

Supplementary Materials

Table S1. Prediction of the stabilizing effect of mutations.

VARIABLE REGION	POSITION	MUT	MCSM PREDICTED STABILITY CHANGE ($\Delta\Delta G$)	SDM PREDICTED STABILITY CHANGE ($\Delta\Delta G$)	DUET PREDICTED STABILITY CHANGE ($\Delta\Delta G$)
II	Glu182	Lys	0.047 Kcal/mol <i>(Stabilizing)</i>	-0.72 Kcal/mol <i>(Destabilizing)</i>	0.383 Kcal/mol <i>(Stabilizing)</i>
	Glu183	Ile	0.501 Kcal/mol <i>(Stabilizing)</i>	1.21 Kcal/mol <i>(Stabilizing)</i>	0.625 Kcal/mol <i>(Stabilizing)</i>
	Gly184	Ile	0.125 Kcal/mol <i>(Stabilizing)</i>	3.29 Kcal/mol <i>(Stabilizing)</i>	0.489 Kcal/mol <i>(Stabilizing)</i>
	Gln185	Ala	0.353 Kcal/mol <i>(Stabilizing)</i>	0.83 Kcal/mol <i>(Stabilizing)</i>	0.54 Kcal/mol <i>(Stabilizing)</i>
	Gln186	Glu	-0.112 Kcal/mol <i>(Destabilizing)</i>	0.76 Kcal/mol <i>(Stabilizing)</i>	0.306 Kcal/mol <i>(Stabilizing)</i>
	Gln187	Lys	-0.156 Kcal/mol <i>(Destabilizing)</i>	-0.47 Kcal/mol <i>(Destabilizing)</i>	0.035 Kcal/mol <i>(Stabilizing)</i>
		Ile	0.227 Kcal/mol <i>(Stabilizing)</i>	1.56 Kcal/mol <i>(Stabilizing)</i>	0.363 Kcal/mol <i>(Stabilizing)</i>
	Gln189	Ile	0.029 Kcal/mol <i>(Stabilizing)</i>	1.29 Kcal/mol <i>(Stabilizing)</i>	0.255 Kcal/mol <i>(Stabilizing)</i>
	Gly190	Ala	-0.367 Kcal/mol <i>(Destabilizing)</i>	-2.76 Kcal/mol <i>(Destabilizing)</i>	-0.327 Kcal/mol <i>(Destabilizing)</i>
	Gln191	Glu	-0.071 Kcal/mol <i>(Destabilizing)</i>	-0.42 Kcal/mol <i>(Destabilizing)</i>	0.077 Kcal/mol <i>(Stabilizing)</i>
	Glu192	Lys	0.46 Kcal/mol <i>(Stabilizing)</i>	-1.59 Kcal/mol <i>(Destabilizing)</i>	0.602 Kcal/mol <i>(Stabilizing)</i>
III	Ser216	Ile	-0.272 Kcal/mol <i>(Destabilizing)</i>	1.22 Kcal/mol <i>(Stabilizing)</i>	-0.078 Kcal/mol <i>(Destabilizing)</i>
	Ser217	Ile	-0.188 Kcal/mol <i>(Destabilizing)</i>	3.07 Kcal/mol <i>(Stabilizing)</i>	0.058 Kcal/mol <i>(Stabilizing)</i>
	Ser218	Ala	-0.304 Kcal/mol <i>(Destabilizing)</i>	2.26 Kcal/mol <i>(Stabilizing)</i>	0.062 Kcal/mol <i>(Stabilizing)</i>
	Lys219	Glu	-0.082 Kcal/mol <i>(Destabilizing)</i>	0.72 Kcal/mol <i>(Stabilizing)</i>	0.288 Kcal/mol <i>(Stabilizing)</i>
	Ser221	Ile	-0.368 Kcal/mol <i>(Destabilizing)</i>	1.25 Kcal/mol <i>(Stabilizing)</i>	-0.425 Kcal/mol <i>(Destabilizing)</i>
		Ile	-0.422 Kcal/mol <i>(Destabilizing)</i>	-1.14 Kcal/mol <i>(Destabilizing)</i>	-0.611 Kcal/mol <i>(Destabilizing)</i>
	Ser223	Ala	-0.215 Kcal/mol <i>(Destabilizing)</i>	0.57 Kcal/mol <i>(Stabilizing)</i>	-0.057 Kcal/mol <i>(Destabilizing)</i>
	Ser224	Glu	-0.234 Kcal/mol <i>(Destabilizing)</i>	0.59 Kcal/mol <i>(Stabilizing)</i>	-0.025 Kcal/mol <i>(Destabilizing)</i>
	Glu225	Lys	-0.204 Kcal/mol <i>(Destabilizing)</i>	-0.81 Kcal/mol <i>(Destabilizing)</i>	-0.218 Kcal/mol <i>(Destabilizing)</i>
IV	Gln306	Ile	1.019 Kcal/mol <i>(Stabilizing)</i>	3.58 Kcal/mol <i>(Stabilizing)</i>	1.117 Kcal/mol <i>(Stabilizing)</i>
	Gln307	Ile	0.324 Kcal/mol <i>(Stabilizing)</i>	0.64 Kcal/mol <i>(Stabilizing)</i>	0.465 Kcal/mol <i>(Stabilizing)</i>
	Glu308	Ala	-0.432 Kcal/mol <i>(Destabilizing)</i>	1.03 Kcal/mol <i>(Stabilizing)</i>	-0.365 Kcal/mol <i>(Destabilizing)</i>
	Gln310	Lys	-0.32 Kcal/mol <i>(Destabilizing)</i>	-0.47 Kcal/mol <i>(Destabilizing)</i>	-0.017 Kcal/mol <i>(Destabilizing)</i>

Table S2. Bile acid-binding capacity of Wt and Mut2 8S α globulin digests.

TYPE OF SAMPLE	BILE ACID BINDING CAPACITY (%)	
	WT	MUT2
2-hour digest	27.41 ± 5.03 ^{a,b,a}	33.44 ± 3.13 ^{a,b,a}
6-hour digest	40.97 ± 5.83 ^{b,b,a}	26.07 ± 0.70 ^{b,b,a}
12-hour digest	24.12 ± 2.23 ^{b,b,b}	42.12 ± 4.13 ^{b,b,b}
24-hour digest	36.83 ± 0.50 ^{a,b,a}	28.02 ± 6.93 ^{a,b,a}
0.1 mg/ml rosuvastatin	7.52 ± 8.82	
1 mg/ml rosuvastatin	98.50 ± 0.06	

The first superscript letters indicate comparison of values between 0.1 mg/ml rosuvastatin and each WT and Mut2 hydrolysate; the second superscript letters indicate comparison of values between 1 mg/ml rosuvastatin and each WT and Mut2 hydrolysate; the third superscript letters indicate comparison of values between WT and Mut2 hydrolysates. (Taken from two-tailed t-test at 95% confidence interval). Superscript a indicates $p>0.05$, while superscript b indicates $p<0.05$ between the samples being compared.

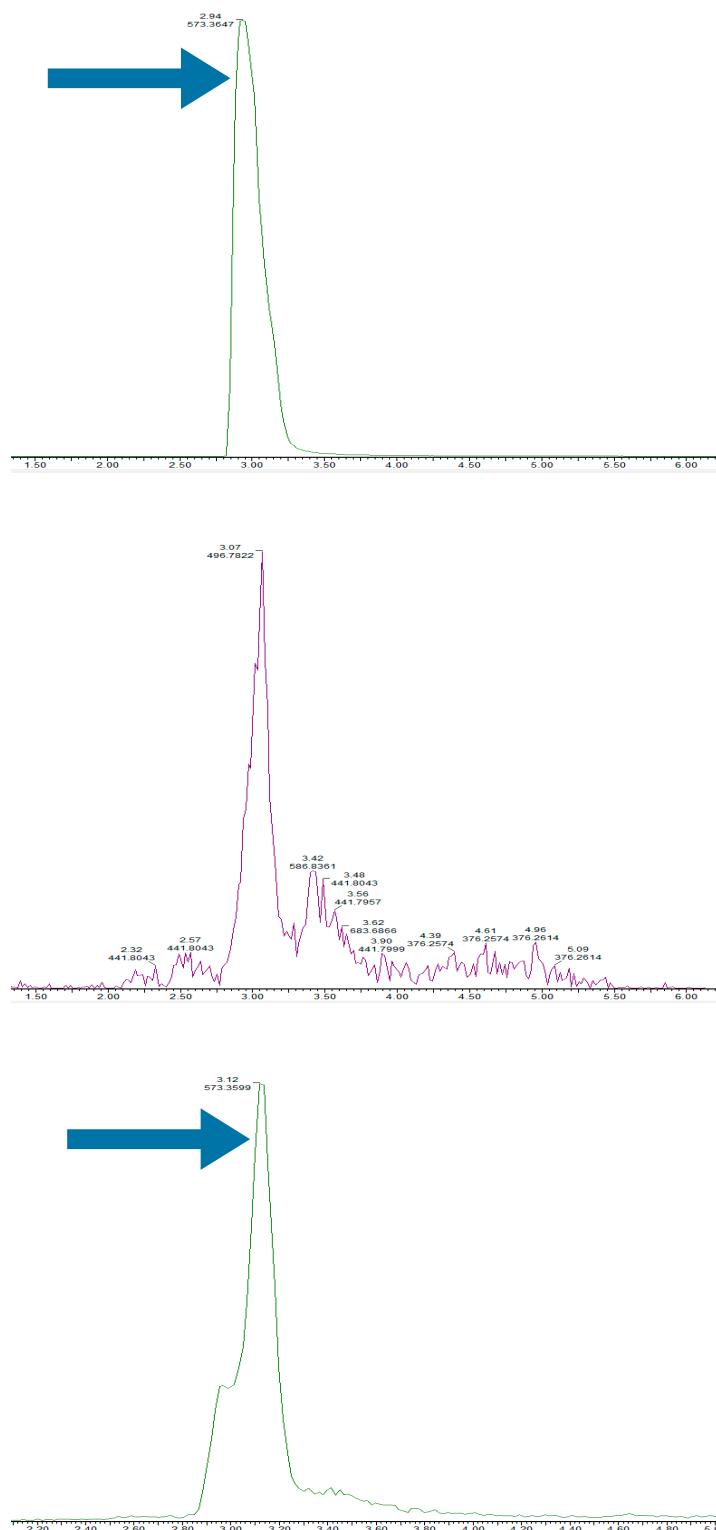


Figure S1. Chromatogram of the 24-hour digests of Wt and Mut2 8S α globulin using LC-MS. From top to bottom: IIAEK peptide standard, 24-hour Wt digest, 24-hour Mut2 digest.

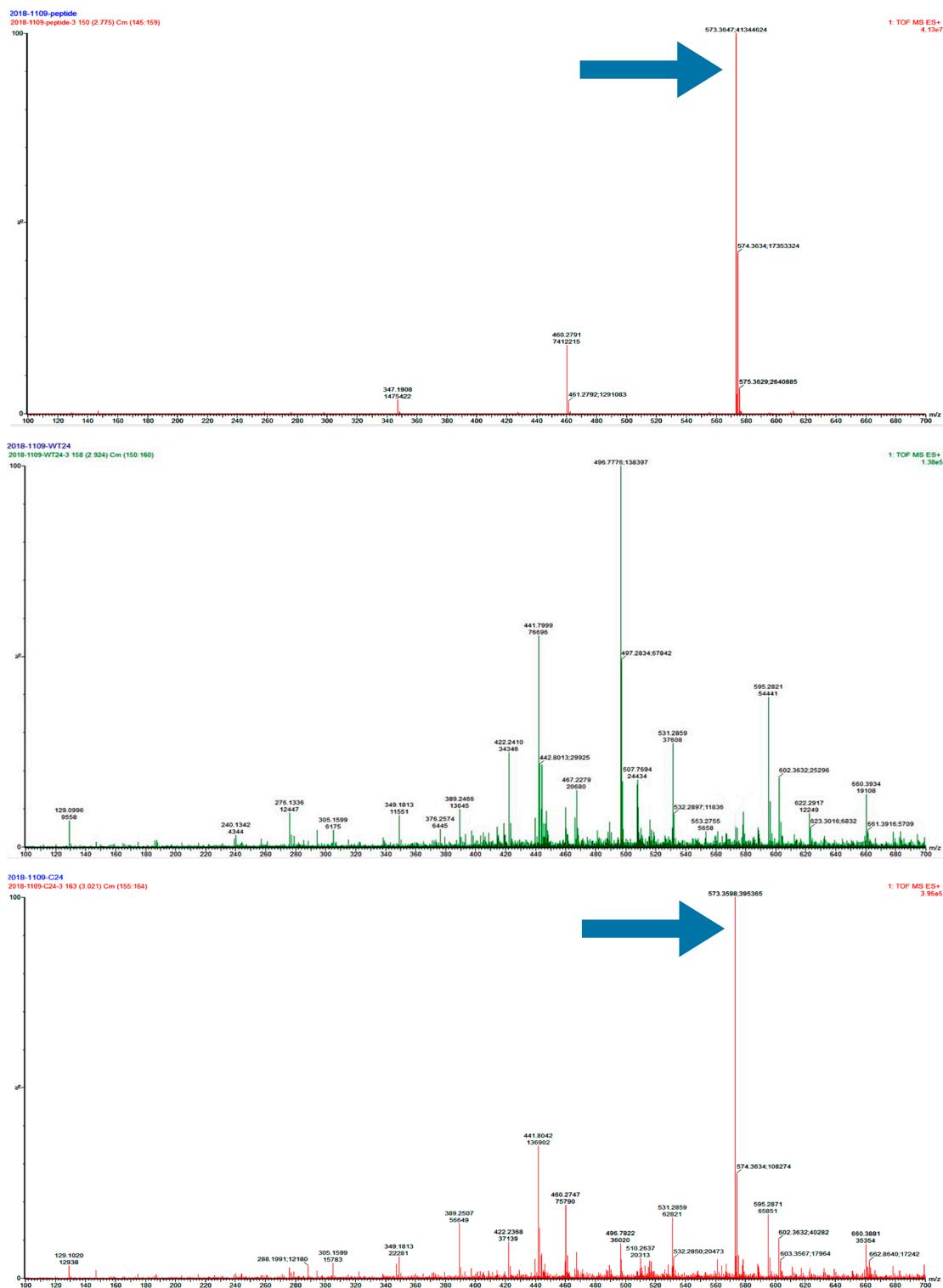


Figure S2. Spectra of the 24-hour digests of Wt and Mut2 8S α globulin using LC-MS. From top to bottom: IIAEK peptide standard, 24-hour Wt digest, and 24-hour Mut2 digests.

