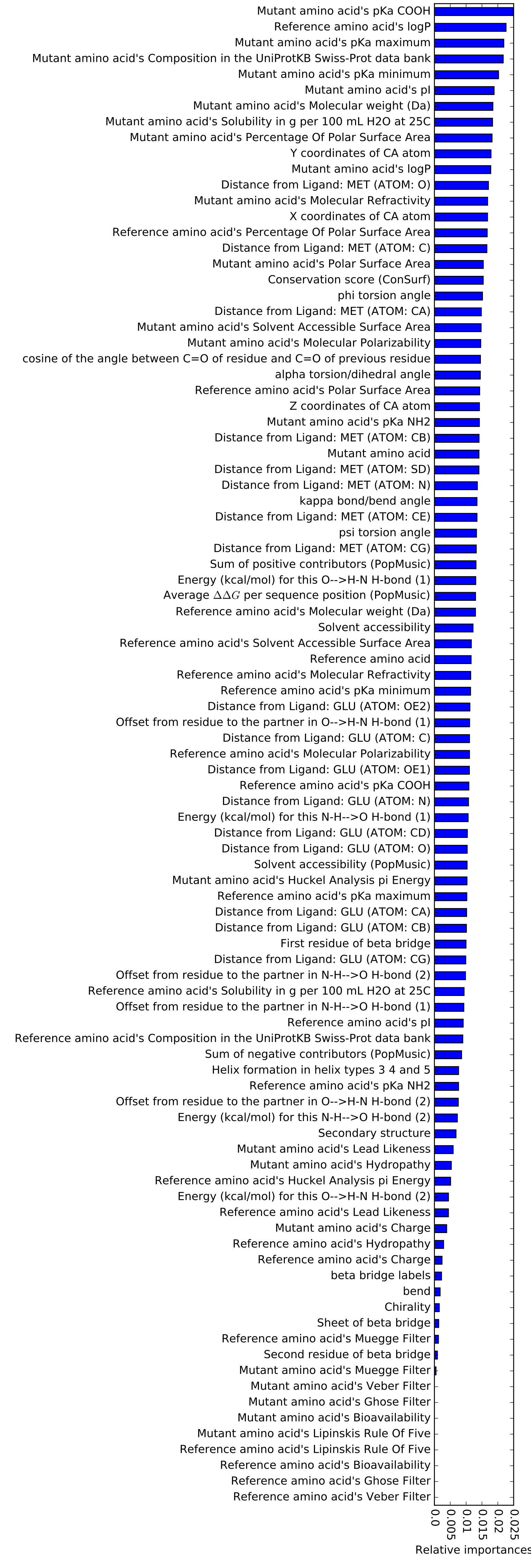
Mutant amino acid's pKa COOH
Reference amino acid's logP
Mutant amino acid's pKa maximum
Mutant amino acid's Composition in the UniProtKB Swiss-Prot data bank
Mutant amino acid's pKa minimum
Mutant amino acid's pI
Mutant amino acid's Molecular weight (Da)
Mutant amino acid's Solubility in g per 100 mL H2O at 25C
Mutant amino acid's Percentage Of Polar Surface Area
Y coordinates of CA atom
Mutant amino acid's logP
Distance from Ligand: MET (ATOM: O)
Mutant amino acid's Molecular Refractivity
X coordinates of CA atom
Reference amino acid's Percentage Of Polar Surface Area
Distance from Ligand: MET (ATOM: C)
Mutant amino acid's Polar Surface Area
Conservation score (ConSurf)
phi torsion angle
Distance from Ligand: MET (ATOM: CA)
Mutant amino acid's Solvent Accessible Surface Area
Mutant amino acid's Molecular Polarizability
cosine of the angle between C=O of residue and C=O of previous residue
alpha torsion/dihedral angle
Reference amino acid's Polar Surface Area
Z coordinates of CA atom
Mutant amino acid's pKa NH2
Distance from Ligand: MET (ATOM: CB)
Mutant amino acid
Distance from Ligand: MET (ATOM: SD)
Distance from Ligand: MET (ATOM: N)
kappa bond/bend angle
Distance from Ligand: MET (ATOM: CE)
psi torsion angle
Distance from Ligand: MET (ATOM: CG)
Sum of positive contributors (PopMusic)
Energy (kcal/mol) for this O-->H-N H-bond (1)
Average $\Delta\Delta G$ per sequence position (PopMusic)
Reference amino acid's Molecular weight (Da)
Solvent accessibility
Reference amino acid's Solvent Accessible Surface Area
Reference amino acid
Reference amino acid's Molecular Refractivity
Reference amino acid's pKa minimum
Distance from Ligand: GLU (ATOM: OE2)
Offset from residue to the partner in O-->H-N H-bond (1)
Distance from Ligand: GLU (ATOM: C)
Reference amino acid's Molecular Polarizability
Distance from Ligand: GLU (ATOM: OE1)
Reference amino acid's pKa COOH
Distance from Ligand: GLU (ATOM: N)
Energy (kcal/mol) for this N-H-->O H-bond (1)
Distance from Ligand: GLU (ATOM: CD)
Distance from Ligand: GLU (ATOM: O)
Solvent accessibility (PopMusic)
Mutant amino acid's Huckel Analysis pi Energy
Reference amino acid's pKa maximum
Distance from Ligand: GLU (ATOM: CA)
Distance from Ligand: GLU (ATOM: CB)
First residue of beta bridge
Distance from Ligand: GLU (ATOM: CG)
Offset from residue to the partner in N-H-->O H-bond (2)
Reference amino acid's Solubility in g per 100 mL H2O at 25C
Offset from residue to the partner in N-H-->O H-bond (1)
Reference amino acid's pI
Reference amino acid's Composition in the UniProtKB Swiss-Prot data bank
Sum of negative contributors (PopMusic)
Helix formation in helix types 3 4 and 5
Reference amino acid's pKa NH2
Offset from residue to the partner in O-->H-N H-bond (2)
Energy (kcal/mol) for this N-H-->O H-bond (2)
Secondary structure
Mutant amino acid's Lead Likeness
Mutant amino acid's Hydropathy
Reference amino acid's Huckel Analysis pi Energy
Energy (kcal/mol) for this O-->H-N H-bond (2)
Reference amino acid's Lead Likeness
Mutant amino acid's Charge
Reference amino acid's Hydropathy
Reference amino acid's Charge
beta bridge labels
bend
Chirality
Sheet of beta bridge
Reference amino acid's Muegge Filter
Second residue of beta bridge
Mutant amino acid's Muegge Filter
Mutant amino acid's Veber Filter
Mutant amino acid's Ghose Filter
Mutant amino acid's Bioavailability
Mutant amino acid's Lipinskis Rule Of Five
Reference amino acid's Lipinskis Rule Of Five
Reference amino acid's Bioavailability
Reference amino acid's Ghose Filter
Reference amino acid's Veber Filter
0.0
0.005
0.01
0.015
0.02
0.025
Relative importances