



Niko Beerenwinkel

Kontakt

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Publikationen (5)

Thorball C, Klimkait T, Yerly S, Battegay M, Rauch A, Schmid P, Bernasconi E, Cavassini M, Kouyos R, Günthard H, Metzner K, Fellay J, Perreau M, Böni J, Wieser M, Borghesi A, Bachmann N, Von Siebenthal C, Vongrad V, Turk T, Neumann K, Beerenwinkel N, Bogojeska J, Roth V, Kok Y, Parbhoo S, Swiss HIV Cohort Study. Host Genomics of the HIV-1 Reservoir Size and Its Decay Rate During Suppressive Antiretroviral Treatment. *J Acquir Immune Defic Syndr* 2020; 85:517-524.

Wan C, Yerly S, Battegay M, Wälti L, Calmy A, Vernazza P, Bernasconi E, Cavassini M, Metzner K, Günthard H, Kouyos R, Klimkait T, Perreau M, Böni J, Bachmann N, Mitov V, Blanquart F, Céspedes S, Turk T, Neumann K, Beerenwinkel N, Bogojeska J, Fellay J, Roth V, Swiss HIV Cohort Study. Heritability of the HIV-1 reservoir size and decay under long-term suppressive ART. *Nat Commun* 2020; 11:5542.

Thorball C, Klimkait T, Yerly S, Battegay M, Rauch A, Schmid P, Bernasconi E, Cavassini M, Kouyos R, Günthard H, Metzner K, Fellay J, Perreau M, Böni J, Wieser M, Borghesi A, Bachmann N, Von Siebenthal C, Vongrad V, Turk T, Neumann K, Beerenwinkel N, Bogojeska J, Roth V, Kok Y, Parbhoo S, Swiss HIV Cohort Study. Host genomics of the HIV-1 reservoir size and its decay rate during suppressive antiretroviral treatment. *J Acquir Immune Defic Syndr* 2020

Carlisle L, Braun D, Rauch A, Calmy A, Cavassini M, Battegay M, Vernazza P, Bernasconi E, Günthard H, Kouyos R, Perreau M, Klimkait T, Yerly S, Turk T, Kusejko K, Metzner K, Leemann C, Schenkel C, Bachmann N, Posada S, Beerenwinkel N, Böni J, Swiss HIV Cohort Study. Viral diversity from next-generation sequencing of HIV-1 samples provides precise estimates of infection recency and time since infection. *J Infect Dis* 2019

Beerenwinkel N, Günthard H, Celleraï C, Klimkait T, Böni J, Yerly S, Bernasconi E, Vernazza P, Cavassini M, Hirschel B, Battegay M, Furrer H, von Wyl V, Knüpfer P, Schuhmacher H, Montazeri H, Swiss HIV Cohort Study. The individualized genetic barrier predicts treatment response in a large cohort of HIV-1 infected patients. *PLoS Comput Biol* 2013; 9:e1003203.

Projekte (0)

Keine Resultate gefunden.

Kantonsspital St.Gallen

Rorschacher Strasse 95

CH-9007 St.Gallen

T: +41 71 494 11 11

support.forschung@kssg.ch