Pharmacogenetic Panel Testing

Policy Number: 2024T0587T
Effective Date: January 1, 2025

⮌ Instructions for Use

Related Commercial/Individual Exchange Policy
• Cardiovascular Disease Risk Tests
Community Plan Policy
• Pharmacogenetic Panel Testing
Medicare Advantage Policy
• Molecular Pathology/Molecular Diagnostics/ Genetic Testing

Application

UnitedHealthcare Commercial

This Medical Policy applies to UnitedHealthcare Commercial benefit plans.

UnitedHealthcare Individual Exchange

This Medical Policy applies to Individual Exchange benefit plans in all states except for Colorado.

Coverage Rationale

The use of pharmacogenetic Multi-Gene Panels (five or more genes) for the evaluation of drug-metabolizer status is unproven and not medically necessary for any indication due to insufficient evidence of efficacy.

The use of the PrismRA® molecular signature test is unproven and not medically necessary for evaluating likelihood of inadequate response to anti-TNF therapies for rheumatoid arthritis due to insufficient evidence of efficacy.

Definitions

Multi-Gene Panel: Genetic tests that use next-generation sequencing to test multiple genes simultaneously. Also called multigene test, multiple-gene panel test and multiple-gene test (National Cancer Institute Dictionary of Genetics Terms, 2024).

Applicable Codes

The following list(s) of procedure and/or diagnosis codes is provided for reference purposes only and may not be all inclusive. Listing of a code in this policy does not imply that the service described by the code is a covered or non-covered health service. Benefit coverage for health services is determined by the member specific benefit plan document and applicable laws that may require coverage for a specific service. The inclusion of a code does not imply any right to reimbursement or guarantee claim payment. Other Policies and Guidelines may apply.

CPT Code	Description
0029U	Drug metabolism (adverse drug reactions and drug response), targeted sequence analysis (i.e., CYP1A2, CYP2C19, CYP2C9, CYP2D6, CYP3A4, CYP3A5, CYP4F2, SLCO1B1, VKORC1 and rs12777823)
0173U	Psychiatry (i.e., depression, anxiety), genomic analysis panel, includes variant analysis of 14 genes
0175U	Psychiatry (e.g., depression, anxiety), genomic analysis panel, variant analysis of 15 genes
0345U	Psychiatry (e.g., depression, anxiety, attention deficit hyperactivity disorder [ADHD]), genomic analysis panel, variant analysis of 15 genes, including deletion/duplication analysis of CYP2D6
0347U	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 16 gene report, with variant analysis and reported phenotypes
0423U	Psychiatry (e.g., depression, anxiety), genomic analysis panel, including variant analysis of 26 genes, buccal swab, report including metabolizer status and risk of drug toxicity by condition
0434U	Drug metabolism (adverse drug reactions and drug response), genomic analysis panel, variant analysis of 25 genes with reported phenotypes
0438U	Drug metabolism (adverse drug reactions and drug response), buccal specimen, gene-drug interactions, variant analysis of 33 genes, including deletion/duplication analysis of CYP2D6, including reported phenotypes and impacted gene-drug interactions
0348U	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 25 gene report, with variant analysis and reported phenotypes
0349U	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 27 gene report, with variant analysis, including reported phenotypes and impacted gene-drug interactions
0350U	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 27 gene report, with variant analysis and reported phenotypes
0380U	Drug metabolism (adverse drug reactions and drug response), targeted sequence analysis, 20 gene variants and CYP2D6 deletion or duplication analysis with reported genotype and phenotype
0392U	Drug metabolism (depression, anxiety, attention deficit hyperactivity disorder [ADHD]), gene-drug interactions, variant analysis of 16 genes, including deletion/duplication analysis of CYP2D6, reported as impact of gene-drug interaction for each drug
0411U	Psychiatry (e.g., depression, anxiety, attention deficit hyperactivity disorder [ADHD]), genomic analysis panel, variant analysis of 15 genes, including deletion/duplication analysis of CYP2D6
0419U	Neuropsychiatry (e.g., depression, anxiety), genomic sequence analysis panel, variant analysis of 13 genes, saliva or buccal swab, report of each gene phenotype
0456U	Autoimmune (rheumatoid arthritis), next-generation sequencing (NGS), gene expression testing of 19 genes, whole blood, with analysis of anti-cyclic citrullinated peptides (CCP) levels, combined with sex, patient global assessment, and body mass index (BMI), algorithm reported as a score that predicts nonresponse to tumor necrosis factor inhibitor (TNFi) therapy
0460U	Oncology, whole blood or buccal, DNA single-nucleotide polymorphism (SNP) genotyping by real-time PCR of 24 genes, with variant analysis and reported phenotypes
0461U	Oncology, pharmacogenomic analysis of single-nucleotide polymorphism (SNP) genotyping by real-time PCR of 24 genes, whole blood or buccal swab, with variant analysis, including impacted gene-drug interactions and reported phenotypes
0476U	Drug metabolism, psychiatry (e.g., major depressive disorder, general anxiety disorder, attention deficit hyperactivity disorder [ADHD], schizophrenia), whole blood, buccal swab, and pharmacogenomic genotyping of 14 genes and CYP2D6 copy number variant analysis and reported phenotypes
0477U	Drug metabolism, psychiatry (e.g., major depressive disorder, general anxiety disorder, attention deficit hyperactivity disorder [ADHD], schizophrenia), whole blood, buccal swab, and pharmacogenomic genotyping of 14 genes and CYP2D6 copy number variant analysis, including impacted gene-drug interactions and reported phenotypes
0516U	Drug metabolism, whole blood, pharmacogenomic genotyping of 40 genes and CYP2D6 copy number variant analysis, reported as metabolizer status

CPT Code	Description
81418	Drug metabolism (e.g., pharmacogenomics) genomic sequence analysis panel, must include testing of at least 6 genes, including CYP2C19, CYP2D6, and CYP2D6 duplication/deletion analysis
81479	Unlisted molecular pathology procedure

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Description of Services

Pharmacogenetics (also called pharmacogenomics) studies how variation in genes impacts the way an individual may respond to certain medications. Differences in genes can account for the reasons why some individuals benefit from a specific medication while others may not. These differences can also influence the side effects some individuals suffer from a medication, while other individuals have none (MedlinePlus, 2023).

A pharmacogenetic test is meant to guide treatment strategies, clinical evaluations, and decisions based on its ability to predict response to treatment in particular clinical contexts. When testing is targeted to evaluate an individual's response to a specific drug, typically only one gene is analyzed. For warfarin, also known as Coumadin, two to three genes are tested. However, laboratories have developed Multi-Gene Panels including five or more genes in order to proactively evaluate an individual's possible response to many drugs. This policy is designed to address Multi-Gene Panel testing.

Clinical Evidence

Psychiatric Indications

Up to 42% of variance in therapy response for major depressive disorders (MDD) may be explained by genetic variation (Tansey et al., 2013), which has led to the development of pharmacogenetic (PGx) tests to inform the use of certain psychiatric medications. Currently, multiple combinatorial PGx tests (panels) are commercially available; however, the existing published evidence does not support the use of combinatorial PGx tools for psychiatric indications. Additional high quality studies utilizing fully blinded designs along with focus on the design of effective, evidence-based tools that assess both likelihood for adverse drug effects as well as efficacy are required.

In 2024, Baum et al. published an update to the 2018 report of the American Psychiatric Association (APA) Council of Research Workgroup on Biomarkers and Novel Treatments on the use of PGx tests in treatment selection for individuals with depression. The workgroup reviewed evidence newly published since the prior report (eleven clinical trials and five meta-analyses), all of which had primary outcomes focused on speed and/or efficacy of response to therapy. Only three trials (using three distinct PGx tests) demonstrated efficacy with statistical significance on the primary outcome measure; two of the studies showing efficacy were small, single-blind trials and one was open-label. Only one of the trials reviewed addressed adverse effects as a primary outcome. All studies examined had significant limitations, such as lack of full blinding. The workgroup concluded that recent published data does not support the use of currently marketed multigene panels for guiding selection of therapies for MDD. They recommend further investigation using fully blinded studies and including the evaluation of promising variants that are not included in currently marketed pharmacogenomic tests. Studies focused on additional purposes of pharmacogenomic testing, such as evaluation of likelihood of adverse drug effects, are also advised.

Saadullah Khani et al. (2024) published a systematic review assessing the influence of PGx testing on individuals undergoing antipsychotic treatment. A total of 13 studies were included in the analysis. The authors determined that while the existing evidence shows either no difference or positive clinical outcomes with PGx-guided prescribing, the studies identified had methodological limitations. Several of the studies were not blinded or randomized and all studies had fewer than 300 participants. The reviewers indicate that confounding factors such as selection bias were underestimated as well. With these limitations, the researchers recommend interpreting the results with caution. High quality studies are needed to evaluate the specific benefits of PGx testing for mental health conditions.

Findings specific to psychiatric-related PGx testing from the PREemptive Pharmacogenomic testing for preventing Adverse drug REactions (PREPARE) study were reported by Skokou et al. (2024). PREPARE was a multicenter, open-label, prospective study of the clinical utility of PGx-guided treatment which employed a 12-gene PGx panel and investigated the occurrence of adverse drug reactions (ADRs). In this publication, outcomes focused specifically on 1076 individuals affected with schizophrenia, MDD, or bipolar disorder are described. The primary goal of this investigation was to evaluate the impact of PGx-guided therapy on incidence of adverse drug reactions in individuals affected with the above noted psychiatric indications. Although each sample was genotyped for 12 genes, only *CYP2C19* and/or *CYP2D6* were considered as part of this analysis, as these are the two pharmacogenes related to metabolism of psychiatric

medications. The researchers found that individuals with an actionable phenotype in the PGx-guided arm of the study (n = 25) showed 34.1% fewer adverse drug reactions when compared to those in the control arm (n = 36). In addition, there were 41.2% fewer hospitalizations and less polypharmacy in the PGx-guided arm (n = 124 individuals prescribed at least 4 psychiatric drugs in the PGx-guided arm versus n = 143 in the control arm). Nine deaths were reported in the control arm compared to only one death in the PGx-guided arm. The authors determined that PGx-guided therapy may have a helpful impact on individuals with psychiatric diagnoses. However, the proportion of individuals with an actionable genotype in this study was small (~25%), which impacted statistical significance. This study focused only on occurrence of adverse drug reactions; drug efficacy was not evaluated. As such, additional study focused on drug efficacy as well as occurrence of adverse drug reactions is recommended. In addition, the study focused only on the impact of *CYP2C19* and *CYP2D6* and did not incorporate findings from other pharmacogenes that may be included in larger PGx panels.

A 2023 meta-analysis and rapid review (Bunka et al.) focused on appraising the impact of PGx testing on clinical outcomes compared to treatment as usual for individuals with MDD. The analysis incorporated results from ten randomized controlled trials (RCTs). All PGx decision-support tools used for depression included *CYP2C19* and *CYP2D6* pharmacogenes, but no specific test or panel was evaluated by this review; rather, the review focused on PGx testing in general. Based on this analysis, the authors determined that PGx-guided care for MDD more often resulted in remission and response than treatment as usual. Despite this finding, there are notable limitations, including high risk of bias and inconsistencies between the various trials; additional high-quality research is needed. Further studies should incorporate diverse populations and address the lack of evidence focused on adverse effects as well as the measurement of long-term efficacy, including rates of recurrence. Studies by Greden et al. (2019), Menchón et al. (2019), Bradley et al. (2018) and Pérez et al. (2017), discussed below, were included in this analysis.

In a 2023 systematic review and meta-analysis of RCTs, Wang et al. investigated the impact of using PGx testing to guide treatment on clinical outcomes of individuals with MDD. A total of eleven studies including 5347 participants were included in the evaluation. Various marketed tests with differing numbers of genes were used in the studies. The authors note that most of the studies were considered to have a high risk of bias as they were funded by the industry. The group of individuals whose treatment was guided by pharmacogenomic testing was associated with increased response rate at week eight (OR 1.32, 95%CI 1.15–1.53, eight studies, 4328 participants) and week 12 (OR 1.36, 95%CI 1.15–1.62, four studies, 2814 participants) when compared with the usual treatment group. In addition, the group with pharmacogenomically guided treatment had an association with increased remission rates at week eight (OR 1.58, 95%CI 1.31–1.92, eight studies, 3971 participants) and week 12 (OR 2.23, 95%CI 1.23–4.04, five studies, 2664 participants). However, no significant differences in either response rate or remission rate were found between the two groups at week four or week 24. The meta-analysis also found that medication congruence in 30 days showed a significant reduction in the pharmacogenomic testing group versus the usual care group (OR 2.07, 95%CI 1.69–2.54, three studies, 2862 participants). Subgroup analysis revealed a significant difference between the Asian subgroup and the Caucasian subgroup, possibly due to the sub-genotype of allele frequencies of gene variants. The authors concluded that in all, the results of this analysis indicate that pharmacogenomically guided treatment led to faster clinical remission or response in individuals with MDD but resulted in no difference in final response or remission at the end of the pharmacogenomically guided treatment. These results differ from those of previous meta-analyses, which showed overall higher response/remission rates in individuals with MDD who underwent pharmacogenomically guided treatment compared to those who underwent usual treatment. The researchers speculate that the lack of significant changes at week four may be due to the long onset time of anti-depressants and the lack of significant changes at week 24 may be due to the pharmacogenomic testing showing an accelerated process of excluding unsuitable anti-depressants for individuals with MDD. Ongoing, high-quality studies are recommended to continue assessment of the benefits of pharmacogenomic testing, especially across differing populations and ethnic groups. Publications by Oslin et al. (2022), Tiwari et al. (2022), Greden et al. (2019), and Bradley et al. (2018), discussed below, and Perlis et al. (2018), previously discussed in this policy, were included this systematic review.

Noting the limited evidence supporting the clinical benefit of pharmacogenomics-informed treatment (PIT) with antidepressants, (specifically tricyclic antidepressants [TCA]), Vos et al. (2023) conducted an RCT designed to ascertain whether PIT leads to faster therapeutic TCA plasma concentrations, when compared with usual treatment, for individuals with MDD. Because treatment with TCAs is often associated with adverse effects, identification of optimal dosing can be time consuming, and therapeutic plasma concentrations are well defined, PIT is of special interest in this class of medication. The study took place in the Netherlands and enrolled 111 individuals with unipolar, nonpsychotic MDD. Participant age ranged from 18 to 65 years and all were eligible for treatment with TCA. Medications use to treat included nortriptyline, clomipramine, or imipramine. In the group receiving PIT (n = 56), initial dose of TCA was based on *CYP2D6* and *CYP2C19* genotypes. The control group (n = 55) was provided with usual treatment including standard initial TCA dosages. Days to attainment of therapeutic TCA plasma concentration was the primary outcome with secondary outcomes that included the severity of depressive symptoms (as measured by the 17-item Hamilton Rating Scale for Depression [HAMD-17]) and the frequency and severity of adverse side effects. In the group receiving PIT, therapeutic

concentrations were reached more quickly than in the control group (mean [SD], 17.3 [11.2] vs 22.0 [10.2] days; Kaplan-Meier $\chi 21$ = 4.30; p = .04), but no significant difference in the reduction of depressive symptoms was captured. The interaction between group and time differed for frequency, severity, and burden of adverse effects via linear mixed-model analysis, which may suggest that adverse effects had a relative decrease for individuals receiving PIT. Overall the researchers assert that the results of this trial show pharmacogenomics-informed dosing of TCAs is safe and may be helpful in personalizing treatment for individuals with MDD.

Brown et al. (2022) performed a systematic review and meta-analysis on 13 clinical trials comprised of 4767 total individuals with MDD. Prescribing recommendations for participants who were in the PGx-guided treatment group were based on their *CYP2C19* and *CYP2D6* genotypes, while treatment recommendations for those in the treatment as usual group were based on current Australian guidelines for the prescribing of antidepressant medications. Study findings revealed that the application of PGx test results for treatment guidance in individuals with MDD resulted in a modest but significant increase in the remission of depressive symptoms. Across all trials, individuals receiving PGx-guided treatment for MDD were 41% (95% CI = 15–74%) more likely to reach remission than those whose treatment was not guided by PGx. The authors point out, however, that the trials included in this systematic review and meta-analysis used tests that assessed for variants in genes beyond *CYP2C19* and *CYP2D6* (e.g. *SLC6A4, HTR2A*), since this additional testing is often included in panels marketed by various commercial laboratories even though there are no dosing guidelines for these genes. In addition, many of the test panels used in these trials included proprietary algorithms that could result in conflicting recommendations, highlighting the need for standardization and regulation of PGx testing in the context of MDD treatment. Publications by Oslin et al. (2022) Tiwari et al. (2022), Bradley et al. (2018) Greden et al. (2019), discussed below, and Perlis et al. (2020), previously discussed in this policy, were included in this systematic review and meta-analysis.

In an RCT including 1944 individuals with MDD, Oslin et al. (2022) assessed the impact of pharmacogenomic testing for drug-gene interactions on the selection of anti-depressant medications and response of depression symptoms, compared to usual care. Eligible participants had MDD and were starting therapy or switching therapy including a single antidepressant. Individuals with active substance disorders, mania, psychosis, or concurrent treatment with other specified medications were excluded. In the pharmacogenomic-guided group (n = 966), results from a commercial pharmacogenomic test (GeneSight, Myriad Genetics) were provided to clinicians overseeing the care for that group. The comparison group (n = 978) received usual care (access to pharmacogenomic results were provided after 24 weeks). Outcomes included the proportion of prescriptions with predicted drug-gene interactions written within 30 days of randomization and remission of the symptoms of depression as assessed by the Patient Health Questionnaire-9 (PHQ-9). Assessment of outcomes was performed at week 4, 8, 12, 18, and 24 by raters who were blinded to clinical care and study randomization. Of the 1944 participants randomized, 79% completed the full 24-week evaluation. Estimated risk of receiving an antidepressant with none, moderate, or substantial drug-gene interactions for the group whose care was guided by PGx testing results were 59.3%, 30.0%, and 10.7%, respectively. In the usual care group, risk was determined to be 25.7%, 54.6%, and 19.7%. Prescriptions with no predicted drug-gene interaction were provided for 45% of individuals in the pharmacogenomically guided group compared with 18% of individuals in the usual care group; a statistically significant difference. Overall, rates of remission over the course of 24 weeks were higher in individuals whose care was directed with pharmacogenomic testing than those receiving usual care (OR, 1.28 [95% CI, 1.05 to 1.57]; p = .02; risk difference, 2.8% [95% CI, 0.6% to 5.1%]). However, remission rates were not significantly higher in the pharmacogenomically guided group at 24 weeks. The authors concluded that for individuals with MDD, offering pharmacogenomic testing for drug-gene interactions decreased prescriptions of medications with predicted drug-gene interactions when compared to usual care. Use of test results had small positive impacts on symptom remission (especially early in the trial) that did not persist at 24 weeks.

In a Canadian participant- and rater-blinded RCT, Tiwari et al. (2022) evaluated clinical outcomes for individuals with a diagnosis of depression whose treatment was guided by combinatorial pharmacogenomic testing (GeneSight[®] Psychotropic or Enhanced GeneSight[®] Psychotropic) as compared to treatment as usual. The GAPP-MDD RCT was a three-arm, 52-week, multi-center trial primarily evaluating symptom improvement using the HAMD-17 at week eight, as well as secondary outcomes including response (≥ 50% decrease in HAMD-17) and remission (HAMD-17 ≤7) at week eight. The participants were randomized 1:1:1 to one of three treatment arms, including two intervention arms and a treatment as usual arm. For the first intervention arm (n = 147), the providers received the standard combinatorial pharmacogenomic test report to guide treatment (GEN arm). The second intervention arm included participants (n = 152) for whom the providers received an enhanced test report to guide treatment (EGEN – 6 additional genes) and the final arm was treatment as usual (n = 138). The researchers found that individuals in the pharmacogenomically guided groups had greater symptom improvement (27.6% versus 22.7%), response (30.3% versus 22.7%) and remission rates (15.7% versus 8.3%) compared to treatment as usual, but the differences found were not statistically significant. Since they felt that this trial was underpowered to detect statistically meaningful differences in outcomes, the authors did a parallel assessment with the U.S. "GUIDED" trial results (discussed in Greden et al., 2019, below). They found consistent results

related to relative improvements in response and remission rates between GAPP-MDD (33.0% response, 89% remission) and GUIDED (31.0% response, 51.0% remission) and concluded that in the context of the Canadian universal healthcare setting, GAPP-MDD and GUIDED RCTs support the use of combinatorial pharmacogenomic testing as an effective tool to help guide treatment of depression. Noted limitations included lack of diversity in the cohort, no assessment of adherence to treatment, lack of assessment of the impact of polypharmacy on outcomes, and lack of blinding of clinicians evaluating participants.

For use of PGx testing to assist with medication or dose selection for individuals diagnosed with ADHD, a Hayes Clinical Utility Evaluation (2022a, updated 2024) found insufficient evidence to support clinical utility/improved clinical outcomes. The authors suggest that future studies to evaluate PGx testing assessing effects on ADHD symptoms, medication side effects and other clinical outcomes are needed.

An Ontario Health Technology Assessment (2021), which included a systematic review of the literature, evaluated the safety, effectiveness, and cost-effectiveness of multi-gene pharmacogenomic tests designed with decision-support tools to aid in treatment of individuals with MDD. Fourteen studies, including evaluation of six multi-gene pharmacogenomic tests (GeneSight, NeuroIDgenetix, CNSdose, Neuropharmagen, Genecept and one unspecified test), were reviewed. Heterogeneity of available multi-gene pharmacogenomic tests as well as study design, populations included and outcomes reported were noted. Effectiveness of the six tests evaluated was inconsistent; clinical utility of one test may not apply to the others. Little to no differences were found in score changes on the HAMD-17 in individuals who underwent pharmacogenomic testing compared to those who were treated with usual care; however some of the tests showed promising results in terms of response to treatment or remission from their symptoms.

A systematic review to summarize and assess the state of evidence regarding the use of PGx testing in individuals with depression was performed by Aboelbaha et al. in 2021. The researchers queried scientific databases from inception through June 30, 2020, for RCTs and systematic reviews which assessed clinical utility of PGx testing for treatment of depression. A total of six systematic reviews and three RCTs ultimately met criteria for inclusion in this study. The results provided evidence on efficacy of PGx testing, with newer RCTs of better quality showing clinical promise regarding efficacy outcomes, especially in participants with gene-drug interactions. The researchers state that PGx testing before initiation of treatment or during therapy may improve efficacy outcome and recommend further studies to assess impact of PGx testing on safety outcomes. Publications by Brown et al. (2020), Bousman et al. (2019), and Rosenblat et al. (2018), previously discussed in this policy, were included in the Aboelbaha systematic review.

A Hayes Clinical Utility Evaluation (2021a, updated 2023) addressed the use of PGx testing to inform selection or dosing of medication for individuals with selected mental health conditions including anxiety disorder, bipolar disorder, depression, schizophrenia spectrum or other psychotic disorder. Hayes concluded that there was lack of consistency in study results and the role of PGx-guided prescribing to improve outcomes in the select mental health disorders detailed above remains uncertain.

In a 2021b (updated 2023) Molecular Test Assessment, Hayes evaluated the GeneSight Psychotropic test. GeneSight is a pharmacogenomic gene panel test that assesses the interaction between genes and certain drugs for the purpose of aiding health care providers in decision-making for treatment of individuals with mental health conditions. Hayes found no peer-reviewed studies addressing analytical or clinical validity but did reference four studies (none of which included the current, 15-gene configuration of the test) reporting on the GUIDED trial. Overall, Hayes found insufficient evidence supporting the use of GeneSight for mental health disorders at this time. Since the original 2021 publication, additional studies addressing the clinical utility of GeneSight have been published, however, the 2023 annual review of the Hayes assessment indicates the newly published studies are unlikely to change the current rating of D2.

Aranz et al. (2019) analyzed the benefits of PGx testing of *CYP* variants for the purpose of adjusting clinical doses of frequently used antipsychotics. Results for individuals using PGx information (PI) were compared with individuals who were treated as usual. Two hundred and ninety participants from three hospitals in Spain with schizophrenia/ schizoaffective/delusional disorders requiring medication were randomized for PI (PharmG+ arm) or treatment as usual (PharmG-arm). Recruitment began when initial treatment was started or when a change in antipsychotic treatment was deemed necessary. One hundred twenty-three participants were genotyped using the commercial Brainchip PGx test; 167 were treated as usual by adhering to standard clinical practices. Positive and negative scale for schizophrenia (PANSS) and UKU-side effect rating scores were gathered at the beginning and again at 12 weeks to assess effectiveness of treatment. PANSS/UKU values were rated by clinical psychiatrists who were also blinded to the participant's arm. No statistically significant differences were observed in side effects between the two groups. When participants had their dose adjusted based on PharmG+ data (n = 123), there was a larger reduction in side effects than those in the PharmG-group, but this was not statistically significant ($p > 0.05$). PharmG+ patients who were carriers of *CYP2D6* UM (ultra-metabolizer) or PM (poor metabolizer) variants showed statistically larger improvements in global, psychic, and other UKU

side effects as compared to PharmG- (p = 0.02, p = 0.05 and p = 0.01, respectively). The authors concluded that PGx interventions may enhance safety by decreasing the side effects of antipsychotic treatments, however the study did not find evidence of greater efficacy. The researchers also concluded that the results were not unexpected as treatment success may be influenced by more than genomic profiles and describe the effect of drug metabolism as a key factor.

Menchón et al. (2019) examined the influence of individual characteristics such as age, baseline severity, and duration of episode on the clinical utility of PGx testing for psychiatric drugs from the AB-GEN study, a randomized 12-week study comparing treatment as usual (TAU) to PGx guided therapy selection in 280 adults with MDD. The primary outcomes analyzed were the Patient Global Impression of Improvement (PGI-I) scale and the HAMD-17. Participants generally showed no difference in sustained response at the 12-week endpoint between the TAU and PGx group (Pérez et al., 2017). However, the PGx group had a higher response rate than TAU, and when subjects whose physicians did not follow the genetic testing recommendations were removed, the response rate improved further. Side effects were less in the PGx group by 6 weeks; this was maintained at week 12. The primary dependent variable identified was the number of previously failed medication trials. In the Menchón et al. reanalysis by patient demographics, additional important variables were identified. Age was important as PGx testing significantly improved outcomes in those under age 60, but not over age 60. Outcomes were also improved in those with moderate to severe depression, but not in those with mild depression. Genetic testing improved PGI-I in one year or less from diagnosis, but not HAMD-17. The effect on HAMD-17 was not significant until the cutoff from time of diagnosis was increased to 5 years. After this, however, a null effect was seen, and individuals who were more than 5 years from their diagnosis were actually worse off in the PGx arm than TAU. To determine which type of patient is most likely to benefit from PGx testing for psychiatric therapies, more prospective, randomized trials are needed.

GUIDED was a 24-week RCT conducted between April 2014 and February 2017 that compared active treatment groups guided by PGx information to active treatment groups receiving TAU for MDD (Greden et al., 2019, included in the Hayes 2021 GeneSight Psychotropic Molecular Test Assessment). Sixty sites participated; individuals were referred to the study when they or their clinician reported inadequate response to at least one antidepressant. The average number of medications failed in the cohort was three, making this a difficult-to-treat population. Genotyping was performed for eight genes: *CYP1A2, CYP2C9, CYP2C19, CYP3A4, CYP2B6, CYP2D6, HTR2A*, and *SLC6A4*. Results were evaluated and reported using a proprietary PGx algorithm from Assurex Health. Participants were blinded to the study arm, but clinicians were not, since they needed to consult the PGx results to guide treatment. Using the results to guide treatment was not mandated. Patients were assessed at 4, 8, 12, and 24 weeks using the HAMD-17, which was administered by blinded raters. A total of 1167 enrolled patients made it through week 8 with 607 in TAU and 560 in PGx guided. HAMD-17 scores decreased in the TAU arm by 24% and in the PGx arm by 27%, but the difference was not statistically significant. Treatment response, defined as ≥ 50% decrease in depression, was greater in the PGx arm (26%) than TAU (20%). The depression remission rate, defined as score of ≤ 7 for HAMD-17, was 10% with TAU and 15% with PGx (p = .007). Additionally, at week 8, there was no difference between the groups in reported side effects. When patients taking incongruent medications were evaluated as a separate cohort, those who switched to congruent medications by week 8 experienced significantly fewer side effects. Medication prescriptions that aligned with PGx results at baseline were 77% in the TAU group and 79% in the PGx group. By week 8, the PGx group rate increased to 91%, and the TAU group was unchanged. After completing 8 weeks, clinicians in the TAU arm were unblinded and could use the PGx results if they chose. A total of 913 participants completed week 24 with 456 in TAU and 457 in the PGx guided arm. Overall, in the PGx group, HAMD-17 scores decreased by 42.5% at week 24 relative to baseline. Response and remission increased by 70% and 100%, respectively, from week 8 to week 24. While the primary outcome being analyzed, symptom improvement at week 8, was not different between the two groups, there was significant difference in response and remission in the PGx group on other measures.

A panel of ten genes with select polymorphisms combined with a proprietary algorithm, the NeuroIDgenetix® Test, was the subject of an RCT to evaluate clinical utility for guiding treatment for depression and anxiety (Bradley et al., 2018). Genes in the test included *CYP1A2, CYP2C9, CYP2C19, CYP2D6, CYP3A4, CYP3A5, SLC6A4, COMT, HTR2A*, and *MTHFR*. Participants were identified from 20 independent clinical sites in the U.S. that represented psychiatry, internal medicine, family medicine, and obstetrics and gynecology. A total of 685 participants were included in the study, ranging in age from 19 to 87, and all had a diagnosis of depression or anxiety using the Diagnostic and Statistical Manual of Mental Disorders, Fifth Edition (DSM-V) criteria and verified by the Mini-International Neuropsychiatric Interview (M.I.N.I.) Most were female (73%) with diagnoses of depression (n = 246), anxiety (n = 235) or both (n = 204). Participants were either 'New to Treatment' (newly diagnosed or taking medications for less than 6 weeks) or 'Inadequately Controlled' with medications as defined by lack of efficacy or treatment discontinuation due to adverse events or intolerability, although the authors did not report the distribution. PGx testing was performed in all subjects but was only shared with the physicians of those in the PGx arm. Patients were assessed at 4, 8 and 12 weeks using the HAMD-17 and the Hamilton Rating Scale for Anxiety (HAM-A), with their physicians blinded to the results. Adverse events were captured via the Adverse Drug Event form developed by external psychiatric consultants, and a blinded clinician ranked the adverse events on a severity scale.

The PGx testing group showed a greater response and remission rate (odds ratios of 4.72 and 3.54 respectively) than the TAU group at 12 weeks. In the anxiety group, those that received testing had a higher response rate at 8 and 12 weeks with an odds ratio of 1.76, compared to the TAU group. At the two-week follow-up, physicians made at least one medication change in 81% of those receiving testing compared with 64% in the control group. No difference was found in adverse drug events between the two treatment groups. In a post-hoc analysis on the 'Inadequately Controlled' cohort, improvement in remission (42% vs. 27%, p = 0.03) and response rates (62% vs. 44%, p = 0.01) were greater with PGx than TAU.

Jung et al. (2017) conducted a genome-wide association study (GWAS) in Generalized Anxiety Disorder (GAD) to identify potential predictors of venlafaxine XR treatment outcome. Ninety-eight European American patients participated in a venlafaxine XR clinical trial for GAD, with HAM-A response/remission at 24 weeks as the primary outcome measure. All participants were genotyped with the Illumina PsychChip, and 266,820 common single nucleotide polymorphisms (SNPs) were analyzed. Although no SNPs reached genome-wide significance, eight SNPs were marginally associated with treatment response/remission and HAM-A reduction at week 12 and 24 (p < 0.00001). The authors concluded that several identified genes may indicate markers crossing neuropsychiatric diagnostic categories. The authors acknowledged that the limitations of this study include small sample size and the lack of statistical power for a GWAS. Areas for future research include the replication of results with larger samples sizes to increase statistical power and further elucidate the treatment effects of antidepressant venlafaxine XR on GAD.

Pérez et al. (2017) enrolled 528 participants (outpatients and inpatients) from 18 hospitals and associated mental health centers in Spain from July 2014 to June 2015 in the AB-GEN study, a 12-week, double-blind, parallel, multi-center RCT to evaluate the effectiveness of PGx testing for drug therapy guidance for MDD. Individuals with a clinical global impression-severity (CGI-S) ≥ 4 and requiring antidepressant medication de novo or changes in their medication were randomized to a PGx or TAU group. PGx testing was conducted, a Neuropharmagen pharmacogenetic report was generated, and results were reported using their web-based clinical decision support tool. Thirty genes and relevant SNPs were analyzed. The primary endpoint was measuring a sustained response on the Patient Global Impression of Improvement (PGI-I) of ≤ 2 within the 12-week follow-up. Follow up was conducted by phone, and the interviewer was blinded to the participant's study arm. A participant was considered to have a sustained response with a PGI-I score of 2 or less if they reported their condition to be "much better" or "very much better." Only 280 of 528 patients completed the study. A difference in sustained response was not observed between PGx and TAU at 12 weeks (38.5% vs 34.4%, p = 0.4735; OR = 1.19 [95%CI 0.74-1.92]). However, the PGx group had a higher responder rate compared to TAU (47.8% vs 36.1%, p = 0.0476; OR = 1.62 [95%CI 1.00-2.61]), and this improved when removing the patients whose physicians did not follow the PGx recommendations (51.3% vs 36.1%, p = 0.0135; OR = 1.86 [95%CI 1.13-3.05]). Effects were greatest in individuals who had failed up to three prior medications. Of those who reported side effects at baseline, the PGx group was more likely to report fewer side effects than the TAU group. This study used real world practices and clinicians, a heterogeneous population with variable disease states and prior treatment failures, and clinicians could choose to not follow the PGx recommendations. Additional studies are needed to replicate these findings across larger, ethnically diverse study groups.

Cardiovascular Disease

The evidence regarding use of multigene PGx testing for cardiac disease is limited at this time. High-quality studies demonstrating improved outcomes related to use of PGx testing in individuals with cardiac conditions and/or undergoing cardiac interventions are required.

Ratner et al. (2022) explored the impact of multigene PGx testing on individuals undergoing percutaneous coronary intervention (PCI) and bone marrow transplant. Frequency of prescription for 65 medications with actionable PGx recommendations were obtained for all participants and a simulation was used to then project the number of opportunities for PGx-guided prescribing. In the PCI group (215 individuals), 66.5% of participants were prescribed at least one medication that had actionable PGx prescribing recommendations available. Using the simulations, if multigene PGx were available, 26.5 prescribing opportunities per 100 individuals undergoing PCI were projected. The authors indicated their belief that multigene PGx testing may offer potential to improve medication prescribing in individuals undergoing PCI. However, additional high quality studies are needed to further investigate the role of PGx testing for individuals undergoing PCI.

Rouby et. al (2020) enrolled two hundred and eleven individuals from the University of Florida (UF) who underwent PCI in a study to analyze the benefits of genotype-guided prescribing of PGx drugs and examine the clinical utility of multigene panel testing. Genotype data for five genes (*CYP2C19, CYP2D6, CYP2C9, VKORC1, SLCO1B1*) was compiled from this cohort. Seventy-seven percent of participants exhibited at least one actionable phenotype for these five genes; 32% had opportunities for genotype-guided prescribing of medications. The data was then used as parameter estimates in a simulation model to predict genotype-guided opportunities among privately insured beneficiaries in the MarketScan

database who had undergone PCI with at least one and five years of follow-up data (n = 105,547 and n = 12,462, respectively). Fifty percent of the individuals who had undergone PCI with over one year and 68% with over five years of follow-up were taking at least one CPIC A/B drug in addition to prescribed antiplatelet therapy. A 39% and 52% incidence of genotype-guided prescribing opportunity at one and five years, respectively, was projected. The authors hypothesized that panel-based testing at the time of PCI could result in genotype-driven prescribing decisions in 1/3 of patients, thereby improving therapy outcomes beyond that of *CYP2C19* alone for antiplatelet therapy.

The real-world clinical utility of PGx testing for managing cardiovascular disease was studied by Billings et al. (2018). A retrospective cohort of individuals was identified through pharmaceutical, medical, and laboratory claims data from a national health insurer from January 2011 through September 2015. Baseline data and outcomes were measured over a 12-month period. Individuals who received PGx testing that included *CYP2C19, CYP2C9, VKORC1, F5, F2*, and *MTHFR* were matched to controls based on demographics and diagnoses. PGx testing was ordered at the physician's discretion and was not influenced by the study. The total number of individuals tested was 11,060 and a total of 178,096 matched controls were identified. Outcomes evaluated through claims data included pharmacy costs, medical costs, emergency room visits, outpatient visits, emergency room stays, controlling for demographics, coverage type, low income, cardiovascular disease, and other co-morbidities, such as diabetes. The PGx test group appeared significantly more likely to experience stroke, pulmonary embolism, deep vein thrombosis, or a composite event than the control group. Real world PGx testing did not appear to improve outcomes based on claims analysis.

Anthracyclines

The routine use of PGx panel testing in assessment of risk related to chemotherapy-induced cardiotoxicity (CIC) is not supported by the evidence at this time. Although the initial research shows promise for potential benefit, additional prospective studies with long-term follow-up are needed for validation of the role of PGx related to CIC.

To ascertain whether previously identified variants associated with anthracycline-induced cardiac dysfunction in children with cancer impacts adolescent and young adults (AYAs) with cancer in the same manner, 253 AYAs who had previously undergone treatment with anthracyclines were assessed for 45 gene variants in a study by Stafford et al. (2024). In these 253 AYA, four variants associated with cardiac dysfunction were detected: *SLC10A2*:rs7319981($p = 0.017$), *SLC22A17*:rs4982753($p = 0.019$), *HAS3*:rs2232228 ($p = 0.023$), and *RARG*:rs2229774 ($p = 0.050$). Interestingly, *HAS3*:rs2232228 and *SLC10A2*:rs7319981 impacted the AYA cancer survivor group in reverse of the manner that has been reported for childhood cancer survivors. Further evaluation of host genes was performed to assess for additional genetic variants associated with cardiotoxicity in AYA cancer survivors and then assessed in a panel of induced pluripotent stem cell-derived cardiomyocytes to evaluate for changes in levels of expression when doxorubicin was used for treatment. The reviewers observed significant upregulation of *HAS3* and *SLC22A17* expression ($p < 0.05$) and non-significant anthracycline-responsivity for *RARG*. Overall, they concluded that there appears to be a genetic influence on cardiac dysfunction in AYA with cancer, but this study suggests that the role of genetics may vary between children and AYAs who survive cancer. Further study is required to better understand the role of PGx in determining risk of anthracycline-induced cardiac dysfunction and the differences in associated variants based on age and other factors.

Yang et al. (2021) conducted a systematic review and meta-analysis to examine the correlation between genomic variants and CIC. The review and analysis included forty-one studies examining the relationship between genetic variants and CIC, including 88 unique genes and 154 SNPs. The results revealed that six variants had an association with increased risk of CIC, including *CYBA* rs4673, *RAC2* rs13058338, *CYP3A5* rs776746, *ABCC1* rs45511401, *ABCC2* rs8187710, and *HER2-Ile655Val* rs1136201. The authors felt that this study revealed promising potential benefits of pharmacogenomic testing prior to chemotherapy to minimize the risk of CIC, however further studies are required to validate the prognostic and diagnostic roles of the six identified variants in predicting CIC. Publication by Sági et al. (2018), discussed below, was included in this systematic review and meta-analysis.

Anthracyclines are an important category of chemotherapeutic agents for hematological and solid tumors but are associated with a high rate of anthracycline associated cardiotoxicity (ACT) that can result in symptoms during therapy or even years after therapy is completed. Sági et al. (2018) conducted genotyping of 26 genes and 70 SNPs associated with anthracycline metabolism and a retrospective review of medical records of 622 children with lymphoblastic leukemia (ALL) and 39 children with osteosarcoma (OSC) treated between 1989 and 2015 in Hungarian pediatric oncology centers. Those with comorbidities such as Down syndrome or prior cardiac findings were excluded. Blood samples were taken on children with ALL in remission. All participants were followed by echocardiography routinely during and after treatment, and retrospective chart review examined the following timepoints: at baseline (used as a control), in the acute phase, during oral maintenance, at the end of treatment, 2-3 years post diagnosis, 5-10 years post diagnosis, and 10-15 years post diagnosis. SNPs in *ABCC2, NQO1, SLC22A6*, and *SLC28A3* were associated with decreased fractional shortening and ejection fraction, particularly in the 5-10-year period after diagnosis. *NQO1* SNP rs1043470 T was associated with lower left ventricular function in the acute phase and 5-10 years post diagnosis. *CYP3A5* rs4646450 TT was found in 17%

of participants with ALL who had anthracycline associated cardiotoxicity (ACT) with a fractional shortening less than 28, and appeared to be more prominent in ACT overall, particularly in boys and the ALL group. Additional prospective studies with long term follow up are needed to further understand how PGx testing can contribute to understanding ACT.

Pain Management

Although the evidence for use of PGx panel testing related to pain management is evolving, the use of multi-gene panel testing for predicting response, side effects, dependence, or improving overall treatment outcomes is currently not supported as safe or efficacious in the peer-reviewed, published literature.

In an effort to help generate a predictive model including PGx markers that could be used by clinicians to predict risk of opioid use disorder in individuals with chronic non-cancer pain (CNCP), Escorial et al. (2024) conducted an observational study of 806 individuals with CNCP and long-term opioid use. The study included 137 participants with opioid use disorder (OUD) and 669 individuals without OUD. The researchers evaluated genetic variants in *OPRM1,* A118G, rs1799971, *COMT*, G472A, rs4680, and *CYP2D6*. The *OPRM1*-AA genotype and *CYP2D6* poor and ultrarapid metabolizers were determined to have acceptable diagnostic accuracy (sensitivity: 0.82 and specificity: 0.85), goodness of fit (p = 0.87), and discrimination (0.89) when considered along with along with three additional predictors: age, work disability, and oral morphine equivalent daily dose (MEDD). Those with OUD were found to have lower incomes, were, on average, ten years younger than those without OUD, had more sleep disturbances, more frequent use of benzodiazepines, and a greater likelihood of a history of substance use disorder. Based on these results, the authors concluded that polymorphisms related to *OPRM1* variants and *CYP2D6* phenotypes may be associated with a higher risk of OUD, along with known risk factors such as elevated MEDD, lower incomes, and age. Additional research including high quality clinical trials is required to establish an accurate and useful clinical predictive model for use in individuals with CNCP who may need long-term use of opioid analgesics.

Kraus et al. (2024) investigated the use of preoperative PGx testing as it relates to postoperative pain control for individuals undergoing total knee arthroplasty in a recent randomized trial. A total of 68 individuals aged 18 to 80 years, all of whom were scheduled to undergo primary TKA under general anesthesia, met inclusion criteria and were evaluated in the study. All participants underwent PGx testing and were then randomly assigned to either the experimental group (n = 38) or the control group (n = 30). Prior to surgery, PGx test results for the experimental group were examined by a pharmacist who made recommendations for perioperative medications. In addition, clinically relevant drug-gene interactions were reviewed by a pharmacist and recommendations specific to drug and dose were made based on CPIC guidelines. Participants were blinded to their PGx test results. Results of PGx tests for individuals in the control group were not considered prior to surgery and standard institutional pathways were followed. Outcomes were measured using the Overall Benefit of Analgesic Score (OBAS) 24 hours after surgery. Secondary outcomes were mean 24-hour pain score, total morphine milligram equivalent and frequency of opioid administration. No differences were found between the two groups in terms of mean OBAS (mean ±SD 4.7 ±3.7 in the control group versus 4.2 ±2.8 in the experimental group, mean difference 0.5 [95% CI -1.1 to 2.1]; p = 0.55), total opioids administered, opioid prescribing patterns, or use of tramadol (41% versus 71%, proportion difference 0.29 [95% CI 0.05 to 0.53]; nominal p = 0.02; adjusted p > 0.99). Although this study was small, the results suggest that use of PGx testing for individuals undergoing TKA does not lead to better pain management or decreased use of opioid analgesics. The authors recommend future study with greater focus on at-risk populations or individuals undergoing complex and especially painful surgeries to determine if PGx may be helpful in specific scenarios.

Agulló et al. (2023) conducted a double-blind, randomized, controlled study to assess the safety and effectiveness of PGx-guided opioid therapy by examining clinical changes in individuals with chronic non-cancer pain (CNCP) after three months of treatment with opioid analgesics. CPIC clinical recommendations for *CYP2D6* phenotypes and *OPRM1* and *COMT* genotypes were the basis for the PGx-guided treatment employed in this study. The trial randomized 60 participants with chronic pain into two arms, both of which were prescribed opioids. The first was guided by *CYP2D6*, *OPRM1* and *COMT* genotypes and the other received routine care. Participants were interviewed in a baseline visit to assess physical status and medical history. Over the course of the three month trial, ten participants were excluded for various reasons; a total of 50 participants completed the full three month trial and follow up. Data was collected with validated scales and questionnaires which were self-administered in the presence of an expert clinician. In the group guided by genotype, pain was reduced in intensity (76 vs. 59 mm, p < 0.01), pain relief was improved (28 vs. 48 mm, p < 0.05), quality of life was improved (43 vs. 56 mm p < 0.001), incidence of clinically relevant adverse effects was reduced (3 [1–5] vs. 1 [0–2], p < 0.01) and opioid dose was reduced by 42% (35 [22–61] vs. 60 [40–80] mg/day, p < 0.05) when compared to the usual prescribing group. The score for health utility was significantly higher in the genotype-guided group due to improving symptoms of sleepiness and depression and a substantial reduction (30-34%) for headaches, nervousness, dry mouth, and constipation. The authors propose that these results support safety and efficacy of the use of genotype-guided CNCP opioid use for both pain and associated psychiatric disorder management. However, the study was limited by its small sample size from a single pain unit during the COVID-19 pandemic. In addition, the opioid fentanyl

was only used in the control arm, creating difficulty in evaluating specific effects of guided treatment when there are differences in the drugs between groups. Lastly, participants were on other medications for additional pathologies which could have contributed to the differences in outcomes. Additional high-quality studies with larger and more diverse populations are recommended.

In a 2022 systematic review, Zobdeh et al. examined the impact of PGx on safety and efficacy of non-steroidal anti-inflammatory drugs (NSAIDs) and antidepressants when they are used for treatment of pain. A total of 25 articles met inclusion criteria and were reviewed in the analysis. Interactions applicable for use in pain management were detected for 10 drug/gene combinations including ibuprofen/*CYP2C9*, celecoxib/*CYP2C*, piroxicam/*CYP2C8, CYP2C9*, diclofenac/*CYP2C9, UGT2B7, CYP2C8, ABCC2*, meloxicam/*CYP2C9*, aspirin/*CYP2C9, SLCO1B1*, and *CHST2*, amitriptyline/*CYP2D6* and *CYP2C19*, imipramine/*CYP2C19*, nortriptyline/*CYP2C19, CYP2D6, ABCB1*, and escitalopram/*HTR2C, CYP2C19*, and *CYP1A2*. The authors note that the PGx studies they identified focused on the role of genes in the CYP family for NSAIDs, but the number of studies that investigated the impact of these variants on pain relief were very limited and detected only small impact of *CYP2C8* and *CYP2C9* on therapeutic effect. Overall, there is a lack of well powered studies investigating PGx in individuals being treated for pain with NSAIDs and antidepressants. Although a higher risk for more severe side effects for *CYP2C9* poor metabolizers and NSAIDs was observed, the researchers concluded that larger in vivo studies are required to further investigate the efficacy regarding use of PGx of NSAIDs and antidepressants in pain management.

To determine whether PGx testing may be used to effectively customize postoperative pain management after a total joint replacement, Hamilton et al. (2022) conducted a prospective RCT including 107 individuals undergoing hip or knee arthroplasty. PGx testing was performed using a panel of 16 genes including *CYP2D6, CYP2C9, OPRM1*, and *CYP1A2*, which have an impact on pharmacodynamics of NSAIDs and many opioids. Participants were blinded and randomized to either a control group (n = 46) or custom group (n = 61). The control group received prescriptions for oxycodone, tramadol, and celecoxib for their postoperative pain. In the custom group, if variants indicating these drugs would not be normally metabolized were found via PGx testing, alternative drugs (hydromorphone, meloxicam) were prescribed. Participants recorded pain levels and medications used for 10 days following surgery and medication used was converted to milligram morphine equivalents (MME). The researchers found that genetic variations impacting medication effects in the standard pain management protocol occurred in 22.4% of participants. The 10-day MME in the control group for those individuals who had genetic variants was 162.6 mg. In the custom group, individuals with variants and custom medications used only 86.7 mg in the same timeframe. The control group also had a higher 10-day average pain level than the custom group (4.2 vs. 3.1, respectively, $p < 0.05$). The authors concluded that with custom postoperative pain medication prescriptions based on results of PGx testing, individuals undergoing hip or knee arthroplasty had better pain control and reduced consumption of pain medication, however they acknowledge that this study was small, especially since the genetic variations of greatest interest are rare.

In a 2021 systematic review, Rodriguez et al. examined the efficacy and safety of opioid therapy guided by PGx testing. Out of 3794 records found, five met inclusion criteria for data extraction. Of the five studies, two reported significant pain improvement related to PGx-guided therapy in individuals with a high risk *CYP2D6* phenotype. The authors concluded that evidence on the safety and efficacy of using PGx testing to guide intervention in opioid therapy for chronic and postoperative pain is very limited.

In 2020 (updated 2023), Hayes published a Clinical Utility Evaluation of PGx and pharmacogenomic testing related to opioid use disorders. Hayes found insufficient evidence to either predict risk of opioid dependence or improve treatment for individuals with opioid use disorder. In addition, a Hayes Clinical Utility Evaluation (2019a, updated 2022) found limited, low-quality evidence addressing PGx testing prior to prescribing codeine, tramadol, and general opioids related to improved opioid related treatment outcomes in adult patients with pain. Lastly, another Hayes Clinical Utility Evaluation (2019b updated 2022) found insufficient evidence to report or refute the clinical utility of *OPRM1* or *COMT* genotyping for pain management in patients with organic causes of pain.

Muriel et al. (2019) conducted a six-month, observational, prospective study on the use of PGx testing for 88 individuals involved in long term opioid deprescription treatment of non-cancer related pain in the Pain Unit of Alicante General Hospital in Spain. Visits were monitored and analyzed based on various genotypes. Visits included baseline, follow-up and final, and other parameters tracked were opioid rotation or discontinuation, adverse drug events and suspected adverse drug reactions (ADRs). Genotyping consisted of the following genes and variants using RT-PCR: *OPRM1* (A118G), *ABCB1* (C3435T), *COMT* (G472A), *OPRD1* (T921C) and *ARRB2* (C8622T). Five participants were lost to follow up. The remaining participants were 64% female and 100% Caucasian. In the baseline visit, a median of 6 adverse events were recorded including dry mouth, constipation, sleep disruption, and depression. There was no difference recorded in ADRs from baseline through final visits. A total of 1659 ADRs were reported in 359 visits for this cohort, and the most common by system classification were psychiatric (21%) and gastrointestinal (20%). At the baseline visit, ADRs varied

between *OPRM1* genotypes, with individuals who were AA at that A118G locus having, on average, two or more ADRs than AG/GG patients. Nausea and other gastrointestinal ADRs followed this same pattern. *COMT* genotyping was similar; with AA/GG patients having more ADRs; those that were *COMT* AG were less likely to have loss of libido, skin redness, vomiting, or sexual dysfunction. The *OPRD-CT* genotype also showed less association with sexual dysfunction and reproductive system disorders. The authors were surprised that the number of ADRs did not change over the course of the study, and they also noted that the use of antidepressants increased from the beginning to end of the study. Antidepressants can have similar ADRs to opioids; this may be a confounding variable. The authors found value in the PGx testing as a predictor of who may experience nausea and gastrointestinal discomfort and highlights the potential promising use of PGx in opioid management.

Rheumatoid Arthritis

The body of evidence supporting the PrismRA® test is limited. For this test to be considered proven with clinical utility, additional larger and independent studies with better study designs are necessary.

Anti-tumor necrosis factor (TNF) medications are the first tier of rheumatoid arthritis (RA) treatment therapy in over 90% of biologic naïve patients whose disease is not controlled by conventional disease modifying anti-rheumatic drugs (DMARDs); 70% of these RA patients do not attain significant clinical improvement (Mellors et al. 2020). Scipher Medicine created PrismRA® as a molecular signature test that evaluates the likelihood that an RA patient may not respond to traditional anti-TNF therapy before treatment is initiated. Twenty-three different assessments are made by PrismRA; the resulting biomarker panel includes 19 gene expression features, anti-cyclic citrullinated protein (anti-CCP) and three clinical metrics (sex, body mass index, patient disease assessment) which stratify patients based on the likelihood of inadequate response to anti-TNF therapies. Scipher predicts that a 40% increase in response to the first targeted DMARD could have been achieved for RA patients using PrismRA and that both responders and non-responders have a greater chance of responding to their first biologic/targeted treatment (Mellors et al. 2020).

To evaluate the impact of a molecular signature response classifier (MSRC) on treatment decisions made by rheumatologists for individuals with RA, Curtis et al. (2024) surveyed physicians to determine if results from MSRC testing guided their selection of biologic and targeted synthetic disease-modifying antirheumatic drugs (b/tsDMARDs). Data from the Study to Accelerate Information of Molecular Signatures (AIMS), a longitudinal, prospective database of individuals with RA and their MSRC results, was used in this evaluation. The rate of b/tsDMARD prescriptions that demonstrated alignment with MSRC results and the total percentage of providers using MSRC results to guide treatment were also included in the results. In total, 1018 participants were included in the analysis, and of those, 70.7% (720/1018) received MSRC results prior to treatment selection. Of the 720, 544 (75.6%) were prescribed a b/tsDMARD that was in alignment with their MSRC results; 84.6% of the prescribing physicians reported that they had used the MSRC results to direct choice of treatment. For those that did not align choice of treatment with MSRC results, the most common reason provided was concerns with health insurance coverage. The researchers determined that the MSRC test appears to provide helpful information for making treatment decisions in individuals with RA but note limitations including the use of a survey, which may have been impacted by individual biases, and potential differences in treatment due to regional variation. The study was funded by the manufacturer of an MSRC test, which introduces additional potential for bias. In addition, potential step-therapy treatments required by insurers were not accounted for in this study. The authors recommend long-term studies which further clarify how MSRC testing is used by treating providers.

A Hayes Molecular Test Assessment (2022b, updated 2024) evaluated the clinical validity, utility, and analytic validity of Scipher's PrismRA test, noting that the test has undergone changes in the number of risk categories and cutoff values for classification. This Hayes Assessment addresses the PrismRA test in its most current form and previously published analyses of PrismRA, which did not evaluate the most current version of the test (or in which the version of the test could not be identified), were excluded from the Hayes assessment. Overall, a very low quality body of evidence was identified to support use of the PrismRA test. Additional studies evaluating PrismRA in larger and more diverse populations are needed. A 2024 update to the initial assessment indicates that although new studies have been published since the 2022 assessment, the rating of D2 is unlikely to change based on these publications.

In a 2022 cohort study, Curtis et al. compared a group of individuals (n = 627) who had been tested using an MSRC with a control group, using propensity score matching applied to balance baseline traits. The individuals in the MSRC-tested group were participants in AIMS, while the control group members (n = 2721) were external; information was obtained from a large, de-identified database of US electronic health records. All participants either began a b/tsDMARD or continued anti-TNF therapy. The researchers calculated odds ratios (ORs) for six-month response based on clinical disease activity index (CDAI) scores for low disease activity/remission (CDAI-LDA/REM), remission (CDAI-REM) and minimally important differences (CDAI-MID). In the group of MSRC-tested participants, a non-response signature was obtained in 59% of the group and MSCR-aligned treatment was provided in 70% of the group. In participants who were treated with anti-TNF therapy, the MSRC had a PPV of 88% and sensitivity of 54% Those individuals who received

MSRC-guided treatment were significantly more likely to respond to b/tsDMARDs than individuals who received standard care (CDAI-LDA/REM: 36.0% vs 21.9%, OR 2.01[1.55-2.60]; CDAI-REM: 10.4% vs 3.6%, OR 3.14 [1.94-5.08]; CDAI-MID: 49.5% vs 32.8%, OR 2.01[1.58-2.55]). Based on these results, the authors assert that the clinical validity of the MSCR test supports high clinical utility since treatment that was guided by MSCR testing led to substantially better outcomes compared to standard care, with almost three times more individuals reaching CDAI remission. Some limitations were noted, however, including the intrinsic limitations in the ability to identify unmeasured confounders in an external control group and the length of time that passed from the baseline assessment and MSRC testing to the beginning of treatment in some members of the MSRC-tested group (up to one year). In addition, several authors had associations with the corporation that manufacturers the MSRC test used and funded the study, which creates potential for bias.

Jones et al. (2021, included in the 2022b Hayes report) conducted a nonrandomized retrospective assay to assess the analytical and clinical validity of the PrismRA test in individuals with RA who have not responded to tumor necrosis factor-α inhibitor (TNFi) therapy. A total of 174 individual samples from the NETWORK-004 clinical study were analyzed for clinical validity. Of these, 100 were had not undergone any targeted RA therapy and 74 had been exposed to TNFi. The test results classified samples according to non-response prediction with a positive predictive value of 87.7% (95% CI: 78–94%), sensitivity of 60.2% (95% CI: 50–69%), and specificity of 77.3% (95% CI: 65–87%). Three thresholds were used: signal not detected, high, and very high. Accuracy of the test under study was found to be 95.8% for threshold concordance; high repeatability was detected (92.6%) as well as high reproducibility (100%). The authors concluded that PrismRA is a "robust assay" that detects molecular non-response signatures in individuals with RA accurately and reproducibly. Limitations to this study include lack of randomization, small population, wide confidence intervals and inability to determine potential for selection bias due to lack of information regarding the original NETWORK-004 study.

To assess provider decision making and outcomes related to treatment following use of the PrismRA test to inform selection of b/tsDMARDs in individuals with RA, a prospective cohort study was undertaken (Strand et al., 2022, included in the 2022b Hayes report). In the decision making cohort, 377 individuals met inclusion criteria and were evaluated according to treatment, treatment modifications and physician questionnaire responses. For the clinical outcomes cohort, 212 individuals completing a 12-week follow up visit and a subset of 85 individuals completing a 24-week follow up visit were included; clinical outcomes were evaluated between the subsets based on test results and b/tsDMARD choice. The researchers report that PrismRA test results informed therapy selection in 73.5% of study participants, noting that when these test results were not incorporated into the decision-making process, 62% of participating providers reported that the deviation from the recommendation was due to insurance-related issues. The American College of Rheumatology criteria for ≥ 50% responses (ACR50) at 24 weeks for individuals prescribed medication according to PrismRA test results were 39.6%. Individuals whose test results indicated non-response had significantly improved responses to non-TNFi therapies compared to TNFi therapies (ACR50 34.8% vs 10.3%, p-value = 0.05), indicating that predicted non-responders to TNFi therapies are not nonresponders to other types of RA therapy. The researchers concluded that incorporating PrismRA into patient care could significantly improve RA treatment outcomes, however, the study was nonrandomized and nonblinded and there was no comparison group of impacted individuals that did not undergo testing with the PrismRA test. There was also limited racial diversity (79-84% of population was white) and there were significant differences in characteristics, such as age, between the groups. Lastly, there is potential for bias related to affiliations with the test laboratory. Longer term data is required to evaluate persistence and treatment patterns along with disease burden.

Mellors et al. (2020) reported on the Scipher cross cohort, cross platform study that developed the molecular test to predict decreased/non-response (ACR < 50) to anti-TNF therapies in biologic-naïve RA patients using the Human Interactome model; 39 RA-associated SNPs were evaluated. Data taken from two cohorts collected from the CERTAIN trial (n = 58/patient discovery cohort and n = 143/training cohort) were evaluated to produce a drug biomarker panel; laboratory studies included CBC, C-reactive protein, rheumatoid factor titer and anti-citrullinated protein. A validation cohort (n = 175) was matched to the training cohort for response rate, age and gender and all individuals in the validation cohort from the CERTAIN study had a clinical disease activity index > 10. Results revealed that the biomarker panel identified non-responders with an 89.8% PPV and 86.8% specificity (OR 6.57%). A limitation of this study is that the researchers did not have a single platform or single cohort to analyze. The authors concluded that development and validation of such algorithms to predict drug non-responsiveness shows promise for advancing RA precision medicine treatment and for other complex autoimmune conditions where patients demonstrate inadequate response to therapeutics.

Bergman et al. (2020) developed a decision-analytic model to examine two treatment strategies to evaluate the clinical and economic outcomes of PrismRA for the first 12 months following initial biologic treatment. They observed clinical decision-making from 175 patients enrolled in the CERTAIN study who received anti-TNF after failing to demonstrate response to conventional synthetic DMARD and modeled clinical decision-making for the same cohort using PrismRA. In total, 69.7% of patients failed to reach goal of ACR50 in response to anti-TNF treatment. A PrismRA score of ≥ 11.8 was

used to identify patients with a high or very high likelihood or poor/non-response to an anti-TNF treatment. Sixty-eight subjects were predicted to be poor responders: 61 were correctly predicted; 7 were misclassified as they did reach ACR50. With the first treatment strategy, 70% of subjects did not reach ACR50 within 6 months. Subsequently, these subjects received a second-line treatment- either a second anti-TNF treatment (60%) or an alternate treatment (40%); these subjects demonstrated a 20% ACR50 response within 12 months. Subjects who reached ACR50 in the first 6 months stayed on therapy for the entire 12 months. Forty-four percent of patients in the 175-subject cohort were predicted to have achieved ACR50 within the first 12 months of treatment. With the second strategy using PrismRA, the 68 subjects who were poor responders were assigned to another treatment therapy; 27 reached ACR50 in the first 6 months and the other 107 subjects were prescribed an anti-TNF treatment. Of 107 responders, 61 did not reach ACR50 and were given another mechanism of action as a second-line therapy; 16/61 then achieved ACR50. Therefore, 57% of subjects from the 175-patient cohort were predicted to reach ACR50 within the first 12 months of treatment. The researchers listed multiple limitations for this study including the lack of sensitivity analysis and the assumption that health care providers will follow with full adherence the PrismRA test results. The authors concluded that precision medicine and biomarker-driven treatment are a necessary step toward advancing clinical effectiveness and cost-saving for all medications in addition to RA patient treatment.

Johnson and Weinblatt (2018) introduced the PrismRA test for Scipher Medicine stating that it predicts non-response to all anti-TNF treatments including Humira, Enbrel and Remicade prior to drug prescription. Scipher Medicine reported that preliminary performance suggests a negative predictive value (NPV) of 92% and a true negative rate (TNR) of 50%. Validation of the predictive accuracy of PrismRA in a clinical trial is ongoing. Scipher is in communication with rheumatologists and payers to determine optimal clinical endpoints. Once the end points are determined from the trial, PrismRA will be offered commercially as a CAP-proficient, CLIA-certified lab. PrismRA will allow more RA patients to achieve good response/remission (ACR50) resulting in improved patient outcome and significant cost savings according to the authors.

Other Pharmacogenetic Multi-Gene Panel Testing

The evidence for use of PGx multi-gene panel testing to guide individualized therapies for indications such as multimorbidity, polypharmacy, cancer treatment toxicity and medication response, inflammatory bowel disease (IBD), and for general use with medication prescription is insufficient at this time.

A 2024 systematic review and meta-analysis by Lingaratnam et al. assessed safety outcomes related to the use of PGx-directed treatment options (Analysis 1) and sought to identify promising genomic variants with the potential to predict medication toxicity and severity of symptoms in individuals with cancer diagnoses who had undergone active cancer treatment (Analysis 2). Primary endpoints included severe adverse effects (SAE) or pain and vomiting, as defined by specific trial procedures and evaluated by trial investigators. A total of six studies met inclusion criteria and were evaluated in Analysis 1; these studies included PGx-guided dosing related to treatment with fluoropyrimidines, irinotecan and a combinations of multiple medications incorporating both anti-cancer and supportive care. The most frequently studied genes were *MTHFR, UGT1A1, ABCB1, TYMS, UGT1A6/UGT1A7/UGT1A9 and HLA-DRB1*. Forty studies were included in a subset analysis (Analysis 2). The reviewers found a lower absolute occurrence of SAEs with evidence-based PGx-guided treatment approaches when compared to TAU (16% vs 34%, respectively, RR = 0.72, 95%CI 0.57–0.91, p = 0.006, I^2 = 34%) in meta-Analysis 1. In meta-Analysis 2, nine variant pairs of interest were detected including genes *TYMS, ABCB1, UGT1A1, HLA-DRB1*, and *OPRM1*. The authors concluded that the use of PGx testing led to a reduction in the rates of SAEs in individuals with cancer undergoing treatment based on the outcome of this analysis. The identification of emerging genetic variations warrants further study focused on the development and improvement of PGx testing for individuals undergoing cancer treatment and on the safety of supportive care treatments. High-quality clinical trials evaluating emerging pharmacogenes (including those identified by this review) and their relationship not only to anti-cancer treatment, but to efficacy outcomes, are recommended.

The use of PGx testing for specific gene-drug interactions has been studied in several RCTs with evidence for improved outcomes, but robust evidence related to PGx panel testing is relatively limited. In 2023, Swen et al. published the results of an open-label, cluster-randomized, controlled, multicenter trial of a 12-gene PGx panel (the PREPARE study). The trial took place in multiple clinical settings across seven European countries and included participants with a broad range of diseases and medication needs. Overall, 39 drugs were used to treat multiple conditions in PREPARE. Though the trial initially enrolled 6944 individuals assigned to receive either PGx-guided treatment (n = 3342) or TAU (n = 3602), 751 of these either withdrew consent or were lost to follow up. Of the remaining participants, a total of 1558 individuals were found to have an actionable test result related to the drug they were being prescribed, and of those, a clinically significant ADR transpired in 21% (152/725) of participants in the experimental group and 27.7% (231/833) of participants in the control group (OR 0·70 [95% CI 0·54–0·91]; p = 0·0075). For the entire population, the incidence of ADRs was 21.5% of 2923 experimental group participants and 28.6% of 3270 control group participants. The most common study drug linked to actionable variant findings was atorvastatin (n = 716); clopidogrel (n = 619) and tacrolimus (n = 472) also had a

significant number of individuals with associated variants identified. The volume and severity of ADRs varied per country, which may have been related to the type of facility from which participants were recruited (e.g., cancer clinic vs primary care). Based on these results, the authors assert that use of the 12-gene PGx panel test to guide treatment selection substantially decreased incidence of ADRs over a diverse populations of individuals in European health care settings and affirm that their findings bolster the existing evidence supporting broad use of panel-based PGx testing for improved safety of drug therapy. They highlight the potential benefit of standardizing a validated PGx testing system for decision-making support related to medication prescription. The study did have noted limitations; these included subjective, patient-reported ADRs (although the assessment was independently validated in 10% of participants that were randomly selected), reliance on participants to contact the research team if a secondary drug was used, and low volumes of participants for some of the drugs included in the study, some of which had high-toxicity profiles (e.g., mercaptopurine, azathioprine, and thioguanine). This study focused only on reduction of adverse effects. Another area requiring further evaluation is the impact of PGx panel testing on drug efficacy. In addition, 97.7% of participants were of European, Mediterranean, or Middle Eastern ancestry. Additional studies incorporating greater ethnic diversity are required before this test can be widely recommended.

Plaza and colleagues (2024) performed a systematic review investigating the status of evidence specific to genetic variants associated with biological agent therapy in inflammatory bowel disease (IBD), contending that PGx is an emerging area of importance for the optimization of IBD treatment. In total, 28 studies were included in the review. In addition, PharmGKB was used to gather evidence on the relationship between known genetic variants and IBD treatment. The researchers indicate that genome-wide association studies have detected SNPs that have a potential relationship with the pathogenesis of IBD. Several studies have also shown a relationship between SNPs and pharmacological response to IBD treatments. The review indicates that the most important SNPs related to biological therapeutics are those linked to immunity, such as immunorecognition and cytokine production. The authors stress the importance of large, high-quality studies designed to investigate the relationship of PGx and biological therapy, which will hopefully lead to the ability to determine the most valuable SNP assessment for incorporation into IBD treatment.

In a 2022 systematic review, O'Shea et al. sought to establish the efficacy of multi-gene, multi-disease, and multi-drug PGx interventions in adults with multiple morbidities and/or prescription polypharmacy in healthcare settings and to inform enactment of PGx-guided treatments in practice. The review included 12 studies assessing multi-medicine PGx in individuals with multiple morbidities or polypharmacy that reported on relevant core outcomes. Studies varied in design and quality; six non-comparative studies, three observational studies and three RCTs were included. Only a narrative analysis was performed due to high levels of heterogeneity in the evidence reviewed, so the results can provide only a high level representation of the impact of PGx testing in multimorbidity and/or polypharmacy. Ultimately, the authors concluded that due to the lack of methodologically robust, high-quality studies with appropriate long term follow-up, no generalized conclusions regarding benefits for patients or health systems could be made based on this review. They assert that there is promise for individualizing therapies through PGx guidance, but further high-quality studies across differing patient care settings are required to establish efficacy.

A systematic review and meta-analysis evaluating the current evidence regarding the impact of PGx testing on hospital admissions and whether PGx leads to changes in medication was published by David et al. in 2021. Five studies focused on hospitalization and five studies focused on medication change were identified for evaluation. The meta-analysis found that changes in medication occurred significantly more often in the PGx test arm in four of five studies, and all-cause hospitalization occurred significantly less often in the PGx test arm than in the TAU comparator. The researchers share their belief that these results show proof of concept for use of PGx in prescribing that may lead to patient benefit but point out the evidence gaps that exist related to introduction of PGx into health care systems. They feel their analysis will assist with identifying areas where further research is needed, including investigation of the perspectives of health care providers and patients to assist in design of patient-centric PGx-guided care.

Borobia et al. (2018) reported on the implementation of a PGx program in 2014 at La Paz University Hospital (LPUH) in Madrid. LPUH is a 1308 bed tertiary-care teaching hospital of the Spanish NHS serving approximately 600,000 people. The goal of the study was to implement PGx into clinical practice and evolve from an ad hoc strategy linked to a prescription to a proactive practice, where genetic information would be obtained prior to a prescription in at-risk populations. The targeted populations were at-risk for IBD, psoriasis, cardiovascular disease, leukemia, colorectal cancer, or had undergone a transplant. The authors utilized a 180 SNP panel (PharmArray) for testing. Ordering providers would submit a recommendation and request for testing to a centralized testing unit which would evaluate the request based on patient demographics if the requested marker fell into one of three categories: Category A for pre-emptive screening of an actionable marker, such as *HLA-B5701* for abacavir response, Category B for drugs with a well-defined protocol for treating certain diseases, such as *TPMT* for thiopurine response in the treatment of IBD, or Category C for drugs without a well-defined protocol. In this situation, the PGx unit would evaluate the therapeutic issue and determine if a PGx test would be clinically useful. From January 2014 through December 2016, the Pharmacogenetic Testing Unit received 2539

consultation requests. The most common tests were *TPMT* and *MTHFR*. There were 1939 requests for treatment selection with well-defined protocols and 711 for drugs with PGx treatment recommendations for certain diseases or with poorly defined recommendations. Of these, 600 were found appropriate and approved, and 32% had a molecular profile that impacted the drug. In this sub-group, 58% (107) had a dose adjustment as a result. The program's total cost was estimated at 216 € ($254) per patient, and 91% of physicians surveyed said they would now use PGx regularly.

O'Donnell et al. (2014) implemented a PGx testing program, The 1200 Patients Project, for adults being seen at the University of Chicago who were regularly taking at least one, but not more than six, prescription drugs. Individuals could be referred by a care provider or self-referred to the program. After completing an informed consent process, participants were tested for PGx variants using a commercially available multi-gene PGx testing panel (Sequenom ADME). Overall, 868 individuals that completed PGx testing had 2279 clinical encounters that were reviewed. Four medical specialties and seventeen providers represented all clinic visits: executive health, nephrology, hepatology, and pulmonology. The most prevalent medications included aspirin, atorvastatin, hydrochlorothiazide, lisinopril, and amlodipine. Of all medications on participants' active drug lists, 34% had associated alerts (n = 2869) that included green (21%), cautionary yellow (13%) and high-risk red (0.5%). The remaining medications had no actionable PGx information. Of the 2869 alerts provided, green alerts were viewed 40% of the time, and 4% had medication changes documented. Yellow alerts were viewed 66% of the time, and 5% had medication changes documented. Red alerts were viewed 89% of the time, and 24% had medication changes documented. Nearly half of all medication changes were for omeprazole and atorvastatin. Simvastatin and rabeprazole had the highest overall percentage of changes influenced by the PGx test results. The authors note that limitations to this study include the small number of providers involved and the modest response to actionable alerts, with only 60 medication changes out of 405 possible actionable red and yellow alerts. In addition, the providers included in the study were also co-investigators which may highlight a bias toward PGx, and they knew their behavior was being examined, which may have altered their choices from what they would have done if they had not known their choices were being monitored.

Clinical Practice Guidelines

American College of Rheumatology (ACR)

In a 2021 ACR guideline (Fraenkel et al.) the PrismRA test is not specifically discussed, however the guideline does reference the following as a "key clinical question requiring further research": Do clinical or biologic markers predict a differential response to DMARDs? They note that the answer to this question is an important gap in knowledge related to management of RA.

ACR has identified eleven measures of disease activity for Rheumatoid Arthritis as a minimum standard for regular use in clinical settings: Disease Activity Score (DAS), Routine Assessment of Patient Index Data 3 (RAPID3), Routine Assessment of Patient Index Data 5(RAPID 5), Clinical Disease Activity Index (CDAI), Disease Activity Score with 28 joints (DAS28-ESR/CP), Patient Derived DAS28, Hospital Universitario La Princesa Index (HUPI), Multibiomarker Disease Activity Score (MBDA score, VectraDA), Rheumatoid Arthritis Disease Activity Index (RADAI), Rheumatoid Arthritis Disease Activity Index D (RADAI-5), Simplified Disease Activity Index (SDAI). **(**England et al., 2019)

Singh et al. (2016) recommended that the primary goal for RA treatment should be low disease activity and/or clinical remission with a goal of ACR50 or 70 achievement. With moderate to high activity despite DMARD monotherapy, combination DMARD or a TNF1 or non-TNF biologic is preferred over DMARD monotherapy. The guideline states that the use of non-TNF biologics has been proven effective in RA treatment.

Clinical Pharmacogenetics Implementation Consortium (CPIC®)

CPIC® is an international organization with membership including clinicians, scientists, laboratorians, and other PGx experts with the purpose of facilitating the use of PGx test results for patient care. CPIC's goal is to address the barrier caused by difficulty translating genetic laboratory test results into actionable prescribing decisions for applicable drugs by creating freely available, peer-reviewed, evidence-based, and updatable gene/drug clinical practice guidelines. CPIC started as a shared project between the Pharmacogenetics Research Network (PGRN) and the Pharmacogenomics Knowledge Base (PharmGKB) in 2009. CPIC guidelines are indexed in PubMed as clinical guidelines, endorsed by the American Society of Health-System Pharmacists (ASHP) and the American Society for Clinical Pharmacology and Therapeutics (ASCPT), and are referenced in ClinGen and PharmGKB (CPIC, 2024).

In an updated guideline (Bousman et al., 2023) CPIC expanded on their existing guideline for *CYP2D6* and *CYP2CD19* genotypes and selective serotonin reuptake inhibitor (SSRI) antidepressant dosing and summarized the effect of *CYP2D6*, *CYP2C19, CYP2B6, SLC6A4* and *HTR2A* genotypes on the dosing, efficacy, and tolerability of antidepressant medications. The guideline states that *CYP2D6*, *CYP2C19*, and/or *CYP2B6* genotype results may be beneficial for detecting individuals who are at a higher risk of either adverse drug reactions or inadequate response to SSRI therapy,

based on moderate to high quality evidence. Risks, including the potential to miss the identification of rare or new variations that are usually not tested on current platforms, have been identified. In such cases, the actual phenotype may be different from the predicted phenotype. Other factors, such as age, diet, comorbidities, smoking, pregnancy, concomitant medications, and epigenetic variation may also apply. CPIC did not provide recommendations for *HTR2A* and *SLC6A4* because the evidence supporting an association between these genotypes and SSRI antidepressants is mixed/insufficient to support clinical validity and utility at this time (CPIC level C: no recommendation). CPIC guidelines (Hicks et al., 2016, updated 2019) also address the use of *CYP2D6* and *CYP2C19* genotyping for dosing of tricyclic antidepressants (moderate to high quality evidence).

No existing CPIC guidelines provide recommendations regarding the use of multi-gene panels including testing of five or more genes.

European League Against Rheumatism (EULAR)

Smolen et al. (2022) updated the EULAR recommendations for the management of rheumatoid arthritis based on evidence from three systematic literature searches on the safety and efficacy of DMARDs and glucocorticoids (GCs). The EULAR task force provided five principles and eleven recommendations regarding the use of conventional synthetic (cs) DMARDs, GCs, biological DMARDs and targeted synthetic DMARDs. Neither the use of molecular signature response classifiers or PrismRA were discussed, but one of the items on the EULAR research agenda is identification of new biomarkers to help stratify individuals with RA and predict therapeutic response or lack of response.

International Society of Psychiatric Genetics (ISPG)

In 2021, a group of experts assembled by the ISPG published a narrative review of PGx evidence, product labeling and existing prescribing guidelines for psychotropic medications and the main considerations and concerns related to psychiatric use of PGx testing (Bousman et al., 2021). The group determined that current published literature, product labeling and prescribing guidelines support the use of PGx testing for *CYP2D6*, and *CYP2C19* to inform selection of medication and dosing of multiple common anti-depressant and anti-psychotic medications. They indicated that the evidence also supports additional testing for human leukocyte antigen genes with use of mood stabilizers including carbamazepine, oxcarbazepine, and phenytoin. Screening for variants in *POLG, OTC*, and *CSP1* is recommended for valproate screening when there is suspicion of a mitochondrial disorder or urea cycle disorder. Noted in this review is the fact that PGx testing is not regulated at present and there are many available tests that include genes with little or no support for clinical implementation which could lead to inappropriate medication selection and dosing. Large PGx studies are currently underway, with the expectation that results will lead to further evolution of evidence supporting the use of PGx testing and removal of barriers for appropriate testing. Overall, the group is optimistic regarding the current direction of research and innovation in the field of PGx testing and believes this testing will ultimately become an important tool for use in individuals with psychiatric disorders.

ISPG updated their statement on genetic testing in 2019. Their recommendation regarding PGx testing is as follows: "Pharmacogenetic testing should be viewed as a decision-support tool to assist in thoughtful implementation of good clinical care. We recommend HLA-A and HLA-B testing prior to use of carbamazepine and oxcarbazepine, in alignment with regulatory agencies and expert groups. Evidence to support widespread use of other pharmacogenetic tests at this time is still inconclusive, but when pharmacogenetic testing results are already available, providers are encouraged to integrate this information into their medication selection and dosing decisions. Genetic information for *CYP2C19* and *CYP2D6* would likely be most beneficial for individuals who have experienced an inadequate response or adverse reaction to a previous antidepressant or antipsychotic trial."

National Comprehensive Cancer Network (NCCN)

NCCN guidelines for adult cancer pain (v2.2024) include a section on Principles of PGx, indicating that PGx testing may be considered before initiation or during treatment of pain when concerns of toxicity or lack of analgesic response are present or suspected. The use of PGx panel testing is not addressed.

Standardizing Laboratory Practices in Pharmacogenomics (STRIPE) Collaborative Community

To provide an overview of the current state of recommendations specific to PGx testing in existing U.S. clinical practice guidelines (CPGs), a clinical subcommittee of the Standardizing Laboratory Practices in Pharmacogenomics (STRIPE) Collaborative Community Study Designs Task Force (SDTF) comprised of experts in PGx testing was formed. This group identified gene-drug pairs with published CPIC guidelines or those included in the FDA table of PGx associations, then reviewed gene-drug pairs that are addressed in current U.S.-based CPGs (Hertz et al., 2024). Overall, 21 gene-drug (or drug class) pairs with well-established associations were identified and categorized into five therapeutic areas (cardiology,

pain/general medicine, infectious disease, psychiatry/neurology, and oncology). All 21 pairs had evidence of "clinical actionability" according to CPIC. The experts found that relatively few CPGs in the U.S. provide recommendations specific to PGx testing, and recommendations for the same gene-drug pairs often varied between organization, sometimes even between different CPGs from the same organization. No information regarding panel tests including five or more genes was provided in this review. The subcommittee concluded that additional effort, both within STRIPE SDTF and in other organizations, is required to develop a standardized approach to analyzing evidence related to clinical utility of PGx in order to provide clear PGx recommendations within CPGs and to direct study designs that will provide this evidence.

U.S. Food and Drug Administration (FDA)

This section is to be used for informational purposes only. FDA approval alone is not a basis for coverage.

Laboratories that perform genetic tests are regulated under the Clinical Laboratory Improvement Amendments (CLIA) Act of 1988. More information is available at:
https://www.fda.gov/medicaldevices/deviceregulationandguidance/ivdregulatoryassistance/ucm124105.htm.
(Accessed August 14, 2024)

The list of genetic tests that have been cleared or approved by the FDA Center for Devices and Radiological Health is available at: https://www.fda.gov/medical-devices/in-vitro-diagnostics/nucleic-acid-based-tests.
(Accessed August 14, 2024)

A full list of FDA-approved or cleared Companion Diagnostics is available at: https://www.fda.gov/medical-devices/in-vitro-diagnostics/list-cleared-or-approved-companion-diagnostic-devices-in-vitro-and-imaging-tools.
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Policy History/Revision Information

Date	Summary of Changes
01/01/2025	**Template Update** • Created shared policy version to support application to UnitedHealthcare West plan membership **Coverage Rationale** *Multi-Gene Panels* • Revised language to indicate the use of pharmacogenetic Multi-Gene Panels (five or more genes) for the evaluation of drug-metabolizer status is unproven and not medically necessary for any indication due to insufficient evidence of efficacy **Supporting Information** • Updated *Description of Services*, *Clinical Evidence*, *FDA*, and *References* sections to reflect the most current information • Removed *Medical Records Documentation Used for Reviews* section (medical records documentation no longer required) • Archived previous policy versions 2024T0587S and MMG157.R

Instructions for Use

This Medical Policy provides assistance in interpreting UnitedHealthcare standard benefit plans. When deciding coverage, the member specific benefit plan document must be referenced as the terms of the member specific benefit plan may differ from the standard plan. In the event of a conflict, the member specific benefit plan document governs. Before using this policy, please check the member specific benefit plan document and any applicable federal or state mandates.

UnitedHealthcare reserves the right to modify its Policies and Guidelines as necessary. This Medical Policy is provided for informational purposes. It does not constitute medical advice.

This Medical Policy may also be applied to Medicare Advantage plans in certain instances. In the absence of a Medicare National Coverage Determination (NCD), Local Coverage Determination (LCD), or other Medicare coverage guidance, CMS allows a Medicare Advantage Organization (MAO) to create its own coverage determinations, using objective evidence-based rationale relying on authoritative evidence (Medicare IOM Pub. No. 100-16, Ch. 4, §90.5).

UnitedHealthcare may also use tools developed by third parties, such as the InterQual® criteria, to assist us in administering health benefits. UnitedHealthcare Medical Policies are intended to be used in connection with the independent professional medical judgment of a qualified health care provider and do not constitute the practice of medicine or medical advice.