~~A~~Claims

1. Migalastat or a salt thereof for use in a method of treating Fabry disease in a subject comprising:

accessing mutation information corresponding to the subject, the mutation information identifying one or more α-galactosidase A mutations;

determining, based on the mutation information, that the subject has at least one mutation as identified in Table 2; and

administering migalastat or a salt thereof to the subject ~~determined to have~~having the at least one mutation as identified in Table 2.

2. ~~The method of~~Migalastat or a salt thereof for use according to claim 1, wherein determining that the subject has at least one mutation as identified in Table 2 includes:

initiating a query of a data store that identifies two or more mutations from a set of mutations identified in Table 2; and

receiving a query result that identifies the at least one mutation is represented in the mutation information and also in Table 2.

3. ~~The method of claim~~Migalastat or a salt thereof for use according to claim 2, wherein the data store further identifies two or more mutations from another set of mutations identified in Table 1.

4. ~~The method of claim~~Migalastat or a salt thereof for use according to claim 2 or 3, wherein the data store includes at least 50% of the set of mutations identified in Table 2.

5. ~~The method of any~~Migalastat or a salt thereof for use according to any of claims 2-4, wherein the query is initiated by accessing a particular webpage hosted by a web server that controls a data store identifying at least some of the mutations in Table 2.

6. ~~The method of any~~Migalastat or a salt thereof for use according to any of claims 2-4, wherein the query is initiated by:

accessing a particular webpage on a website;

providing input at the particular webpage that identifies at least part of the mutation information; and

selecting an option at the webpage to submit, to a web server, an electronic request to perform the query, the electronic request including a representation of the input;

wherein the query result is received from the web server in response to the query and is displayed at the particular webpage or another webpage on the website.

7. ~~The method of any~~Migalastat or a salt thereof for use according to any of claims 1-6, wherein the at least one mutation includes one or more mutations of α-galactosidase A at amino acid residues 5-14, 17-18, 20-30, 32-33, 36-39, 41, 43, 45-46, 48, 50-51, 53-56, 58-62, 64-89, 91, 96-99, 101-102, 104-110, 113-117, 121, 123-131, 133, 135-141, 143-153, 156-162, 164-167, 169, 171, 173, 175-178, 180-182, 184-201, 203, 204, 206-222, 224, 227- 230, 232-233, 235, 237-261, 263-265, 267-270, 272-273, 275, 277-278, 280-286, 288-289, 291-292, 294-295, 297-300, 302-304, 306-322, 324-327, 329-339, 341, 343-344, 346-357, 359, 362-371, 373-377, 379-381, 383-388, 391-425, 427, 429, or any combination thereof, wherein the residues are numbered relative to SEQ ID NO:2.

~~8. The method of any of claims 1-6, wherein the at least one mutation includes one or more mutations of α-galactosidase A at amino acid residues -14, 17-18, 20-30, 32-33, 36-39, 41, 43, 45-46, 48, 50-51, 53-56, 58-62, 64-89, 91, 96-99, or any combination thereof, wherein the residues are numbered relative to SEQ ID NO:2.~~

~~9. The method of any of claims 1-6, wherein the at least one mutation includes one or more mutations of α-galactosidase A at amino acid residues 101-102, 104-110, 113-117, 121, 123-131, 133, 135-141, 143-153, 156-162, 164-167, 169, 171, 173, 175-178, 180-182, 184-201, or any combination thereof, wherein the residues are numbered relative to SEQ ID NO:2.~~

~~10. The method of any of claims 1-6, wherein the at least one mutation includes one or more mutations of α-galactosidase A at amino acid residues 203, 204, 206-222, 224, 227-230, 232-233, 235, 237-261, 263-265, 267-270, 272-273, 275, 277-278, 280-286, 288-289, 291-~~

~~292, 294-295, 297-300, or any combination thereof, wherein the residues are numbered relative to SEQ ID NO:2.~~

~~11. The method of any of claims 1-6, wherein the at least one mutation includes one or more mutations of α-galactosidase A at amino acid residues 302-304, 306-322, 324-327, 329-339, 341, 343-344, 346-357, 359, 362-371, 373-377, 379-381, 383-388, or any combination thereof, wherein the residues are numbered relative to SEQ ID NO:2.~~

~~12. The method of any of claims 1-6, wherein the at least one mutation includes one or more mutations of α-galactosidase A at amino acid residues 391-425, 427, 429, or any combination thereof, wherein the residues are numbered relative to SEQ ID NO:2.~~

~~13.~~8. ~~The method of any of claims 1-12~~ Migalastat or a salt thereof for use according to any of claims 1-7, wherein the at least one mutation includes a mutation:

at amino acid residue 5 that comprises N5D or N5K;

at amino acid residue 6 that comprises P6L, P6Q, P6R, P6S, or P6T;

at amino acid residue 7 that comprises E7D, E7K, E7V;

at amino acid residue 8 that comprises, L8I, L8P, L8Q;

at amino acid residue 9 that comprises H9L, H9Q, H9R, or H9Y;

at amino acid residue 10 that comprises, L10M, L10P, L10Q,, L10R, or L10V;

at amino acid residue 11 that comprises G11C, G11D, G11R, G11S, or G11V;

at amino acid residue 12 that comprises C12G, C12R, C12S, or C12Y;

at amino acid residue 13 that comprises A13E or A13G;

at amino acid residue 14 that comprises L14F, L14H, or L14V

at amino acid residue 17 that comprises R17C, R17G, R17H, R17P, or R17S;

at amino acid residue 18 that comprises, F18I or F18L;

at amino acid residue 20 that comprises A20G;

at amino acid residue 21 that comprises L21H;

at amino acid residue 22 that comprises V22A, V22F, V22I, or V22L;

at amino acid residue 23 that comprises S23P orS23T;

at amino acid residue 24 that comprises W24S; or

at amino acid residue 25 that comprises D25H;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~14. The method of any of claims 1-13, wherein the at least one mutation includes a mutation:~~

at amino acid residue 26 that comprises I26N;

at amino acid residue 27 that comprises P27A, P27L, P27S, or P27T;

at amino acid residue 28 that comprises G28E, G28R or G28W;

at amino acid residue 29 that comprises A29G, A29P, or A29V;

at amino acid residue 30 that comprises R30G

at amino acid residue 32 that comprises L32M, L32Q, L32R, or L32V;

at amino acid residue 33 that comprises D33A, D33E, or D33V;

at amino acid residue 36 that comprises L36M or L36V;

at amino acid residue 37 that comprises A37E, A37G, or A37S;

at amino acid residue 38 that comprises R38G, R38M, or, R38W;

at amino acid residue 39 that comprises, T39A, T39K, T39M, T39R, or T39S;

at amino acid residue 41 that comprises T41A, T41N, or T41S;

at amino acid residue 43 that comprises G43A;

at amino acid residue 45 that comprises L45M or L45V;

at amino acid residue 46 that comprises H46D, H46N, or H46Q;

at amino acid residue 48 that comprises E48A; or

at amino acid residue 50 that comprises F50Y;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~15. The method of any of claims 1-14, wherein the at least one mutation includes a mutation:~~

at amino acid residue 51 that comprises M51R, M51T, or M51V;

at amino acid residue 53 that comprises N53H;, N53I, N53S, or N53T;

at amino acid residue 54 that comprises L54H, L54R, or L54V;

at amino acid residue 55 that comprises D55A, D55E, D55H, or D55Y;

at amino acid residue 56 that comprises C56W;

at amino acid residue 58 that comprises E58K;

at amino acid residue 59 that comprises E59A, E59D, E59G, E59Q, or E59V;

at amino acid residue 60 that comprises P60A, P60Q, or P60R;

at amino acid residue 61 that comprises D61E, or D61V;

at amino acid residue 62 that comprises S62A, S62C, S62F, S62P, or S62Y;

at amino acid residue 64 that comprises I64L, or I64V;

at amino acid residue 65 that comprises S65C, S65G, or S65R;

at amino acid residue 66 that comprises E66D or E66V;

at amino acid residue 67 that comprises K67E, K67M, K67N, K67Q, or K67T;

at amino acid residue 68 that comprises L68I;

at amino acid residue 69 that comprises F69I or F69Y;

at amino acid residue 70 that comprises M70I,, M70K, M70L, or M70R;

at amino acid residue 71 that comprises E71A, E71D, E71G, E71Q, or E71V;

at amino acid residue 72 that comprises M72L or M72T;

at amino acid residue 73 that comprises A73S or A73T;

at amino acid residue 74 that comprises, E74D, E74G, E74K, or E74V; or

at amino acid residue 75 that comprises L75F or L75P;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~16. The method of any of claims 1-15, wherein the at least one mutation includes a mutation:~~

at amino acid residue 76 that comprises M76V;

at amino acid residue 77 that comprises V77I orV77L;

at amino acid residue 78 that comprises S78L or S78P;

at amino acid residue 79 that comprises E79A, E79D, E79G, E79K, E79Q, or E79V;

at amino acid residue 80 that comprises G80A, G80C, or G80S;

at amino acid residue 81 that comprises W81L;

at amino acid residue 82 that comprises K82E, K82M, K82N, K82R, or K82T;

at amino acid residue 83 that comprises D83A, D83E, D83G, or D83V;

at amino acid residue 84 that comprises A84E, A84G, A84P, A84S, A84T, or A84V;

at amino acid residue 85 that comprises G85A, G85C, or G85R;

at amino acid residue 86 that comprises Y86F;

at amino acid residue 87 that comprises E87G;

at amino acid residue 88 that comprises Y88H, or Y88N;

at amino acid residue 89 that comprises L89V

at amino acid residue 91 that comprises I91F, I91L, I91M, or I91S;

at amino acid residue 96 that comprises M96L orM96T;

at amino acid residue 97 that comprises A97D, A97S, or A97T;

at amino acid residue 98 that comprises P98H, P98L, or P98R; or

at amino acid residue 99 that comprises Q99E, Q99L, Q99P, or Q99R;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~17. The method of any of claims 1-16, wherein the at least one mutation includes a mutation:~~

at amino acid residue 101 that comprises D101A, D101E, D101G, D101H, D101V;

at amino acid residue 102 that comprises S102A, S102P, or S102T;

at amino acid residue 104 that comprises G104A, G104D, or G104S;

at amino acid residue 105 that comprises R105G, R105I, R105K, or R105T

at amino acid residue 106 that comprises L106H, L106I, L106P, or L106V;

at amino acid residue 107 that comprises Q107E, Q107H, or Q107K;

at amino acid residue 108 that comprises A108E or A108V;

at amino acid residue 109 that comprises D109A, D109E, D109H, D109N, or D109Y;

at amino acid residue 110 that comprises P110T;

at amino acid residue 113 that comprises F113V, or F113Y;

at amino acid residue 114 that comprises P114L;

at amino acid residue 115 that comprises H115D or H115N;

at amino acid residue 116 that comprises G116R;

at amino acid residue 117 that comprises I117M or I117T;

at amino acid residue 121 that comprises A121V;

at amino acid residue 123 that comprises Y123D, Y123F, Y123N, or Y123S;

at amino acid residue 124 that comprises V124I; or

at amino acid residue 125 that comprises H125D, H125N, or H125R;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~18. The method of any of claims 1-17, wherein the at least one mutation includes a mutation:~~

~~at amino acid residue 126 that comprises S126C or S126I,;~~

at amino acid residue 127 that comprises K127E;

at amino acid residue 128 that comprises G128A;

at amino acid residue 129 that comprises L129V;

at amino acid residue 130 that comprises K130M, K130N, or K130Q;

at amino acid residue 131 that comprises L131V;

at amino acid residue 133 that comprises, I133L, I133T, or I133V;

at amino acid residue 135 that comprises A135E, A135G, A135S, or A135T;

at amino acid residue 136 that comprises D136A, D136N or D136V;

at amino acid residue 137 that comprises V137A, V137D, V137G, V137I or V137L;

at amino acid residue 138 that comprises G138A;

at amino acid residue 139 that comprises N139H N139I, N139K, or N139Y;

at amino acid residue 140 that comprises K140E, K140I, K140N, K140Q, or K140R;

at amino acid residue 141 that comprises T141S;

at amino acid residue 143 that comprises, A143E, or A143G;

at amino acid residue 144 that comprises G144A, G144C, G144R, or G144S;

at amino acid residue 145 that comprises F145C, F145L, F145V or F145Y;

at amino acid residue 146 that comprises P146A, P146H, P146L, or P146T;

at amino acid residue 147 that comprises G147A;

at amino acid residue 148 that comprises S148C, S148G, or S148T;

at amino acid residue 149 that comprises F149C; or

at amino acid residue 150 that comprises G150E or G150V;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~19. The method of any of claims 1-18, wherein the at least one mutation includes a mutation:~~

at amino acid residue 151 that comprises Y151C, Y151D, or Y151S

at amino acid residue 152 that comprises Y152F, or Y152S;

at amino acid residue 153 that comprises D153A, D153H, D153N D153V, or D153Y;

at amino acid residue 156 that comprises A156G;

at amino acid residue 157 that comprises Q157E, Q157K, Q157L, or Q157P;

at amino acid residue 158 that comprises T158A, T158I, T158N, or T158S;

at amino acid residue 159 that comprises F159I, F159L, F159V, or F159Y;

at amino acid residue 160 that comprises A160G, A160S, A160T or A160V;
at amino acid residue 161 that comprises D161H, D161N, D161V, or D161Y;
at amino acid residue 162 that comprises W162S;
at amino acid residue 164 that comprises V164A, V164I, or V164L;
at amino acid residue 165 that comprises D165A or D165E;
at amino acid residue 166 that comprises L166M or L166Q;
at amino acid residue 167 that comprises L167I;
at amino acid residue 169 that comprises F169C, F169L, F169V, or F169Y;
at amino acid residue 171 that comprises G171A or G171V;
at amino acid residue 173 that comprises Y173C, Y173F, Y173H, or Y173S; or
at amino acid residue 175 that comprises D175G, D175H, D175V, or D175Y;
~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~20. The method of any of claims 1-19, wherein the at least one mutation includes a mutation:~~
at amino acid residue 176 that comprises S176C or S176R;
at amino acid residue 177 that comprises L177F, L177M, L177S, L177V, or L177W;
at amino acid residue 178 that comprises E178A, E178G, E178K, or E178Q;
at amino acid residue 180 that comprises L180M, or L180S;
at amino acid residue 181 that comprises A181P, A181T, or A181V
at amino acid residue 182 that comprises D182A, D182E, D182V, or D182Y;
at amino acid residue 184 that comprises Y184F, Y184H, or Y184S;
at amino acid residue 185 that comprises K185M, K185N, K185Q, or K185T ;
at amino acid residue 186 that comprises H186D, H186L, H186N, H186Q, or H186Y;
at amino acid residue 187 that comprises M187L;
at amino acid residue 188 that comprises S188A, S188C S188F, S188P, S188T, or S188Y;
at amino acid residue 189 that comprises L189S or L189V;
at amino acid residue 190 that comprises A190D, A190G, A190S, A190T, or A190V;
at amino acid residue 191 that comprises L191M or L191V;
at amino acid residue 192 that comprises N192D, N192H, N192K, N192S, or N192T;
at amino acid residue 193 that comprises R193G, R193M, R193T or R193W;
at amino acid residue 194 that comprises T194N, T194P, or T194S;

at amino acid residue 195 that comprises G195C, G195R, or G195S;

at amino acid residue 196 that comprises R196I,or R196K;

at amino acid residue 197 that comprises S197C, S197G, S197I, S197N, or S197T;

at amino acid residue 198 that comprises I198M or I198S;

at amino acid residue 199 that comprises V199E or V199L; or

at amino acid residue 200 that comprises Y200N or Y200S;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~21. The method of any of claims 1-20, wherein the at least one mutation includes a mutation:~~

at amino acid residue 201 that comprises S201A, S201C, or S201T;

at amino acid residue 203 that comprises E203A, E203G, or E203Q;

at amino acid residue 204 that comprises W204S;

at amino acid residue 206 that comprises L206F, L206H, L206I, L206R, or L206V;

at amino acid residue 207 that comprises Y207F;

at amino acid residue 208 that comprises M208K;

at amino acid residue 209 that comprises W209C, or W209G;

at amino acid residue 210 that comprises P210H or P210T;

at amino acid residue 211 that comprises F211C, F211L, F211S, F211V, or F211Y;

at amino acid residue 212 that comprises Q212H, or Q212P;

at amino acid residue 213 that comprises K213E, or K213Q;

at amino acid residue 214 that comprises P214A, P214H, P214R, or P214T;

at amino acid residue 215 that comprises N215H, N215K, N215T, or N215Y;

at amino acid residue 216 that comprises Y216F, Y216H, , or Y216N;

at amino acid residue 217 that comprises T217A, T217I, T217K, T217P, T217R, or T217S;

at amino acid residue 218 that comprises E218A, E218D, E218G, E218K, E218Q, or E218V

at amino acid residue 219 that comprises I219F, I219M, or I219S;

at amino acid residue 220 that comprises R220L;

at amino acid residue 221 that comprises Q221E, Q221H, Q221K.,Q221L, or Q221R

at amino acid residue 222 that comprises Y222C, Y222D, Y222H, Y222N, or Y222S; or

at amino acid residue 224 that comprises N224H;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~22. The method of any of claims 1-21, wherein the at least one mutation includes a mutation:~~

at amino acid residue 227 that comprises R227G;

at amino acid residue 228 that comprises N228H, N228I, or N228T;

at amino acid residue 229 that comprises F229I, F229S, or F229Y;

at amino acid residue 230 that comprises A230D, A230G, A230P, or A230V;

at amino acid residue 232 that comprises I232L, I232M, or I232V;

at amino acid residue 5 that comprises D233A, D233E, D233G, or D233V;

at amino acid residue 235 that comprises S235A or S235T;

at amino acid residue 237 that comprises K237I;

at amino acid residue 238 that comprises S238C, S238I, or S238T;

at amino acid residue 239 that comprises I239L;

at amino acid residue 240 that comprises K240E, K240M, or K240R;

at amino acid residue 241 that comprises S241C, S241I, or S241T;

at amino acid residue 242 that comprises I242L, I242M, or I242S;

at amino acid residue 243 that comprises L243M, L243S, or L243V;

at amino acid residue 244 that comprises D244A, D244E, D244G, D244V, or D244Y;

at amino acid residue 245 that comprises W245C,

at amino acid residue 246 that comprises T246A, T246I, T246K, or T246R;

at amino acid residue 247 that comprises S247A, S247F, S247T, or S247Y;

at amino acid residue 248 that comprises F248C, F248L, F248V, or F248Y;

at amino acid residue 249 that comprises N249D, N249H, N249I, N249S, N249T, or N249Y;

at amino acid residue 250 that comprises Q250E or Q250L;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~23. The method of any of claims 1-22, wherein the at least one mutation includes a mutation:~~

at amino acid residue 251 that comprises E251G, E251K, E251Q, or E251V;

at amino acid residue 252 that comprises R252G;

at amino acid residue 253 that comprises I253F, I253N, or I253V;

at amino acid residue 254 that comprises V254A, V254D, V254F, or V254G;

at amino acid residue 255 that comprises D255A. D255E, D255H, D255N, D255V, or D255Y;

at amino acid residue 256 that comprises V256D, V256G, or V256L;

at amino acid residue 257 that comprises A257S;

at amino acid residue 258 that comprises G258E;

at amino acid residue 259 that comprises P259A, or P259T;

at amino acid residue 260 that comprises G260W;

at amino acid residue 261 that comprises G261A;

at amino acid residue 263 that comprises N263H or N263T;

~~at amino acid residue 264 that comprises D264H or D264N;~~

at amino acid residue 265 that comprises P265A or P265Q;

at amino acid residue 267 that comprises M267L or M267V;

at amino acid residue 268 that comprises L268F or L268I;

at amino acid residue 269 that comprises V269L;

at amino acid residue 270 that comprises I270L, I270S, or I270V;

at amino acid residue 272 that comprises N272D;

at amino acid residue 273 that comprises F273Y; or

at amino acid residue 275 that comprises L275I;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~24. The method of any of claims 1-23, wherein the at least one mutation includes a mutation:~~

at amino acid residue 277 that comprises W277L;

at amino acid residue 278 that comprises N278I,;

at amino acid residue 280 that comprises Q280L or Q280R;

at amino acid residue 281 that comprises V281A, V281E, , V281G, or V281L

at amino acid residue 282 that comprises T282S;

at amino acid residue 283 that comprises Q283E, Q283H, or Q283L;

at amino acid residue 284 that comprises M284I or M284L;

at amino acid residue 285 that comprises A285G, A285T, or A285V;

at amino acid residue 286 that comprises L286F, L286H, or L286V;

at amino acid residue 288 that comprises A288G, A288S, or A288V;

at amino acid residue 289 that comprises I289L, I289T or I289V;

at amino acid residue 291 that comprises A291G;

at amino acid residue 292 that comprises A292G or A292S;

at amino acid residue 294 that comprises L294F, L294I, or L294V

at amino acid residue 295 that comprises F295I, F295S, F295V, or F295Y,;

at amino acid residue 297 that comprises S297T;

at amino acid residue 298 that comprises N298D, N298I, or N298T;

at amino acid residue 299 that comprises D299H or D299N; or

at amino acid residue 300 that comprises L300I or L300V;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~25. The method of any of claims 1-24, wherein the at least one mutation includes a mutation:~~

at amino acid residue 302 that comprises H302D, H302L, H302N, or H302Y;

at amino acid residue 303 that comprises I303S;

at amino acid residue 304 that comprises S304I;

at amino acid residue 306 that comprises Q306E, Q306L, or Q306P;

at amino acid residue 307 that comprises A307D, A307G, A307P, A307S, or A307V;

at amino acid residue 308 that comprises K308I, K308Q, or K308R;

at amino acid residue 309 that comprises A309D or A309T;

at amino acid residue 310 that comprises L310I;

at amino acid residue 311 that comprises L311I;

at amino acid residue 312 that comprises Q312E, Q312K, or Q312L;

at amino acid residue 313 that comprises D313E or D313V;

at amino acid residue 314 that comprises K314E, K314M, K314N, or K314T;

at amino acid residue 315 that comprises D315A, D315G, D315H, D315N, D315V, or D315Y;

at amino acid residue 316 that comprises V316A or V316L;

at amino acid residue 317 that comprises I317L, I317M, or I317V;

at amino acid residue 318 that comprises A318D, A318P, A318T, or A318V;

at amino acid residue 319 that comprises I319M;

at amino acid residue 320 that comprises N320S or N320T;

at amino acid residue 321 that comprises Q321K;

at amino acid residue 322 that comprises D322A or D322V;

at amino acid residue 324 that comprises L324V or L324W; or

at amino acid residue 325 that comprises G325A, G325C, or G325V;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~26. The method of any of claims 1-25, wherein the at least one mutation includes a mutation:~~

at amino acid residue 326 that comprises K326E, K326M, K326Q, K326R, or K326T;

at amino acid residue 327 that comprises Q327H or Q327P;

at amino acid residue 329 that comprises Y329C, Y329D, Y329F, Y329H, or Y329N;

at amino acid residue 330 that comprises Q330E, Q330H, or Q330K;

at amino acid residue 331 that comprises L331H, L331P, L331R, or L331V;

at amino acid residue 332 that comprises R332G, R332I, R332S, or R332T;

at amino acid residue 333 that comprises Q333E, Q333L, Q333P, or G334R;

at amino acid residue 334 that comprises G334V;

at amino acid residue 335 that comprises D335A, D335E, D335G, D335V, or D335Y;

at amino acid residue 336 that comprises N336D, N336I, N336S, N336T, or N336Y;

at amino acid residue 337 that comprises F337C, F337L, F337V, or F337Y;

at amino acid residue 338 that comprises E338A, E338D, or E338G;

at amino acid residue 339 that comprises V339M;

at amino acid residue 341 that comprises E341A, E341Q;

at amino acid residue 343 that comprises P343A or P343S;

at amino acid residue 344 that comprises L344F, L344R, or L344V;

at amino acid residue 346 that comprises G346A, G346C, G346D, or G346V;

at amino acid residue 347 that comprises L347I;

at amino acid residue 348 that comprises A348D;

at amino acid residue 349 that comprises W349C or W349L; or

at amino acid residue 350 that comprises A350G, A350S, A350T, A350V;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~27. The method of any of claims 1-26, wherein the at least one mutation includes a mutation:~~

at amino acid residue 351 that comprises V351A or V351E;

at amino acid residue 352 that comprises A352S or A352T;

at amino acid residue 353 that comprises M353K, M353L, or M353T;

at amino acid residue 354 that comprises I354R;

at amino acid residue 355 that comprises N355D, N355H, N355S, or N355Y;

at amino acid residue 356 that comprises R356L;

at amino acid residue 357 that comprises Q357E;

at amino acid residue 359 that comprises I359F, I359L, I359N, I359S, or I359V;

at amino acid residue 362 that comprises P362A, P362H, P362R, or P362S;

at amino acid residue 363 that comprises R363G, R363L, or R363S;

at amino acid residue 364 that comprises S364C or S364P;

at amino acid residue 365 that comprises Y365D, Y365F, Y365N, or Y365S;

at amino acid residue 366 that comprises T366I, T366N, T366P, or T366S

at amino acid residue 367 that comprises I367F, I367L, or I367M;

at amino acid residue 368 that comprises A368G or A368P;

at amino acid residue 369 that comprises V369A, V369F, V369G, V369I, or V369L;

at amino acid residue 370 that comprises A370D, A370G, A370P, A370T, or A370V;

at amino acid residue 371 that comprises S371C or S371T;

at amino acid residue 373 that comprises G373A or G373C;

at amino acid residue 374 that comprises K374E, K374I, K374R, or K374T; or

at amino acid residue 375 that comprises G375R;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~28. The method of any of claims 1-27, wherein the at least one mutation includes a mutation:~~

at amino acid residue 376 that comprises V376E, V376G, V376L or V376M;

at amino acid residue 377 that comprises A377G, A377P, A377S, or A377T;

at amino acid residue 379 that comprises N379D, N379I, N379K, or N379T;

at amino acid residue 380 that comprises P380A, P380H, P380R, or P380T;

at amino acid residue 381 that comprises A381D;

at amino acid residue 383 that comprises F383C, F383I, or F383Y;

at amino acid residue 384 that comprises I384F, I384M, or I384T;

at amino acid residue 385 that comprises T385I;

at amino acid residue 386 that comprises Q386H, Q386K, or Q386L;

at amino acid residue 387 that comprises L387F, L387H, L387I, or L387R;

at amino acid residue 388 that comprises L388F, L388H, L388I, L388R, or L388V;

at amino acid residue 391 that comprises K391I, K391N, K391Q, or K391R;

at amino acid residue 392 that comprises R392G, R392K, R392M or R392W;

at amino acid residue 393 that comprises s K393E, K393N, K393Q, or K393T;

at amino acid residue 394 that comprises L394I, L394Q, or L394R;

at amino acid residue 395 that comprises G395R;

at amino acid residue 396 that comprises F396C, F396I, F396L, or F396V;

at amino acid residue 397 that comprises Y397C, Y397F, Y397H, Y397N, or Y397S; or

at amino acid residue 398 that comprises E398G or E398Q;

at amino acid residue 394 that comprises W399G or W399R;

at amino acid residue 400 that comprises T400A, T400I, T400N, T400P, or T400S;

~~wherein the residues are numbered relative to SEQ ID NO:2.~~

~~29. The method of any of claims 1-28, wherein the at least one mutation includes a mutation:~~

at amino acid residue 401 that comprises S401A, S401L, or S401T;

at amino acid residue 402 that comprises R402G, R402M, R402S, R402T, or R402W;

at amino acid residue 403 that comprises L403F or L403V;

at amino acid residue 404 that comprises R404G, R404I, R404K, R404S, or R404T;

at amino acid residue 405 that comprises S405G;

at amino acid residue 406 that comprises H406D, H406L, or H406Q;

at amino acid residue 407 that comprises I407L, I407M, or I407T;

at amino acid residue 408 that comprises N408D, N408H or N408T;

at amino acid residue 409 that comprises P409L;

at amino acid residue 410 that comprises T410S;

at amino acid residue 411 that comprises G411A, G411C, or G411V;

at amino acid residue 412 that comprises T412A, T412I, or T412S;

at amino acid residue 413 that comprises V413F, V413G, or V413I;

at amino acid residue 414 that comprises L414F or L414V;
at amino acid residue 415 that comprises L415H or L415I;
at amino acid residue 416 that comprises Q416E, Q416H, or Q416L;
at amino acid residue 417 that comprises L417I;
at amino acid residue 418 that comprises E418A, E418D, E418K, or E418Q;
at amino acid residue 419 that comprises N419I, N419S, N419T, or N419Y;
at amino acid residue 420 that comprises T420K, T420P, T420R, or T420S;
at amino acid residue 421 that comprises M421I, M421K, M421L, M421R, or M421T;
at amino acid residue 422 that comprises Q422P;
at amino acid residue 423 that comprises M423I, M423K, M423L or M423T;
at amino acid residue 424 that comprises S424L;
at amino acid residue 425 that comprises L425F;
at amino acid residue 427 that comprises D427N; or
at amino acid residue 429 that comprises L429R;
wherein the residues are numbered relative to SEQ ID NO:2.

~~30. The method of any of the preceding claims, wherein administering migalastat or salt thereof that comprises administering migalastat or salt thereof to the subject every other day.~~

~~31. The method of any of the preceding claims, wherein administering migalastat or salt thereof that comprises administering to the subject a dose of about 100 to about 150 mg free base equivalent of the migalastat or salt thereof.~~

~~32. The method of any of the preceding claims, wherein administering migalastat or salt thereof that comprises administering to the subject a dose of about 123 mg free base equivalent of the migalastat or salt thereof.~~

~~33. The method of any of the preceding claims, wherein the migalastat or salt thereof enhances α-galactosidase A activity in the subject.~~

34. The method of any of the preceding claims, wherein the at least one mutation includes an HEK assay amenable mutation in α-galactosidase A

35. The method of any of the preceding claims, wherein the migalastat or salt thereof is administered orally.

36. The method of any of claims 1-34, wherein the migalastat or salt thereof is administered by injection.

37. A computer-implemented method comprising:

receiving an electronic communication that corresponds to an identification of a particular mutation;

querying a data store medium using the identification of the particular mutation, wherein the data store medium includes an identification of each of a set of amenable mutations, and wherein each of the set of amenable mutations corresponds to a mutation listed in Table 2;

detecting a result of the query, wherein the result is indicative of whether the particular mutation is represented in the set of amenable mutations;

generating, based on the response, an output that is indicative of a suitability of treating a subject with the particular mutation with migalastat or a migalastat salt; and

transmitting the output.

38. The method of claim 37, wherein the electronic communication includes the identification of the particular mutation in a first format, and wherein the method further that comprises:

determining that the first format differs from a second format used by the data store;

extracting one or more components from the identification;

generating a second identification based on the components, the second identification being in the second format;

transmitting the second identification; and

receiving a second electronic communication that indicates that the second identification corresponds to the first identification, wherein the data store medium is queried in response to receiving the second electronic communication.

39. The method of claim 37 or 38, wherein the data store medium further includes an identification of a second set of amenable mutations, wherein each of the second set of amenable mutations corresponds to a mutation listed in Table 1, and wherein the result is further indicative of whether the particular mutation is represented in the second set of amenable mutations.

40. The method of any of claims 37-39, wherein the result includes a binary indication as to whether migalastat or migalastat salt is a suitable treatment for a condition attributed to the particular mutation.

41. The method of any of claims 37-40, further comprising:

transmitting webpage data to a user device, wherein the electronic communication is received from the user device, wherein the webpage data corresponds to a webpage, and wherein the identification of the particular mutation corresponds to input detected at the webpage.

42. The method of any of claims 37-41, wherein the data store medium identifies at least 90% of the mutations listed in Table 2.

43. A system comprising:

one or more data processors; and

a non-transitory computer readable storage medium containing instructions which, when executed on the one or more data processors, cause the one or more data processors to perform actions including:

receiving an electronic communication that corresponds to an identification of a particular mutation;

querying a data store medium using the identification of the particular mutation, wherein the data store medium includes an identification of each of a set of amenable mutations, and wherein each of the set of amenable mutations corresponds to a mutation listed in Table 2;

detecting a result of the query, wherein the result is indicative of whether the particular mutation is represented in the set of amenable mutations;

generating, based on the response, an output that is indicative of a suitability of treating a subject with the particular mutation with migalastat or a migalastat salt; and

transmitting the output.

44. The system of claim 43, wherein the electronic communication includes the identification of the particular mutation in a first format, and wherein the actions further include:

determining that the first format differs from a second format used by the data store;

extracting one or more components from the identification;

generating a second identification based on the components, the second identification being in the second format;

transmitting the second identification; and

receiving a second electronic communication that indicates that the second identification corresponds to the first identification, wherein the data store medium is queried in response to receiving the second electronic communication.

45. The system of claim 43 or 44, wherein the data store medium further includes an identification of a second set of amenable mutations, wherein each of the second set of amenable mutations corresponds to a mutation listed in Table 1, and wherein the result is further indicative of whether the particular mutation is represented in the second set of amenable mutations.

46. The system of any of claims 43-45, wherein the result includes a binary indication as to whether migalastat or migalastat salt is a suitable treatment for a condition attributed to the particular mutation.

47. The system of any of claims 43-46, wherein the actions further include:

transmitting webpage data to a user device, wherein the electronic communication is received from the user device, and the identification of the particular mutation corresponds to input detected at the webpage.

48. The system of any of claims 43-47, wherein the data store medium identifies at least 90% of the mutations listed in Table 2.

49. A computer-program product tangibly embodied in a non-transitory machine-readable storage medium, including instructions configured to cause one or more data processors to perform actions including:

receiving an electronic communication that corresponds to an identification of a particular mutation;

querying a data store medium using the identification of the particular mutation, wherein the data store medium includes an identification of each of a set of amenable mutations, and wherein each of the set of amenable mutations corresponds to a mutation listed in Table 2;

detecting a result of the query, wherein the result is indicative of whether the particular mutation is represented in the set of amenable mutations;

generating, based on the response, an output that is indicative of a suitability of treating a subject with the particular mutation with migalastat or a migalastat salt; and

transmitting the output.

50. The computer-program product of claim 49, wherein the electronic communication includes the identification of the particular mutation in a first format, and wherein the actions further include:

determining that the first format differs from a second format used by the data store;

extracting one or more components from the identification;

generating a second identification based on the components, the second identification being in the second format;

transmitting the second identification; and

receiving a second electronic communication that indicates that the second identification corresponds to the first identification, wherein the data store medium is queried in response to receiving the second electronic communication.

51. The computer-program product of claim 49 or 50, wherein the data store medium further includes an identification of a second set of amenable mutations, wherein each of the second set of amenable mutations corresponds to a mutation listed in Table 1, and wherein the result is further indicative of whether the particular mutation is represented in the second set of amenable mutations.

52. The computer-program product of any of claims 49-51, wherein the result includes a binary indication as to whether migalastat or migalastat salt is a suitable treatment for a condition attributed to the particular mutation.

53. The computer-program product of any of claims 49-52, wherein the actions further include:

transmitting webpage data to a user device, wherein the electronic communication is received from the user device, and the identification of the particular mutation corresponds to input detected at the webpage.

54. The computer-program product of any of claims 49-53, wherein the data store medium identifies at least 90% of the mutations listed in Table 2.

55. A computer-implemented method comprising:

accessing a data store medium storing a data set unit storing a data set that identifies, for each mutation of a set of mutations, a degree to which α Gal A activity is responsive to migalastat or a migalastat salt when the mutation is present, wherein the set of mutations includes one or more mutations listed in Table 2;

receiving a communication that identifies one or more particular mutations;

querying the data store medium using a representation of the one or more particular mutations;

detecting a result of the query that indicates, for each particular mutation of the one or more particular mutations, the degree to which α Gal A activity is responsive to migalastat or a migalastat salt when the particular mutation is present;

determining a metric corresponding to a predicted efficacy of treating a subject having the one or more particular mutations with migalastat or a migalastat salt; and

outputting the metric.

56. The computer-implemented method of claim 55, wherein the one or more particular mutations include a plurality of particular mutations, and wherein determining the metric includes identifying a minimum or maximum of the degrees to which α-Gal A activity is responsive to migalastat or a migalastat salt across the plurality of particular mutations.

57. The computer-implemented method of claim 55 or 56, wherein the metric is a binary indication as to whether a condition associated with the one or more particular mutations is amenable to treatment with migalastat or a migalastat salt.

58. The computer-implemented method of any of claims 55-57, wherein the metric includes a number, category or descriptor indicating a predicted extent to which a condition associated with the one or more particular mutations is amenable to treatment with migalastat or a migalastat salt.

59. The computer-implemented method of any of claims 55-58, wherein the result of the query indicates, for a particular mutation of the one or more particular mutations and as a result of the particular mutation not being detected within the data set, that the α-Gal A activity corresponding to the particular mutation is not responsive to migalastat or a migalastat salt.

60. The computer-implemented method of any of claims 55-59, wherein the set of mutations further includes one or more mutations listed in Table 1.

61. The computer-implemented method of any of claims 55-60, wherein the one or more particular mutations include a plurality of particular mutations, and wherein determining the metric includes identifying a minimum or maximum of the degrees to which α-Gal A activity is responsive to migalastat or a migalastat salt across the plurality of particular mutations.

62. A system comprising:

one or more data processors; and

a non-transitory computer readable storage medium containing instructions which, when executed on the one or more data processors, cause the one or more data processors to perform actions including:

accessing a data set unit storing a data set that identifies, for each mutation of a set of mutations, a degree to which α-Gal A activity is responsive to migalastat or a migalastat salt when the mutation is present, wherein the set of mutations includes one or more mutations listed in Table 2;

receiving a communication that identifies one or more particular mutations;

querying the data set unit using a representation of the one or more particular mutations;

detecting a result of the query that indicates, for each particular mutation of the one or more particular mutations, the degree to which α-Gal A activity is responsive to migalastat or a migalastat salt when the particular mutation is present;

determining a metric corresponding to a predicted efficacy of treating a subject having the one or more particular mutations with migalastat or a migalastat salt; and

outputting the metric.

63. The system of claim 62, wherein the one or more particular mutations include a plurality of particular mutations, and wherein determining the metric includes identifying a minimum or maximum of the degrees to which α-Gal A activity is responsive to migalastat or a migalastat salt across the plurality of particular mutations.

64. The system of claim 62 or 63, wherein the metric is a binary indication as to whether a condition associated with the one or more particular mutations is amenable to treatment with migalastat or a migalastat salt.

65. The system of any of claims 62-64, wherein the metric includes a number, category or descriptor indicating a predicted extent to which a condition associated with the one or more particular mutations is amenable to treatment with migalastat or a migalastat salt.

66. The system of any of claims 62-65, wherein the result of the query indicates, for a particular mutation of the one or more particular mutations and as a result of the particular mutation not

being detected within the data set, that the α-Gal A activity corresponding to the particular mutation is not responsive to migalastat or a migalastat salt.

67. The system of any of claims 62-66, wherein the set of mutations further includes one or more mutations listed in Table 1.

68. The system of any of claims 62-67, wherein the one or more particular mutations include a plurality of particular mutations, and wherein determining the metric includes identifying a minimum or maximum of the degrees to which α-Gal A activity is responsive to migalastat or a migalastat salt across the plurality of particular mutations.

69. A computer-program product tangibly embodied in a non-transitory machine-readable storage medium, including instructions configured to cause one or more data processors to perform actions including:

accessing a data set unit storing a data set that identifies, for each mutation of a set of mutations, a degree to which α-Gal A activity is responsive to migalastat or a migalastat salt when the mutation is present, wherein the set of mutations includes one or more mutations listed in Table 2;

receiving a communication that identifies one or more particular mutations;

querying the data set unit using a representation of the one or more particular mutations;

detecting a result of the query that indicates, for each particular mutation of the one or more particular mutations, the degree to which α-Gal A activity is responsive to migalastat or a migalastat salt when the particular mutation is present;

determining a metric corresponding to a predicted efficacy of treating a subject having the one or more particular mutations with migalastat or a migalastat salt; and

outputting the metric.

70. The computer-program product of claim 69, wherein the one or more particular mutations include a plurality of particular mutations, and wherein determining the metric includes identifying a minimum or maximum of the degrees to which α-Gal A activity is responsive to migalastat or a migalastat salt across the plurality of particular mutations.

~~71. The computer-program product of claim 69 or 70, wherein the metric is a binary indication as to whether a condition associated with the one or more particular mutations is amenable to treatment with migalastat or a migalastat salt.~~

~~72. The computer-program product of any of claims 69-71, wherein the metric includes a number, category or descriptor indicating a predicted extent to which a condition associated with the one or more particular mutations is amenable to treatment with migalastat or a migalastat salt.~~

~~73. The computer-program product of any of claims 69-72, wherein the result of the query indicates, for a particular mutation of the one or more particular mutations and as a result of the particular mutation not being detected within the data set, that the α-Gal A activity corresponding to the particular mutation is not responsive to migalastat or a migalastat salt.~~

~~74. The computer-program product of any of claims 69-73, wherein the set of mutations further includes one or more mutations listed in Table 1.~~

~~75. The computer-program product of any of claims 69-74, wherein the one or more particular mutations include a plurality of particular mutations, and wherein determining the metric includes identifying a minimum or maximum of the degrees to which α-Gal A activity is responsive to migalastat or a migalastat salt across the plurality of particular mutations.~~

~~76. A method of treating Fabry disease in a subject comprising:~~

accessing mutation information corresponding to the subject, the mutation information identifying one or more α-galactosidase A mutations;

~~determining, based on the mutation information, that the subject has a mutation for which α-Gal A activity in lysates prepared from HEK-293 cells transiently transfected with a mutant form of α-Gal A and incubated for 5 days in the presence of 10 μM migalastat is greater than a reference α-Gal A activity in other lysates prepared from other HEK-293 cells transiently~~

~~transfected with the mutant form of α-Gal A and incubated for 5 days in the absence of 10 μM migalastat, the mutant form of α-Gal A corresponding to the mutation; and~~

~~in response to the determination, administering migalastat or a salt thereof to the subject.~~

~~77. The method of claim 76, wherein the α-Gal A activity is defined as the nmoles of free 4-MU released per milligram of protein per hour.~~

~~78. The method of claim 76 or 77, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 1% greater than the reference α-Gal A activity.~~

~~79. The method of claim 76 or 77, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 5% greater than the reference α-Gal A activity.~~

~~80. The method of claim 76 or 77, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 10% greater than the reference α-Gal A activity.~~

~~81. The method of claim 76 or 77, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 20% greater than the reference α-Gal A activity.~~

~~82. The method of any of claims 76-81, wherein the determination includes:~~

~~querying a data store medium with an identification of the one or more α-galactosidase A mutations;~~

~~receiving a result of the query.~~

~~83. The method of claim 82, wherein the result indicates that representation of the mutation is included in the data store.~~

84. The method of claim 82, wherein the result includes one or more values associated with a representation of the mutation in the data store, and wherein the method further includes comparing the one or more values or a processed version thereof to a predefined threshold.

85. A method comprising:

accessing mutation information corresponding to a subject, the mutation information identifying one or more α galactosidase A mutations;

determining, based on the mutation information, that the subject has a mutation for which α Gal A activity in lysates prepared from HEK 293 cells transiently transfected with a mutant form of α Gal A and incubated for 5 days in the presence of 10 μM migalastat is greater than a reference α Gal A activity in other lysates prepared from other HEK 293 cells transiently transfected with the mutant form of α-Gal A and incubated for 5 days in the absence of 10 μM migalastat, the mutant form of α Gal A corresponding to the mutation; and

in response to the determination, outputting an indication that the mutation is amenable to treatment with migalastat or a salt thereof.

86. The method of claim 85, wherein the α Gal A activity is defined as the nmoles of free 4-MU released per milligram of protein per hour.

87. The method of claim 85 or 86, wherein the determination includes determining that the subject has a mutation for which α Gal A activity is at least 1% greater than the reference α-Gal A activity.

88. The method of claim 85 or 86, wherein the determination includes determining that the subject has a mutation for which α Gal A activity is at least 5% greater than the reference α-Gal A activity.

89. The method of claim 85 or 86, wherein the determination includes determining that the subject has a mutation for which α Gal A activity is at least 10% greater than the reference α-Gal A activity.

90. The method of claim 85 or 86, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 20% greater than the reference α-Gal A activity.

91. The method of any of claims 85-90, wherein the determination includes:

querying a data store medium with an identification of the one or more α-galactosidase A mutations; and

receiving a result of the query.

92. The method of claim 91, wherein the result indicates that representation of the mutation is included in the data store.

93. The method of claim 91, wherein the result includes one or more values associated with a representation of the mutation in the data store, and wherein the method further includes comparing the one or more values or a processed version thereof to a predefined threshold.

94. The method of any of claims 85-93, further comprising:

receiving, from a user device, a first communication that includes the mutation information;

wherein outputting the indication includes, transmitting a second communication to the user device, the second communication including the indication.

95. A system comprising:

one or more data processors; and

a non-transitory computer readable storage medium containing instructions which, when executed on the one or more data processors, cause the one or more data processors to perform actions including:

accessing mutation information corresponding to a subject, the mutation information identifying one or more α-galactosidase A mutations;

determining, based on the mutation information, that the subject has a mutation for which α-Gal A activity in lysates prepared from HEK-293 cells transiently transfected with

~~a mutant form of α-Gal A and incubated for 5 days in the presence of 10 μM migalastat is greater than a reference α-Gal A activity in other lysates prepared from other HEK-293 cells transiently transfected with the mutant form of α-Gal A and incubated for 5 days in the absence of 10 μM migalastat, the mutant form of α-Gal A corresponding to the mutation; and~~

~~in response to the determination, outputting an indication that the mutation is amenable to treatment with migalastat or a salt thereof.~~

~~96. The system of claim 95, wherein the α-Gal A activity is defined as the nmoles of free 4-MU released per milligram of protein per hour.~~

~~97. The system of claim 95 or 96, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 1% greater than the reference α-Gal A activity.~~

~~98. The system of claim 95 or 96, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 5% greater than the reference α-Gal A activity.~~

~~99. The system of claim 95 or 96, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 10% greater than the reference α-Gal A activity.~~

~~100. The system of claim 95 or 96, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 20% greater than the reference α-Gal A activity.~~

~~101. The system of any of claims 95-100, wherein the determination includes:~~

~~querying a data store medium with an identification of the one or more α-galactosidase A mutations; and~~

~~receiving a result of the query.~~

~~102. The system of claim 101, wherein the result indicates that representation of the mutation is included in the data store.~~

~~103. The system of claim 101, wherein the result includes one or more values associated with a representation of the mutation in the data store, and wherein the actions further include comparing the one or more values or a processed version thereof to a predefined threshold.~~

~~104. The system of any of claims 95-103, wherein the actions further include:~~

~~receiving, from a user device, a first communication that includes the mutation information;~~

~~wherein outputting the indication includes, transmitting a second communication to the user device, the second communication including the indication.~~

~~105. A computer program product tangibly embodied in a non-transitory machine-readable storage medium, including instructions configured to cause one or more data processors to perform actions including:~~

~~accessing mutation information corresponding to a subject, the mutation information identifying one or more α-galactosidase A mutations;~~

~~determining, based on the mutation information, that the subject has a mutation for which α-Gal A activity in lysates prepared from HEK-293 cells transiently transfected with a mutant form of α-Gal A and incubated for 5 days in the presence of 10 μM migalastat is greater than a reference α-Gal A activity in other lysates prepared from other HEK-293 cells transiently transfected with the mutant form of α-Gal A and incubated for 5 days in the absence of 10 μM migalastat, the mutant form of α-Gal A corresponding to the mutation; and~~

~~in response to the determination, outputting an indication that the mutation is amenable to treatment with migalastat or a salt thereof.~~

~~106. The computer program product of claim 105, wherein the α-Gal A activity is defined as the nmoles of free 4-MU released per milligram of protein per hour.~~

~~107. The computer-program product of claim 105 or 106, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 1% greater than the reference α-Gal A activity.~~

~~108. The computer-program product of claim 105 or 106, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 5% greater than the reference α-Gal A activity.~~

~~109. The computer-program product of claim 105 or 106, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 10% greater than the reference α-Gal A activity.~~

~~110. The computer-program product of claim 105 or 106, wherein the determination includes determining that the subject has a mutation for which α-Gal A activity is at least 20% greater than the reference α-Gal A activity.~~

~~111. The computer-program product of any of claims 105-110, wherein the determination includes:~~

~~querying a data store medium with an identification of the one or more α-galactosidase A mutations; and~~

~~receiving a result of the query.~~

~~112. The computer-program product of claim 111, wherein the result indicates that representation of the mutation is included in the data store.~~

~~113. The computer-program product of claim 111, wherein the result includes one or more values associated with a representation of the mutation in the data store, and wherein the actions further include comparing the one or more values or a processed version thereof to a predefined threshold.~~

~~114. The computer-program product of any of claims 105-113, wherein the actions further include:~~

~~receiving, from a user device, a first communication that includes the mutation information;~~

~~wherein outputting the indication includes, transmitting a second communication to the user device, the second communication including the indication.~~

~~115. A method for treatment of Fabry disease in a human patient in need thereof, the method comprising administering to the patient a therapeutically effective dose of migalastat or a salt thereof, wherein the patient has an α-galactosidase A mutation selected from the group consisting of those mutations provided in Table 2.~~

~~116. A method of enhancing α-galactosidase A in a patient diagnosed with or suspected of having Fabry disease, the method comprising administering to the patient a therapeutically effective dose of migalastat or a salt thereof, wherein the patient has an α-galactosidase A mutation selected from the group consisting of those mutations provided in Table 2.~~

~~117. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: N5D, N5K, P6L, P6Q, P6R, P6S, P6T, E7D, E7K, E7V, L8I, L8P, L8Q, H9L, H9Q, H9R, H9Y, L10M, L10P, and L10Q.~~

~~118. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: L10R, L10V, G11C, G11D, G11R, G11S, G11V, C12G, C12R, C12S, C12Y, A13E, A13G, L14F, L14H, L14V, R17C, R17G, R17H, and R17P.~~

~~119. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: R17S, F18I, F18L, A20G, L21H, V22A, V22F, V22I, V22L, S23P, S23T, W24S, D25H, I26N, P27A, P27L, P27S, P27T, G28E, and G28R.~~

~~120. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: G28W, A29G, A29P, A29V, R30G, L32M, L32Q, L32R, L32V, D33A, D33E, D33V, L36M, L36V, A37E, A37G, A37S, R38G, R38M, and R38W.~~

~~121. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: T39A, T39K, T39M, T39R, T39S, T41A, T41N, T41S, G43A, L45M, L45V, H46D, H46N, H46Q, E48A, F50Y, M51R, M51T, M51V and N53H.~~

~~122. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: N53I, N53S, N53T, L54H, L54R, L54V, D55A, D55E, D55H, D55Y, C56W, E58K, E59A, E59D, E59G, E59Q, E59V, P60A, P60Q, and P60R.~~

~~123. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: D61E, D61V, S62A, S62C, S62F, S62P, S62Y, I64L, I64V, S65C, S65G, S65R, E66D, E66V, K67E, K67M, K67N, K67Q, K67T, and L68I.~~

~~124. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: F69I, F69Y, M70I, M70K, M70L, M70R, E71A, E71D, E71G, E71Q, E71V, M72L, M72T, A73S, A73T, E74D, E74G, E74K, E74V, and L75F.~~

~~125. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: L75P, M76V, V77I, V77L, S78L, S78P, E79A, E79D, E79G, E79K, E79Q, E79V, G80A, G80C, G80S, W81L, K82E, K82M, K82N, and K82R.~~

~~126. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: K82T, D83A, D83E, D83G, D83V, A84E, A84G, A84P, A84S, A84T, A84V, G85A, G85C, G85R, Y86F, E87G, Y88H, Y88N, L89V, and I91F.~~

~~127. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: I91L, I91M, I91S, M96L, M96T, A97D, A97S, A97T, P98H, P98L, P98R, Q99E, Q99L, Q99P, Q99R, D101A, D101E, D101G, D101H, and D101V.~~

~~128. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: S102A, S102P, S102T, G104A, G104D, G104S, R105G, R105I, R105K, R105T, L106H, L106I, L106P, L106V, Q107E, Q107H, Q107K, A108E, A108V, and D109A.~~

~~129. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: D109E, D109H, D109N, D109Y, P110T, F113V, F113Y, P114L, H115D, H115N, G116R, I117M, I117T, A121V, Y123D, Y123F, Y123N, Y123S, V124I, and H125D.~~

~~130. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: H125N, H125R, S126C, S126I, K127E, G128A, L129V, K130M, K130N, K130Q, L131V, I133L, I133T, I133V, A135E, A135G, A135S, A135T, D136A, and D136N.~~

~~131. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: D136V, V137A, V137D, V137G, V137I, V137L, G138A, N139H, N139I, N139K, N139Y, K140E, K140I, K140N, K140Q, K140R, T141S, A143E, A143G, and G144A.~~

~~132. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: G144C, G144R, G144S, F145C, F145L, F145V, F145Y, P146A, P146H, P146L, P146T, G147A, S148C, S148G, S148T, F149C, G150E, G150V, Y151C, and Y151D.~~

~~133. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: Y151S, Y152F, Y152S, D153A, D153H, D153N, D153V, D153Y, A156G, Q157E, Q157K, Q157L, Q157P, T158A, T158I, T158N, T158S, F159I, F159L, and F159V.~~

~~134. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: F159Y, A160G, A160S, A160T, A160V, D161H, D161N, D161V, D161Y, W162S, V164A, V164I, V164L, D165A, D165E, L166M, L166Q, L167I, F169C, and F169L.~~

~~135. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: F169V, F169Y, G171A, G171V, Y173C, Y173F, Y173H, Y173S, D175G, D175H, D175V, D175Y, S176C, S176R, L177F, L177M, L177S, L177V, L177W, and E178A.~~

~~136. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: E178G, E178K, E178Q, L180M, L180S, A181P, A181T, A181V, D182A, D182E, D182V, D182Y, Y184F, Y184H, Y184S, K185M, K185N, K185Q, K185T, and H186D.~~

~~137. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: H186L, H186N, H186Q, H186Y, M187L, S188A, S188C, S188F, S188P, S188T, S188Y, L189S, L189V, A190D, A190G, A190S, A190T, A190V, L191M, and L191V.~~

~~138. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: N192D, N192H, N192K, N192S, N192T, R193G, R193M, R193T, R193W, T194N, T194P, T194S, G195C, G195R, G195S, R196I, R196K, S197C, S197G, and S197I.~~

~~139. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: S197N, S197T, I198M, I198S, V199E, V199L, Y200N, Y200S, S201A, S201C, S201T, E203A, E203G, E203Q, W204S, L206F, L206H, L206I, L206R, and L206V.~~

~~140. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: Y207F, M208K, W209C, W209G, P210H, P210T, F211C, F211L, F211S, F211V, F211Y, Q212H, Q212P, K213E, K213Q, P214A, P214H, P214R, P214T, and N215H.~~

~~141. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: N215K, N215T, N215Y, Y216F, Y216H, Y216N, T217A, T217I, T217K, T217P, T217R, T217S, E218A, E218D, E218G, E218K, E218Q, E218V, I219F, and I219M.~~

~~142. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: I219S, R220L, Q221E, Q221H, Q221K, Q221L, Q221R, Y222C, Y222D, Y222H, Y222N, Y222S, N224H, R227G, N228H, N228I, N228T, F229I, F229S, and F229Y.~~

~~143. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: A230D, A230G, A230P, A230V, I232L, I232M, I232V, D233A, D233E, D233G, D233V, S235A, S235T, K237I, S238C, S238I, S238T, I239L, K240E, and K240M.~~

~~144. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: K240R, S241C, S241I, S241T, I242L, I242M, I242S, L243M, L243S, L243V, D244A, D244E, D244G, D244V, D244Y, W245C, T246A, T246I, T246K, and T246R.~~

~~145. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: S247A, S247F, S247T, S247Y, F248C, F248L, F248V, F248Y, N249D, N249H, N249I, N249S, N249T, N249Y, Q250E, Q250L, E251G, E251K, E251Q, and E251V.~~

~~146. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: R252G, I253F, I253N, I253V, V254A, V254D, V254F, V254G, D255A, D255E, D255H, D255N, D255V, D255Y, V256D, V256G, V256L, A257S, G258E, and P259A.~~

~~147. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: P259T, G260W, G261A, N263H, N263T, D264H, D264N, P265A, P265Q, M267L, M267V, L268F, L268I, V269L, I270L, I270S, I270V, N272D, F273Y, and L275I.~~

~~148. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: W277L, N278I, Q280L, Q280R, V281A, V281E, V281G, V281L, T282S, Q283E, Q283H, Q283L, M284I, M284L, A285G, A285T, A285V, L286F, L286H, and L286V.~~

~~149. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: A288G, A288S, A288V, I289L, I289T, I289V, A291G, A292G, A292S, L294F, L294I, L294V, F295I, F295S, F295V, F295Y, S297T, N298D, N298I, and N298T.~~

~~150. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: D299H, D299N, L300I, L300V, H302D, H302L, H302N, H302Y, I303S,~~

~~S304I, Q306E, Q306L, Q306P, A307D, A307G, A307P, A307S, A307V, K308I, and K308Q.~~

~~151. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: K308R, A309D, A309T, L310I, L311I, Q312E, Q312K, Q312L, D313E, D313V, K314E, K314M, K314N, K314T, D315A, D315G, D315H, D315N, D315V, and D315Y.~~

~~152. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: V316A, V316L, I317L, I317M, I317V, A318D, A318P, A318T, A318V, I319M, N320S, N320T, Q321K, D322A, D322V, L324V, L324W, G325A, G325C, and G325V.~~

~~153. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: K326E, K326M, K326Q, K326R, K326T, Q327H, Q327P, Y329C, Y329D, Y329F, Y329H, Y329N, Q330E, Q330H, Q330K, L331H, L331P, L331R, L331V, and R332G.~~

~~154. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: R332I, R332S, R332T, Q333E, Q333L, Q333P, G334R, G334V, D335A, D335E, D335G, D335V, D335Y, N336D, N336I, N336S, N336T, N336Y, F337C, and F337L.~~

~~155. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: F337V, F337Y, E338A, E338D, E338G, V339M, E341A, E341Q, P343A, P343S, L344F, L344R, L344V, G346A, G346C, G346D, G346V, L347I, A348D, and W349C.~~

~~156. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: W349L, A350G, A350S, A350T, A350V, V351A, V351E, A352S, A352T, M353K, M353L, M353T, I354R, N355D, N355H, N355S, N355Y, R356L, Q357E, and I359F.~~

~~157. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: I359L, I359N, I359S, I359V, P362A, P362H, P362R, P362S, R363G, R363L, R363S, S364C, S364P, Y365D, Y365F, Y365N, Y365S, T366I, T366N, and T366P.~~

~~158. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: T366S, I367F, I367L, I367M, A368G, A368P, V369A, V369F, V369G, V369I, V369L, A370D, A370G, A370P, A370T, A370V, S371C, S371T, G373A, and G373C.~~

~~159. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: K374E, K374I, K374R, K374T, G375R, V376E, V376G, V376L, V376M, A377G, A377P, A377S, A377T, N379D, N379I, N379K, N379T, P380A, P380H, and P380R.~~

~~160. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: P380T, A381D, F383C, F383I, F383Y, I384F, I384M, I384T, T385I, Q386H, Q386K, Q386L, L387F, L387H, L387I, L387R, L388F, L388H, L388I, and L388R.~~

~~161. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: L388V, K391I, K391N, K391Q, K391R, R392G, R392K, R392M, R392W, K393E, K393N, K393Q, K393T, L394I, L394Q, L394R, G395R, F396C, F396I, and F396L.~~

~~162. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: F396V, Y397C, Y397F, Y397H, Y397N, Y397S, E398G, E398Q, W399G, W399R, T400A, T400I, T400N, T400P, T400S, S401A, S401L, S401T, R402G, and R402M.~~

~~163. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: R402S, R402T, R402W, L403F, L403V, R404G, R404I, R404K, R404S, R404T, S405G, H406D, H406L, H406Q, I407L, I407M, I407T, N408D, N408H, and N408T.~~

~~164. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: P409L, T410S, G411A, G411C, G411V, T412A, T412I, T412S, V413F, V413G, V413I, L414F, L414V, L415H, L415I, Q416E, Q416H, Q416L, L417I, and E418A.~~

~~165. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: E418D, E418K, E418Q, N419I, N419S, N419T, N419Y, T420K, T420P, T420R, T420S, M421I, M421K, M421L, M421R, M421T, Q422P, M423I, M423K, and M423L.~~

~~166. The method of claim 115 or 116, wherein the mutation is selected from the group consisting of: M423T, S424L, L425F, D427N, and L429R.~~

~~167. The method of any one of claims 115-166, wherein the migalastat or salt thereof is administered to the patient every other day.~~

~~168. The method of any one of claims 115-167, wherein the patient is administered about 100 to about 150 mg free base equivalent of the migalastat or salt thereof every other day.~~

~~169. The method of any one of claims 115-168, wherein the patient is administered about 123 mg free base equivalent of the migalastat or the salt thereof every other day.~~

~~170. The method of any one of claims 115-169, wherein the patient is administered about 123 mg of migalastat free base every other day.~~

~~171. The method of one of claims 115-169, wherein the patient is administered about 150 mg of migalastat hydrochloride every other day.~~

~~172. The method of any one of claims 115-171, wherein the migalastat or salt thereof enhances α-galactosidase A activity.~~

~~173. The method of one of claims 115-172, wherein the mutation is disclosed in a pharmacological reference table.~~

~~174. The method of claim 173, wherein the pharmacological reference table is provided in a product label for a migalastat product approved for the treatment of Fabry disease.~~

~~175. The method of claim 173, wherein the pharmacological reference table is provided in a product label for GALAFOLD®.~~

~~176. The method of claim 173, wherein the pharmacological reference table is provided at a website.~~

~~177. The method of claim 176, wherein the website is one or more of www.galafoldamenabilitytable.com or www.fabrygenevariantsearch.com.~~

~~178. The method of any one of claims 115-177, wherein the migalastat or salt thereof is administered orally.~~

~~179. The method of any one of claims 115-177, wherein the migalastat or salt thereof is administered by injection.~~

~~180. The method of any one of claims 115-179, wherein the patient is male.~~

~~181. The method of any one of claims 115-179, wherein the patient is female.~~

~~182. A method for treatment of Fabry disease in a human patient in need thereof, the method comprising administering to the patient a therapeutically effective dose of migalastat or a salt thereof, wherein the patient has a HEK assay amenable mutation in α-galactosidase A disclosed in a pharmacological reference table, wherein the pharmacological reference table includes one or more mutations from Table 2.~~

~~183. A method of enhancing α-galactosidase A in a patient diagnosed with or suspected of having Fabry disease, the method comprising administering to the patient a therapeutically effective dose of migalastat or a salt thereof, wherein the patient has a HEK assay amenable~~

~~mutation in α-galactosidase A disclosed in a pharmacological reference table, wherein the pharmacological reference table includes one or more mutations from Table 2.~~

~~184. The method of claim 182 or 183, wherein the pharmacological reference table includes all of the mutations from Table 2.~~

~~185. The method of any one of claims 182-184, wherein the pharmacological reference table includes one or more mutations from Table 1.~~

~~186. The method of any one of claims 182-185, wherein the pharmacological reference table includes all of the mutations from Table 1.~~

~~187. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: N5D, N5K, P6L, P6Q, P6R, P6S, P6T, E7D, E7K, E7V, L8I, L8P, L8Q, H9L, H9Q, H9R, H9Y, L10M, L10P, and L10Q.~~

~~188. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: L10R, L10V, G11C, G11D, G11R, G11S, G11V, C12G, C12R, C12S, C12Y, A13E, A13G, L14F, L14H, L14V, R17C, R17G, R17H, and R17P.~~

~~189. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: R17S, F18I, F18L, A20G, L21H, V22A, V22F, V22I, V22L, S23P, S23T, W24S, D25H, I26N, P27A, P27L, P27S, P27T, G28E, and G28R.~~

~~190. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: G28W, A29G, A29P, A29V, R30G, L32M, L32Q, L32R, L32V, D33A, D33E, D33V, L36M, L36V, A37E, A37G, A37S, R38G, R38M, and R38W.~~

~~191. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: T39A, T39K, T39M, T39R, T39S, T41A, T41N, T41S, G43A, L45M, L45V, H46D, H46N, H46Q, E48A, F50Y, M51R, M51T, M51V and N53H.~~

~~192. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: N53I, N53S, N53T, L54H, L54R, L54V, D55A, D55E, D55H, D55Y, C56W, E58K, E59A, E59D, E59G, E59Q, E59V, P60A, P60Q, and P60R.~~

~~193. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: D61E, D61V, S62A, S62C, S62F, S62P, S62Y, I64L, I64V, S65C, S65G, S65R, E66D, E66V, K67E, K67M, K67N, K67Q, K67T, and L68I.~~

~~194. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: F69I, F69Y, M70I, M70K, M70L, M70R, E71A, E71D, E71G, E71Q, E71V, M72L, M72T, A73S, A73T, E74D, E74G, E74K, E74V, and L75F.~~

~~195. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: L75P, M76V, V77I, V77L, S78L, S78P, E79A, E79D, E79G, E79K, E79Q, E79V, G80A, G80C, G80S, W81L, K82E, K82M, K82N, and K82R.~~

~~196. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: K82T, D83A, D83E, D83G, D83V, A84E, A84G, A84P, A84S, A84T, A84V, G85A, G85C, G85R, Y86F, E87G, Y88H, Y88N, L89V, and I91F.~~

~~197. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: I91L, I91M, I91S, M96L, M96T, A97D, A97S, A97T, P98H, P98L, P98R, Q99E, Q99L, Q99P, Q99R, D101A, D101E, D101G, D101H, and D101V.~~

~~198. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: S102A, S102P, S102T, G104A, G104D, G104S, R105G, R105I, R105K, R105T, L106H, L106I, L106P, L106V, Q107E, Q107H, Q107K, A108E, A108V, and D109A.~~

~~199. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: D109E, D109H, D109N, D109Y, P110T, F113V, F113Y, P114L, H115D, H115N, G116R, I117M, I117T, A121V, Y123D, Y123F, Y123N, Y123S, V124I, and H125D.~~

~~200. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: H125N, H125R, S126C, S126I, K127E, G128A, L129V, K130M, K130N, K130Q, L131V, I133L, I133T, I133V, A135E, A135G, A135S, A135T, D136A, and D136N.~~

~~201. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: D136V, V137A, V137D, V137G, V137I, V137L, G138A, N139H, N139I, N139K, N139Y, K140E, K140I, K140N, K140Q, K140R, T141S, A143E, A143G, and G144A.~~

~~202. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: G144C, G144R, G144S, F145C, F145L, F145V, F145Y, P146A, P146H, P146L, P146T, G147A, S148C, S148G, S148T, F149C, G150E, G150V, Y151C, and Y151D.~~

~~203. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: Y151S, Y152F, Y152S, D153A, D153H, D153N, D153V, D153Y, A156G, Q157E, Q157K, Q157L, Q157P, T158A, T158I, T158N, T158S, F159I, F159L, and F159V.~~

~~204. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: F159Y, A160G, A160S, A160T, A160V, D161H, D161N, D161V, D161Y, W162S, V164A, V164I, V164L, D165A, D165E, L166M, L166Q, L167I, F169C, and F169L.~~

~~205. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: F169V, F169Y, G171A, G171V, Y173C, Y173F, Y173H, Y173S, D175G, D175H, D175V, D175Y, S176C, S176R, L177F, L177M, L177S, L177V, L177W, and E178A.~~

~~206. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: E178G, E178K, E178Q, L180M, L180S, A181P, A181T, A181V, D182A, D182E, D182V, D182Y, Y184F, Y184H, Y184S, K185M, K185N, K185Q, K185T, and H186D.~~

~~207. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: H186L, H186N, H186Q, H186Y, M187L, S188A, S188C, S188F, S188P, S188T, S188Y, L189S, L189V, A190D, A190G, A190S, A190T, A190V, L191M, and L191V.~~

~~208. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: N192D, N192H, N192K, N192S, N192T, R193G, R193M, R193T, R193W, T194N, T194P, T194S, G195C, G195R, G195S, R196I, R196K, S197C, S197G, and S197I.~~

~~209. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: S197N, S197T, I198M, I198S, V199E, V199L, Y200N, Y200S, S201A, S201C, S201T, E203A, E203G, E203Q, W204S, L206F, L206H, L206I, L206R, and L206V.~~

~~210. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: Y207F, M208K, W209C, W209G, P210H, P210T, F211C, F211L, F211S, F211V, F211Y, Q212H, Q212P, K213E, K213Q, P214A, P214H, P214R, P214T, and N215H.~~

~~211. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: N215K, N215T, N215Y, Y216F, Y216H, Y216N, T217A, T217I,~~

~~T217K, T217P, T217R, T217S, E218A, E218D, E218G, E218K, E218Q, E218V, I219F, and I219M.~~

~~212. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: I219S, R220L, Q221E, Q221H, Q221K, Q221L, Q221R, Y222C, Y222D, Y222H, Y222N, Y222S, N224H, R227G, N228H, N228I, N228T, F229I, F229S, and F229Y.~~

~~213. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: A230D, A230G, A230P, A230V, I232L, I232M, I232V, D233A, D233E, D233G, D233V, S235A, S235T, K237I, S238C, S238I, S238T, I239L, K240E, and K240M.~~

~~214. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: K240R, S241C, S241I, S241T, I242L, I242M, I242S, L243M, L243S, L243V, D244A, D244E, D244G, D244V, D244Y, W245C, T246A, T246I, T246K, and T246R.~~

~~215. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: S247A, S247F, S247T, S247Y, F248C, F248L, F248V, F248Y, N249D, N249H, N249I, N249S, N249T, N249Y, Q250E, Q250L, E251G, E251K, E251Q, and E251V.~~

~~216. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: R252G, I253F, I253N, I253V, V254A, V254D, V254F, V254G, D255A, D255E, D255H, D255N, D255V, D255Y, V256D, V256G, V256L, A257S, G258E, and P259A.~~

~~217. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: P259T, G260W, G261A, N263H, N263T, D264H, D264N, P265A,~~

P265Q, M267L, M267V, L268F, L268I, V269L, I270L, I270S, I270V, N272D, F273Y, and L275I.

218. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: W277L, N278I, Q280L, Q280R, V281A, V281E, V281G, V281L, T282S, Q283E, Q283H, Q283L, M284I, M284L, A285G, A285T, A285V, L286F, L286H, and L286V.

219. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: A288G, A288S, A288V, I289L, I289T, I289V, A291G, A292G, A292S, L294F, L294I, L294V, F295I, F295S, F295V, F295Y, S297T, N298D, N298I, and N298T.

220. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: D299H, D299N, L300I, L300V, H302D, H302L, H302N, H302Y, I303S, S304I, Q306E, Q306L, Q306P, A307D, A307G, A307P, A307S, A307V, K308I, and K308Q.

221. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: K308R, A309D, A309T, L310I, L311I, Q312E, Q312K, Q312L, D313E, D313V, K314E, K314M, K314N, K314T, D315A, D315G, D315H, D315N, D315V, and D315Y.

222. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: V316A, V316L, I317L, I317M, I317V, A318D, A318P, A318T, A318V, I319M, N320S, N320T, Q321K, D322A, D322V, L324V, L324W, G325A, G325C, and G325V.

223. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: K326E, K326M, K326Q, K326R, K326T, Q327H, Q327P, Y329C, Y329D, Y329F, Y329H, Y329N, Q330E, Q330H, Q330K, L331H, L331P, L331R, L331V, and R332G.

224. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: R332I, R332S, R332T, Q333E, Q333L, Q333P, G334R, G334V, D335A, D335E, D335G, D335V, D335Y, N336D, N336I, N336S, N336T, N336Y, F337C, and F337L.

225. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: F337V, F337Y, E338A, E338D, E338G, V339M, E341A, E341Q, P343A, P343S, L344F, L344R, L344V, G346A, G346C, G346D, G346V, L347I, A348D, and W349C.

226. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: W349L, A350G, A350S, A350T, A350V, V351A, V351E, A352S, A352T, M353K, M353L, M353T, I354R, N355D, N355H, N355S, N355Y, R356L, Q357E, and I359F.

227. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: I359L, I359N, I359S, I359V, P362A, P362H, P362R, P362S, R363G, R363L, R363S, S364C, S364P, Y365D, Y365F, Y365N, Y365S, T366I, T366N, and T366P.

228. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: T366S, I367F, I367L, I367M, A368G, A368P, V369A, V369F, V369G, V369I, V369L, A370D, A370G, A370P, A370T, A370V, S371C, S371T, G373A, and G373C.

229. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: K374E, K374I, K374R, K374T, G375R, V376E, V376G, V376L, V376M, A377G, A377P, A377S, A377T, N379D, N379I, N379K, N379T, P380A, P380H, and P380R.

~~230. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: P380T, A381D, F383C, F383I, F383Y, I384F, I384M, I384T, T385I, Q386H, Q386K, Q386L, L387F, L387H, L387I, L387R, L388F, L388H, L388I, and L388R.~~

~~231. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: L388V, K391I, K391N, K391Q, K391R, R392G, R392K, R392M, R392W, K393E, K393N, K393Q, K393T, L394I, L394Q, L394R, G395R, F396C, F396I, and F396L.~~

~~232. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: F396V, Y397C, Y397F, Y397H, Y397N, Y397S, E398G, E398Q, W399G, W399R, T400A, T400I, T400N, T400P, T400S, S401A, S401L, S401T, R402G, and R402M.~~

~~233. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: R402S, R402T, R402W, L403F, L403V, R404G, R404I, R404K, R404S, R404T, S405G, H406D, H406L, H406Q, I407L, I407M, I407T, N408D, N408H, and N408T.~~

~~234. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: P409L, T410S, G411A, G411C, G411V, T412A, T412I, T412S, V413F, V413G, V413I, L414F, L414V, L415H, L415I, Q416E, Q416H, Q416L, L417I, and E418A.~~

~~235. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: E418D, E418K, E418Q, N419I, N419S, N419T, N419Y, T420K, T420P, T420R, T420S, M421I, M421K, M421L, M421R, M421T, Q422P, M423I, M423K, and M423L.~~

~~236. The method of any one of claims 182-186, wherein the mutation is selected from the group consisting of: M423T, S424L, L425F, D427N, and L429R.~~

~~237. The method of any one of claims 182-236, wherein the migalastat or salt thereof is administered to the patient every other day.~~

~~238. The method of any one of claims 182-237, wherein the patient is administered about 100 to about 150 mg free base equivalent of the migalastat or salt thereof every other day.~~

~~239. The method of any one of claims 182-238, wherein the patient is administered about 123 mg free base equivalent of the migalastat or the salt thereof every other day.~~

~~240. The method of any one of claims 182-239, wherein the patient is administered about 123 mg of migalastat free base every other day.~~

~~241. The method of any one of claims 182-239, wherein the patient is administered about 150 mg of migalastat hydrochloride every other day.~~

~~242. The method of any one of claims 182-241, wherein the migalastat or salt thereof enhances α-galactosidase A activity.~~

~~243. The method of any one of claims 182-242, wherein the pharmacological reference table is provided in a product label for a migalastat product approved for the treatment of Fabry disease.~~

~~244. The method of any one of claims 182-243, wherein the pharmacological reference table is provided in a product label for GALAFOLD®.~~

~~245. The method of any one of claims 182-243, wherein the pharmacological reference table is provided at a website.~~

~~246. The method of claim 182-245, wherein the website is one or more of www.galafoldamenabilitytable.com or www.fabrygenevariantsearch.com.~~

~~247. The method of any one of claims 182-246, wherein the migalastat or salt thereof is administered orally.~~

~~248. The method of any one of claims 182-246, wherein the migalastat or salt thereof is administered by injection.~~

~~249. The method of any one of claims 182-248, wherein the patient is male.~~

~~250. The method of any one of claims 182-248, wherein the patient is female.~~

9. Migalastat or a salt thereof for use according to any one of claims 1 to 8, wherein the mutation is disclosed in a pharmacological reference table.

10. Migalastat or a salt thereof for use according to claim 9, wherein the pharmacological reference table includes all of the mutations from Table 2.

11. Migalastat or a salt thereof for use according to claim 10, wherein the pharmacological reference table further includes all of the mutations from Table 1.

12. Migalastat or a salt thereof for use according to any one of claims 9 to 11, wherein the pharmacological reference table is provided in a product label for a migalastat product approved for the treatment of Fabry disease.

13. Migalastat or a salt thereof for use according to claim any one of claims 9 to 11, wherein the pharmacological reference table is provided at a website.

14. Migalastat or a salt thereof for use according to claim 13, wherein the website is www.galafoldamenabilitytable.com or www.fabrygenevariantsearch.com.

15. A package comprising migalastat or a salt thereof for use according to any one of the preceding claims 1 to 14; and a product label providing a pharmacological reference table that discloses the mutations provided in Table 2.

16. A package comprising

migalastat or a salt thereof for use in treating Fabry disease by:

accessing mutation information corresponding to the subject, the mutation information identifying one or more α-galactosidase A mutations;

administering migalastat or a salt thereof to the subject having at least one mutation as identified in Table 2; and

an indication that the at least one mutation as identified in table 2 is amenable to treatment with migalastat.

17. A package according to claim 16, wherein the indication comprises a pharmacological reference table that discloses the mutations provided in Table 2.

18. A package according to claim 15 or claim 17, wherein the pharmacological reference table is in written form and comprises HEK assay amenable mutations, including the mutations provided in Table 2.

19. A package according to claim 15 or claim 17, wherein the pharmacological reference table is in electronic form and comprises a website comprising a table of HEK assay amenable mutations, including the mutations provided in Table 2.

20. A package according to claim 19, wherein the website is www.galafoldamenabilitytable.com or www.fabrygenevariantsearch.com.