Gene names	Protein names	bestbest (kcal/mol)	Num in Largest Cluster
1 BCAT2 BCATM BCT2 ECA40	Branched-chain-amino-acid aminotransferase, mitochondrial (BCAT(m)) (EC 2.6.1.42) (Placental protein 18) (PP18)	-8.450000	40.000000
2 AADAT KAT2	Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial (KAT/AadAT) (2-aminoadipate aminotransferase) (2-aminoadipate transaminase) (EC 2.6.1.39) (Alpha-aminoadipate aminotransferase) (AadAT) (Kynurenine aminotransferase II) (Kynurenineoxoglutarate transaminase 2) (EC 2.6.1.7) (Kynurenineoxoglutarate transaminase II)	-8.340000	82.000000
3 GOT2	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine-oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	-8.200000	36.000000
4 GOT1	Aspartate aminotransferase, cytoplasmic (cAspAT) (EC 2.6.1.1) (EC 2.6.1.3) (Cysteine aminotransferase, cytoplasmic) (Cysteine transaminase, cytoplasmic) (cCAT) (Glutamate oxaloacetate transaminase 1) (Transaminase A)	-8.100000	36.000000
5 KYAT1 CCBL1	Kynurenineoxoglutarate transaminase 1 (EC 2.6.1.7) (Cysteine-S-conjugate beta-lyase) (EC 4.4.1.13) (Glutamine transaminase K) (GTK) (Glutaminephenylpyruvate transaminase) (EC 2.6.1.64) (Kynurenine aminotransferase I) (Kynurenine aminotransferase I) (Kynurenineoxoglutarate transaminase I)	-8.020000	79.000000
6 KYAT3 CCBL2 KAT3	Kynurenineoxoglutarate transaminase 3 (EC 2.6.1.7) (Cysteine-S-conjugate beta-lyase 2) (EC 4.4.1.13) (Kynurenine aminotransferase 3) (Kynurenine aminotransferase III) (KATIII) (Kynurenineglyoxylate transaminase) (EC 2.6.1.63) (Kynurenineoxoglutarate transaminase III)	-7.800000	66.000000
7 AGXT AGT1 SPAT	Serinepyruvate aminotransferase (SPT) (EC 2.6.1.51) (Alanineglyoxylate aminotransferase) (AGT) (EC 2.6.1.44)	-7.750000	48.000000
PHYKPL 8 AGXT2L2 PP9286	5-phosphohydroxy-L-lysine phospho-lyase (EC 4.2.3.134) (Alanineglyoxylate aminotransferase 2-like 2)	-7.650000	20.000000
9 BCAT1 BCT1 ECA39	Branched-chain-amino-acid aminotransferase, cytosolic (BCAT(c)) (EC 2.6.1.42) (Protein ECA39)	-7.320000	42.000000
10 SEPSECS TRNP48	O-phosphoseryl-tRNA(Sec) selenium transferase (EC 2.9.1.2) (Liver-pancreas antigen) (LP) (SLA-p35) (SLA/LP autoantigen) (Selenocysteine synthase) (Sec synthase) (Sec synthase) (Sep-tRNA:Sec-tRNA synthase) (SepSecS) (Soluble liver antigen) (SLA) (UGA suppressor tRNA-associated protein) (tRNA(Ser/Sec)-associated antigenic protein)	-7.250000	24.000000
11 CTH		-7.200000	14.000000
12 ODC1			17.000000
13 GPT AAT1 GPT1 14 PSAT1 PSA		-7.090000 -7.080000	55.000000
15 GPT2 AAT2 ALT2 GAD1 GAD			32.000000
$16_{\mathrm{GAD67}}^{\mathrm{GAD1\ GAD}}$			17.000000
17 PYGL			31.000000
18 TAT 19 CSAD CSD			27.000000 29.000000
20 SDSL			15.000000
21 THNSL1	Threonine synthase-like 1 (TSH1)	-6.710000	67.000000
22 SRR	Serine racemase (EC 5.1.1.18) (D-serine ammonia-lyase) (D-serine dehydratase) (EC 4.3.1.18) (L-serine ammonia-lyase) (L-serine dehydratase) (EC 4.3.1.17)	-6.640000	50.000000
23 SGPL1 KIAA1252	Sphingosine-1-phosphate lyase 1 (S1PL) (SP-lyase 1) (SPL 1) (hSPL) (EC 4.1.2.27) (Sphingosine-1-phosphate aldolase)	-6.630000	37.000000
ALAS1 ALAS3 24 ALASH OK/SW- cl.121	5-aminolevulinate synthase, nonspecific, mitochondrial (ALAS-H) (EC 2.3.1.37) (5-aminolevulinic acid synthase 1) (Delta-ALA synthase 1) (Delta-aminolevulinate synthase 1)	-6.610000	56.000000
25 SDS SDH			49.000000
26 DDC AADC 27 SHMT2			14.000000 44.000000
SPTLC3	Serme nyuroxymethymansierase, mitochonuriai (SHMT) (EC 2.1.2.1) (Glychie nyuroxymethymansierase) (Serme methylase)	-0.390000	44.000000
28 C20orf38 SPTLC2L		-6.360000	91.000000
29 OAT	Ornithine aminotransierase, renai form		25.000000
30 GAD2 GAD65 31 ACCS PHACS			22.000000 61.000000
32 GADL1	Acidic amino acid decarboxylase GADL1 (Aspartate 1-decarboxylase) (ADC) (HuADC) (EC 4.1.1.11) (Cysteine sulfinic acid decarboxylase) (CSADC) (HuCSADC) (EC 4.1.1.29) (Glutamate		21.000000
33 ALAS2 ALASE ASB	decarboxylase-like protein 1)		100.00000
34 PYGM 35 ACCSL			47.000000 24.000000
36 NFS1 NIFS HUSSY-08			20.000000
	A aminabuturata aminatranafarasa, mitaabandrial (EC 2.6.1.10) ((S) 2 amina 2 matbularanianata transaminasa) (EC 2.6.1.22) (CABA aminatranafarasa) (CABA AT) (Camma amina N. buturata		
37 ABAT GABAT 38 PYGB	transaminase) (GABA transaminase) (GABA-T) (L-AIBAT)		35.000000 24.000000
39 SHMT1			19.000000
40 GCAT KBL			29.000000
41 SCLY SCL		-5.940000	19.000000
42 GOT1L1 43 CBSL			37.000000 25.000000
44 SPTLC2 KIAA0526 LCB2			31.000000
45 THNSL2			63.000000
46 ETNPPL AGXT2L1			17.000000
			57.000000
47 HDC 48 KYNU			32.000000
49 PLPBP PROSC			21.000000
50 MOCOS	Molybdenum cofactor sulfurase (MCS) (MOS) (MoCo sulfurase) (hMCS) (EC 2.8.1.9) (Molybdenum cofactor sulfurtransferase)		18.000000
51 AGXT2 AGT2	Alanineglyoxylate aminotransferase 2, mitochondrial (AGT 2) (EC 2.6.1.44) ((R)-3-amino-2-methylpropionatepyruvate transaminase) (EC 2.6.1.40) (Beta-ALAAT II) (Beta-alanine-pyruvate aminotransferase) (D-AIBAT)	-4.820000	21.000000
ED OLDO COOD	Chairm debada area (decade adative) with the adrial (EC 4.4.4.9) (Chairm decade adaptive) (Chairm debada (Chair	4 740000	22 000000

Glycine dehydrogenase (decarboxylating), mitochondrial (EC 1.4.4.2) (Glycine cleavage system P protein) (Glycine decarboxylase) (Glycine dehydrogenase (aminomethyl-transferring))

-4.740000 23.000000

-4.390000 16.000000

 $\mathbf{52}\,\mathrm{GLDC}\,\mathrm{GCSP}$

 $\mathbf{53}_{\ \mathrm{OAZIN}}^{\ \mathrm{AZIN1}\ \mathrm{OAZI}}$

Antizyme inhibitor 1 (AZI) (AZI1) (Ornithine decarboxylase antizyme inhibitor)