Human genes associated with disease / syndromes by missense mutations

In the list below, some variants are known to cause detrimental phenotypes, others are known to be neutral, or a phenotype is currently not known (neutral or deleterious). All the proteins below are known to be associated with disease / syndromes when mutations disrupt their function. The condition is followed by the protein name; in parenthesis is the official human gene abbreviation; then the accession number for the version of the human protein to use.

Nomenclature example for AA variants: I65T – at position 65 (65th amino acid in the protein), there is usually or normally an I (isoleucine); in the variant, there is a T (threonine). Note that this may or may not affect the function of the protein.

Condition/Syndrome: Protein (enzyme) name (Human gene abbreviation) – Accession No.
List of variants

Phenylketonuria: Phenylalanine hydroxylase (PAH) - P00439 [Crystal structure: 6HYC]

D59Y
I65T
R158Q
Q160P
L255V
R261Q
M276K
P281L
P314S
Y343F
S349P
K363N
R408W

Segawa Syndrome, Dopa-responsive Dystonia, Infantile Parkinsonism: Tyrosine Hydroxylase (TH) - P07101 [Crystal structure: 7PIM – numbering of protein is altered; subtract 31 to find AA in crystal structure; e.g., R233 - 31 = R201.]

R233H
L236P
T276P
G280R
E284V
V306I
T314M
R337H
C359F
I440T

Tay Sachs disease: Beta-Hexosaminidase A (HEXA) - P06865 [Crystal structure: 2GJX – note that this is a dimeric co-crystal of both HEXA & HEXB (one chain of each), see below]

L39R
S59L

L127R
R170Q
R178H
V192A
K197T
H204R
S293I
G367D
N370S
W420C
R424H

Sandhoff disease, GM2-Gangliosidosis: Beta-hexosaminidase B (HEXB) - P07686 (condition is clinically indistinguishable from Tay-Sachs) [Crystal structure: 2GJX – note that this is a dimeric co-crystal of both HEXA & HEXB (one chain of each), see above]

W57C
L62S
R100P
H113R
T150N
K217T
Y266D
P417L
I420V
Y456S
L498F
R505Q

Ehlers-Danlos syndrome with short stature and limb anomalies (EDSSLA): 4-Beta-Galactosyltransferase (B4GALT7) - Q9UBV7 [Crystal structure: 4IRP]

H136L
R141W
A180T
A186D
L206P
C214Y
D229N
D260G
R270C
C307Y

Gaucher disease: Acid beta-glucocerebrosidase aka Beta-glucosidase (GBA) - P04062 [Crystal structure: 3GXF – numbering of protein is altered; subtract 44 to find AA in crystal structure; e.g., S281- 39 = S242.]

S281N
L353R
V391L
V394L

T408M
N409S
P415R
A423V
K480N
L483P
S504P

Glycine Encephalopathy: Aminomethyltransferase (AMT) - P48728
[Crystal structure: 1WSR – numbering of protein is altered; subtract 28 to find AA in crystal structure; e.g., H42 - 28 = H14.]

H42R
G47R
R62P
S117L
D197H
G269D
N275K
Q317P
R320H

BH4-deficient hyperphenylalaninemia (HPA) D [HPABH4D]: Pterin carbinolamine dehydratase (PCBD1) - P61457 [Crystal structure: 1DCO – note this is the Rat protein structure; however, the proteins are 100% identical in sequence!]

D14Y
N19K
K36R
H39R
F40L
L60P
H63P
D42G
T79I
C82R
A83T
S86A
R88Q
R88W
I90T
E97K

BH4-deficient hyperphenylalaninemia (HPA) C [HPABH4C]: Quinoid dihydropteridine reductase (QDPR) - P09417 [Crystal structure: 1HDR – numbering of protein is altered; subtract 1 to find AA in crystal structure; e.g., W36 – 1 = W35.]

G23D
W36R

K55T
A91T
W108G
H120R
A139S
Y150C
H158Y
L164V
S193P