Supplementary Table 5. In silico pathogenicity prediction scores and classifications for CYP21A2 variants across fourteen computational tools.
This table summarizes the numerical scores and categorical pathogenicity classifications generated by fourteen commonly used in silico prediction tools for all CYP21A2 missense variants analyzed in this study. Each tool provides a quantitative score (upper row) and a corresponding predicted functional impact or pathogenicity category (lower row) for each variant. Higher scores generally reflect stronger predicted functional impact for Alpha Missense, PolyPhen-2, CADD, MutPred2, DANN, FATHMM, Meta-SNP, SNAP, PhD-SNP, PANTHER , SNPs&GO and S3Ds&GO, whereas lower scores indicate stronger predicted deleteriousness for SIFT and PredictSNP2. Classification labels follow the terminology used by each tool (e.g., “Likely benign”, “Benign”, “Possibly damaging”, “Deleterious”, “Neutral”). A dash (–) indicates that a classification is not provided by the respective tool.
These data correspond to the values visualized in Figure 6 (Heatmap of In Silico Pathogenicity Predictions for Ten CYP21A2 Missense Variants).

	Variant		R76K	E162G	S274Y	L308V	S373N	P387L	H393Q	R401G	R436C	S494N	L10del
In silico tools	Alpha Missense	Score	0.086	0.192	0.156	0.458	0.304	0.591	0.471	0.26	0.393	-	-
		Class	Likely benign	Likely benign	Likely benign	Uncertain	Likely benign	Likely pathogenic	Uncertain	Likely benign	Uncertain	-	-
	PolyPhen-2 (HumDiv)	Score	0.013	0.568	0.946	1	0.665	1	0.934	0.973	1	0.003	-
		Class	Benign; sensitivity: 0.96; specificity: 0.78	Possible damaging; sensitivity: 0.88; specificity: 0.91	Possibly damaging; sensitivity: 0.80; specificity: 0.95	Probably damaging	Possible damaging	Probably damaging; sensitivity: 0.00; specificity: 1.00	Possibly damaging; sensitivity: 0.80; specificity: 0.94	Probably damaging	Probably damaging	Benign; sensitivity: 0.98; specificity: 0.44	-
	SIFT	Score	0.52	0.52	0.04	0	0.07	0.67	0.09	0.13	0	0.2	-
		Class	Tolerated/Likely benign	Tolerated/Likely benign	Affect protein function /Damaging	Affect protein function /Damaging	Affect protein function /Damaging	Tolerated/Likely benign	Affect protein function /Damaging	Tolerated/Likely benign	Affect protein function /Damaging	Tolerated/Likely benign	-
	CADD	Score	12.56	19.73	3.621	22.4	35	24.7	16.45	20.1	28.6	0.156	-
		Class	-	Possibly damaging	-	Likely benign	Very likely damaging	-	-	Possibly damaging	Likely damaging	-	-

MutPred2	Score	0.145	0.504	0.43	0.489	0.25	0.633	0.58	0.241	0.776	0.057	-
	Class	Benign / Likely neutral	Uncertain / Possibly damaging	Benign / Likely neutral	Benign / Likely neutral	Benign / Likely neutral	Uncertain / Possibly damaging	Uncertain / Possibly damaging	Benign / Likely neutral	Pathogenic	Benign / Likely neutral	-
PredictSNP2	Score	0.89	0.89	0.91	0.63	0.87	0.65	0.89	0.89	0.63	0.89	-
	Class	Neutral	Neutral	Neutral	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral	-
DANN	Score	0.95	0.973	0.98	0.997	0.998	1.00	0.97	0.964	0.999	0.60	-
	Class	Neutral	Neutral	Neutral	Deleterious	Deleterious	Deleterious	Neutral	Neutral	Deleterious	Neutral	-
FATHMM	Score	0.01048	0.098	0.04114	0.832	0.985	0.48629	0.1479	0.009	0.283	0.02061	-
	Class	Neutral	Neutral	Neutral	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral	-
Meta-SNP	Score	0.277	0.293	0.517	0.573	0.489	0.531	0.479	0.437	0.749	0.04	-
	Class	-	-	-	-	-	-	-	-	-	-	-
SNAP	Score	0.195	0.42	0.615	0.645	0.345	0.4	0.65	0.42	0.675	0.585	-
	Class	-	-	-	-	-	-	-	-	-	-	-
PhD-SNP	Score	0.126	0.132	0.481	0.624	0.22	0.55	0.57	0.298	0.843	0.062	-
	Class	-	-	-	-	-	-	-	-	-	-	-
PANTHER	Score	0.121	0.262	-	0.43	0.589	0.761	0.237	0.192	0.83	-	-

SNPs&GO	Class	Neutral	Neutral	-	Neutral	Disease	Disease	Neutral	Neutral	Disease	-	-
	Score	0.087	0.101	0.221	0.647	0.669	0.842	0.405	0.196	0.814	0.04	-
	Class	Neutral	Neutral	Neutral	Disease	Disease	Disease	Neutral	Neutral	Disease	Neutral	-
S3Ds&GO	Score	0.074	0.354	-	0.789	0.735	0.952	0.81	0.584	0.883	-	-
	Class	Neutral	Neutral	-	Disease	Disease	Disease	Disease	Disease	Disease	-	-