

Amino acid	% abundance	ln (% abundance)	Cost	(ATP)	Cost	(ATP/t)	ln (% abundance)	Organism	Genomic GC c	R % abundance	R ln(% abundance)
A	8.2554	2.11086753	11.7	11.7	11.7	11.7	1.177	<i>A. thaliana</i>	0.36	-0.5998612	-0.6451639
C	1.226	0.20375684	24.7	741	1.058						
D	5.6055	1.72374826	12.7	114.3	1.058						
E	7.263	1.98279297	15.3	76.5	1.058						
F	3.9496	1.37361431	52	208	1.632						
G	7.6919	2.04016783	11.7	11.7	1.177						
H	1.8889	0.63599465	38.3	536.2	1.058						
I	5.276	1.66316823	32.3	64.6	2.127						
K	7.1432	1.96616086	30.3	242.4	1.632						
L	8.505	2.14065423	27.3	54.6	2.387						
M	2.2663	0.81814855	34.3	445.9	0.611						
N	3.8493	1.34789131	14.7	147	1.632						
P	4.7738	1.56314263	20.3	60.9	1.177						
Q	3.3873	1.22003314	16.3	130.4	1.058						
R	4.7941	1.567386	27.3	109.2	1.813						
S	7.5431	2.02063324	11.7	70.2	2.157						
T	5.4449	1.69543211	18.7	112.2	1.751						
V	7.3239	1.99114297	23.3	46.6	1.751						
W	1.0416	4.08E-02	74.3	891.6	3.70E-02						
Y	2.767	1.0177637	50	350	1.632						
A	8.0216	2.0821379	11.7	11.7	1.987	T. gammaole	0.54	-0.4243748	-0.3894329		
C	0.5011	-0.6909496	24.7	741	1.133						
D	5.4069	1.68767592	12.7	114.3	1.133						
E	8.8216	2.17720326	15.3	76.5	1.133						
F	3.6787	1.30255943	52	208	0.973						
G	7.7964	2.05366209	11.7	11.7	1.987						
H	1.7692	0.57052747	38.3	536.2	1.133						
I	7.0663	1.955337	32.3	64.6	1.351						
K	7.5457	2.02097786	30.3	242.4	0.973						
L	8.2096	2.1053042	27.3	54.6	2.181						
M	2.5658	0.94227032	34.3	445.9	0.356						
N	3.2444	1.17693043	14.7	0.973							

R % abundance R ln(% abundance), observed vs predicted  
-0.8150534 -0.9302527 0.62952057

P	4.9656	1.60253414	20.3	60.9	1.987
Q	2.2364	0.80486743	16.3	130.4	1.133
R	5.3622	1.67937434	27.3	109.2	2.341
S	4.0297	1.39369193	11.7	70.2	2.232
T	5.0234	1.614107	18.7	112.2	1.826
V	8.7146	2.16499978	23.3	46.6	1.826
W	1.3682	0.31349601	74.3	891.6	0.517
Y	3.6726	1.30089986	50	350	0.973
A	7.29	1.98650355	11.7	11.7	1.284
C	0.747	-0.2916901	24.7	741	L. interrogans
D	5.3931	1.68512036	12.7	114.3	1.08
E	7.695	2.04057077	15.3	76.5	1.08
F	4.0547	1.3998767	52	208	1.57
G	7.4426	2.00722025	11.7	11.7	1.284
H	1.617	0.48057258	38.3	536.2	1.08
I	7.6019	2.02839822	32.3	64.6	2.052
K	8.5321	2.14383552	30.3	242.4	1.57
L	8.6561	2.15826427	27.3	54.6	2.37
M	2.274	0.8215404	34.3	445.9	0.602
N	4.6349	1.53361462	14.7	147	1.57
P	3.883	1.35660805	20.3	60.9	1.284
Q	3.3046	1.19531544	16.3	130.4	1.08
R	4.2217	1.44023789	27.3	109.2	1.88
S	6.856	1.92512418	11.7	70.2	2.179
T	5.3129	1.67013783	18.7	112.2	1.773
V	6.6977	1.90176418	23.3	46.6	1.773
W	0.7331	-0.3104732	74.3	891.6	0.113
Y	3.0526	1.11599369	50	350	1.57
A	10.3131	2.33341493	11.7	11.7	1.906 S. typhimurium
C	0.748	-0.2903523	24.7	741	0.52
D	5.8981	1.77463027	12.7	114.3	-0.590483
E	7.0475	1.95267294	15.3	76.5	-0.630423

-0.7932245 -0.9275999 0.67601055

-0.8013338 -0.934277 0.61776515



-0.796752 -0.9331608 0.62554931

V	8.0204	2.0819883	23.3	46.6	1.832			
W	0.828	-0.1887421	74.3	891.6	0.457			
Y	2.5226	0.92529012	50	350	1.119			
A	12.3175	2.51102102	11.7	11.7	2.376	M. tuberculosis	0.66	-0.5837622
C	0.5577	-0.5839341	24.7	741	1.037			-0.594927
D	6.4482	1.86380102	12.7	114.3	1.037			
E	6.4772	1.86828832	15.3	76.5	1.037			
F	2.8656	1.05277775	52	208	0.391			
G	8.9621	2.19300457	11.7	11.7	2.376			
H	1.7419	0.55497647	38.3	536.2	1.037			
I	4.6759	1.54242166	32.3	64.6	0.686			
K	4.1219	1.41631422	30.3	242.4	0.391			
L	8.6897	2.16213842	27.3	54.6	1.963			
M	1.993	0.68964104	34.3	445.9	-3.10E-02			
N	2.7075	0.9960257	14.7	147	0.391			
P	5.5531	1.71435633	20.3	60.9	2.376			
Q	3.3782	1.21734302	16.3	130.4	1.037			
R	6.0804	1.80507048	27.3	109.2	2.609			
S	5.3305	1.67344504	11.7	70.2	2.135			
T	6.2626	1.83459543	18.7	112.2	1.73			
V	8.6902	2.16219595	23.3	46.6	1.73			
W	0.9986	-1.40E-03	74.3	891.6	0.615			
Y	2.1481	0.76458373	50	350	0.391			
A	8.4457	2.13365744	11.7	11.7	1.178	S. pombe	0.36	-0.5983103
C	1.2224	0.20081614	24.7	741	1.058			-0.647442
D	5.492	1.70329249	12.7	114.3	1.058			
E	6.8818	1.92888025	15.3	76.5	1.058			
F	3.8797	1.35575783	52	208	1.632			
G	7.0034	1.94639575	11.7	11.7	1.178			
H	2.0788	0.7317908	38.3	536.2	1.058			
I	6.0113	1.79364103	32.3	64.6	2.126			
K	7.0027	1.94629579	30.3	242.4	1.632			

-0.7592226 -0.9141458 0.62695515

-0.8388065 -0.942812 0.67568717

L	8.2989	2.11612298	27.3	54.6	2.387
M	2.1517	0.76625823	34.3	445.9	0.611
N	4.3802	1.47709439	14.7	147	1.632
P	4.7254	1.55295221	20.3	60.9	1.178
Q	3.3389	1.20564141	16.3	130.4	1.058
R	4.9995	1.60933791	27.3	109.2	1.813
S	7.1768	1.9708536	11.7	70.2	2.157
T	5.6051	1.7236769	18.7	112.2	1.752
V	7.2858	1.98592725	23.3	46.6	1.752
W	0.9373	-6.48E-02	74.3	891.6	3.80E-02
Y	3.0826	1.1257734	50	350	1.632
A	8.0799	2.0893795	11.7	11.7	1.555
C	0.6805	-0.3849275	24.7	741	1.122
D	5.3465	1.67644214	12.7	114.3	1.122
E	8.4383	2.13278087	15.3	76.5	1.122
F	3.674	1.30128099	52	208	1.384
G	7.5312	2.01905439	11.7	11.7	1.555
H	2.0501	0.71788857	38.3	536.2	1.122
I	6.7368	1.90758503	32.3	64.6	1.831
K	8.1398	2.09676561	30.3	242.4	1.384
L	8.3242	2.11916694	27.3	54.6	2.316
M	2.607	0.95820013	34.3	445.9	0.551
N	4.1032	1.41176716	14.7	147	1.384
P	3.5767	1.27444059	20.3	60.9	1.555
Q	3.6622	1.29806406	16.3	130.4	1.122
R	4.6948	1.54645551	27.3	109.2	2.055
S	5.5591	1.71543622	11.7	70.2	2.221
T	5.4274	1.6914602	18.7	112.2	1.816
V	7.7471	2.04731858	23.3	46.6	1.816
W	0.7215	-0.3264229	74.3	891.6	0.29
Y	2.8999	1.06467625	50	350	1.384
A	7.477	2.01183164	11.7	11.7	1.402
					H. sapiens
				0.4	-0.611998
					-0.706061

-0.7897507 -0.9227579 0.63715069

-0.7716967 -0.8825331 0.70376406

C	2.2954	0.83090712	24.7	741	1.101
D	5.3598	1.67892666	12.7	114.3	1.101
E	7.5366	2.01977115	15.3	76.5	1.101
F	3.8375	1.34482111	52	208	1.494
G	6.8345	1.92198331	11.7	11.7	1.402
H	2.2076	0.79190595	38.3	536.2	1.101
I	3.9002	1.36102783	32.3	64.6	1.962
K	7.0759	1.95669464	30.3	242.4	1.494
L	9.3303	2.23326717	27.3	54.6	2.348
M	2.0387	0.711231235	34.3	445.9	0.585
N	3.7699	1.32704848	14.7	147	1.494
P	5.1794	1.64468922	20.3	60.9	1.402
Q	4.3717	1.47515195	16.3	130.4	1.101
R	4.7851	1.56550692	27.3	109.2	1.956
S	7.0607	1.9545442	11.7	70.2	2.2
T	5.8144	1.7603376	18.7	112.2	1.794
U	6.7645	1.91168835	23.3	46.6	1.794
V	1.2269	0.20449066	74.3	891.6	0.193
W	3.1339	1.14227824	50	350	1.494
Y					
A	10.6028	2.36111812	11.7	11.7	2.405
C	0.9587	-4.22E-02	24.7	741	1.023
D	5.4092	1.68810121	12.7	114.3	1.023
E	5.7294	1.74561081	15.3	76.5	1.023
F	3.7703	1.32715457	52	208	0.335
G	8.113	2.09346771	11.7	11.7	2.405
H	1.0258	2.55E-02	38.3	536.2	1.023
I	6.1249	1.81236243	32.3	64.6	0.623
K	4.7423	1.55652225	30.3	242.4	0.335
L	8.8773	2.18349746	27.3	54.6	1.94
M	2.3828	0.86827627	34.3	445.9	-7.20E-02
N	4.3376	1.4673212	14.7	147	0.335
P	4.2797	1.45388291	20.3	60.9	2.405
Q	4.1635	1.42635607	16.3	130.4	1.023

*M. aeruginosæ*

0.67 -0.5928878 -0.6198083

-0.8300464 -0.9471387 0.48797002

R	5.1598	1.64089782	27.3	109.2	2.629
S	6.8403	1.92283159	11.7	70.2	2.122
T	5.9117	1.77693344	18.7	112.2	1.716
V	7.2046	1.97471971	23.3	46.6	1.716
W	0.9185	-8.50E-02	74.3	891.6	0.616
Y	3.448	1.23779435	50	350	0.335
A	8.3471	2.12191417	11.7	11.7	1.292
C	0.9509	-5.03E-02	24.7	741	1.082
D	5.7909	1.75628772	12.7	114.3	1.082
E	6.8401	1.92280235	15.3	76.5	1.082
F	3.9724	1.37937045	52	208	1.565
G	6.7993	1.91681967	11.7	11.7	1.292
H	1.9844	0.6853166	38.3	536.2	1.082
I	6.1477	1.81607803	32.3	64.6	2.046
K	8.126	2.0950688	30.3	242.4	1.565
L	8.3443	2.12157867	27.3	54.6	2.368
M	1.9355	0.66036569	34.3	445.9	0.601
N	4.7318	1.55430568	14.7	147	1.565
P	4.2877	1.45575046	20.3	60.9	1.292
Q	3.4779	1.24642866	16.3	130.4	1.082
R	4.4848	1.5006939	27.3	109.2	1.885
S	6.8481	1.92397124	11.7	70.2	2.18
T	5.759	1.75076385	18.7	112.2	1.775
V	7.2299	1.9782252	23.3	46.6	1.775
W	0.9429	-5.88E-02	74.3	891.6	0.118
Y	2.9994	1.09841227	50	350	1.565
A	8.6446	2.15693485	11.7	11.7	1.144
C	1.1908	0.17462535	24.7	741	1.051
D	5.8275	1.76258809	12.7	114.3	1.051
E	7.454	2.0087508	15.3	76.5	1.051
F	3.6902	1.30568066	52	208	1.651
G	6.972	1.94190213	11.7	11.7	1.144

C. elegans

0.35 -0.6246407 -0.6794239

-0.814094 -0.9303567 0.68244709

-0.8284969 -0.9423982 0.61372416

H	2.1177	0.75033059	38.3	536.2	1.051
I	5.425	1.6910179	32.3	64.6	2.149
K	7.7763	2.05108065	30.3	242.4	1.651
L	7.9571	2.07406461	27.3	54.6	2.392
M	2.248	0.81004093	34.3	445.9	0.613
N	4.3176	1.46269969	14.7	147	1.651
P	4.3895	1.47921533	20.3	60.9	1.144
Q	4.2407	1.44472835	16.3	130.4	1.051
R	5.3654	1.67997093	27.3	109.2	1.792
S	6.3341	1.84594774	11.7	70.2	2.149
T	5.4846	1.70194416	18.7	112.2	1.744
V	6.9435	1.93780597	23.3	46.6	1.744
W	0.8902	-0.1163091	74.3	891.6	1.30E-02
Y	2.731	1.00466784	50	350	1.651
A	8.5558	2.14660942	11.7	11.7	1.495
C	1.273	0.24137632	24.7	741	1.115
D	5.8041	1.75856456	12.7	114.3	1.115
E	7.2161	1.97631464	15.3	76.5	1.115
F	3.478	1.24645742	52	208	1.428
G	6.9697	1.94157218	11.7	11.7	1.495
H	1.9788	0.6824906	38.3	536.2	1.115
I	5.3257	1.67254416	32.3	64.6	1.884
K	7.8746	2.06364239	30.3	242.4	1.428
L	8.2715	2.11281587	27.3	54.6	2.329
M	2.2067	0.79149819	34.3	445.9	0.566
N	4.4719	1.49781337	14.7	147	1.428
P	4.5759	1.15208034	20.3	60.9	1.495
Q	4.477	1.49895318	16.3	130.4	1.115
R	5.4143	1.6890436	27.3	109.2	2.016
S	6.4158	1.8587637	11.7	70.2	2.214
T	5.347	1.67653566	18.7	112.2	1.808
V	6.7783	1.91372633	23.3	46.6	1.808
W	0.8047	-0.2172857	74.3	891.6	0.253

-0.8309994 -0.9455694 0.70077172

Y	2.7609	1.01555671	50	350	1.428	
A	7.8315	2.05815406	11.7	11.7	1.448	M. musculus
C	1.6824	0.52022135	24.7	741	1.108	
D	5.3894	1.68443406	12.7	114.3	1.108	
E	7.2169	1.9764255	15.3	76.5	1.108	
F	3.637	1.29115917	52	208	1.462	
G	7.4357	2.00629272	11.7	11.7	1.448	
H	2.2143	0.79493633	38.3	536.2	1.108	
I	4.8985	1.58892904	32.3	64.6	1.924	
K	7.2677	1.98343987	30.3	242.4	1.462	
L	8.8486	2.18025925	27.3	54.6	2.339	
M	2.4293	0.88760315	34.3	445.9	0.576	
N	3.823	1.34103545	14.7	147	1.462	
P	5.0688	1.6231041	20.3	60.9	1.448	
Q	4.297	1.4579171	16.3	130.4	1.108	
R	5.5858	1.72022766	27.3	109.2	1.986	
S	6.7039	1.90268945	11.7	70.2	2.207	
T	5.3565	1.67831078	18.7	112.2	1.801	
U	6.5157	1.87421465	23.3	46.6	1.801	
V	0.9851	-1.50E-02	74.3	891.6	0.223	
W	2.8128	1.03418043	50	350	1.462	
X	7.995	2.07881635	11.7	11.7	1.484	B. taurus
Y	2.3278	0.84492362	24.7	741	1.114	
Z	5.1828	1.64534545	12.7	114.3	1.114	
A	7.6465	2.03424803	15.3	76.5	1.114	
C	3.6564	1.29647906	52	208	1.436	
D	6.2101	1.826177	11.7	11.7	1.484	
E	2.2243	0.79944226	38.3	536.2	1.114	
F	4.6997	1.54749868	32.3	64.6	1.894	
G	7.4404	2.00692461	30.3	242.4	1.436	
H	9.92	2.29455292	27.3	54.6	2.332	
I	2.1788	0.77877427	34.3	445.9	0.569	

0.42 -0.5899417 -0.7194498

-0.821106 -0.932148 0.71419077

-0.7536695 -0.8837632 0.71652091

N	3.4877	1.24924249	14.7	147	1.436	
P	5.572	1.71775406	20.3	60.9	1.484	
Q	4.608	1.52779392	16.3	130.4	1.114	
R	4.0552	1.40000001	27.3	109.2	2.009	
S	6.9309	1.93598967	11.7	70.2	2.212	
T	5.2381	1.65595884	18.7	112.2	1.807	
V	6.6675	1.89724498	23.3	46.6	1.807	
W	0.9763	-2.40E-02	74.3	891.6	0.246	
Y	2.9822	1.09266128	50	350	1.436	
A	10.0677	2.30933228	11.7	11.7	1.336	S. pyogenes
C	0.318	-1.1457039	24.7	741	1.09	
D	5.9946	1.79085906	12.7	114.3	1.09	
E	7.9177	2.06910076	15.3	76.5	1.09	
F	3.3364	1.20489238	52	208	1.537	
G	7.6573	2.03565944	11.7	11.7	1.336	
H	1.5742	0.453374721	38.3	536.2	1.09	
I	6.367	1.8511284	32.3	64.6	2.013	
K	8.0933	2.09103656	30.3	242.4	1.537	
L	7.9674	2.07535822	27.3	54.6	2.361	
M	2.337	0.84886806	34.3	445.9	0.596	
N	4.4748	1.49846166	14.7	147	1.537	
P	3.3167	1.19897031	20.3	60.9	1.336	
Q	3.5511	1.26725741	16.3	130.4	1.09	
R	4.4969	1.50338827	27.3	109.2	1.913	
S	5.474	1.70000961	11.7	70.2	2.188	
T	5.8921	1.77361247	18.7	112.2	1.783	
V	7.9199	2.06937858	23.3	46.6	1.783	
W	0.556	-0.586987	74.3	891.6	0.148	
Y	2.688	0.98879742	50	350	1.537	
A	8.228	2.10754297	11.7	11.7	1.484	G. gallus
C	1.4166	0.34825963	24.7	741	1.114	
D	5.4153	1.68922828	12.7	114.3	1.114	

0.42 -0.6166312 -0.6895094

-0.7886328 -0.9215407 0.58719613

-0.8191444 -0.9363247 0.70847817

E	7.3495	1.99463228	15.3	76.5	1.114
F	3.5913	1.27851425	52	208	1.436
G	7.7212	2.04396979	11.7	11.7	1.484
H	2.0332	0.70961091	38.3	536.2	1.114
I	5.2442	1.6571227	32.3	64.6	1.894
K	7.5956	2.02756913	30.3	242.4	1.436
L	8.5171	2.14207591	27.3	54.6	2.332
M	2.442	0.89281738	34.3	445.9	0.569
N	3.8641	1.3517288	14.7	147	1.436
P	4.85	1.5789787	20.3	60.9	1.484
Q	3.9229	1.36683118	16.3	130.4	1.114
R	5.4784	1.70081309	27.3	109.2	2.009
S	6.6432	1.89359378	11.7	70.2	2.212
T	5.3958	1.68562087	18.7	112.2	1.807
V	6.5154	1.87416861	23.3	46.6	1.807
W	0.9138	-9.01E-02	74.3	891.6	0.246
Y	2.8622	1.05159056	50	350	1.436