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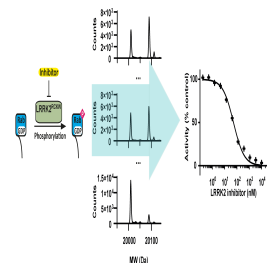
In vitro LRRK2 kinase activity assay using mass-spectrometry as readout V.2

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dx.doi.org/10.17504/protocols.io.6qpvr385ovmk/v2Verena Dederer^{1,2}, Deep Chatterjee^{1,2}, Sebastian Mathea^{1,2}, Stefan Knapp^{1,2}¹Institute of Pharmaceutical Chemistry, Goethe University Frankfurt, Max-von-Laue-Straße 9, Frankfurt 60438, Germany;²Structural Genomics Consortium, Buchman Institute for Molecular Life Science (BMLS), Max-von-Laue-Straße 15, Frankfurt 60438, Germany**Verena Dederer**

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We use this protocol and it's working

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Abstract

This protocol can be used in this form or with small adjustments regarding concentration and reaction time to determine in vitro substrate phosphorylation for any purified kinase substrate pair.

It can be used to determine inhibition curves by addition of concentration series of kinase inhibitors.

Reaction is carried out in 50 μ L reaction mix containing final concentration of 50 nM kinase and 5 μ M substrate.



Materials

Purified proteins

kinase: LRRK2^{RCKW}

protein sequence:

KKAVPYNRMKLMIVGNTGSGKTTLLQQLMKTKKSDLGMQSATVGIDVKDWPIQIRDKRKRDVLNVWDFAGREEFYSTHPH
FMTQRALYLAVYDL SKGQAEVDAMKPWLFNIKARASSSPVILVGTHLDVSDEKQRKACMSKITKELLNKRGFPAIRDYHFVN
ATEESDALAKLRKTIINESLNFKIRDQLVVGQLIPDCYVELEKIILSERKNVPIEFVIDRKRLQLVRENQLQLDENELPHAVHFL
NESGVLLHFQDPALQLSDLYFVEPKWLCKIMAQILTVKVEGCPKHPKGIISRRDVEKFLSKKRKFPKNYMSQYFKLLEKFQIAL
PIGEEYLLVPSSLSDRPVIELPHCENSEIIIRLYEMPYFPMGFW SRLINRLLEISPYMLSGRERALRPNRM YWRQGIYLNWSPE
AYCLVGSEVLDNHPESFLKITVPSCRKGCILLGQVVDHIDSLMEEWFPGLLEIDICGEGETLLKKWALYSFNDGEEHQKILLDD
LMKKAEEGDLLVNPDQPRLTIPISQIAPDLILADLPRNIMLNNDELEFEQAPEFLLGDGSGFSVYRAAYEGEEVAVKIFNKHTSL
RLLRQELVVLCHLHHPSLISLLAAGIRPRMLVME LASKGSLDRLLQQDKASLRTLQHRIALHVADGLRYLHSAMIIYRDLKPH
NVLLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTPGFRAPEVARGNVIYNQQADVVSFGLLLYDILTTGGRIVEGLKFPNEF
DELEIQGKLDPVKEYGCAPWPMVEKLIKQCLKENPQERPTSAQVFDILNSAELVCLTRRILLPKNVIVECMVATHHNSRNASI
WLGC GHTDRGQLSFLDLNTEGYTSEEVADSRILCLALVHLPVEKESWIVSGTQSGTLLVINTEDGKKRHTLEKMTDSVTCLY
CNSFSKQSKQKNFLLVGTADGKLAIFEDKTVKLKGAAPLKILNIGNVSTPLMCLSESTNSTERNVMWGGCGTKIFSFSNDFTI
QKLIETRTSQLFSYAAFSDSNIITVVVD TALYIAKQNSPVVEVWDKKTEKLCGLIDCVHFLREVMVKENKESKHKMSYSGRVK
TLCLQKNTALWIGTGGGHILLDLSTRRLIRVIYNFCNSVRVMMTAQLGSLKNVMLVLGYNRKNTEGTQKQKEIQSCLTVWDI
NLPHEVQNLEKHIEVRKELAEKMRRTSVE

substrate: Rab8A

protein sequence:

GHMDYLFKLLLLIGDSGVGKTCVLF RFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQIWDTAGQERFRTITTAYYRGAMGIMLVY
DITNEKSFDNIRNWIRNIEEHASADVEKMILGNKCDVNDKRQVSKERGEK LALDYGIKFMETSAKANINVENAFFTLARDIKAK
MDKK

Buffers and Reagents

reaction buffer: 20 mM Hepes pH 7.4, 150 mM NaCl, 5% glycerol, 0.5 mM TCEP, 20 μ M GDP, 2.5 mM MgCl_2

ATP 100 mM stock in dH_2O

mass spec buffer: dH_2O + 0.1% formic acid

Troubleshooting

Step-by-Step Protocol

- 1 Prepare 50 μL reaction mix I: 50 nM purified LRRK2^{RCKW} and 5 μM Rab8 substrate in buffer containing 20 mM Hepes pH 7.4, 150 mM NaCl, 5% glycerol, 0.5 mM TCEP, 20 μM GDP, 2.5 mM MgCl_2 .
Aliquot 25 μL per tube.

Note

If you want to run multiple reactions prepare a master mix and aliquot 25 μL per tube.

- 2 Prepare 25 μL reaction mix II: 2 mM ATP + 2.5 mM MgCl_2 in buffer containing 20 mM Hepes pH 7.4, 150 mM NaCl, 5% glycerol, 0.5 mM TCEP, 20 μM GDP, 2.5 mM MgCl_2 .

Note

Multiply if you want to run more than one reaction.

- 3 Prepare 25 μL reaction mix III: same as reaction mix II but no ATP as negative control.
- 4 Start reaction by adding 25 μL reaction II to reaction mix I.
Note: for negative control add 25 μL reaction mix III to second aliquot of reaction mix I.
- 5 Mix by vortexing and brief centrifugation for 30 sec with 500xg.
- 6 Incubate reaction for 3 h at room temperature.
Note: depending on kinase this may be shorter or longer.
- 7 Stop reaction by adding 50 μL mass spec buffer (dH_2O +0.1% formic acid).
- 8 Store at -80°C or proceed directly with mass spectrometry analysis.



Note

For determination of inhibition curves, prepare a concentration series of inhibitor in DMSO. Prepare a master mix of kinase and substrate pair and aliquot 25 μ L per tube. Add the desired amount of inhibitor to each of the tube and incubate all reactions at room temperature.

Note

For analysis: substrate phosphorylation/turnover can be determined as ratio between phosphorylated and unphosphorylated peak intensity for each sample analyzed.