Scipher Medicine Bibliography

Pub. Date	1st Author	Title	Reference	Online Access
Nov-2022	Curtis JR	Patient outcomes improve when a molecular signature test guides treatment decision making in rheumatoid arthritis	Curtis JR, Strand V, Golombek S, et al. Patient outcomes improve when a molecular signature test guides treatment decision-making in rheumatoid arthritis. Expert Rev Mol Diagn. 2022 Nov 3:1-10. doi: 10.1080/14737159.2022.2140586.	Link
Aug-2022	Ghiassian SD	Network-based response module comprised of gene expression biomarkers predicts response to infliximab at treatment initiation in ulcerative colitis.	Ghiassian GD, Voitalov I, Withers JB, et al. Network-based response module comprised of gene expression biomarkers predicts response to infliximab at treatment initiation in ulcerative colitis. *Transl Res*. 2022 Aug;246:78-86. doi:10.1016/j.trsl.2022.03.006.	Link
Jun-2022	Strand V	Improvement in clinical disease activity index when treatment selection is informed by thetumor necrosis factor-α inhibitor molecular signature response classifier: analysis from the study to accelerate information of molecular signatures in rheumatoid arthritis	Strand V, Zhang L, Arnaud A, et al. Improvement in clinical disease activity index when treatment selection is informed by the tumor necrosis factor-α inhibitor molecular signature response classifier: analysis from the study to accelerate information of molecular signatures in rheumatoid arthritis. *Expert Opin Biol Ther*. 2022 Jun;22(6):801-807. doi: 10.1080/14712598.2022.2066972.	Link
Apr-2022	Bergman M	Budget impact and clinical outcomes of a molecular signature to inform TNFi treatment selection in commercial patients with rheumatoid arthritis.	Bergman M, Connolly-Strong E, Guldoboni A, et al. Budget impact and clinical outcomes of a molecular signature to inform TNFi treatment selection in commercial patients with rheumatoid arthritis. Poster presented at AMCP. April 2022.	Link
Mar-2022	Connolly-Strong E	Evaluation of physician global assessment in patients with b/tsDMARD therapy selection aligned with a molecular signature response classifier results: an analysis from the study to accelerate information of molecular signatures (AIMS) in rheumatoid arthritis	Connolly-Strong E, Zhang L, Asgarian S. POS0548 Evaluation of physician global assessment in patients with b/tsDMARD therapy selection aligned with a molecular signature response classifier results: an analysis from the study to accelerate information of molecular signatures (AIMS) in rheumatoid arthritis. *Annals of the Rheumatic Diseases*. 2022;81:538.	Link
Feb-2022	Cohen S	A response to: letter to the editor regarding a molecular signature response classifier to predict inadequate response to tumor necrosis factor-α inhibitors: the NETWORK-005 prospective observational study	Cohen S, Akmaev VR, Withers JB, et al. A Response to: Letter to the Editor Regarding A Molecular Signature Response Classifier to Predict Inadequate Response to Tumor Necrosis Factor-α Inhibitors: The NETWORK-004 Prospective Observational Study. Rheumatol Ther. 2022 Feb;9(1):309-311. doi: 10.1007/s40744-021-00387-9.	Link

Jan-2022	Strand V	Clinical utility of therapy selection informed by predicted nonresponse to tumor necrosis factor-α inhibitors: an analysis from the Study to Accelerate Information of Molecular Signatures (AIMS) in rheumatoid arthritis	Strand V, Cohen SB, Curtis JR, et al. Clinical utility of therapy selection informed by predicted nonresponse to tumor necrosis factor-α inhibitors: an analysis from the Study to Accelerate Information of Molecular Signatures (AIMS) in rheumatoid arthritis. *Expert Rev Mol Diagn*. 2022 Jan;22(1):101-109. doi: 10.1080/14737159.2022.2020648.	Link
Dec-2021	Arnell C	Guided therapy selection in rheumatoid arthritis using a molecular signature response classifier: an assessment of budget impact and clinical utility	Arnell C, Bergman M, Basu D, et al. Guided therapy selection in rheumatoid arthritis using a molecular signature response classifier: an assessment of budget impact and clinical utility. *J Manag Care Spec Pharm*. 2021 Dec;27(12):1734-1742. doi: 10.18553/jmcp.2021.21120.	Link
Nov-2021	Jones A	Analytical and clinical validation of an RNA sequencing-based assay for quantitative, accurate evaluation of a molecular signature response classifier in rheumatoid arthritis	Jones A, Rapisardo S, Zhang L, et al. Analytical and clinical validation of an RNA sequencing-based assay for quantitative, accurate evaluation of a molecular signature response classifier in rheumatoid arthritis. *Expert Rev Mol Diagn*. 2021 Nov;21(11):1235-1243. doi: 10.1080/14737159.2021.2000394	Link
Nov-2021	Cohen S	A molecular signature response classifier predicts the likelihood of non-response to TNF inhibitor therapies in RA at 3 months	Cohen S, Mellors T, Zhang L, et al. A molecular signature response classifier predicts the likelihood of non-response to TNF inhibitor therapies in RA at 3 months [abstract]. *Arthritis Rheumatol*. 2021;73(suppl 9).	Link
Nov-2021	Curtis J	Discontinuation of TNFi treatment among rheumatoid arthritis patients with a molecular signature of non-response to tumor necrosis factor-α inhibitor therapies	Curtis J, Kremer J, Pappas D, et al. Discontinuation of TNFi treatment among rheumatoid arthritis patients with a molecular signature of non-response to tumor necrosis factor-α inhibitor therapies [abstract]. *Arthritis Rheumatol*. 2021;73(suppl 9).	Link
Oct-2021	Ghiassian SD	A network medicine approach to discover common novel drug target mechanisms across autoimmune diseases	Ghiassian S, Withers J, Akmaev J. S913 A network medicine approach to discover common novel drug target mechanisms across autoimmune disease. *Am J Gastroenterol*. 2021 Oct;116:S431-S432. doi:10.14309/01.ajg.0000777184.25987.8b.	Link
Sep-2021	Cohen S	A Molecular Signature Response Classifier to Predict Inadequate Response to Tumor Necrosis Factor-α Inhibitors: The NETWORK-004 Prospective Observational Study	Cohen S, Wells AF, Curtis JR, et al. A Molecular Signature Response Classifier to Predict Inadequate Response to Tumor Necrosis Factor-α Inhibitors: The NETWORK-004 Prospective Observational Study. *Rheumatol Ther*. 2021 Sep;8(3):1159-1176. doi: 10.1007/s40744-021-00330-y.	Link
Aug-2021	Cohen S	Use of precision medicine to guide treatment of patients with rheumatoid arthritis: comment on the article by Tao et al.	Cohen SB, Mellors T, Bergman MJ. Use of Precision Medicine to Guide Treatment of Patients With Rheumatoid Arthritis: Comment on the Article by Tao et al. Arthritis Rheumatol. 2021 Aug;73(8):1567-1569. doi: 10.1002/art.41712.a	Link
May-2021	Gysi DM	Network medicine framework for identifying drug-repurposing opportunities for COVID-19	Morselli Gysi D, do Valle Í, Zitnik M, et al. Network medicine framework for identifying drug-repurposing opportunities for COVID-19. *Proc Natl Acad Sci USA*. 2021 May 11;118(19):e2025581118. doi: 10.1073/pnas.2025581118.	Link

May-2021	Zhang L	A molecular signature response classifier predicts the likelihood of EULAR non-response to TNF inhibitor therapies in RA: results from a retrospective cohort analysis	Zhang L, van der Tog C, den Broeder A, et al. POS0492 A molecular signature response classifier predicts the likelihood of EULAR non-response to TNF inhibitor therapies in RA: results from a retrospective cohort analysis. *Annals of the Rheumatic Diseases.* 2021;80:478-479.	Link
May-2021	Cohen S	A molecular signature response classifier stratifies seropositive rheumatoid arthritis patients based on their likelihood of inadequate response to TNF inhibitor therapies	Cohen S, Strand V, Connolly-Strong E, et al. AB0138 A molecular signature response classifier stratifies seropositive rheumatoid arthritis patients based on their likelihood of inadequate response to TNF inhibitor therapies. *Annals of the Rheumatic Diseases.* 2021;80:1096-1097.	Link
May-2021	Strand V	A high-confidence definition of therapeutic response in rheumatoid arthritis using a monte carlo stimulation approach	Strand V, Cohen S, Zhang L, et al. AB0140 A high-confidence definition of therapeutic response in rheumatoid arthritis using a monte carlo simulation approach. *Annals of the Rheumatic Diseases*. 2021;80:1097-1098.	Link
Mar-2021	Pappas DA	Perceived clinical utility of a test for predicting inadequate response to TNF inhibitor therapies in rheumatoid arthritis: results from a decision impact study	Pappas DA, Brittle C, Mossell JE 3rd, et al. Perceived clinical utility of a test for predicting inadequate response to TNF inhibitor therapies in rheumatoid arthritis: results from a decision impact study. *Rheumatol Int*. 2021 Mar;41(3):585-593. doi: 10.1007/s00296-020-04746-7.	Link
Feb-2021	Wang M	A system-based method to repurpose marketed therapeutics for antiviral use: a SARS-CoV-2 case study	Wang M, Withers JB, Ricchiuto P, et al. A systems-based method to repurpose marketed therapeutics for antiviral use: a SARS-CoV-2 case study. *Life Sci Alliance*. 2021 Feb 16;4(5):e202000904. doi: 10.26508/lsa.202000904.	Link
Dec-2020	Bergman MJ	Clinical Utility and Cost Savings in Predicting Inadequate Response to Anti-TNF Therapies in Rheumatoid Arthritis	Bergman MJ, Kivitz AJ, Pappas DA, et al. Clinical Utility and Cost Savings in Predicting Inadequate Response to Anti-TNF Therapies in Rheumatoid Arthritis. *Rheumatol Ther*. 2020 Dec;7(4):775-792. doi: 10.1007/s40744-020-00226-3.	Link
Jul-2020	Mellors T	Clinical Validation of a Blood-Based Predictive Test for Stratification of Response to Tumor Necrosis Factor Inhibitor Therapies in Rheumatoid Arthritis Patients	Mellors T, Withers JB, Ameli A, et al. Clinical Validation of a Blood-Based Predictive Test for Stratification of Response to Tumor Necrosis FactorInhibitor Therapies in Rheumatoid Arthritis Patients. *Netw Syst Med.* 2020 July;3(1):91-104. doi:10.1089/nsm.2020.0007.	Link
Feb-2020	Jeter A	Markov chain economic impact model for anti-TNF non-response stratification of patients with moderate to severe ulcerative colitis	Jeter A, Sanchez H, Withers J, et al. P055 Markov chain economic impact model for anti-TNF non-response stratification of patients with moderate to severe ulcerative colitis. *Gastroenterology*. 2020 Feb;158(3);S23-S24.	Link
Nov-2019	Johnson KJ	Defining response to TNF-inhibitors in rheumatoid arthritis: the negative impact of anti-TNF cycling and the need for a personalized medicine approach to identify primary non-responders	Johnson KJ, Sanchez HN, Schoenbrunner N. Defining response to TNF-inhibitors in rheumatoid arthritis: the negative impact of anti-TNF cycling and the need for a personalized medicine approach to identify primary non-responders. *Clin Rheumatol.* 2019 Nov;38(11):2967-2976. doi: 10.1007/s10067-019-04684-1.	Link
Apr-2019	Cheng F	Network-based prediction of drug combinations	Cheng F, Kovács IA, Barabási AL. Network-based prediction of drug combinations. *Nat Commun*. 2019 Mar 13;10(1):1197. doi: 10.1038/s41467-019-09186-x. Erratum in: Nat Commun. 2019 Apr 15;10(1):1806.	Link

Oct-2018	Johnson K	PRISM-RA: A personalized medicine test that accurately predicts rheumatoid arthritis patients who will not respond adequately to tumor necrosis factor inhibitors	Johnson K, Schoenbrunner N, Ghiassian D. PRISM-RA: A personalized medicine test that accurately predicts rheumatoid arthritis patients who will not respond adequately to tumor necrosis factor inhibitors [abstract]. *Arthritis Rheumatol*. 2018;70(suppl 10).	Link
Oct-2018	Johnson K	Precision medicine in complex disease: use of the PrismRA test to stratify patients for response to anti-TNF therapy in rheumatoid arthritis	Johnson K, Weinblatt M. Precision medicine in complex disease: use of the PrismRA test to stratify patients for response to anti-TNF therapy in rheumatoid arthritis. *J Precis Med*. 2018 Oct: https://www.thejournalofprecisionmedicine.com/wp-content/uploads/Johnson-online.pdf.	Link
July-2018	Cheng F	Network-based approach to prediction and population-based validation of in silico drug repurposing	Cheng F, Desai RJ, Handy DE, et al. Network-based approach to prediction and population-based validation of in silico drug repurposing. *Nat Commun*. 2018 Jul 12;9(1):2691. doi: 10.1038/s41467-018-05116-5.	Link
Mar-2017	Menche J	Integrating personalized gene expression profiles into predictive disease-associated gene pools	Menche J, Guney E, Sharma A, et al. Integrating personalized gene expression profiles into predictive disease-associated gene pools. *NPJ Syst Biol Appl*. 2017 Mar 13;3:10. doi:10.1038/s41540-017-0009-0.	Link
Oct-2016	Kitsak M	Tissue specificity of human disease module	Kitsak M, Sharma A, Menche J, et al. Tissue Specificity of Human Disease Module. *Sci Rep*. 2016 Oct 17;6:35241. doi: 10.1038/srep35241.	Link
June-2016	Ghiassian SD	Endophenotype network models: common core of complex disease	Ghiassian SD, Menche J, Chasman DI, Giulianini F, Wang R, Ricchiuto P, Aikawa M, Iwata H, Müller C, Zeller T, Sharma A, Wild P, Lackner K, Singh S, Ridker PM, Blankenberg S, Barabási AL, Loscalzo J. Endophenotype Network Models: Common Core of Complex Diseases. *Sci Rep*. 2016 Jun 9;6:27414. doi:10.1038/srep27414.	Link
Feb-2016	Guney E	Network-based in silico drug efficacy screening	Guney E, Menche J, Vidal M, et al. Network-based in silico drug efficacy screening. Nat Commun. 2016 Feb 1;7:10331. doi: 10.1038/ncomms10331.	Link
Jun-2015	Sharma A	A disease module in the interactome explains disease heterogeneity, drug response and captures novel pathways and genes in asthma	Sharma A, Menche J, Huang CC, et al. A disease module in the interactome explains disease heterogeneity, drug response and captures novel pathways and genes in asthma. *Hum Mol Genet*. 2015 Jun 1;24(11):3005-20. doi: 10.1093/hmg/ddv001.	Link
Apr-2015	Ghiassian SD	A DIseAse Module Detection (DIAMOnD) algorithm derived from a systematic analysis of connectivity patterns of disease proteins in the human interactome	Ghiassian SD, Menche J, Barabási AL. A DIseAse MOdule Detection (DIAMOnD) algorithm derived from a systematic analysis of connectivity patterns of disease proteins in the human interactome. *PLoS Comput Biol*. 2015 Apr 8;11(4):e1004120. doi:10.1371/journal.pcbi.1004120.	Link
Feb-2015	Menche J	Disease networks. Uncovering disease-disease relationships through the incomplete interactome	Menche J, Sharma A, Kitsak M, et al. Disease networks. Uncovering disease-disease relationships through the incomplete interactome. *Science*. 2015 Feb 20;347(6224):1257601. doi:10.1126/science.1257601.	Link
Nov-2014	Rolland T	A proteome-scale map of the human interactome network	Rolland T, Taşan M, Charloteaux B, et al. A proteome-scale map of the human interactome network. *Cell*. 2014 Nov 20;159(5):1212-1226. doi:10.1016/j.cell.2014.10.050.	Link
Jan-2013	Silverman EK	Developing new drug treatments in the era of network medicine	Silverman EK, Loscalzo J. Developing new drug treatments in the era of network medicine. *Clin Pharmacol Ther*. 2013 Jan;93(1):26-8. doi:10.1038/clpt.2012.207.	Link

Last updated November 15th, 2022