A

	species	ΔG vs acc		Controlling size		Controlling GC		controlling GC, size		Controlling AA-content		Controlling AA groups		Controlling codon bias	
		SP		SP		SP		SP		SP		SP		SP	
ΔGmean	HSA	0.28	**6.3E-11**	0.13	**2.54E-03**	0.41	**<1E-16**	0.11	**1.37E-02**	0.09	**4.30E-02**	0.11	**9.77E-03**	0.23	**8.03E-07**
	SCE	0.15	**4.1E-02**	0.03	6.68E-01	0.34	**1.01E-06**	0.11	1.33E-01	0.07	3.89E-01	0.10	2.03E-01	0.12	1.96E-01
	BSU	0.54	**<1E-16**	0.18	**3.21E-02**	0.42	**4.96E-08**	0.09	3.06E-01	0.42	**5.67E-07**	0.40	**4.61E-07**	0.33	**1.84E-03**
	ECO	0.43	**<1E-16**	0.09	**7.39E-02**	0.26	**6.09E-08**	-0.02	6.26E-01	0.29	**1.95E-09**	0.36	**1.53E-14**	0.03	5.58E-01
	TGA	0.41	**3.0E-05**	0.11	2.83E-01	0.41	**1.56E-05**	0.11	2.79E-01	0.37	**6.84E-04**	0.32	**1.19E-03**	0.46	**2.38E-03**
ΔGmin	HSA	0.38	**<1E-16**	0.05	2.18E-01	0.39	**<1E-16**	-0.03	4.89E-01	0.22	**5.98E-07**	0.26	**2.23E-09**	0.22	**1.61E-06**
	SCE	0.49	**3.0E-12**	0.13	7.45E-02	0.57	**<1E-16**	0.19	**1.09E-02**	0.27	**4.10E-04**	0.35	**1.06E-06**	0.14	1.10E-01
	BSU	0.60	**2.9E-15**	0.20	**1.45E-02**	0.51	**3.99E-12**	0.14	1.09E-01	0.41	**9.34E-07**	0.44	**1.54E-08**	0.30	**6.02E-03**
	ECO	0.53	**<1E-16**	0.09	6.69E-02	0.43	**<1E-16**	0.03	5.76E-01	0.36	**8.73E-14**	0.43	**<1E-16**	0.19	**3.79E-04**
	TGA	0.38	**1.3E-04**	-0.01	9.15E-01	0.36	**1.62E-04**	-0.02	8.74E-01	0.27	**1.65E-02**	0.34	**5.90E-04**	-0.01	9.65E-01
ΔGmax	HSA	-0.08	5.6E-02												
	SCE	-0.32	**8.0E-06**												
	BSU	-0.05	5.8E-01												
	ECO	-0.18	**3.2E-04**												
	TGA	-0.21	**4.0E-02**												

B

		ΔGmin vs acc		
		SP		n
Fold	HSA	0.44	**4.69E-10**	187
	SCE	0.42	**7.83E-05**	84
	BSU	0.63	**9.91E-11**	84
	ECO	0.56	**3.14E-18**	204
	TGA	0.36	**6.06E-03**	56
Superfam	HSA	0.42	**1.90E-10**	207
	SCE	0.43	**2.43E-05**	90
	BSU	0.60	**2.48E-10**	91
	ECO	0.56	**<1E-16**	226
	TGA	0.39	**1.83E-03**	60

C

	ACC vs GC	
	SP	
HSA	-0.13	**2.41E-03**
SCE	0.16	**2.96E-02**
BSU	-0.37	**4.88E-06**
ECO	-0.35	**1.99E-13**
TGA	-0.13	**2.18E-01**

Supplementary Table 1: A, Correlations between mRNA folding energy (using ΔGmean, ΔGmin and ΔGmax – rows from top to bottom, see **Methods**) and protein solvent accessibility (ACC) controlling protein size (size) and messenger GC content (GC), amino acids content (AA) and the fractions of 6 groups of amino acids (see Methods) (AA-group). Column 4 shows the partial correlation controlling both GC content and protein size. B, correlation between ΔGmin and ACC after removing SCOP Fold or SCOP Superfamily (Superfam) redundancy and number of protein (n). C, Correlation between ACC and GC. Correlation and partial correlation is computed using Spearman's rank correlation (SP). Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. HSA, SCE, BSU, ECO, TGA correspond respectively to *H. sapiens*, *S. cerevisiae*, *B. subtilis*, *E. coli* and *T. gammatolerans*. As protein solvent accessibility requires protein structures, we used here the structural dataset.

		ΔG vs GC		Controlling size		ΔG vs size		Controlling GC		GC vs size	
	species	**SP**		**SP**		**SP**		**SP**		**SP**	
ΔGmean	CEL	-0.69	**<1E-16**	-0.75	**<1E-16**	-0.19	**<1E-16**	-0.42	**<1E-16**	-0.15	**<1E-16**
	HSA	-0.92	**<1E-16**	-0.94	**<1E-16**	-0.18	**<1E-16**	-0.44	**<1E-16**	0.01	5.43E-01
	DME	-0.76	**<1E-16**	-0.79	**<1E-16**	-0.13	**<1E-16**	-0.38	**<1E-16**	-0.15	**<1E-16**
	SCE	-0.61	**<1E-16**	-0.66	**<1E-16**	-0.09	**1.46E-09**	-0.34	**<1E-16**	-0.27	**<1E-16**
	ASP	-0.59	**<1E-16**	-0.61	**<1E-16**	-0.17	**<1E-16**	-0.25	**<1E-16**	-0.06	**6.55E-09**
	NEU	-0.59	**<1E-16**	-0.62	**<1E-16**	-0.16	**<1E-16**	-0.30	**<1E-16**	-0.13	**<1E-16**
	BSU	-0.79	**<1E-16**	-0.76	**<1E-16**	-0.53	**<1E-16**	-0.42	**<1E-16**	0.36	**<1E-16**
	MET	-0.72	**<1E-16**	-0.70	**<1E-16**	-0.41	**<1E-16**	-0.33	**<1E-16**	0.26	<1E-16
	ECO	-0.80	**<1E-16**	-0.77	**<1E-16**	-0.48	**<1E-16**	-0.34	**<1E-16**	0.36	**<1E-16**
	TGA	-0.67	**<1E-16**	-0.67	**<1E-16**	-0.45	**<1E-16**	-0.44	**<1E-16**	0.19	5.11E-11
	HAL	-0.81	**<1E-16**	-0.81	**<1E-16**	-0.30	**<1E-16**	-0.25	**<1E-16**	0.19	**<1E-16**
	DEI	-0.83	**<1E-16**	-0.83	**<1E-16**	-0.25	**<1E-16**	-0.30	**<1E-16**	0.10	1.24E-05
ΔGmin	CEL	-0.34	**<1E-16**	-0.51	**<1E-16**	-0.53	**<1E-16**	-0.63	**<1E-16**		
	HSA	-0.71	**<1E-16**	-0.78	**<1E-16**	-0.43	**<1E-16**	-0.60	**<1E-16**		
	DME	-0.35	**<1E-16**	-0.52	**<1E-16**	-0.54	**<1E-16**	-0.64	**<1E-16**		
	SCE	-0.23	**<1E-16**	-0.45	**<1E-16**	-0.51	**<1E-16**	-0.61	**<1E-16**		
	ASP	-0.33	**<1E-16**	-0.42	**<1E-16**	-0.49	**<1E-16**	-0.55	**<1E-16**		
	NEU	-0.29	**<1E-16**	-0.42	**<1E-16**	-0.53	**<1E-16**	-0.59	**<1E-16**		
	BSU	-0.58	**<1E-16**	-0.49	**<1E-16**	-0.66	**<1E-16**	-0.59	**<1E-16**		
	MET	-0.47	**<1E-16**	-0.41	**<1E-16**	-0.66	**<1E-16**	-0.63	**<1E-16**		
	ECO	-0.57	**<1E-16**	-0.46	**<1E-16**	-0.66	**<1E-16**	-0.59	**<1E-16**		
	TGA	-0.36	**<1E-16**	-0.32	**<1E-16**	-0.62	**<1E-16**	-0.61	**<1E-16**		
	HAL	-0.58	**<1E-16**	-0.60	**<1E-16**	-0.60	**<1E-16**	-0.62	**<1E-16**		
	DEI	-0.53	**<1E-16**	-0.57	**<1E-16**	-0.52	**<1E-16**	-0.56	**<1E-16**		

Supplementary Table 2: A, partial correlation analysis between mRNA folding energy (ΔGmean and ΔGmin), protein size (size) and messenger GC content (GC). B, correlation between GC and size. CEL, HSA, DME, SCE, ASP, NEU, BSU, MET, ECO, TGA, HAL, DEI correspond respectively to *Caenorhabditis elegans* , *Homo sapiens, Drosophila melanogaster, Saccharomyces cerevisiae, Aspergillus orizae, Neurospora crassa, Bacillus subtilis, Methanosarcina. Marzei, Escherichia coli, Thermococcus gammatolerans, Haloferax volcanii, Deinococcus radiodurans.* Correlation and partial correlation were estimated using Spearman's rank correlation (SP). Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. We used the transcriptome dataset.

		ΔGmean vs ACC				ΔGmin vs ACC			
		Order		Disorder		Order		Disorder	
	species	**SP**		**SP**		**SP**		**SP**	
SEGHCA	HSA	0.29	**1.48E-11**	0.13	**3.40E-02**	0.39	**<1E-16**	0.16	**9.95E-03**
	SCE	0.15	**3.71E-02**	0.05	6.51E-01	0.50	**7.31E-13**	0.11	3.19E-01
	BSU	0.51	**1.77E-10**	0.04	7.70E-01	0.59	**2.05E-14**	0.25	7.64E-02
	ECO	0.43	**<1E-16**	0.22	**9.55E-04**	0.53	**<1E-16**	0.29	**1.12E-05**
	TGA	0.37	**1.73E-04**	0.16	4.10E-01	0.39	**7.55E-05**	0.31	9.82E-02
IUPRED	HSA	0.28	**6.76E-11**	0.12	**1.16E-02**				
	SCE	0.14	6.00E-02	0.06	4.34E-01				
	BSU	0.49	**7.28E-10**	0.11	2.00E-01				
	ECO	0.40	**<1E-16**	0.19	**1.02E-04**				
	TGA	0.39	**1.01E-04**	-0.01	9.20E-01				

Supplementary Table 3: Correlations between mRNA folding energy (ΔGmean and ΔGmin) and protein solvent accessibility (ACC) in ordered and disordered part of the protein define using SEGHCA and IUPRED. Correlations were estimated using Spearman's rank correlation (SP). Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. HSA, SCE, BSU, ECO, TGA correspond respectively to *H. sapiens*, *S. cerevisiae*, *B. subtilis*, *E. coli* and *T. gammatolerans*. As protein solvent accessibility requires protein structures, we used here the structural dataset.

	whole protein		order		disorder	
	ΔG3mean vs acc		ΔG3mean vs acc		ΔG3mean vs acc	
species	**SP**		**SP**		**SP**	
HSA	0.30	**4.08E-12**	0.30	**4.08E-12**	0.15	**7.02E-03**
ECO	0.45	**<1E-16**	0.43	**<1E-16**	0.21	**1.70E-04**

Supplementary Table 4: Correlation between mRNA folding energy (ΔG3mean) estimated from a 3-nt window and protein solvent accessibility (ACC) considering the whole protein, ordered and disordered part of the protein in HSA (*H. sapiens*) and ECO (*E. coli*). Correlations were estimated using Spearman's rank correlation (SP). Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. We used here the structural dataset.

		dG vs GC		Controlling size		GC vs size		dGmean vs size		Controlling GC		
	species	SP		SP		SP		SP		SP		
ΔGmean	HSA	-0.91	**<1E-16**	-0.93	**<1E-16**	0.08	8.92E-02	-0.26	**1.21E-09**	-0.48	**<1E-16**	Order
	SCE	-0.65	**<1E-16**	-0.70	**<1E-16**	-0.15	**4.16E-02**	-0.18	**1.35E-02**	-0.37	**5.91E-08**	
	BSU	-0.73	**<1E-16**	-0.71	**<1E-16**	0.28	**7.30E-04**	-0.54	**7.35E-12**	-0.50	**8.11E-12**	
	ECO	-0.71	**<1E-16**	-0.67	**4.75E-74**	0.32	**2.29E-11**	-0.49	**1.39E-25**	-0.39	**4.30E-17**	
	TGA	-0.55	**5.02E-09**	-0.53	**1.41E-09**	0.20	**4.60E-02**	-0.50	**2.11E-07**	-0.47	**2.03E-07**	
	HSA	-0.67	**<1E-16**	-0.67	**<1E-16**	0.13	**1.06E-02**	-0.03	6.04E-01	0.01	8.52E-01	Disorder
	SCE	-0.19	5.48E-02	-0.18	7.31E-02	0.02	8.40E-01	-0.22	**2.71E-02**	-0.21	**3.49E-02**	
	BSU	-0.51	**8.25E-05**	-0.53	**9.00E-06**	0.19	**4.74E-02**	0.03	8.17E-01	0.16	2.38E-01	
	ECO	-0.43	**1.23E-11**	-0.42	**1.35E-11**	0.09	**1.04E-01**	-0.23	**4.65E-04**	-0.19	**4.44E-03**	
	TGA	-0.15	4.22E-01	-0.18	3.22E-01	-0.09	**4.43E-01**	-0.12	5.02E-01	-0.16	3.75E-01	
ΔGmin	HSA	-0.67	**<1E-16**	-0.72	**<1E-16**			-0.47	**<1E-16**	-0.56	**<1E-16**	Order
	SCE	-0.28	**1.00E-04**	-0.45	**1.44E-11**			-0.56	**<1E-16**	-0.64	**<1E-16**	
	BSU	-0.58	**<1E-16**	-0.54	**2.37E-14**			-0.62	**<1E-16**	-0.58	**<1E-16**	
	ECO	-0.51	**<1E-16**	-0.42	**<1E-16**			-0.63	**<1E-16**	-0.57	**<1E-16**	
	TGA	-0.25	**1.35E-02**	-0.16	1.11E-01			-0.61	**2.79E-11**	-0.59	**1.10E-12**	
	HSA	-0.63	**<1E-16**	-0.65	**<1E-16**			-0.34	**1.76E-09**	-0.39	**2.79E-13**	Disorder
	SCE	-0.23	**2.18E-02**	-0.22	**2.71E-02**			-0.55	**2.37E-09**	-0.54	**9.64E-11**	
	BSU	-0.52	**5.72E-05**	-0.49	**6.61E-05**			-0.36	**8.40E-03**	-0.30	**2.65E-02**	
	ECO	-0.38	**7.42E-09**	-0.36	**9.32E-09**			-0.60	**<1E-16**	-0.59	**<1E-16**	
	TGA	0.06	7.34E-01	-0.04	8.36E-01			-0.42	**1.54E-02**	-0.42	**1.21E-02**	

Supplementary Table 5: Partial correlation analysis between mRNA folding energy (ΔGmean and ΔGmin), protein size (size) and messenger GC content (GC) in ordered and disordered parts of the proteins. HSA, SCE, BSU, ECO, TGA correspond respectively to *H. sapiens*, *S. cerevisiae*, *B. subtilis*, *E. coli* and *T. gammatolerans*. Correlations were estimated using Spearman's rank correlation (SP). Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. We used the structural set.

	ACC vs dN		ACC vs dS		ACC vs dN		ACC vs dS		ACC vs dN		ACC vs dS	
species	SP		SP		SP		SP		SP		SP	
HSA	-0.17	**9.77E-05**	-0.03	5.04E-01	-0.17	**1.14E-04**	-0.03	4.42E-01	-0.09	1.44E-01	-0.14	**2.75E-02**
SCE	-0.30	**3.76E-05**	-0.24	**9.69E-04**	-0.33	**6.79E-06**	-0.23	**1.64E-03**	-0.28	**8.95E-03**	-0.21	5.24E-02
BSU	-0.30	**3.46E-04**	-0.32	**1.16E-04**	-0.33	**8.72E-05**	-0.32	**1.52E-04**	0.04	7.86E-01	-0.03	8.42E-01
ECO	-0.19	**1.20E-04**	-0.25	**3.16E-07**	-0.19	**1.35E-04**	-0.25	**5.10E-07**	-0.05	4.70E-01	-0.19	**6.23E-03**
TGA	-0.23	**2.83E-02**	-0.33	**1.18E-03**	-0.23	**2.78E-02**	-0.32	**1.76E-03**	0.00	9.96E-01	-0.39	**3.58E-02**

Supplementary Table 6: Correlations between protein solvent accessibility (ACC) and evolutionary rates (non-synonymous *dN* and synonymous *dS* rates). HSA, SCE, BSU, ECO, TGA correspond respectively to *H. sapiens*, *S. cerevisiae*, *B. subtilis*, *E. coli* and *T. gammatolerans*. Correlation was estimated using Spearman's rank correlation (SP). Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. We used the structural set.

		dG vs dN		dG vs dS		dG vs dN/dS	
	species	SP		SP		SP	
ΔGmean	CEL	0.16	**<1E-16**	0.21	**<1E-16**	0.05	**1.41E-04**
	HSA	-0.12	**1.03E-08**	-0.36	**<1E-16**	0.00	9.48E-01
	DME	0.19	**<1E-16**	0.16	**<1E-16**	0.14	**<1E-16**
	SCE	0.36	**<1E-16**	0.25	**<1E-16**	0.33	**<1E-16**
	ASP	0.12	**<1E-16**	0.04	**3.83E-04**	0.14	**<1E-16**
	NEU	0.20	**<1E-16**	-0.10	**<1E-16**	0.27	**<1E-16**
	BSU	-0.02	3.43E-01	-0.14	**8.51E-15**	0.05	1.11E-02
	MET	0.20	**<1E-16**	0.10	**5.67E-06**	0.20	**<1E-16**
	ECO	-0.03	1.18E-01	-0.02	2.67E-01	0.01	7.53E-01
	TGA	-0.06	**4.51E-02**	-0.01	7.55E-01	-0.05	8.10E-02
	HAL	-0.36	**<1E-16**	-0.34	**<1E-16**	-0.19	**<1E-16**
	DEI	-0.22	**4.13E-05**	-0.28	**5.77E-08**	-0.05	3.14E-01
ΔGmin	CEL	0.02	8.55E-02	-0.02	1.63E-01	0.03	**2.37E-02**
	HSA	-0.12	**4.78E-09**	-0.27	**<1E-16**	-0.04	**6.65E-02**
	DME	0.01	6.33E-01	0.05	**1.70E-03**	-0.01	3.75E-01
	SCE	0.06	**1.14E-04**	-0.01	6.72E-01	0.07	**1.34E-06**
	ASP	0.12	**<1E-16**	0.14	**<1E-16**	0.06	**2.10E-06**
	NEU	0.10	**<1E-16**	-0.07	**4.28E-08**	0.14	**<1E-16**
	BSU	-0.06	**4.03E-04**	-0.20	**<1E-16**	0.02	3.77E-01
	MET	0.03	1.90E-01	-0.05	**1.13E-02**	0.08	**8.17E-05**
	ECO	-0.06	**4.84E-03**	-0.11	**1.00E-06**	0.04	1.03E-01
	TGA	-0.10	**6.91E-04**	-0.08	**4.88E-03**	-0.06	**4.96E-02**
	HAL	-0.15	**2.81E-12**	-0.24	**<1E-16**	0.02	2.88E-01
	DEI	-0.05	3.42E-01	-0.23	**1.10E-05**	0.10	**6.89E-02**

		dN vs dS	
species	GC	SP	
CEL	0.44	0.48	**<1E-16**
HSA	0.53	0.43	**<1E-16**
DME	0.55	0.42	**<1E-16**
SCE	0.40	0.53	**<1E-16**
ASP	0.52	0.73	**<1E-16**
NEU	0.57	0.42	**<1E-16**
BSU	0.44	0.48	**<1E-16**
MET	0.45	0.55	**<1E-16**
ECO	0.52	0.68	**<1E-16**
TGA	0.55	0.43	**<1E-16**
HAL	0.68	0.60	**<1E-16**
DEI	0.65	0.39	**3.02E-14**

Supplementary Table 7: A, correlation between mRNA folding energy (ΔGmean and ΔGmin) and evolutionary rates (non-synonymous *dN* and synonymous *dS* rates). B, correlation between *dN* and *dS*. HSA, SCE, BSU, ECO, TGA correspond respectively to *H. sapiens, S. cerevisiae, B. subtilis*, *E. coli* and *T. gammatolerans*. Correlation was estimated using Spearman's rank correlation (SP). Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. We used the transcriptome set.

		ΔGmean vs TE		ΔGmin vs TE		GC vs TE		Size vs TE		dN vs TE		dS ve TE		Abundance vs TE	
	condition	SP		SP		SP		SP		SP		SP		SP	
ECO	lb	0.37	**<1E-16**	0.28	**<1E-16**	-0.26	**<1E-16**	-0.25	**<1E-16**	-0.06	**2.14E-02**	-0.01	6.27E-01	0.27	**<1E-16**
	heat	0.36	**<1E-16**	0.29	**<1E-16**	-0.31	**<1E-16**	-0.27	**<1E-16**	-0.05	5.12E-02	0.01	7.31E-01	0.27	**<1E-16**
	mm	0.34	**<1E-16**	0.25	**<1E-16**	-0.24	**<1E-16**	-0.16	**1.89E-11**	-0.07	**4.77E-03**	0.02	5.36E-01	0.36	**<1E-16**
	osm	0.33	**<1E-16**	0.25	**<1E-16**	-0.24	**<1E-16**	-0.22	**<1E-16**	-0.05	**3.47E-02**	-0.01	6.26E-01	0.37	**<1E-16**
HSA	g2	0.43	**<1E-16**	0.41	**<1E-16**	-0.35	**<1E-16**	-0.39	**<1E-16**	-0.04	1.65E-01	-0.13	6.39E-05	0.15	**1.22E-06**
	m	0.01	8.49E-01	0.11	**6.38E-04**	0.08	**8.59E-03**	-0.39	**<1E-16**	-0.02	4.45E-01	0.03	2.80E-01	0.25	**1.36E-15**
	g1	-0.04	2.20E-01	-0.01	7.62E-01	0.12	**2.21E-04**	-0.23	**3.71E-13**	-0.06	**6.55E-02**	0.05	9.96E-02	0.19	**4.93E-09**
SCE	ypd	-0.01	4.68E-01	0.02	1.11E-01	0.19	**<1E-16**	-0.08	**4.41E-08**	-0.36	**<1E-16**	-0.23	**<1E-16**	0.60	**<1E-16**
	nochx	-0.03	**4.96E-02**	0.01	4.32E-01	0.19	**<1E-16**	-0.08	**8.92E-07**	-0.39	**<1E-16**	-0.25	**<1E-16**	0.62	**<1E-16**
	diamide	-0.06	**4.49E-05**	0.06	**3.09E-04**	0.24	**<1E-16**	-0.19	**<1E-16**	-0.39	**<1E-16**	-0.24	**<1E-16**	0.60	**<1E-16**
	rapamycin	0.11	**1.71E-13**	0.13	**<1E-16**	0.02	**2.25E-01**	-0.15	**<1E-16**	-0.34	**<1E-16**	-0.19	**<1E-16**	0.56	**<1E-16**

Supplementary Table 8: Correlations analysis between translation efficiency (TE), mRNA folding energy (ΔGmean and ΔGmin), protein size (size), *dN*, *dS* and protein abundance. ECO, HAS, SCE correspond respectively to *E. coli*, *H. sapiens*, and *S. cerevisiae*. Conditions are described in **Materials.** Correlation and partial correlations were estimated using the Spearman's rank correlation (SP). Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. We used the transcriptome set restricted to translation efficiency and protein abundance available data.

	ACC vs Abundance	
species	**SP**	
HSA	0.17	**1.01E-04**
SCE	0.10	1.66E-01
BSU	0.36	**1.12E-05**
ECO	0.19	**1.45E-04**
TGA	-0.13	1.89E-01

Supplementary Table 9: Correlations between protein solvent accessibility (ACC) and protein abundance (abundance). HSA, SCE, BSU, ECO, TGA correspond respectively to *H. sapiens, S. cerevisiae, B. subtilis, E. coli* and *T. gammatolerans*. Correlations were estimated using the Spearman's rank correlation (SP). Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. We used the structural database restricted to the protein abundance available data.

		dG vs Abundance		Controlling GC		Controlling size		Controlling GC and size	
	species	**SP**		**SP**		**SP**		**SP**	
ΔGmean	CEL	-0.23	**<1E-16**	0.05	**2.35E-06**	-0.27	**<1E-16**	-0.01	3.42E-01
	HSA	0.10	**1.81E-06**	0.01	5.87E-01	0.07	**4.90E-04**	-0.06	**1.47E-03**
	DME	-0.06	**2.09E-05**	0.13	**7.75E-25**	-0.10	**4.23E-14**	0.03	**8.18E-03**
	SCE	-0.26	**<1E-16**	-0.10	**4.77E-11**	-0.28	**<1E-16**	-0.13	**<1E-16**
	BSU	0.13	**1.06E-13**	0.15	**1.02E-16**	0.07	**4.82E-05**	0.11	**3.79E-09**
	ECO	0.19	**<1E-16**	0.23	**<1E-16**	0.14	**3.59E-11**	0.19	**<1E-16**
	TGA	-0.02	5.04E-01	0.16	**4.71E-09**	-0.04	1.37E-01	0.14	**4.13E-07**
ΔGmin	CEL	-0.01	1.85E-01	0.13	**<1E-16**	-0.14	**<1E-16**	0.05	**1.27E-06**
	HSA	0.14	**2.42E-12**	0.10	**6.54E-07**	0.08	**2.94E-05**	0.01	5.97E-01
	DME	0.13	**<1E-16**	0.22	**<1E-16**	-0.03	**1.05E-02**	0.05	**4.19E-05**
	SCE	-0.03	**3.46E-02**	0.04	**6.18E-03**	-0.13	**<1E-16**	0.00	7.61E-01
	BSU	0.14	**6.73E-15**	0.13	**8.65E-14**	0.07	**1.87E-04**	0.07	**3.72E-05**
	ECO	0.19	**<1E-16**	0.18	**<1E-16**	0.13	**2.98E-09**	0.13	**6.82E-10**
	TGA	0.03	3.38E-01	0.11	**7.63E-05**	0.00	9.54E-01	0.08	**6.44E-03**

Supplementary Table 10: Correlations between mRNA folding energy (ΔGmean and ΔGmin) and protein abundance (abundance) controlling GC content (GC) and protein size (size). CEL, HSA, DME, SCE, BSU, ECO and TGA correspond, respectively to *C. elegans, H. sapiens, D. melanogaster, S. cerevisiae, B. subtilis, E. coli* and *T. gammatolerans*. Correlations and partial correlations were estimated using the Spearman's rank correlation (SP). Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. We used the transcriptome set.

			ΔG vs TE		Controlling GC		Controlling size		Controlling abundance		Controlling GC, size, abundance	
		condition	SP		SP		SP		SP		SP	
ΔGmean	ECO	lb	0.38	**<1E-16**	0.28	**<1E-16**	0.30	**<1E-16**	0.35	**<1E-16**	0.20	**<1E-16**
		heat	0.38	**<1E-16**	0.21	**<1E-16**	0.28	**<1E-16**	0.35	**<1E-16**	0.11	**1.19E-06**
		mm	0.35	**<1E-16**	0.26	**<1E-16**	0.31	**<1E-16**	0.31	**<1E-16**	0.19	**<1E-16**
		osm	0.34	**<1E-16**	0.25	**<1E-16**	0.26	**<1E-16**	0.29	**<1E-16**	0.15	**8.83E-11**
	HSA	g2	0.42	**<1E-16**	0.28	**<1E-16**	0.41	**<1E-16**	0.43	**<1E-16**	0.14	**3.76E-06**
		m	0.02	6.22E-01	0.24	**6.89E-15**	-0.04	2.43E-01	0.02	5.58E-01	0.11	**3.20E-04**
		g1	-0.04	2.11E-01	0.19	**2.74E-10**	-0.07	**2.69E-02**	-0.04	2.24E-01	0.13	**2.79E-05**
	SCE	ypd	-0.01	6.28E-01	0.14	**<1E-16**	-0.01	3.29E-01	0.19	**<1E-16**	0.26	**<1E-16**
		nochx	-0.03	7.01E-02	0.11	**1.02E-13**	-0.03	**2.34E-02**	0.18	**<1E-16**	0.24	**<1E-16**
		diamide	-0.06	7.32E-05	0.11	**8.87E-14**	-0.08	**2.76E-07**	0.12	**<1E-16**	0.18	**<1E-16**
		rapamycin	0.12	**3.19E-14**	0.16	**<1E-16**	0.11	**6.36E-12**	0.33	**<1E-16**	0.24	**<1E-16**
ΔGmin	ECO	lb	0.31	**<1E-16**	0.19	**<1E-16**	0.19	**1.38E-15**	0.27	**<1E-16**	0.08	**3.88E-04**
		heat	0.31	**<1E-16**	0.17	**1.28E-12**	0.16	**6.64E-12**	0.28	**<1E-16**	0.03	1.89E-01
		mm	0.27	**<1E-16**	0.16	**1.46E-11**	0.20	**<1E-16**	0.22	**<1E-16**	0.09	**2.95E-04**
		osm	0.27	**<1E-16**	0.17	**6.04E-13**	0.16	**2.55E-11**	0.22	**<1E-16**	0.05	**4.06E-02**
	HSA	g2	0.41	**<1E-16**	0.25	**<1E-16**	0.31	**<1E-16**	0.40	**<1E-16**	0.00	9.01E-01
		m	0.12	**1.03E-04**	0.25	**<1E-16**	-0.03	3.04E-01	0.10	**8.25E-04**	0.04	2.06E-01
		g1	-0.01	7.52E-01	0.11	**5.45E-04**	-0.10	**7.89E-04**	-0.02	4.22E-01	-0.02	4.70E-01
	SCE	ypd	0.03	5.58E-02	0.07	**1.03E-06**	-0.02	2.32E-01	0.06	**1.30E-04**	0.08	**5.07E-08**
		nochx	0.02	2.75E-01	0.06	**5.24E-05**	-0.03	6.68E-02	0.05	**3.13E-03**	0.07	**1.11E-06**
		diamide	0.06	**9.89E-05**	0.12	**2.43E-15**	-0.04	**3.46E-03**	0.10	**2.81E-10**	0.06	**2.86E-05**
		rapamycin	0.13	**<1E-16**	0.14	**<1E-16**	0.06	**6.02E-05**	0.18	**<1E-16**	0.07	**1.96E-06**

		GC vs TE		Size vs TE		TE vs abundance	
		SP		SP		SP	
ECO	lb	-0.27	**<1E-16**	-0.26	**<1E-16**	0.26	**<1E-16**
	heat	-0.32	**<1E-16**	-0.30	**<1E-16**	0.26	**<1E-16**
	mm	-0.25	**<1E-16**	-0.18	**<1E-16**	0.35	**<1E-16**
	osm	-0.24	**<1E-16**	-0.24	**<1E-16**	0.37	**<1E-16**
HSA	g2	-0.35	**<1E-16**	-0.39	**<1E-16**	0.15	**8.84E-07**
	m	0.08	**9.49E-03**	-0.39	**<1E-16**	0.24	**1.09E-15**
	g1	0.12	**9.15E-05**	-0.22	**4.24E-13**	0.18	**1.05E-08**
SCE	ypd	0.19	**<1E-16**	-0.09	**5.63E-09**	0.59	**<1E-16**
	nochx	0.19	**<1E-16**	-0.08	**1.24E-07**	0.62	**<1E-16**
	diamide	0.24	**<1E-16**	-0.19	**<1E-16**	0.59	**<1E-16**
	rapamycin	0.02	2.45E-01	-0.15	**<1E-16**	0.56	**<1E-16**

Supplementary Table 11: A, correlation and partial correlation analysis between Translation efficiency (TE) and mRNA folding energy (ΔGmean) controlling GC content (GC), protein size (size), and protein abundance (abundance). B, correlation between TE and GC, size and abundance. Correlation and partial correlations were estimated using the Spearman's rank correlation (SP). ECO, HSA, SCE correspond respectively to *E. coli*, *H. sapiens*, *S. cerevisiae.*

Significance is indicated by pvalue inferior to 0.05 and is displayed in bold. Conditions are described in **Materials**. We used the transcriptome set restricted to translation efficiency available data.

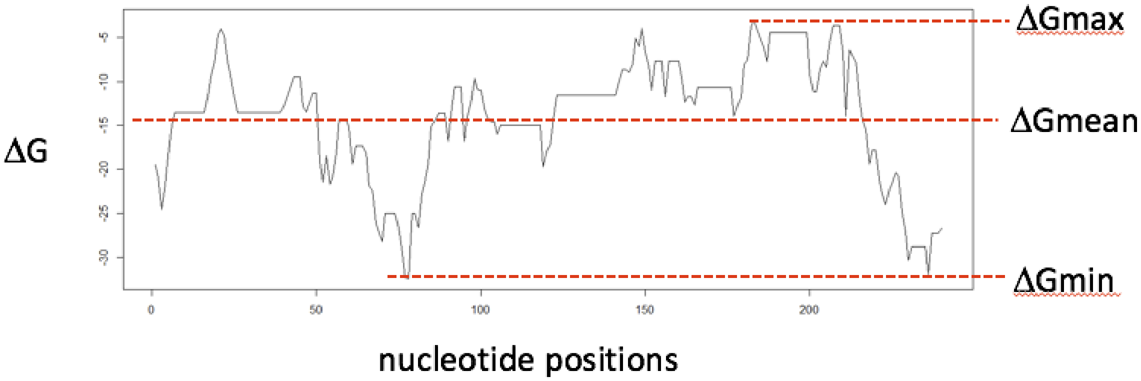
		Controlling ALL	
		SP	
dGmean	HSA	0.04	3.91E-01
	SCE	0.14	7.42E-02
	BSU	0.11	2.39E-01
	ECO	-0.05	3.25E-01
	TGA	0.10	3.81E-01
dGmin	HSA	-0.06	2.08E-01
	SCE	0.10	1.86E-01
	BSU	0.09	3.33E-01
	ECO	-0.02	7.52E-01
	TGA	-0.05	6.50E-01

Supplementary Table 12: Partial correlation analysis between ΔG (ΔGmean and ΔGmin) and protein solvent accessibility controlling for GC content, protein size, *dN*, *dS*, protein abundance and the fractions of 6 groups of amino acids (see Methods). We used the structural set.

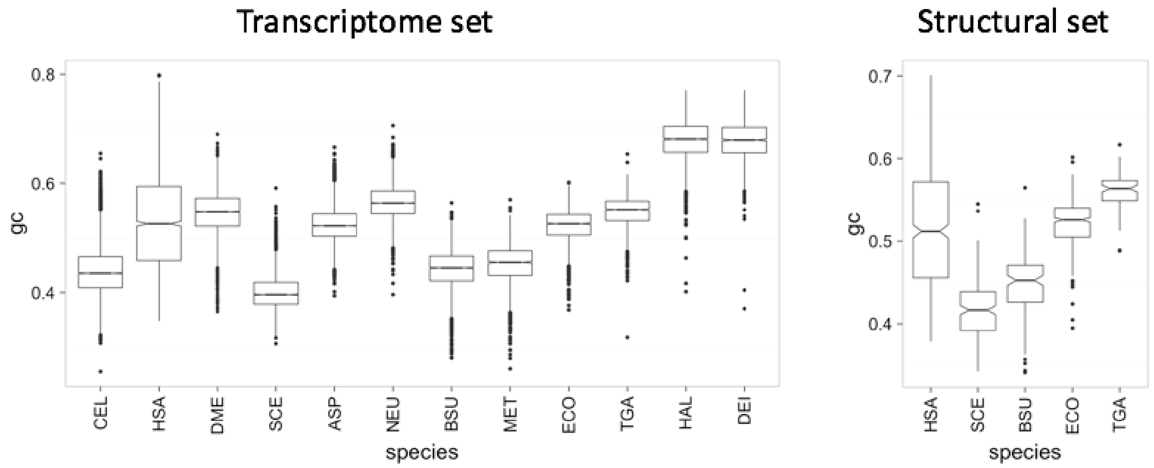
Species	Abbreviation		Close species for ortholog identification	Orthologous Database	Nb messenger	Nb structure
C.elegans	CEL	Eukaryote	*C.briggsae*	OMA	8333	
H.sapiens	HSA	Eukaryote	*M. musculus*	OMA	2432	512
D.melanogaster	DME	Eukaryote	*D.pseudoobscura*	OMA	5710	
S.cerevisiae	SCE	Eukaryote	*S. paradoxus, S. mikitae, S. kudriavzevii and S. bayanus var. uravum*	SensuStricto	4441	184
A.orizae	ASP	Eukaryote	*A.flavus*	OMA	9371	
N.crassa	NEU	Eukaryote	*N.tetrasperma*	OMA	6624	
B.subtilis	BSU	Bacteria	*B. subtilis sbsp. Sprizizenii*	OMA	3059	141
M.mazei	MET	Bacteria	*M.acetivorans*	OMA	2262	
E.coli	ECO	Bacteria	*S. typhi*	OMA	2133	407
T.gammatolerans	TGA	Archeae	*T.AM4_iu54 735*	ACGT	1236	97
H.volcanii	HAL	Bacteria	*H.mediterranei*	OMA	2558	
D.radiodurans	DEI	Bacteria	*D.deserti*	OMA	1936	

Abbreviations	
ACC	Solvent Accessibility value
dN	Rate of non-synonymous mutation
dS	Rate of synonymous mutation
size	protein length
TE	Translation Efficiency
GC	Guanine Cytosine content
ER	Evolutionary Rate
dG	mRNA folding energy
RSA	Relative solvent accessibility
MLR	Multiple Linear Regression

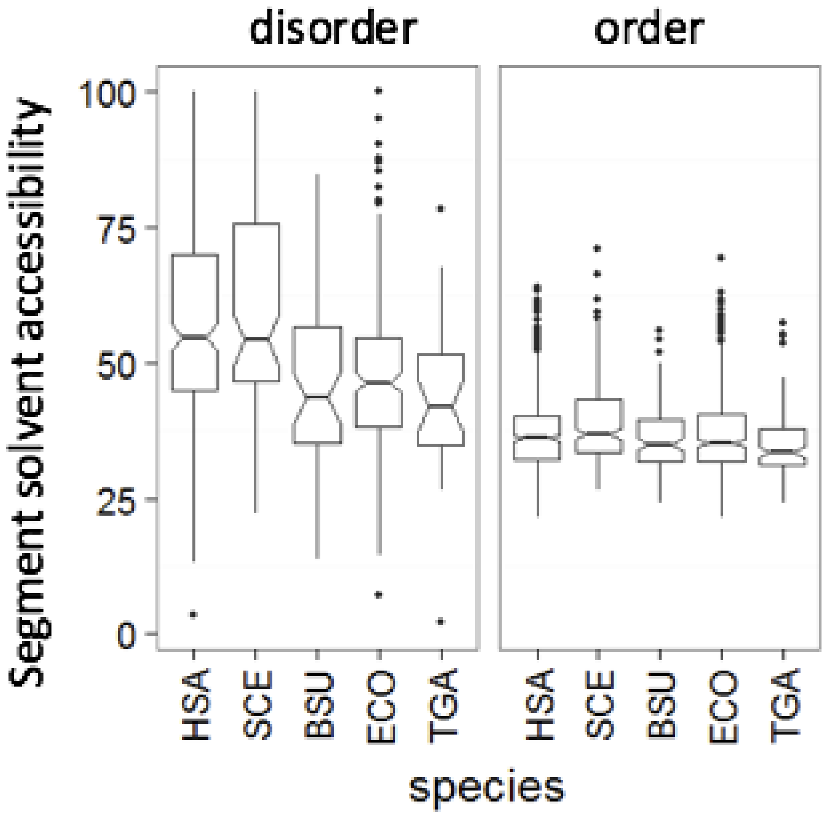
Supplementary Dataset 1. Name of the species used in the study with their abbreviations. Close species used to estimate evolutionary rates (see **Methods**), and orthologous databases used. Number of messenger used in the transcriptome and number of protein used in the structural set. Second table shows the abbreviations used in the main text.



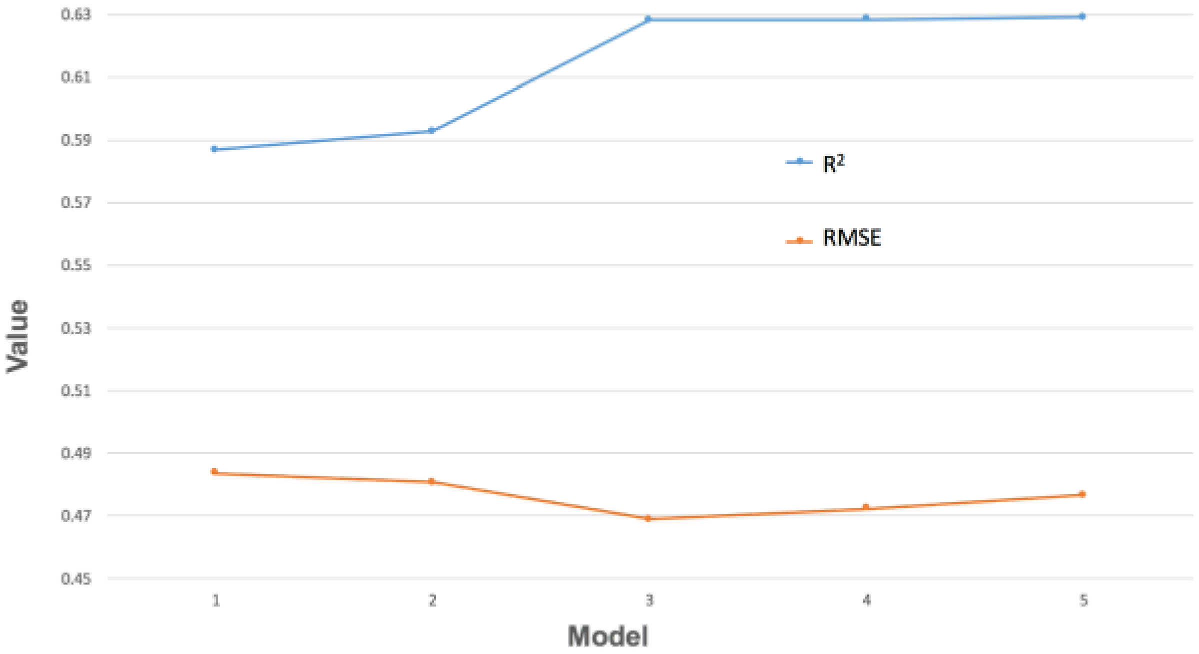
Supplementary Figure 1: A: ΔG profile of TIM9 Human messenger. Average of ΔG (ΔGmean) is -13.7 kcal/mol while the most stable part of the messenger (ΔGmin) has an energy below -30 kcal/mol around position 75.



Supplementary Figure 2: Distribution of the mRNA GC-content for each species among the transcriptome set and the structural set. SCE, CEL, BSU, MET, ASP, ECO, HSA, DME, TGA, NEU, DEI, HAL denote, respectively, *S. cerevisiae, C. elegans, B. subtilis, M.mazei, A.orizae, E. coli, H. sapiens, D. melanogaster, T. gammatolerans, D. radiodurans, H. volvanii.*

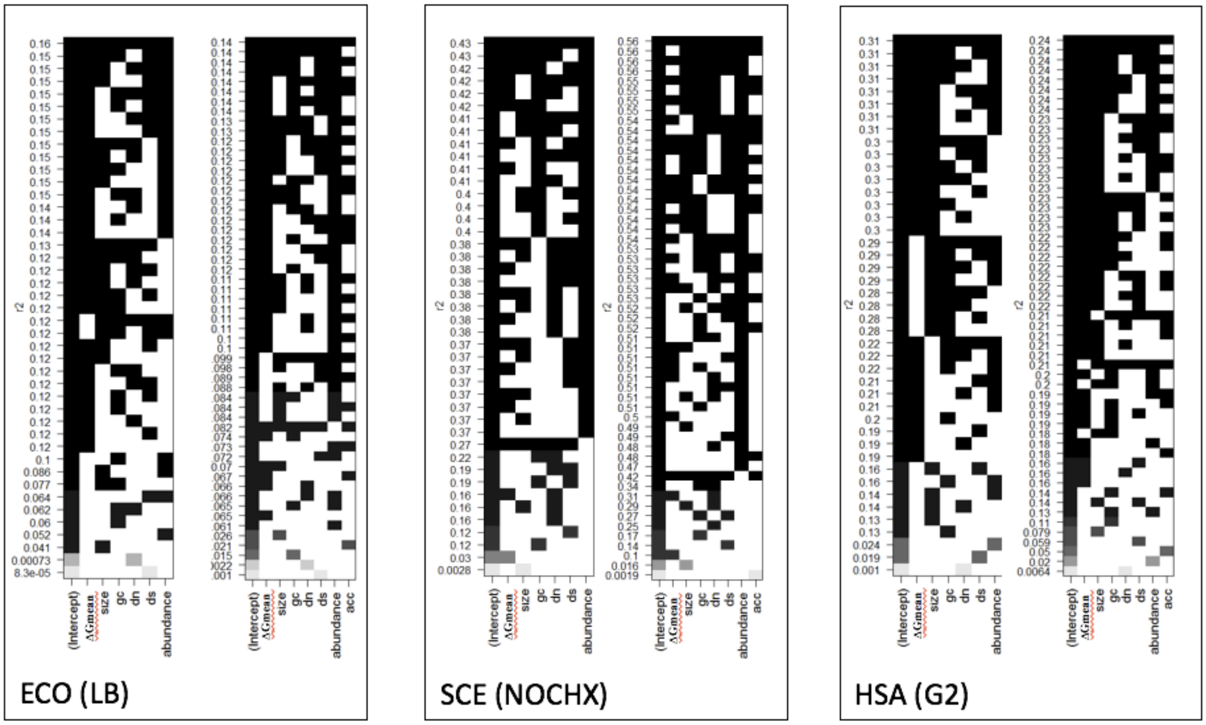


Supplementary Figure 3: Distribution of protein solvent accessibility among disordered and ordered part of the protein. HSA, SCE, BSU, ECO, TGA correspond respectively to *H. sapiens, S. cerevisiae, B. subtilis, E. coli* and *T. gammatolerans.*

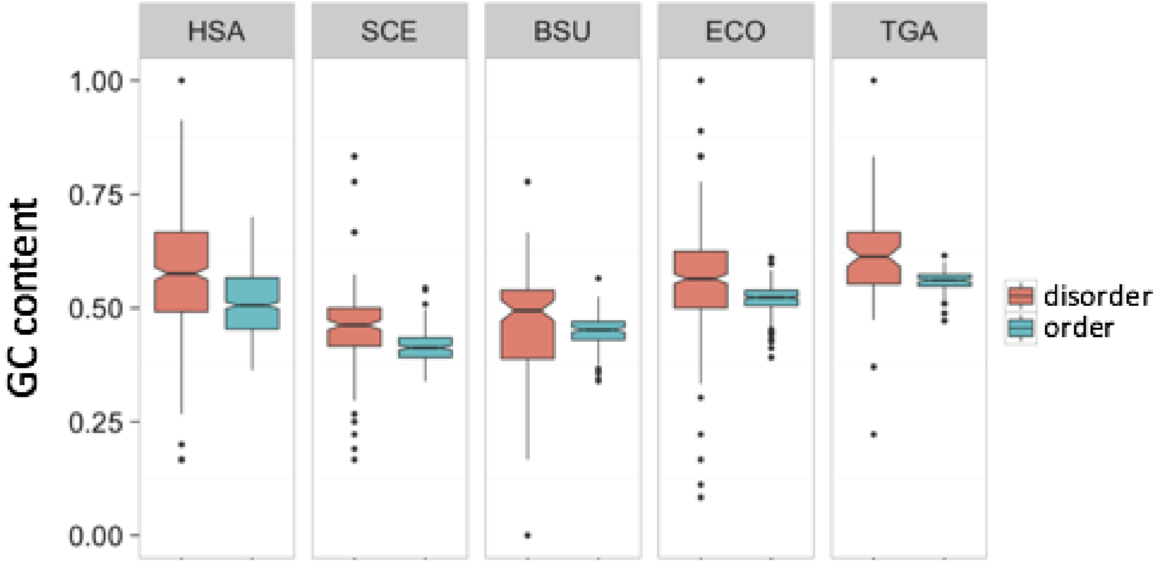


Supplementary Figure 4. Cross validation of multiple regression models. The vertical axis shows the fraction of the protein solvent accessibility variance (R^2) that is explained by the models including different combinations of variables and the root mean squared error (RMSE) values for 5 different models: 1 – size; 2 – size and ΔG; 3- size, ΔG and *dS*; 4 – size, ΔG, *dS* and *dN*; 5 – size, ΔG, *dS*, *dN* and GC-content. The optimal model includes the first three variables whereas the remaining two variables should be discarded.

Y=TE



Supplementary Figure 5: Multiple regression models to predict translation efficiency. For ECO, SCE and HSA (respectively *E. coli*, *S. cerevisiae*, and *H. sapiens*), we selected respectively LB, NOCHX and G2 conditions so each species have only one condition presented. For each species, we predicted independently the translation efficiency from the transcriptome database using mRNA folding energy (ΔGmean) GC content, protein size, *dN*, *dS* and protein abundance and from the structural database using mRNA folding energy (ΔGmean), GC content, protein size, *dN*, *dS*, protein abundance and the protein solvent accessibility. Each line represent a model associated to its R2 and where the composition is noted by colored squared.



Supplementary Figure 6: Distribution of the mRNA GC-content encoded the disordered (red boxes) and ordered (blue boxes) parts of the protein. HSA, SCE, BSU, ECO, TGA correspond respectively to *H. sapiens*, *S. cerevisiae*, *B. subtilis*, *E. coli* and *T. gammatolerans*. We used the structural set.