of treatment is Amphotericin B, a very potent but highly toxic antifungal drug. This compound creates pores targeting ergosterol only present in the plasma membrane of parasites but not in that of mammalian cells. Its less toxic lipid formulation is extremely expensive and thus incompatible with treatment in developing countries (3, 4). Among the other drugs that have been recently developed, miltefosine was a major breakthrough in leishmaniasis therapy as this anticancer drug is the first oral treatment against VL.

Unfortunately, its teratogenicity excludes the treatment of pregnant women and its slow turnover could promote the emergence of clinical parasite resistance (4). Miltefosine plays a role in the perturbation of the lipid metabolism, the induction of apoptosis-like cell death and has immuno-stimulatory effects; however its mode of action has not been precisely identified (5). The activity of miltefosine is due to its accumulation inside the parasite (6), which is prevented in resistant lines generated *in vitro* by the overexpression of members of the ABC (ATP-binding cassette) transporter family and/or mutation of the flippase LdMT (6) (7). Three more drugs complete the list of available treatments for Leishmaniasis: (i) pentamidine, which has been used for VL, CL and MCL treatment, induces the inhibition of polyamine biosynthesis and a decrease of the mitochondrial inner membrane potential, (ii) the aminoglycosidic antibiotic paromomycin, which is restricted to endemic areas, cures both VL and CL efficiently by targeting mitochondria, and (iii) sitamaquine, an 8-aminoquinoline, which intercalates within biological membranes to accumulate in *Leishmania* cytosolic acidic compartments (4).

Despite the various drugs available, none of these treatments are ideal because of two main aspects: (i) their side effects, due mainly to off-target effects that cannot be eliminated by drug optimization as the target responsible for the anti-leishmanial effect is unknown, and (ii) the emergence of parasite resistance, due to the plasticity of the parasite. Therefore there is an urgent need to discover new molecules and to develop new drug discovery pipelines that take these two aspects into consideration. First, the use of known validated targets for drug screening represents a major advantage as the compound could be optimized to fit exclusively the target, avoiding off-target effects mainly responsible for side effects. Protein kinases are among the best candidates as drug

92 targets for leishmaniasis because: (i) kinase inhibitors are one of the most important
93 group of FDA-approved drugs for the treatment of diseases such as cancer or Alzheimer
94 disease, (ii) they are considered as valid targets for diseases caused by unicellular
95 parasites, such as malaria, and (iii) kinases regulate many key processes, such as cell
96 cycle or signal transduction and thus the inhibition of their activity decreases cell viability
97 (8) (9-14). Second, targeting proteins secreted by the parasite could delay the emergence
98 of drug resistance. Indeed it has been recently shown that parasitic proteins could be
99 exported, via exosomes, into the host cell to modify its biology or its innate immune
100 response (15) (16). To perform their function in the host, these proteins need to interact
101 with host proteins and thus any mutations could abrogate their functions in the host cell,
102 which could be detrimental for the intracellular parasite survival.
103
104 Among the proteins identified in the recent proteomic analysis of *Leishmania* exosomes,
105 13 could qualify as good drug targets as defined above because they are excreted kinases.
106 Most of these kinases are involved in purine or glucose metabolism, and only one is
107 involved in signal transduction, casein kinase 1. Member of a highly conserved Ser/Thr
108 protein kinase family (17), casein kinase I contains six isoforms in *Leishmania* (15, 18-
109 20). LmjF35.1010 (LmCK1.2), the major isoform, has been validated pharmacologically
110 as a drug target based on the findings that the inhibition of CK1 activity by the specific
111 inhibitor D4476 strongly compromises axenic amastigote viability and decreases the
112 percentage of infected macrophages (21). We hypothesize that the capacity of LmCK1.2
113 to recognize and phosphorylate host proteins could allow the parasite to regulate essential
114 host cell processes (22) and therefore to survive. This hypothesis is based on our previous

115 findings showing that (i) the protein sequence of LmCK1.2 kinase domain is 100%
116 identical in all sequenced *Leishmania* species (except the lizard-isolated *L. tarentolae* and
117 unclassified *L. sp. MAR LEM2494*), suggesting that there is a selection pressure to
118 maintain the integrity of the protein sequence, and (ii) LmCK1.2 is the most closely
119 related kinase to its human orthologs in *Leishmania*. These two elements suggest that
120 LmCK1.2 cannot be mutated without compromising the survival of the intracellular
121 parasite, which would render the emergence of drug resistant parasites expressing
122 mutated LmCK1.2 unlikely (21).
123 Here we present a four-step pipeline that allows the discovery of novel lead compounds.
124 First, we generated an active recombinant LmCK1.2 and purified mammalian CK1 from
125 porcine brain (SsCK1, (23)). We developed an enzymatic assay to screen 4030
126 compounds from kinase-biased and focused libraries as well as 988 analogs with both
127 *Leishmania* and mammalian kinases in order to identify hit compounds and assess their
128 specificity. We selected 88 compounds with an IC_{50} below 10 μM. Second, we tested the
129 anti-leishmanial effect of these compounds on cultured parasites using a rezasurin-based
130 assay as well as on intracellular parasites using a high content phenotypic screen. We
131 retained seventy-five compounds with an anti-leishmanial activity. Third, after evaluation
132 of the toxicity of the selected anti-leishmanial compounds against mouse macrophages
133 and human cell lines, only four compounds had a selectivity index (SI) above 10. Fourth,
134 the affinity for LmCK1.2 for these compounds was tested using a target deconvolution
135 approach. Two compounds for which LmCK1.2 seems to be the primary target were
136 eventually selected. The identification of these two lead compounds validates our

pipeline, which will be used to screen diversified libraries to identify more lead compounds.

MATERIAL AND METHODS

L. donovani culture and axenic amastigote differentiation.

L. donovani 1S2D (MHOM/SD/62/1S-CL2D), clone LdB, was obtained from Steve Beverley, Washington University School of Medicine, St. Louis, USA and cultured as described (24-26).

Parasite growth inhibition assay.

L. donovani promastigotes and axenic amastigotes ($2x10^6$ cells/ml) in their respective media were distributed in 96 well plates (125 µl/well). An equal volume of medium containing inhibitor at the indicated concentrations (in 1% of dimethyl sulfoxide final concentration, DMSO) was added. After 24h incubation in the dark at 26°C (promastigotes) or 37°C (amastigotes), 25 µl of resazurin solution at 0.001% was added and the plates were incubated for an additional 24h in the dark at appropriate temperatures. The plates were read (λex: 544 nm; λem: 590 nm) using a fluorescent microplate reader (Safas xenius XML) (27).

Human cell lines MTT.

HFF1, SH-SY5Y and U-2 OS cells were cultured in Dulbecco's modified Eagle's medium (DMEM), hTERT RPE-1 were cultured in DMEM:F12 medium. All media were supplemented with 10% fetal calf serum, 2 mM L-glutamine, 50 IU penicillin and

streptomycin. Cell viability was assayed using the 'CellTiter96 AQueous non-radioactive cell proliferation assay' test (MTS) from PROMEGA according to manufacturer's instructions.

Macrophage infection and assessment of intracellular parasite survival.

A high content, biologically relevant cell-based assay was used to determine the anti-leishmanial activity of D4476 as previously described (21, 28). Briefly, the assay combines (1) the use of primary bone marrow-derived mouse macrophages as natural host cells and *Ds*Red2-expressing amastigotes of *L. amazonensis* (MPRO/BR/1972/M1841), the clinically relevant parasite stage of *Leishmania* with (2) the detection of fluorescent markers as reporter molecules. 10,000 macrophages were counted per well depending on the number of replicates per tested compound.

Ethics statement.

All animals were housed in our A3 animal facilities in compliance with the guidelines of the A3 animal facilities at the Institut Pasteur, which is a member of Committee 1 of the "Comité d'Ethique pour l'Expérimentation Animale" (CEEA) - Ile de France - Animal housing conditions and the protocols used in the work described herein were approved by the "Direction des Transports et de la Protection du Public, Sous-Direction de la Protection Sanitaire et de l'Environnement, Police Sanitaire des Animaux under number B75-15-27 and B75-15-28 in accordance with the Ethics Charter of animal experimentation that includes appropriate procedures to minimize pain and animal suffering. GS and EP are authorized to perform experiment on vertebrate animals (licence

183 B75-1159 and 75-1265, respectively) issued by the "Direction Départementale de la
184 Protection des Populations de Paris" and is responsible for all the experiments conducted
185 personally or under his supervision as governed by the laws and regulations relating to
186 the protection of animals.
187
188 **Automated microtiter plate CK-S kinase assay.**
189 A mixture of native CK1 isoforms (essentially CK1δ and CK1ε) was extracted from
190 porcine brain (SsCK1) and purified by affinity chromatography on immobilised axin
191 (23). LmCK1.2 was produced and purified as previously described (21). Both SsCK1 and
192 recombinant LmCK1.2 were assayed, with 27 μM CK-specific peptide substrate CK-S
193 (RRKHAAIGpSAYSITA) synthesized by Proteogenix (Oberhausbergen, France), in
194 buffer C pH 7 (60 mM β-glycerophosphate, 30 mM p-nitrophenyl phosphate, 25 mM
195 MOPS, 5 mM EGTA, 15 mM $MgCl_2$, 1 mM dithiothreitol, 0.1 mM sodium vanadate),
196 with 15 μM [γ-^{33}P] ATP in a final volume of 30 μl. After 30 min incubation at 30°C, 30
197 μL aliquots were filtered onto whatman P81 phosphocellulose paper. The filters were
198 washed with a solution of 1% phosphoric acid then counted in the presence of 20 μl
199 scintillation fluid per well. Blank values were subtracted and activities calculated as
200 pmoles of phosphate incorporated during the 30 min incubation. The activities were
201 expressed in percent of maximal activity, i.e. in the absence of inhibitors. Controls were
202 performed with appropriate dilutions of DMSO.
203
204 **ATP depletion and competition**

Seven mg of axenic amastigote total protein extract were dialyzed overnight at 4°C in dialysis solution (1X PBS, 1 mM EDTA, 1 mM DTT) using a Slide-A-Lyzer 10kD dialysis cassette (Pierce) to eliminate free ATP. One mg of dialyzed extract per condition was mixed with the binding solution (1X Binding solution, 1mM DTT, 1X Protease inhibitor) of the ATP affinity test kit (Jena Bioscience) and 500 µM of inhibitor. The samples were incubated 30 min at 4°C and added to a mixture of 12.5 µl of each ATP agarose (ATP affinity test kit from Jena Bioscience). ATP binding proteins from the assay and the competition samples were enriched according to the manufacturer's instructions. Finally, eluted samples were concentrated using Amicon Ultra 10K centrifugal filters (Millipore) to a final volume of approximately 100 µl.

12.5 µl of the flow through and 30 µl of the eluate were separated on Novex NuPAGE 4-12% bis tris gel (Life technologies) from both the assay and the competition. The gel was stained with SYPRO Ruby (Life technologies) according to the manufacturer's instructions and revealed using a Typhoon scanner. Alternatively, proteins separated by SDS-PAGE were transferred onto a PVDF membrane and probed with SY3535 antibody (21). Signals were revealed by Super Signal ECL (Pierce).

Compound libraries

We screened 5018 compounds from the Roscoff library including 588 purine derivatives (29) and 400 indirubin derivatives (30) (31) (32).

Homology modeling and structural alignment

The amino acid sequence of *L. major* CK1.2 was retrieved from NCBI database (Accession number: XP_003722496) in FASTA format. The homology modeling of the sequence was performed by SWISS-MODEL program (33) and the protein with PDB code 3SV0 was selected as a template. PyMOL program (34) was used for the structural alignment of *Schizosaccharomyces pombe* casein kinase 1 in complex with the specific CK1 inhibitor, IC261 (PDB code: 1EH4) and *Homo sapiens* casein kinase 1δ (PDB code: 4KB8) to the generated *L. major* CK1.2 homology model. The figures were also prepared using PyMOL (34).

RESULTS

We present below, a comprehensive drug discovery pipeline encompassing four steps.

STEP 1: Identification of specific LmCK1.2 inhibitors.

Primary screening comparing SsCK1 and LmCK1.2

We purified recombinant LmCK1.2-V5-His_6 from *E. coli* and a mixture of *Sus scrofa* CK1δ and CK1ε (SsCK1) from porcine brain (21) (23). The conditions used previously for the manual kinase assay were adapted to an automated 96-well plate format (23) (21). We used CK-S as substrate for both kinases, and 15 μM [γ-^{33}P] ATP (23) (21). We screened 4030 compounds at 10 μM from a kinase-biased library that has been previously tested on mammalian kinases, such as Cyclin-Dependent Kinases (CDK) (29). For each compound, the percentage of inhibition of LmCK1.2 versus that of SsCK1 is presented in Figure 1A. We classified as hit compounds those that decreased the kinase activity by more than 40% (Figure 1A a and b). We obtained twice as much hit compounds for the mammalian CK1 than for LmCK1.2 (Figure 1B). Indeed, we identified 245 hit

compounds against SsCK1 (6.1% Hit rate) and 128 against LmCK1.2 (3.2% Hit rate) with only 37 compounds with a similar potency against both kinases. This finding, which is surprising considering the high similarity between the protein sequences of LmCK1.2 and the mammalian CK1s (about 70% (21)), suggests that the ATP binding pocket of the two kinases is sufficiently divergent to accommodate different inhibitors. We next classified the compounds according to their potency and specificity (Class 1 corresponds to compounds that inhibit the kinase activity between 80-100%, Class 2 between 60-80%, and Class 3 between 40-60%, Figure 1C). We obtained a similar number and distribution of hit compounds active on SsCK1 (30 compounds) and on LmCK1.2 (31 compounds) in Class 1. In contrast, we observed an increased number of compounds inhibiting specifically SsCK1 in Class 2 and 3 (Figure 1C). This could suggest that the ATP binding pocket of SsCK1 could be more permissive than that of LmCK1.2. We selected 45 compounds either belonging to Class 1 that inhibited LmCK1.2 activity by more than 90% or that belong to Class 2 and were specific to LmCK1.2 to determine their IC_{50}. As shown in Figure 2, all the compounds with an IC_{50} below 1.3 μM (most potent) were not specific, whereas all the specific compounds had an IC_{50} above 1.3 μM.

Among the 45 compounds that were potent against LmCK1.2, we identified several inhibitors described to have anti-leishmanial activity, including known CK1 inhibitors, such as anthraquinone (35-37), or compounds for which we revealed CK1 as a new target, such as Gossypol, purpurogallin and some flavonoids (38-41) (42) (43). These compounds, identified from several libraries, were found at least twice with similar IC_{50}, indicating that our assay is reproducible (data not shown). Altogether, these data demonstrate the efficiency of using CK1 as a target to identify compounds with anti-

273 leishmanial activities and confirm LmCK1.2 as a valid drug target. However we did not
274 retain these compounds for subsequent characterization as they have been already
275 extensively studied.

276 *Secondary screening of purine and indirubin libraries*

277 Out of the 45 compounds for which we determined the IC_{50}, we selected 2 compounds
278 with low IC_{50} but only moderate specificity towards LmCK1.2, purvalanol B and
279 indirubin-3'-monoxime, and tested analog libraries to perform SAR analysis in order to
280 identify more specific compounds. We chose purvalanol B because we showed
281 previously that *Leishmania* CK1.2 binds to purvalanol B better than its mammalian
282 counterpart, suggesting that the sensitivity to purvalanol B could be higher for LmCK1.2
283 than for SsCK1 (44). Confirming this finding, the IC_{50} of purvalanol B towards LmCK1.2
284 (2 +/- 0.3 μM) is slightly lower than that towards SsCK1 (2.9 +/- 1.2 μM). We tested the
285 potency of 588 purine analogs (Figure 3A) at 10 μM against LmCK1.2 and SsCK1 to
286 identify compounds with better potency and/or specificity. As shown in Figure 3B and
287 3C, most compounds were more potent against mammalian CK1 than against LmCK1.2
288 (below the black line, Figure 3B and dark grey in Figure 3C). Next, we determined the
289 IC_{50} of the 21 most potent purine derivatives against LmCK1.2 (Figure 3D). For all the
290 compounds, except one, the IC_{50} was systematically higher against LmCK1.2 (0.44 to 2.4
291 μM) than against mammalian CK1 (0.081 to 1.6 μM). Only compound **26** had a lower
292 IC_{50} against LmCK1.2 (1 +/- 0.4 μM) than against SsCK1 (3.7 +/- 1.2 μM), which could
293 be due to the presence of a long carbon chain, a unique feature compared to the other
294 derivatives. Thus although the purines were very potent towards LmCK1.2, they present a
295 higher affinity for SsCK1.

296 The second family of compounds we screened are the indirubins (Figure 4A). We showed
297 that the IC_{50} of indirubin-3'-monoxime is lower against LmCK1.2 (0.13 +/- 0.03; Table
298 S1) than against mammalian CK1 (0.39 +/- 0.08 μM; Table S1). To identify better
299 compounds with higher selectivity, we tested 400 indirubin derivatives (Figure 4B).
300 Contrary to the purine analogs, the indirubins were globally more potent against
301 LmCK1.2 than SsCK1 (Figure 4B). For instance, in Class 1, forty-six compounds were
302 more specific toward LmCK1.2 than SsCK1 versus only 9 were more specific towards
303 SsCK1 than LmCK1.2 (Figure 4C). Indeed, the most active compounds were the most
304 selective toward LmCK1.2, whereas compounds with lower potency (Class 3) were more
305 specific toward SsCK1 (Figure 4C). We selected the 55 most potent compounds to
306 measure their IC_{50}. They were comprised between 0.08 and 10 μM, and for almost all the
307 compounds, the IC_{50} against LmCK1.2 was systematically lower than that against
308 mammalian CK1 (Figure 4D), suggesting that the indirubin compounds have more
309 affinity towards LmCK1.2 than SsCK1.
310 The differences in specificity observed with the purine and indirubin compound families
311 confirm that important differences exist between the ATP binding pocket of both kinases
312 (21). It also suggests that due to the strong affinity of the purine for the mammalian CK1,
313 it is likely that these compounds will be toxic for the host cell.
314 Among all the compounds identified in the primary and secondary screenings, we
315 eliminated all the compounds for which the chemical optimization was unfeasible and
316 selected 12 compounds from the main library, 21 compounds from the purine library and
317 55 compounds from the indirubin library to assess their anti-leishmanial activity.
318

STEP 2: Evaluation of the anti-leishmanial activity of selected compounds.

We evaluated the anti-leishmanial activity of the 88 compounds selected in STEP 1 on cultured *L. donovani* promastigotes and axenic amastigotes by measuring the percentage of metabolically active parasites in liquid culture using the rezasurin-based assay (27) (Table S1). As a positive control, we treated the parasites with 1 μM of the anti-leishmanial reference drug, AMB and obtained a growth inhibition of 90.4 ± 1.5 % and 79.9 ± 1.3 % for promastigotes and amastigotes, respectively, with excellent reproducibility as reported by the small standard deviation values.

We then tested the compounds against intracellular *L. amazonensis* using a visual high content phenotypic assay (21, 28). We measured three parameters: (i) the percentage of cells remaining after treatment compared to the vehicle control (DMSO) to evaluate cell detachment (Total Macrophages, TM), (ii) the percentage of healthy cells compared to the total number of cells remaining after treatment to evaluate cell mortality (Viability Index, VI), and (iii) the percentage of parasitophorous vacuoles per healthy cell to evaluate the parasite burden (PB). We used AMB at 0.5 μM and cycloheximide (CHX) at 150 μM as anti-leishmanial and cytotoxic control compounds, respectively. Figure S1 presents the data of all the controls performed during the screening campaign. As expected, AMB is reducing parasite burden without affecting the number of macrophages or their viability, whereas CHX does not affect significantly the number of macrophages but decreases dramatically the viability, as it is extremely toxic to macrophages. The data were reproducible as judged by the small standard deviation values, (Figure S1).

For each of the 88 compounds, we plotted the percentage of metabolically active promastigotes or amastigotes at 10 μM versus the percentage of parasite burden at 10 μM

(Figure 5). We considered as efficient, those compounds that decreased the percentage of metabolically active parasites or the percentage of parasite burden by 40%. We eliminated compounds that had no effect on the percentage of intracellular parasites; remarkably those compounds were also mainly inefficient on cultured parasites (Figure 5, b and d). Among the 65 compounds that were potent towards the intracellular parasites, we identified two categories: compounds equally efficient on cultured and intracellular parasites (Figure 5, c) and compounds that were only efficient on intracellular parasites, which represent the majority of the compounds (43 out of 65 for promastigotes and 57 out of 65 for amastigotes, Figure 5, a). This finding suggests that the exclusion of compounds based on their lack of efficacy on cultured parasites could lead to the elimination of compounds very efficient on intracellular parasites, among which, inhibitors that kill indirectly parasites by targeting host cell proteins.

Main library

We selected seven out of twelve compounds from the main library including i) Rottlerin, NSC 146771, gefitinib and sunitinib, all potent against intracellular parasites at 10 µM, and ii) 5'ITu, PP2 (1-tert-butyl-3-(4-chlorophenyl)-1h-pyrazolo[3,4-d]pyrimidin-4-amine,(45)) and NSC 699479 that were efficient against intracellular parasites at 10 and 1 µM as well as against cultured parasites (Table S1). 5'ITu, which is described as a general kinase inhibitor (46), is potent against promastigotes and axenic amastigotes, with an EC_{50} of 0.4 ± 0.1 and 5.4 ± 1.8 µM respectively (Table S1). It has also a strong effect at 10 and 1 µM on intracellular parasites with only 10 ± 1% and 13 ± 4.5% remaining PB, respectively, which is similar to 0.5 µM AMB. PP2 is potent against intracellular

amastigotes at 1 μM (54 ± 3% PB; Table S1). NSC 699479 (4-[(E)-[2-(4-chlorophenyl)-1-methylpyrazolo[1,5-a]indol-1-ium-4-ylidene]methyl]-N,N-dimethylaniline;tri-fluoromethane-sulfonate) is known for anti-cancer activity and has been shown to target a wide range of proteins including the DNA polymerase iota (47). It is extremely potent against promastigotes and axenic amastigotes, with an EC_{50} below 1 μM as well as intracellular parasites at 10 μM (3.6 ± 1.9% PB), and 1 μM (11 ± 1.4% PB; Table S1), activity which is comparable to AMB.

Purine library

We selected 13 out of 21 purine compounds that were able to kill efficiently intracellular parasites at either 1 μM or 10 μM (compound 21 and 30, Table S1). Consistent with their high potency against recombinant LmCK1.2, most compounds were active against intracellular parasites. Surprisingly the purine derivatives were not very potent against promastigotes and axenic amastigotes. With the exception of compound **22** and **30**, which present an EC_{50} of 0.72 ± 0.03 μM and 6.2 ± 0.8 μM against promastigotes respectively, most of the compounds were weakly active against promastigotes and inactive against axenic amastigotes at 50 μM (Table S1). This lack of potency against cultured parasites cannot be explained by cell permeability as these compounds efficiently decrease the parasite burden of infected macrophages.

Indirubin library

Fifty-five indirubins were tested against promastigotes and axenic amastigote. Twenty-one compounds showed an EC_{50} below 10 μM against promastigotes (ranging from 0.4 to

388 2 μM) whereas only 6 showed an EC_{50} below 10 μM against amastigotes (ranging from
389 3.5 to 8 μM). These compounds were all members of a subfamily of indirubins,
390 containing a diethanolamine substitution in position-3', suggesting that the presence of
391 this substitution could be important for their anti-leishmanial activity against cultured
392 parasites. It is remarkable that the EC_{50} against promastigotes was systematically lower
393 than that against axenic amastigotes (21). We next tested all the indirubin derivatives
394 against intracellular parasites. In contrast to purine derivatives, all indirubin compounds
395 were efficient against intracellular parasites at 10 μM, with 9 also efficient at 1 μM
396 (Table S1). The most efficient indirubin is compound **42** with a remaining 22 ± 5% PB,
397 corresponding to a decrease of 78% compared to the DMSO-treated controls. Altogether,
398 these data confirm what we observed with recombinant LmCK1.2 (Figure 4C and D) that
399 the indirubin compound family, which has a stronger affinity for LmCK1.2 is also
400 showing a higher anti-leishmanial activity.
401
402 **STEP 3: Evaluation of the toxicity of the compounds.**
403 *Cytotoxicity against mouse Bone Marrow Derived Macrophages*
404 We first assessed the toxicity towards mouse bone marrow-derived macrophages of the
405 75 compounds that displayed anti-leishmanial activity against intracellular parasites
406 (Table S1, column VI%). We plotted the percentage of parasite burden versus the
407 percentage of viable macrophages for each of the three libraries (Figure 6). As shown in
408 Figure 6A, 3 compounds out of the 7 selected from the main library were toxic towards
409 macrophages at 10 μM (Figure 6A, c, black dots) but none were toxic at 1 μM (Figure
410 6A, b and d, grey dots). However, decreasing their concentration from 10 μM to 1 μM to

411 prevent cytotoxicity led, in some cases such as with sunitinib, to a decrease in potency
412 against intracellular parasites. Nevertheless, we identified compounds that were not toxic
413 and able to efficiently decrease PB (Figure 6A d). We obtained a similar result with the
414 indirubin derivatives (Figure 6B, b and d) as we identified compounds with anti-
415 leishmanial activity and no toxicity against macrophages: 35 compounds at 10 μM and 9
416 compounds at 1 μM (Figure 6B d). These results are in contrast to the results obtained for
417 the purine library, as most of the 21 purine derivatives that we tested led to cell death,
418 preventing proper analysis of their effect on intracellular parasites. Indeed, we did not
419 identify any compound that decreased the percentage of parasite burden without
420 cytotoxicity (Figure 6C, d). To investigate whether these derivatives could be efficient
421 toward intracellular parasites at lower concentration, we tested compound **16**, **22** and **30**
422 at 0.01 μM and 0.1 μM (data not shown). These compounds were no longer toxic to host
423 cells at 0.1 μM, 0.1 μM and 0.01 μM respectively, and no longer active against
424 intracellular parasites. It seems that the efficient concentration to kill intracellular
425 parasites could be similar to the cytotoxic concentration. This finding could be explained
426 by the higher affinity of this compound family for the mammalian CK1 compared to
427 *Leishmania* CK1.2 (Figure 3B and C).
428 Based on these results, we eliminated the sunitinib from the main library, all the
429 remaining compounds from the purine library and 11 compounds from the indirubin
430 library because of their toxicity against macrophages. We thus retained 6 compounds
431 from the main library and 7 indirubins from those with anti-leishmanial activity at 1 μM
432 and without cytotoxicity against BMDM.
433 *Cytotoxicity against human cell lines*

To establish the selectivity index (SI, this unit corresponds to the ratio between the EC_{50} against intracellular parasites and the EC_{50} against mammalian cells), we determined the EC_{50} against intracellular parasites, macrophages as well as human cell lines (RPE-1, SHSY-5Y, HFF-1 and U2OS, Table S1) for the remaining 13 compounds (Table S1). The SI ranged from 0.15 to 50, which is consistent with small molecules being able to discriminate between *Leishmania* CK1.2 and mammalian CK1, as we identified compounds that show leishmanicidal activity without cytotoxicity (Table S1). We eliminated all the compounds with a SI below 10, as they were likely to lead to side effects, retaining only five compounds: 5'ITu, PP2, NSC 699479 from the main library and compound **38** and **42** from the indirubin library. The EC_{50} of 5'ITu against intracellular parasites is in the nanomolar range (0.06 ± 0.01 μM) while that against mouse macrophages is in the micromolar range (3.5 μM ± 0), which represents a 60-fold difference between the cytotoxic and the anti-leishmanial concentrations (Table S1). The toxicity of this compound towards the human cell lines seems to be cell-dependent; indeed the EC_{50} against RPE-1 and U2OS is 1.2 μM, whereas it is above 25 μM against SHSY-5Y and HFF-1 (Table S1). Taking in account both cell lines and macrophages the minimum SI is thus 20, indicating that the leishmanicidal concentration is 20 fold lower than the toxic concentration. NSC699479 has also an EC_{50} against intracellular parasites in the nanomolar range (0.33 ± 0.05 μM) but a SI of only 10, due to the low EC_{50} towards macrophages and U2OS, respectively at 3.5 ± 0.24 μM and 3 ± 0.5 μM. Indirubin **38** has an EC_{50} of 0.6 ± 0.1 with a SI above 17, whereas compound 42, more potent, has an EC_{50} of 0.06 ± 0.005 μM, with a high SI of 50 (Table S1). For PP2, it was impossible to determine the exact EC_{50}, because the parasite burden at 10 μM of PP2 was 98 ± 8.5%,

457 whereas it was only 54 ± 3% at 1 μM. This result could be explained by the detachment
458 of non-infected macrophages. Indeed, we showed that treatment of infected BMDM with
459 10 μM of PP2 led to cell detachment as judged by the percentage of total remaining cells
460 in the well (60 ± 1%, Table S1). We cannot completely exclude that cell detachment
461 could be the consequence of cell mortality, but it seems unlikely, as the cells that
462 remained attached were viable in the presence of the drug (VI of 83 ± 4%). This is
463 consistent with what has been previously observed for other cell types, as PP2 is known
464 to directly interfere with cell attachment (48). We estimated the EC_{50} of PP2 around 1
465 μM as the PB is 54.3 ± 3.2 % at 1 μM (Table S1), with a SI above 10. For STEP4, we
466 only selected 5'ITu, NSC699479, PP2 and compound **42** (Table 1).
467
468 **STEP 4: Target deconvolution.**
469 To confirm that 5'ITu, NSC699479, PP2 and compound **42** (Table 1) target *Leishmania*
470 CK1.2 in the parasite and to estimate their affinity for this kinase, we investigated
471 whether they could prevent the binding of CK1.2 to ATP-agarose (21). We treated
472 amastigote lysates with PP2, 5'ITu, compound **42**, NSC699479 or D4476 (positive
473 control) before performing an affinity chromatography; we used an untreated sample as
474 negative control. The proteins eluted from the ATP-agarose were separated by SDS-
475 PAGE and either stained with SYPRO-Ruby or analyzed by Western blotting using an
476 anti-LmCK1.2 antibody (21). By comparing the protein elution profiles obtained with the
477 untreated sample (Ama) to that obtained with the treated samples (D4476, PP2, Iodo, **73**
478 and **42**) we were able to assess compound selectivity (Figure 7A). Most of the treated
479 samples showed a profile similar to that of the untreated sample, except for the 5'ITu

480 (Figure 7A). As judged by the disappearance of several bands, 5'ITu could be targeting
481 many ATP-binding proteins aside CK1.2. Because this absence of selectivity prevents
482 any possibility for compound optimization, which could in turn lead to side effects, we
483 eliminated 5'ITu. Based on the Western blot analysis, we also discarded NSC699479, as
484 LmCK1.2 could still bind to the ATP beads in presence of this compound, suggesting that
485 this kinase is not the primary target of NSC699479 (Figure 7B). This is consistent with
486 the fact that the IC_{50} of NSC699479 against LmCK1.2 is 8 μM, which is higher than that
487 of the other compounds (Table S1). However because of its strong anti-leishmanial
488 activity, it would be interesting to identify the primary target of NSC699479. As shown
489 in Figure 7B, similarly to D4476, only PP2 and compound **42** prevent the binding of
490 LmCK1.2 to the ATP beads without affecting the elution profile. This result suggests that
491 LmCK1.2 could be one of the primary targets of these two compounds.
492
493 **DISCUSSION**
494 The anti-leishmanial drugs currently available are compromised mostly because they lead
495 to parasite resistance and have important side effects. Considering these parameters early
496 in the process of drug development is therefore crucial to discover more efficient drugs.
497 We established a pipeline consisting of 4 steps from target-based screening to target
498 deconvolution. In order to integrate these parameters, we used LmCK1.2 (a *Leishmania*
499 exo-kinase) as a target to address parasite resistance, and excluded compounds based on
500 their absence of anti-leishmanial activity, on their lack of specificity or on their poor
501 affinity for LmCK1.2 to address side effects. Our pipeline introduces two improvements
502 compared to previous screening campaigns. First, as *Leishmania* and mammalian CK1s

503 are closely related and to limit the possibility of cell toxicity, which leads to side effects,
504 we screened, in parallel, the leishmanial and mammalian CK1 to assess specificity. Using
505 this approach we could discriminate between compounds with low and high specificity.
506 For instance, we showed that the purine derivatives displayed a better potency against
507 mammalian CK1 than against LmCK1.2, which led to toxicity against mammalian host
508 cells. Reversely, compounds of the indirubin family displayed a better potency against
509 LmCK1.2 than mammalian CK1, which was subsequently confirmed by their absence of
510 toxicity toward the mammalian host cell at 1 μM. This finding suggests that a strong
511 correlation between the specificity toward the target and the subsequent effect on
512 intracellular parasite survival. Moreover, our results also confirm that LmCK1.2 has an
513 ATP binding pocket sufficiently divergent from that of mammalian CK1 to identify
514 discriminating compounds (21). Indeed, more than 70% of the small molecules that we
515 tested showed a differential potency against both kinases. We modelled the structure of
516 *Leishmania* CK1.2 based on existing crystal structures of CK1s found in Protein Data
517 Bank and noticed a few differences between the LmCK1.2 model (green, Figure S2) and
518 the crystal structure of human CK1δ or of *Schizosaccharomyces pombe* CK1 (magenta or
519 cyan (SpCK1) respectively, Figure S2) that could account for the specificity of LmCK1.2
520 towards certain compounds. Indeed, residues in the active site of LmCK1.2 such as F22
521 and K40 could be positioned differently, which could overall change the shape of the
522 active site. Moreover, the structural alignment of LmCK1.2, human CK1δ and SpCK1
523 (49), which is in complex with IC261 (specific CK1 inhibitor) shows that the position of
524 K40 in the active site of LmCK1.2 compared to that of K41 or K38 in the active site of
525 CK1δ and SpCK1 respectively, may account for the differential response to compound

526 inhibition. Indeed, contrary to K38 and K41, K40 could lead to conformational clash with
527 IC261. This finding supports our previous results showing that the IC_{50} of IC261 towards
528 LmCK1.2 is above 10 μM whereas it is 0.47 μM towards mammalian CK1 (21). Our
529 results demonstrate that *Leishmania* CK1.2, which would have been rejected based on the
530 strong identity to its mammalian orthologs, is a good drug target.
531 A second improvement was to assess whether compounds have multiple targets or low
532 affinity for LmCK1.2. To address this issue, we performed target deconvolution. This
533 strategy, which depends on affinity purification and competition, allowed the elimination
534 of compounds based on their lack of specificity or their lack of affinity towards
535 LmCK1.2. Indeed, we excluded 5'ITu that could be targeting many proteins as revealed
536 by their depletion following competition assay and ATP-affinity chromatography. This
537 finding is consistent with recent publications showing that 5'ITu is a general kinase
538 inhibitor due to its broad inhibitory activity (46). Although this compound could be a
539 good lead compound purely based on its SI, its optimisation could be difficult as the
540 target responsible for the leishmanicidal activity is unknown. We also excluded
541 NSC699479 because of its weak affinity towards LmCK1.2, suggesting that this kinase
542 might not be its primary target. Based on previous results in mammalian cells, the
543 primary target of NSC699479 could be topoisomerases in *Leishmania*, enzymes already
544 known as good drug targets (50) (51) (52).
545
546 Using this pipeline, we screened 5018 compounds in total and identified two lead
547 compounds, PP2 and compound **42**. PP2 is an inhibitor for which no anti-leishmanial
548 activity against intracellular parasites in THP-1 cells *in vitro* has been previously

549 described but appears to be efficient in animal model (53). It has an EC_{50} on intracellular
550 parasites around 1 μM, but a selectivity index above 10 for murine macrophages and
551 above 25 for human cell lines. The known targets of PP2 are tyrosine kinases, Src, Lck,
552 Csk, Rip2 and Gak, for which there are no orthologs identified in *Leishmania* (54, 55).
553 The two other kinases that are targeted by PP2 are p38 (52% of inhibition at 1 μM (54))
554 and CK1δ (93% of inhibition at 1 μM (54)), suggesting that the anti-leishmanial activity
555 of PP2 is more likely mediated by the inhibition of CK1.2 in *Leishmania*. This finding is
556 consistent with our experimental data showing that *Leishmania* CK1.2 is one of the
557 primary targets of PP2. However, treatment with high concentrations of PP2 leads to
558 macrophage detachment (40% at 10 μM) similarly to what has been shown previously for
559 other cell types (48). Our results seem to indicate that most of the macrophages that
560 detach from the slides are those non-infected by *Leishmania*. This hypothesis is supported
561 by Tejle *et al*, which showed that the presence of *L. donovani* affect the detachment of
562 monocyte-derived dendritic cells, suggesting that the presence of the parasite could
563 promote cell adhesion (56).
564 Indirubins are particularly potent against cultured as well as intracellular parasites and
565 among the 55 indirubin derivatives showing leishmanicidal activity at 10 μM, only 37%
566 were cytotoxic against macrophages. Compound **42** is our best lead compound, with an
567 EC_{50} on intracellular parasites of 60 ± 5 nM and a SI of 50. Although several authors
568 have already described the anti-leishmanial effect of indirubins (57-59), this particular
569 derivative has not been previously tested on intracellular parasites. From previous
570 published work, we already know some of the targets of the indirubins, such as
571 *Leishmania* CRK3 or GSK3 (57, 58). In our study, we reveal for the first time CK1.2 as a

novel target for this family of compounds. This is particularly striking as in higher eukaryotes GSK3 and CK1 are often involved in similar signalling pathways such as the Wnt/β-catenin or the Hedgehog pathways, where they act as priming kinases for one another (60, 61) (62) (63). Using affinity purification, we found that GSK-3 is also a target of compound **42** (data not shown). We will determine precisely, using biochemical approaches, whether this compound targets other kinases and which one causes the anti-leishmanial effect.

In conclusion, we have established a comprehensive pipeline that identify and select LmCK1.2 inhibitors based on their specificity, anti-leishmanial activity, absence of cytotoxicity and selectivity. As a proof of principle, we identified two lead compounds, PP2 and compound 42 that will be studied further to understand their mode of action and could also be used as pharmacological tools to study parasite-specific signal transduction. We will use this pipeline to screen diversified libraries that have not yet been screened against *Leishmania* kinases, in order to identify lead compounds.

FUNDING INFORMATIONS

This work was supported by the 7th Framework Program of the European Commission through grants to the LEISHDRUG project (223414), by the ANR-11-RPIB-0016 TRANSLEISH, the French Government's Investissements d'Avenir program Laboratoire d'Excellence Integrative Biology of Emerging Infectious Diseases (grant no. ANR-10-LABX-62-IBEID). The Imagopole-CiTech is part of the FranceBioImaging infrastructure supported by the French National Research Agency (ANR-10-INSB-04-01, "Investments

for the future") and is grateful to be supported by Conseil de la Region Ile-de-France (program Sesame 2007, project Imagopole, S. Shorte) and by the Fondation Française pour la Recherche Médicale (FRM, Programme Grands Equipements) to N. Aulner.

ACKNOWLEDGMENTS

We thank all members of the FP7 LEISHDRUG consortium for fruitful discussions, in particular Geneviève Milon. Additional thanks go to Olivier Helynck and Hélène Munier-Lehmann for providing access to the TECAN Freedom EVOware platform for automatic distribution of cells, parasites, and chemicals in a biosafety level 2 facility.

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FIGURE LEGENDS

FIGURE 1. Differential target-based screen of 4030 compounds from various libraries. A. Representation of the percentage of inhibition towards LmCK1.2 activity versus the percentage of inhibition toward SsCK1 activity. Compounds in a and b are potent toward LmCK1.2 as they show more than 40% inhibition, whereas compounds in b and d are potent toward SsCK1. **B.** 336 hit compounds were identified in the screen from which 245 inhibit SsCK1 (6.1 % hit rate) and 128 inhibit LmCK1.2 (3.2% hit rate). Only 37 compounds showed equal potency against both CK1s. **C.** Compounds were classified according to their specificity: compounds only potent against SsCK1 (only SsCK1), more potent against SsCK1 than LmCK1.2 (SsCK1 > LmaCK1.2), equally potent on both kinases (SsCK1 = LmCK1.2), more potent against LmCK1.2 than SsCK1 (SsCK1 < LmaCK1.2) and only potent on LmCK1.2 (only LmCK1.2). Compounds were also classified according to their % of inhibition: Class 1 corresponds to compounds that inhibit the kinases activity between 80-100%, Class 2 between 60-80% and class 3 between 40-60%. Twenty-three compounds are more potent toward LmCK1.2 than SsCK1 and 68 compounds are specific to LmCK1.2 (the numbers in the histograms indicate the percentage of compounds in each category).

814

815 **FIGURE 2. Determination of the IC_{50} of the 45 compounds belonging to Class 1 that**
816 **have a percentage of inhibition above 90%.** Each point represents the IC_{50} of a
817 particular compound towards LmCK1.2. Non-specific compounds have a potency below
818 10 μM towards both kinases, whereas specific compounds have a potency below 10 μM
819 only towards LmCK1.2.

820

821 **FIGURE 3. Screening of the purine derivative library. A.** Structure of the purine
822 backbone. R1, R2 and R3 represent different substitutions of the purines. **B.** We
823 performed a target-based screening of 588 derivatives. Each point represents the
824 percentage of inhibition towards LmCK1.2 activity versus the percentage of inhibition
825 towards SsCK1 activity of each compound. The compounds in the top left are more
826 potent toward LmCK1.2 whereas the compounds in the bottom right are more potent
827 towards SsCK1. **C.** Compounds were classified according to their specificity: only potent
828 on SsCK1, more potent on SsCK1 than LmCK1.2 (SsCK1 > LmCK1.2), equally on both
829 kinases (SsCK1 = LmCK1.2), more potent on LmCK1.2 than SsCK1 (SsCK1 <
830 LmCK1.2) and only potent on LmCK1.2. Compounds were also classified according to
831 their % of inhibition: Class 1 corresponds to compounds that inhibit the kinases between
832 80-100%, Class 2 between 60-80% and class 3 between 40-60%. Only 4 percent of the
833 compounds are more potent toward LmCK1.2 than SsCK1 or specific to LmCK1.2. **D.**
834 We determined the IC_{50} of the 21 compounds belonging to class 1 that have a percentage
835 of inhibition above 90%. Each point represents the IC_{50} of a particular compound towards
836 LmCK1.2 versus SsCK1. The IC_{50} are lower towards SsCK1 than LmCK1.2.

837

838 **FIGURE 4. Screening of the indirubin derivative library. A.** Structure of the indirubin
839 backbone. **B.** Target-based screening of 400 derivatives. Each point represents the
840 percentage of inhibition towards LmCK1.2 activity versus the percentage of inhibition
841 toward SsCK1 activity for each compound. The compounds in the top left are more
842 potent towards LmCK1.2 whereas the compounds in the bottom right are more potent
843 towards SsCK1. **C.** Compounds were classified according to their specificity: only potent
844 on SsCK1, more potent on SsCK1 than LmCK1.2 (SsCK1 > LmaCK1.2), equally on both
845 kinases (SsCK1 = LmCK1.2), more potent on LmCK1.2 than SsCK1 (SsCK1 <
846 LmaCK1.2) and only potent on LmCK1.2. Compounds were also classified according to
847 their % of inhibition: Class 1 corresponds to compounds that inhibit the kinases between
848 80-100%, Class 2 between 60-80% and class 3 between 40-60%. Fifty-seven percent of
849 the compounds are more potent towards LmCK1.2 than SsCK1 and 46% are specific to
850 LmCK1.2. **D.** IC_{50} of the 55 compounds that are specific to LmCK1.2 or that belong to
851 class 1 with a percentage of inhibition above 90%. Each point represents the IC_{50} of a
852 particular compound towards LmCK1.2 versus SsCK1. The IC_{50} are lower against
853 LmCK1.2 than SsCK1.

854

855 **FIGURE 5. Comparaison of the anti-leishmanial activity of compounds on cultured**
856 **and intracelular parasites.** We performed a screening of 88 compounds from the main,
857 the purine and the indirubine libraries on cultures promastigotes, axenic amastigotes and
858 intracellular parasites. Each point represents the percentage of metabolically active
859 promastigotes or amastigotes at 10 μM versus the percentage of parasite burden at 10 μM

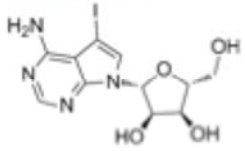
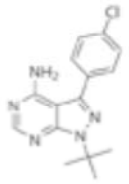
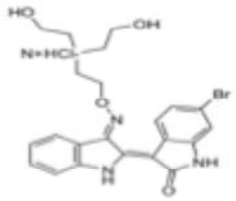
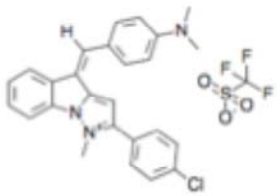
for each compound. Black squares correspond to the percentage of metabolically active promastigotes at 10 μM versus the percentage of parasite burden at 10 μM and grey dots correspond to the percentage of metabolically active amastigotes at 10 μM versus the percentage of parasite burden at 10 μM. a: compounds that are potent against intracellular parasites but not against cultured parasites, b: compounds that are not potent against intracellular and cultured parasites, c: compounds that are potent against intracellular and cultured parasites and d: compounds that are not potent against intracellular but potent against cultured parasites.

FIGURE 6. Parasite burden versus macrophage viability. Using a visual high content phenotypic assay, we calculated the percentage of viable macrophages and the percentage of infected cells. We analysed the anti-leishmanial effect of the selected compounds from the main library (**A)**, the indirubin library **(B)** and the purine library **(C)** versus their toxicity against macrophages. a: compounds that are not potent against intracellular parasites but cytotoxic, b: compounds that are not potent against intracellular parasites and not cytotoxic, c: compounds that are potent against intracellular but cytotoxic and d: compounds that are potent against intracellular and not cytotoxic.

FIGURE 7. PP2 and compound 42 are the most specific compounds towards CK1.2. Competitive ATP affinity chromatography assays were performed on amastigote cell lysates in presence or not of D4476, PP2, 5'ITu (Iodo), NSC699479 (73) and 42. ATP-binding proteins (Elution) were eluted with an excess of ATP, resolved by SDS-PAGE

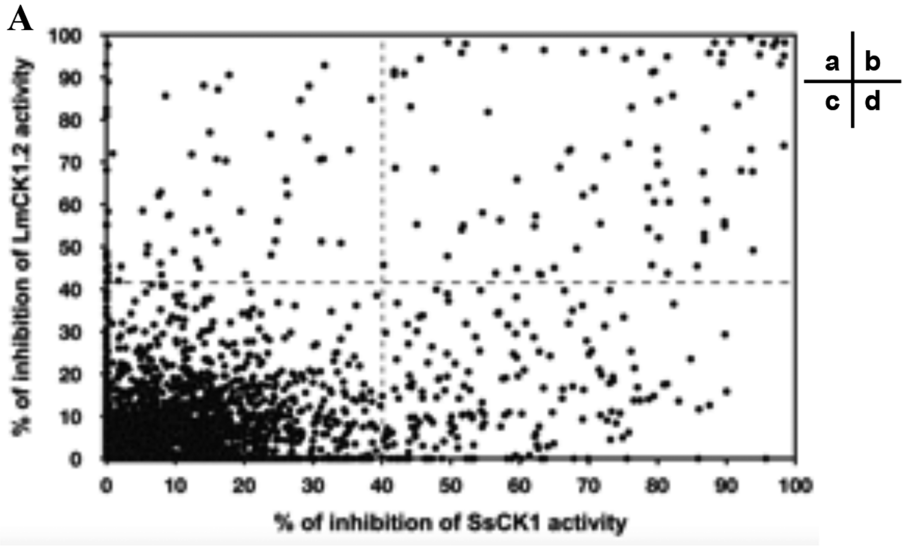
882 electrophoresis and stained by SYPRO Ruby (**A**). CK1.2 was revealed by Western blot
883 using an anti-LmCK1.2 antibody (SY3535, **B**).
884
885 **FIGURE S1. Controls for the phenotypic screen.** We analysed the effect of DMSO,
886 AMB and CHX on intracellular parasites using a visual high content phenotypic assay.
887 We assessed several parameters including the percentage of total cells compared to
888 control cells with DMSO (TM%), the percentage of viable cells (VI%) and the
889 percentage of viable cells with parasitophorous vacuoles that is considered as an
890 indication of parasite burden (PB%).
891
892 **FIGURE S2. Model of the ATP binding pocket of LmCK1.2 compared to that of**
893 **human and yeast CK1s**. Comparison of yeast (cyan) and human (magenta) CK1 crystal
894 structures with a structural model of LmCK1.2 (green). IC261 is represented in the ATP-
895 binding pocket.
896
897

Table 1: Selected compounds against intracellular parasites tested for target deconvolution.

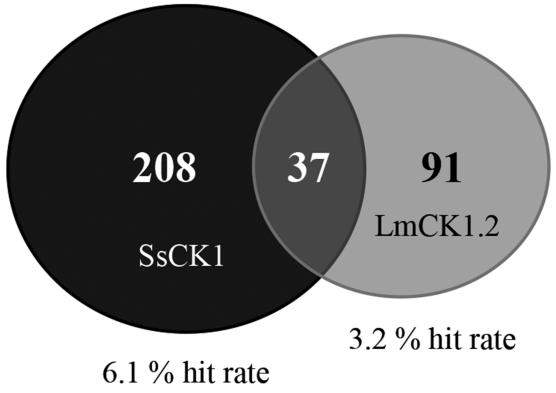
Compound name and structure	LmCK1.2 IC_{50} in µM	EC_{50} on cultured Promastigote in µM	EC_{50} on cultured Amastigote in µM	EC_{50} on intracellular parasites in µM	SI
5' Iodotubercidin 	0.18 ± 0.04	0.40 ± 0.10	5.40 ± 1.80	0.06 ± 0.01	20
PP2 	1.60 ± 0.30	> 10	> 50	1*	> 10
42 	0.93 ± 0.20	2.00 ± 0.00	> 10	0.06 ± 0.00	50
NSC699479 	8.00 ± 0.30	<1	<1	0.33 ± 0.05	10

*: Estimation of the EC_{50}.

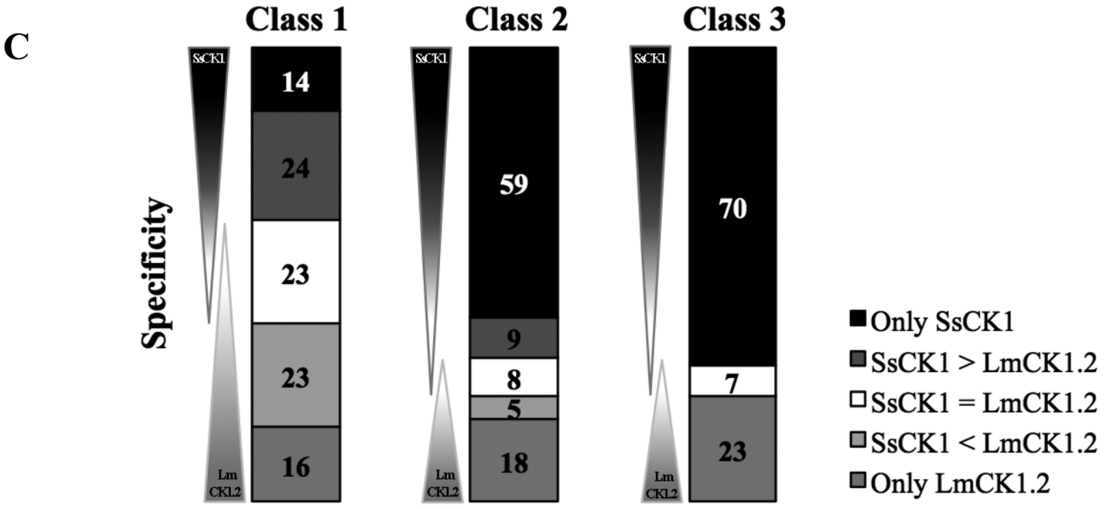
A

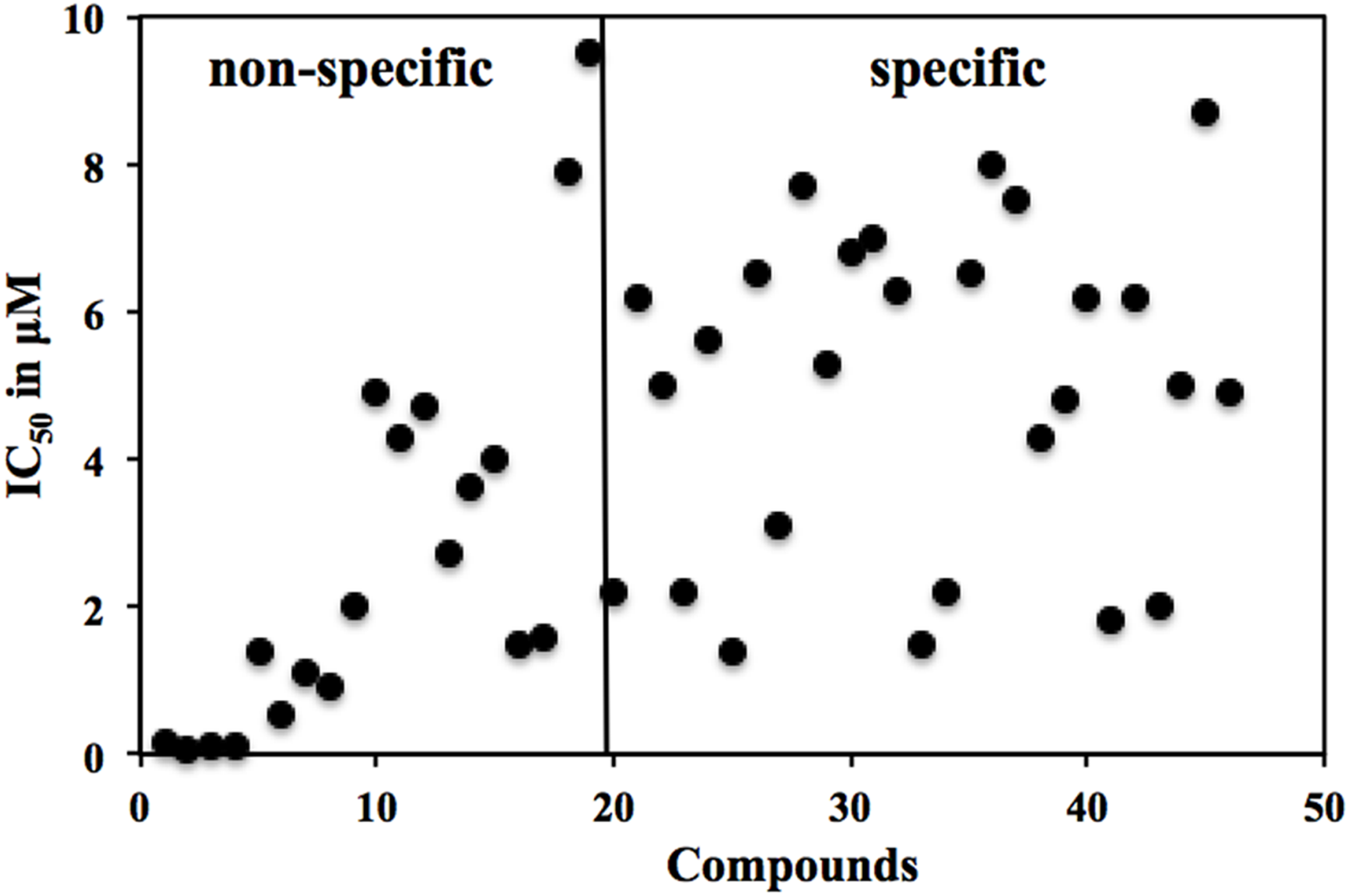

a
b
c
d
% of inhibition of LmCK1.2 activity
% of inhibition of SsCK1 activity
0
10
20
30
40
50
60
70
80
90
100

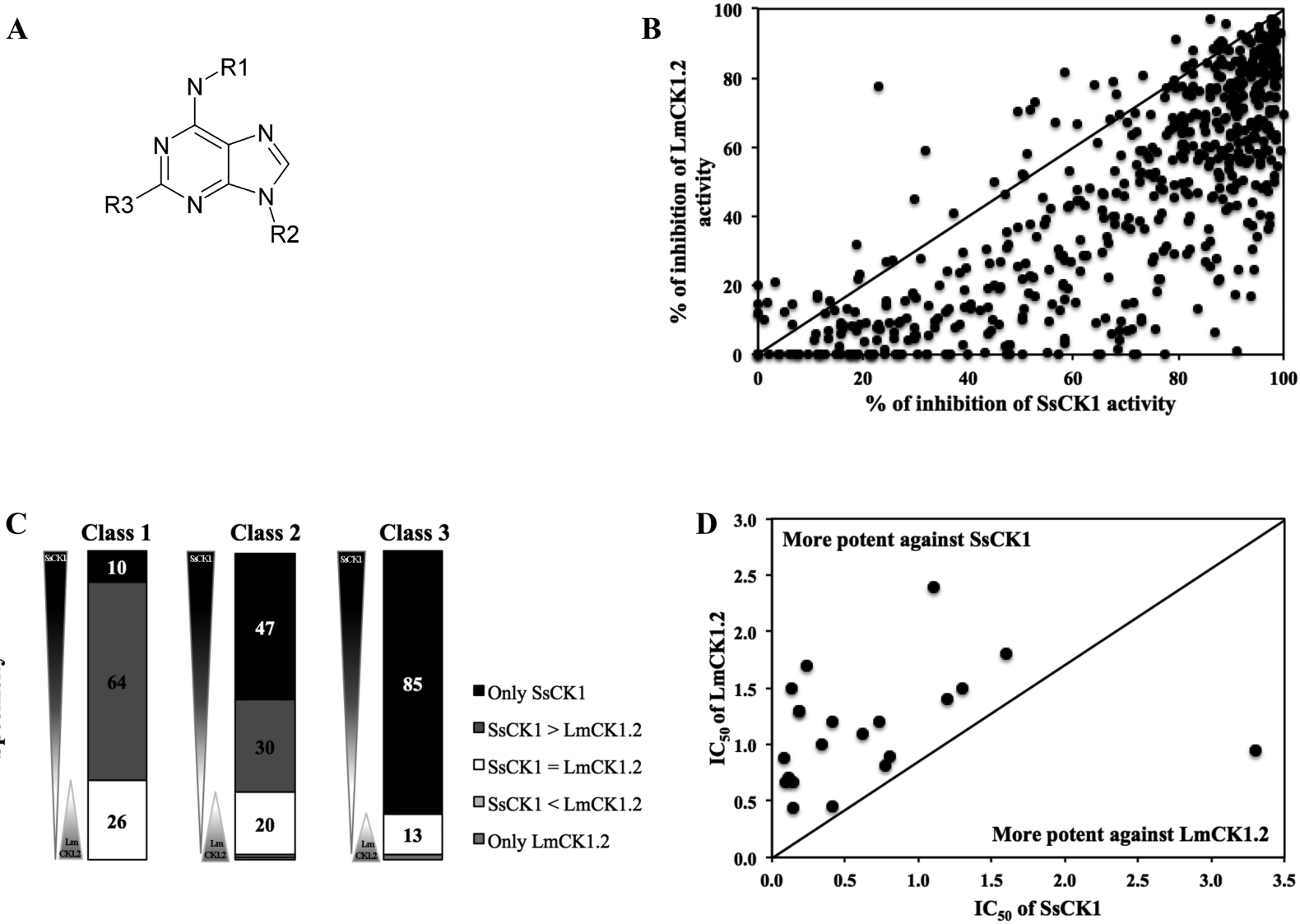
B

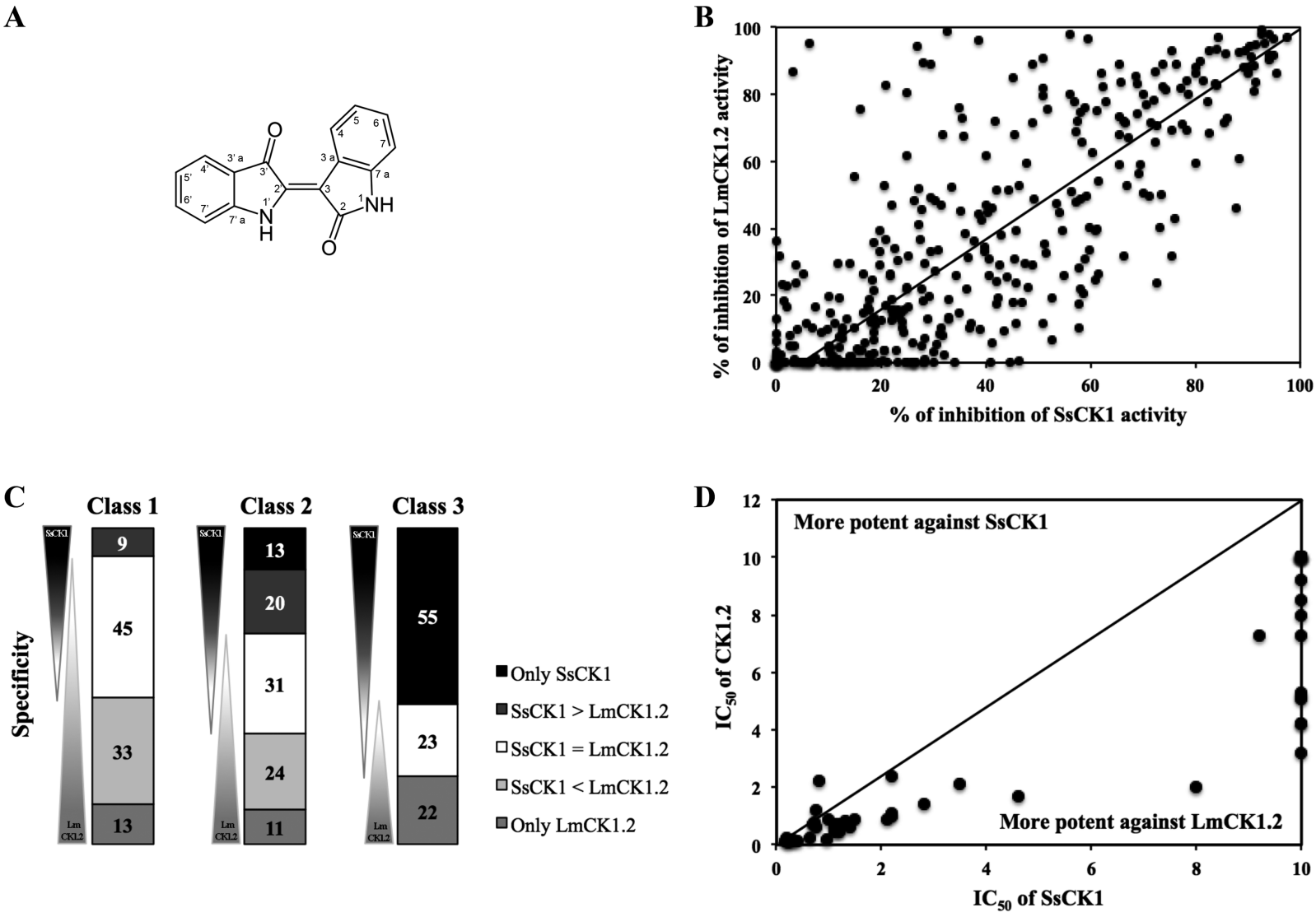

208
37
91
SsCK1
LmCK1.2
6.1 % hit rate
3.2 % hit rate

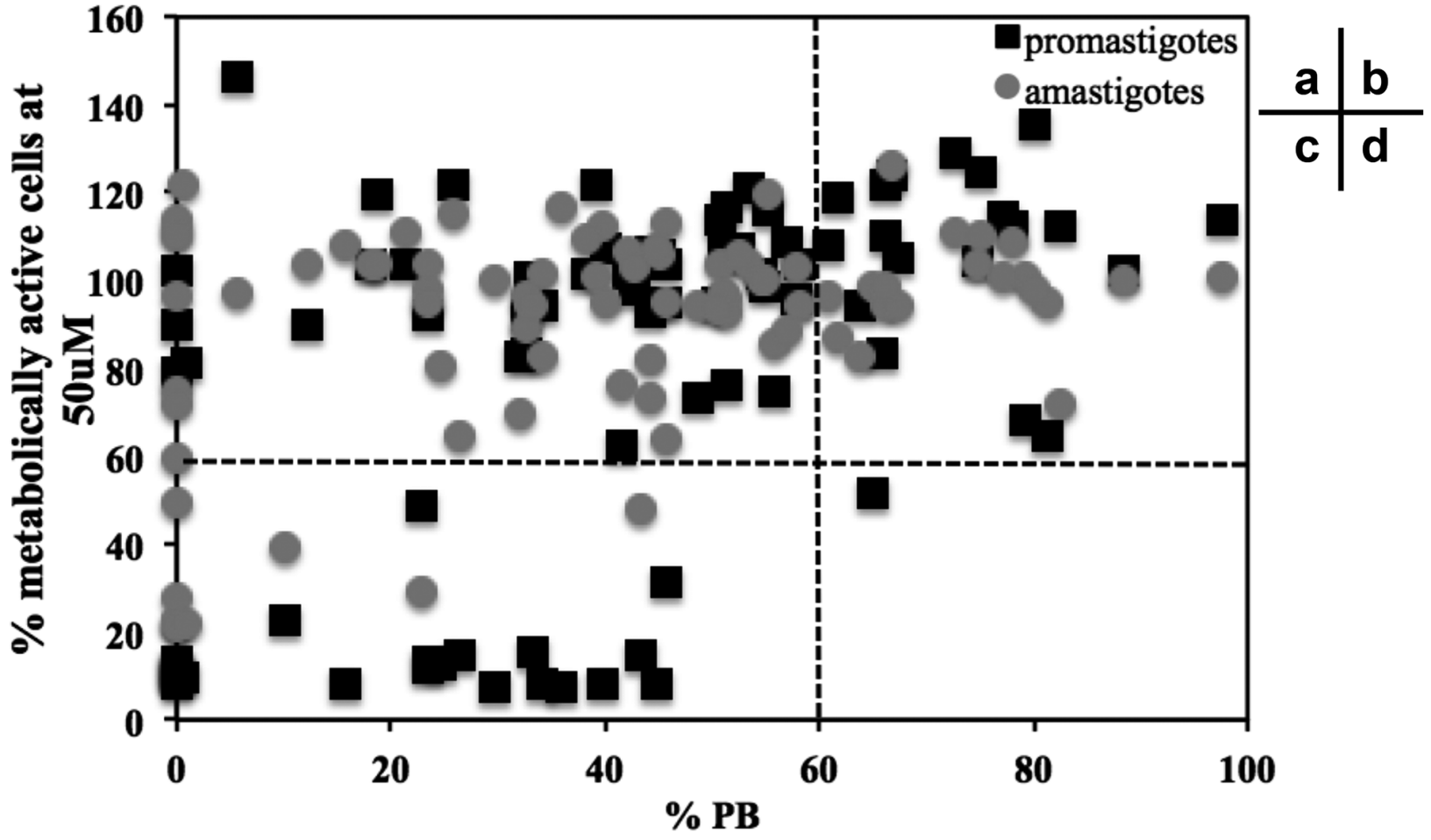
C

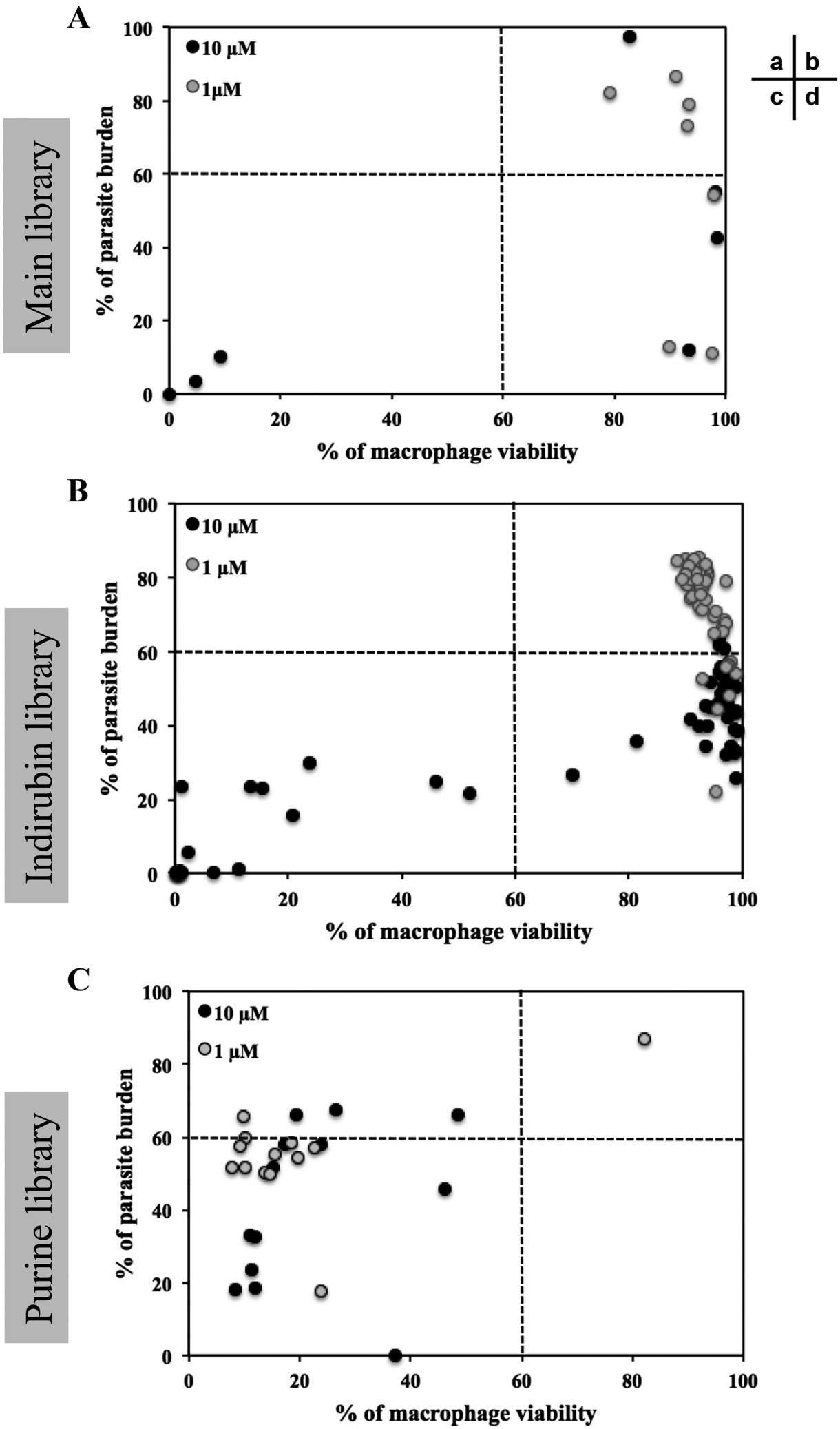

Class 1
Class 2
Class 3
Specificity
SsCK1
Lm CK1.2
14
24
23
23
16
59
9
8
5
18
70
7
23
Only SsCK1
SsCK1 > LmCK1.2
SsCK1 = LmCK1.2
SsCK1 < LmCK1.2
Only LmCK1.2

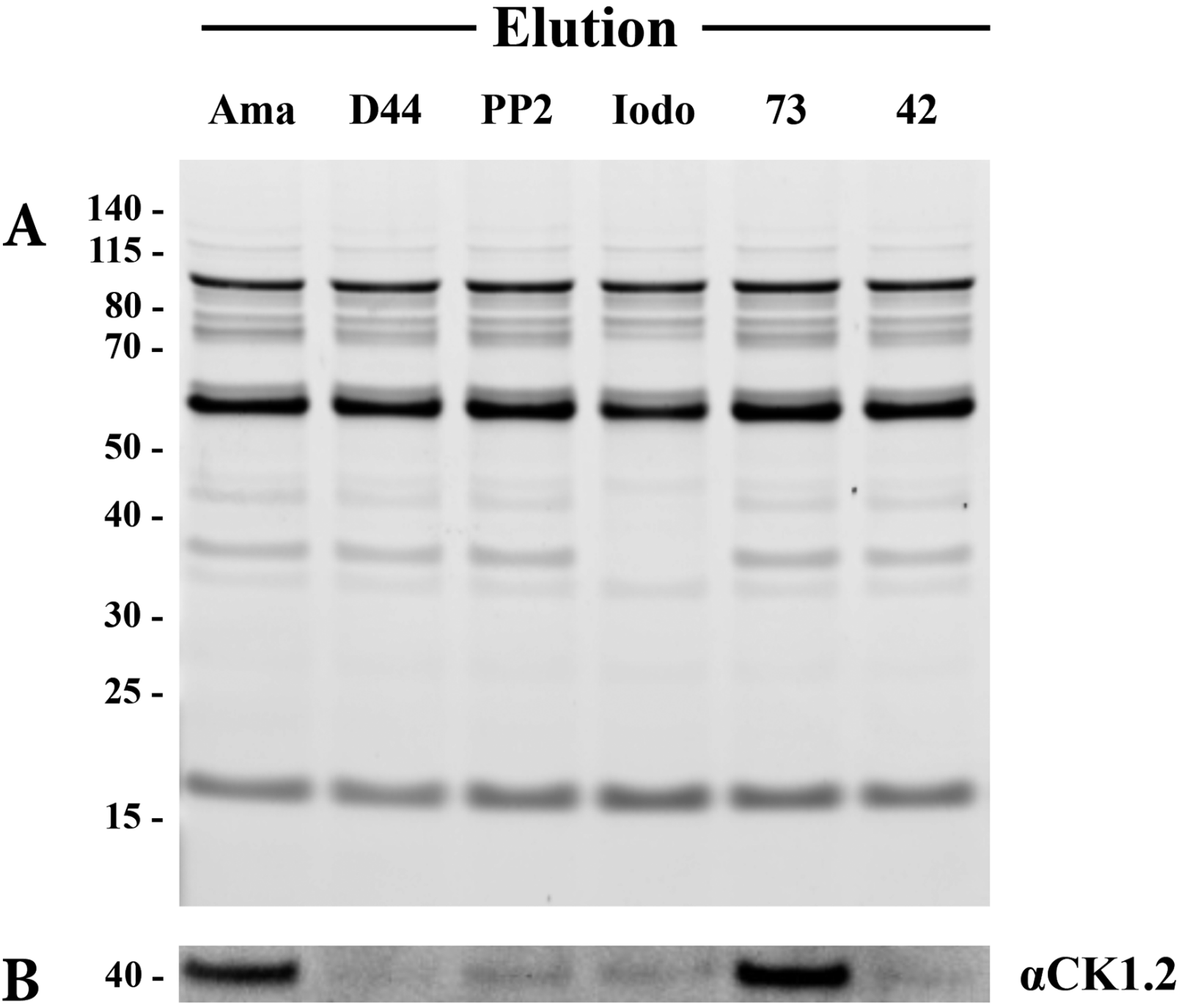

non-specific
specific
IC50 in µM
Compounds
0
2
4
6
8
10
0
10
20
30
40
50


A
R1
N
N
N
N
R3
N
N
R2
B
% of inhibition of LmCK1.2 activity
% of inhibition of SsCK1 activity
0
20
40
60
80
100
C
Class 1
Class 2
Class 3
Specificity
SsCK1
Lm CK1.2
10
64
26
47
30
20
85
13
Only SsCK1
SsCK1 > LmCK1.2
SsCK1 = LmCK1.2
SsCK1 < LmCK1.2
Only LmCK1.2
D
More potent against SsCK1
More potent against LmCK1.2
IC50 of LmCK1.2
IC50 of SsCK1
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5


A
B
% of inhibition of LmCK1.2 activity
% of inhibition of SsCK1 activity
C
Class 1
Class 2
Class 3
Specificity
SsCK1
Lm CK1.2
9
45
33
13
13
20
31
24
11
55
23
22
Only SsCK1
SsCK1 > LmCK1.2
SsCK1 = LmCK1.2
SsCK1 < LmCK1.2
Only LmCK1.2
D
More potent against SsCK1
More potent against LmCK1.2
IC50 of CK1.2
IC50 of SsCK1


% metabolically active cells at 50uM
160
140
120
100
80
60
40
20
0
0
20
40
60
80
100
% PB
promastigotes
amastigotes
a
b
c
d


A
Main library
10 μM
1μM
% of parasite burden
% of macrophage viability
a
b
c
d
B
Indirubin library
10 μM
1 μM
% of parasite burden
% of macrophage viability
C
Purine library
10 μM
1 μM
% of parasite burden
% of macrophage viability


Elution
Ama
D44
PP2
Iodo
73
42
A
140 -
115 -
80 -
70 -
50 -
40 -
30 -
25 -
15 -
B
40 -
αCK1.2

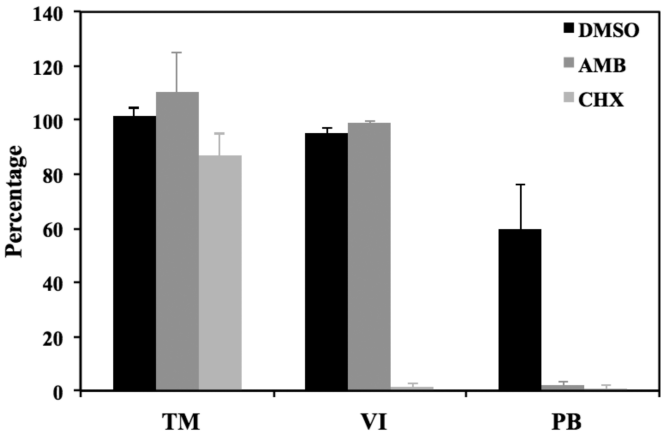


FIGURE S1. Controls for the phenotypic screen. We analysed the effect of DMSO, AMB and CHX on intracellular parasites using a visual high content phenotypic assay. We assessed several parameters including the percentage of total cells compared to control cells with DMSO (TM%), the percentage of viable cells (VI%) and the percentage of viable cells with parasitophorous vacuoles that is considered as an indication of parasite burden (PB%).

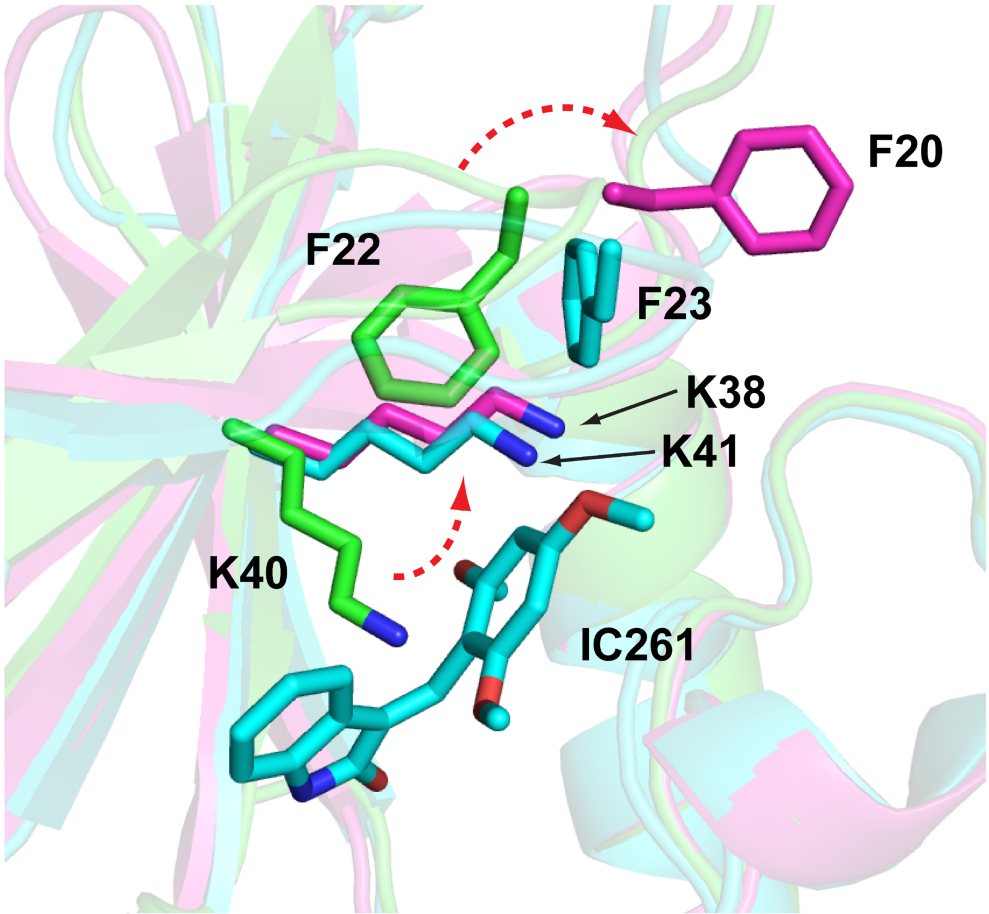


FIGURE S2. Model of the ATP binding pocket of LmCK1.2 compared to that of human and yeast CK1s. Comparison of yeast (cyan) and human (magenta) CK1 crystal structures with a structural model of LmCK1.2 (green). IC261 is represented in the ATP-binding pocket.

	Compound		IC_{50} (µM)		Metabolically active cells (%)				EC_{50} (µM)		intracellular parasites						EC_{50} (µM)	Macrophage viability EC_{50} (µM)	EC_{50} against human cells (µM)				Selectivity Index (SI)
					Promastigote (%)		amastigote (%)				10 µM			1 µM									
	Number	Name	SsCK1	LmCK1.2	50 µM	10 µM	50 µM	10 µM	proma-stigote	ama-stigote	TM %	PB %	VI %	TM %	PB %	VI %			RPE-1	SHSY-5Y	HFF-1	U2OS	
Main Library	1	PKC-412	>10	≥10	63.8	85.0	102.2	93.0	> 50	> 50	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.							
	2	Hypericin	>10	6.2	76.5	127.4	92.9	106.0	> 50	> 50	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.							
	3	5-Iodotubercidin	0.1	0.2	14.5	22.7	25.2	39.0	0.4	5.0	77.0	10.2	9.3	68.0	13.0	90.0	0.1	3.5	1.2	> 25	> 25	1.2	20
	4	SB-202190	0.4	0.1	69.0	129.4	112.3	111.0	> 50	> 50	87.7	72.8	89.4	94.9	83.6	93.5							
	5	PP2	0.5	1.4	41.2	114.0	99.1	101.0	> 10	> 50	59.9	97.6	82.9	83.7	54.3	97.8	1*	> 10	> 25	> 25	> 25	> 25	> 10
	6	GW 5074	4.3	4.9	27.5	112.8	20.3	72.0	> 10	> 10	102.9	82.5	97.6	101.7	79.1	94.1	3*	> 10	> 50	> 50	> 50	39.0	> 3.3
	7	Rottlerin	≥10	4.9	15.7	90.2	32.2	104.0	> 10	> 10	58.5	12.1	93.4	101.8	82.0	79.1							
	8	Indirubin-3'-monoxime	0.4	0.1	70.1	125.0	85.2	110.0	> 50	> 50	99.6	75.2	96.5	104.9	80.5	95.9							
	9	BML-265	2.2	0.9	36.9	124.0	87.2	126.0	> 10	> 50	96.1	66.8	95.6	104.0	80.9	96.4							
Purine Library	10		0.1	0.4	13.8	51.8	49.8	99.0	> 10	> 10	54.5	64.9	65.8	105.1	80.4	87.4							
	11		1.6	1.8	27.9	68.4	83.2	101.0	> 10	> 50	67.5	79.1	90.0	98.9	83.1	95.3							
	12		0.2	1.3	18.1	83.3	56.4	97.0	> 10	> 50	90.9	65.8	89.7	108.2	79.7	88.7							
	13		0.8	0.9	61.9	102.6	104.3	100.0	> 50	> 50	100.5	88.4	96.4	104.3	83.8	94.3							
	14		0.4	0.5	90.7	104.3	109.1	104.0	> 50	> 50	88.1	74.8	94.6	94.6	81.8	95.7							
	15		0.8	0.8	26.1	64.8	77.9	95.0	> 10	> 50	84.8	81.4	95.8	103.6	87.9	95.6							
	16		0.1	0.7	54.3	114.6	100.3	101.0	> 10	> 50	64.3	77.0	27.6	52.1	74.0	48.5							
	17		0.3	1.0	35.0	116.5	78.5	96.0	> 10	> 50	61.7	51.5	15.2	61.2	58.6	18.6							
	18		0.1	0.9	43.1	95.8	81.0	103.0	> 10	> 50	62.7	57.8	17.3	67.8	50.5	13.6							
	19		0.1	0.7	31.2	110.1	86.3	94.0	> 10	> 50	64.8	66.2	19.3	65.0	55.2	15.6							
	20		0.6	1.1	44.2	105.0	92.9	94.0	> 10	> 50	55.6	67.4	26.6	57.1	54.6	19.6							
	21		1.1	2.4	10.6	104.0	99.8	104.0	> 10	> 50	85.1	18.1	8.5	79.5	87.0	82.2							
	22		0.7	1.2	9.9	12.1	19.6	75.0	0.8	> 10	106.9	0.0	37.1	115.2	17.6	23.9							
	23		0.2	1.3	18.3	83.7	70.5	89.0	> 10	> 50	70.5	32.5	12.0	69.0	51.5	7.8							
	24		0.1	1.5	19.7	92.5	61.1	98.0	> 10	> 10	71.5	23.4	11.5	69.2	59.9	10.3							
	25		0.2	1.7	15.3	119.3	58.2	104.0	> 10	> 50	71.0	18.8	12.1	72.7	51.7	10.1							
	26		3.7	1.0	89.9	135.9	78.2	98.0	> 50	> 50	95.0	80.0	90.4	102.1	84.5	92.8							
	27		1.2	1.4	16.9	100.5	74.5	94.0	> 10	> 50	78.6	33.1	11.0	79.0	57.5	9.3							
	28		0.4	1.2	27.6	103.4	84.1	94.0	> 10	> 50	59.3	58.2	23.7	68.9	49.6	14.7							
	29		0.1	0.7	84.8	121.8	101.4	99.0	> 50	> 50	49.0	66.2	48.5	56.8	57.0	22.6							
	30		1.3	1.5	15.0	31.7	27.5	64.2	6.5	> 10	58.9	45.8	46.2	77.8	65.5	9.8							
Indirubin Library	31		2.2	1.0	39.3	75.9	57.0	93.0	> 10	> 50	95.6	51.5	94.5	103.9	81.1	93.3							
	32		0.7	0.6	71.8	73.6	63.2	94.3	> 50	> 50	92.7	48.7	96.2	104.2	84.8	92.0							
	33		3.5	2.1	69.2	113.7	59.7	103.7	> 50	> 50	80.1	50.7	96.8	104.2	81.5	93.7							
	34		0.3	0.2	69.9	92.0	58.3	96.8	> 50	> 50	87.8	32.6	98.6	104.9	78.7	92.6							
	35		1.0	0.2	81.7	105.7	86.9	105.6	> 50	> 50	79.3	45.2	93.6	103.6	78.2	90.2							
	36		0.6	0.2	79.8	101.3	92.8	106.8	> 50	> 50	83.9	42.0	97.3	101.4	85.4	92.2							
	37		0.7	0.7	122.5	121.3	101.2	103.7	> 50	> 50	107.9	53.3	96.5	105.3	77.0	93.0							
	38		0.7	1.2	56.5	122.0	72.8	115.1	> 10	> 50	106.6	25.9	98.8	110.5	68.1	95.5	0.6	> 10	> 25	> 25	> 25	> 25	> 17
	39		1.1	0.5	32.0	121.8	32.9	100.9	> 10	> 10	97.7	39.2	98.6	106.7	82.3	93.4							
	40		0.3	0.1	38.4	93.2	48.8	82.2	> 10	> 10	96.9	44.1	98.2	103.8	79.1	93.0							
	41		1.3	0.7	131.9	146.7	118.9	97.4	> 50	> 50	101.3	5.5	2.3	98.6	81.0	93.9							
	42		2.1	0.9	9.3	11.6	19.3	59.6	2.0	> 10	106.0	0.0	0.5	107.1	46.7	95.4	0.1	3.0	7.0	18.0	7.7	7.3	50
	43		0.7	0.7	10.9	48.7	26.6	29.6	1.0	8.0	83.9	22.8	15.3	102.6	72.0	92.3							
	44		1.2	0.5	8.8	10.5	19.9	22.8	0.9	4.5	106.9	0.0	0.7	96.0	71.4	93.1							
	45		1.2	0.4	9.4	10.7	20.5	22.1	0.7	4.5	106.6	0.0	1.2	103.0	74.4	90.8							
Indirubin Library	46		>10	4.2	10.1	106.7	25.3	73.6	> 10	> 10	103.2	44.1	99.0	105.1	81.6	93.4							
	47		>10	5.2	9.7	13.0	23.0	95.2	2.0	> 10	75.6	23.4	13.5	107.5	79.2	97.2							
	48		10.0	5.1	9.5	10.5	19.6	27.5	0.4	7.0	74.1	0.0	0.3	112.6	53.9	99.0							
	49		1.2	0.7	9.7	12.7	23.5	80.8	2.0	>10	83.5	24.6	46.1	106.0	66.2	96.5							
	50		1.1	0.7	7.9	10.4	19.7	21.0	0.7	3.5	107.4	0.0	0.2	108.7	68.6	96.9							
	51		>10	8.5	98.0	106.3	96.0	97.1	> 50	> 50	111.7	51.0	98.0	104.1	74.8	91.2							
	52		0.2	0.1	106.9	118.6	90.0	86.9	> 50	> 50	103.6	61.6	95.9	102.4	85.1	89.9							
	53		>10	10.0	67.3	103.5	64.3	94.7	> 50	> 10	81.8	45.8	95.7	105.0	84.8	91.4							
	54		1.3	0.8	68.0	95.2	84.2	93.3	> 50	> 50	114.7	50.4	98.8	111.6	81.9	92.6							
	55		>10	5.3	99.0	107.7	88.2	96.3	> 50	> 50	118.1	60.9	96.8	111.2	83.2	93.0							
	56		>10	8.0	96.0	101.8	98.7	100.4	> 50	> 50	106.2	54.6	95.8	111.8	80.1	93.3							
	57		>10	10.0	9.4	90.3	19.2	72.2	> 10	> 10	97.0	0.1	6.8	114.4	81.9	90.7							
	58		9.2	7.3	79.3	94.2	26.9	83.0	> 50	> 10	106.8	63.7	95.8	109.8	81.2	92.2							
	59		0.2	0.1	85.7	94.6	57.7	82.5	> 50	> 10	86.5	34.3	98.0	106.8	77.8	92.7							
	60		>10	3.2	10.2	15.0	27.6	64.4	2.0	>10	70.7	26.5	70.1	105.9	69.5	95.0							
	61		>10	7.3	20.2	81.5	14.8	21.9	n.d.	5.0	43.8	1.0	11.3	110.1	81.4	91.6	2.0	2.0	n.d.	n.d.	n.d.	n.d.	1
Main Library	71	NSC 146771	>10	1.5	59.2	116.3	108.9	119.4	> 10	> 50	104.3	55.2	98.2	102.6	73.3	93.0							
	72	NSC 610744	>10	7.0	104.2	112.6	99.7	109.1	> 50	> 50	104.0	78.1	88.0	105.1	84.3	93.1							
	73	NSC 699479	>10	8.0	n.d	n.d	n.d	n.d	< 1	< 1	107.9	3.6	4.7	105.4	10.9	97.5	0.3	3.5	10.5	36.5	12.0	3.0	12
	74	NSC 715055 (gefitinib)	>10	2.0	19.7	97.9	111.3	102.7	> 10	> 50	93.0	42.7	98.4	102.5	79.2	93.4	8.0	> 10	n.d.	n.d.	n.d.	n.d.	> 1.3
	75	NSC 750690 (sunitinib)	0.8	0.6	8.5	13.1	96.3	111.5	4.0	> 50	88.3	0.0	0.1	79.1	86.6	91.1	2.5	3.0	n.d.	n.d.	n.d.	n.d.	1.2
	77	purvalanol B	2.9	2.0	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	91.76	88.27	82.84	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
Indirubin Library	80		4.6	1.7	7.6	8.0	21.1	112.6	1.8	> 10	66.7	39.7	92.2	105.7	67.5	97.0							
	81		8.0	2.0	5.9	8.0	18.7	108.3	2.3	> 10	80.8	15.8	20.9	109.8	57.1	98.0							
	82		>10	4.2	7.9	9.3	39.7	122.1	2.5	> 10	103.3	0.7	0.8	109.2	65.2	96.6							
	84		≥10	9.2	7.0	8.1	17.9	49.8	0.7	> 10	86.3	0.0	0.3	113.3	56.1	97.8	1.5	2.5	2.3	6.0	2.2	2.0	1.5
	85		-(10)	>10	36.7	104.0	19.3	111.2	> 10	> 10	110.7	21.5	52.0	107.4	79.5	90.9							
	86		2.2	1.1	5.7	7.2	16.4	100.3	2.0	> 10	87.0	29.7	23.7	106.3	56.1	97.4	2.0	4.5	n.d.	n.d.	n.d.	n.d.	2.3
	87		2.8	1.4	7.2	7.4	20.3	116.9	1.7	> 10	64.6	35.9	81.4	99.8	65.1	95.0							
	88		>10	>10	92.6	107.7	104.1	105.9	> 50	> 50	115.6	52.6	98.4	108.4	79.2	93.6							
	89		1.4	0.6	8.0	12.1	39.8	114.0	2.0	> 10	113.2	0.0	0.7	110.2	81.6	91.7							
	90		>10	>10	18.3	94.8	104.8	112.9	> 10	> 50	108.5	45.7	97.3	111.1	84.2	90.8							
	91		1.0	0.9	8.6	79.5	81.6	110.5	> 10	> 50	117.3	0.0	0.5	112.5	55.7	97.2	1.5	3.0	2.2	4.5	2.3	0.8	0.5
	92		>10	>10	30.6	101.7	94.5	109.6	> 10	> 50	98.0	38.3	99.1	113.2	85.2	91.5							
	93		≥10	>10	7.6	8.5	22.3	107.2	1.6	> 10	91.3	44.9	94.4	109.8	83.6	93.4							
	94		0.2	0.3	7.6	11.8	75.6	103.5	1.8	> 50	98.8	23.4	1.0	103.0	47.9	97.8	0.7	3.0	2.0	14.0	10.0	0.7	1
	95		2.2	2.4	64.8	98.5	63.3	100.4	> 50	> 50	85.3	54.9	97.2	101.7	83.1	90.5							
	96		0.8	2.2	6.4	74.7	18.3	85.4	> 10	> 10	96.7	55.9	96.1	105.4	81.1	90.1							
	97		>10	>10	8.4	15.1	19.7	48.0	8.0	> 10	102.8	43.4	98.8	111.5	84.4	88.5	4.0	> 10	> 25	> 25	15.0	> 25	> 2.5
	98		>10	>10	35.7	107.3	21.4	94.7	> 10	> 10	108.4	39.9	93.7	106.3	79.3	92.1							
	99		0.7	0.8	8.0	82.6	59.6	69.5	> 10	> 10	114.6	32.0	97.1	110.5	71.1	95.3							
	100		>10	>10	18.2	108.6	101.9	88.7	> 10	> 50	120.3	57.1	97.7	113.5	80.9	90.0							
	101		1.1	0.6	7.2	15.7	33.0	94.3	6.5	> 10	123.9	33.2	98.9	114.4	74.1	93.6							
	102		0.2	0.2	39.7	62.6	66.2	76.0	> 10	> 10	65.5	41.6	91.0	93.3	52.7	92.9	2.0	> 10	0.8	> 25	9.0	0.3	0.15
	103		0.4	0.2	7.8	102.5	76.8	96.3	> 10	> 50	99.1	0.0	0.5	100.3	75.3	92.5							
	104		1.5	0.9	6.1	8.3	18.7	101.4	5.0	> 10	66.0	34.2	93.6	103.4	79.4	89.3							