

Superkingdom	Phylum	AA	% in all proteins	% in proteins with disorder regions L>=11	% in disorder region L>=11
Archaea	Crenarchaeota	Ala	7.03	0.75	5.99
		Arg	5.36	0.97	7.73
		Asn	4.02	0.43	3.43
		Asp	4.59	0.56	4.52
		Cys	0.68	0.06	0.46
		Gln	2.07	0.36	2.87
		Glu	7.02	1.65	13.26
		Gly	7.05	0.81	6.48
		His	1.37	0.15	1.24
		Ile	8.33	0.58	4.67
		Leu	10.47	0.99	7.94
		Lys	6.83	1.44	11.52
		Met	2.13	0.28	2.24
		Phe	4.06	0.22	1.73
		Pro	4.27	0.76	6.11
		Ser	6.35	1.19	9.55
		Thr	4.63	0.58	4.63
		Trp	1.15	0.05	0.39
		Tyr	4.52	0.24	1.92
		Val	8.10	0.63	5.02
	Euryarchaeota	Ala	7.63	1.40	7.39
		Arg	5.23	1.29	6.82
		Asn	3.96	0.70	3.71
		Asp	5.89	1.37	7.22
		Cys	0.96	0.10	0.55
		Gln	2.18	0.55	2.91
		Glu	8.03	2.50	13.19
		Gly	7.37	1.29	6.81
		His	1.69	0.30	1.56
		Ile	7.46	0.79	4.15
		Leu	9.32	1.26	6.65
		Lys	6.10	1.60	8.42
		Met	2.38	0.43	2.25
		Phe	4.08	0.38	1.98
		Pro	4.12	1.00	5.29
		Ser	6.03	1.66	8.72
		Thr	5.22	1.11	5.84
		Trp	1.00	0.07	0.36
		Tyr	3.66	0.32	1.70
		Val	7.69	0.96	5.07
	Nanoarchaeota	Ala	5.19	0.59	4.16
		Arg	3.90	0.70	4.95
		Asn	5.26	0.63	4.44
		Asp	4.97	0.63	4.45
		Cys	0.81	0.06	0.41
		Gln	2.22	0.43	3.00
		Glu	7.88	2.22	15.62
		Gly	5.30	0.59	4.17
		His	1.34	0.16	1.15
		Ile	10.46	1.04	7.32
		Leu	10.42	1.23	8.66
		Lys	10.82	2.68	18.87
		Met	1.71	0.29	2.01
		Phe	4.43	0.28	1.95
		Pro	4.01	0.65	4.59
		Ser	4.63	0.80	5.60
		Thr	4.11	0.51	3.60
		Trp	0.96	0.05	0.36
		Tyr	5.65	0.38	2.68
		Val	5.95	0.51	3.59
Bacteria	Actinobacteria	Ala	12.61	3.06	13.28
		Arg	7.33	2.17	9.45
		Asn	2.38	0.53	2.30
		Asp	5.97	1.50	6.53
		Cys	0.82	0.11	0.47
		Gln	3.03	0.84	3.64
		Glu	5.53	1.68	7.30

Superkingdom	Phylum	AA	% in all proteins	% in proteins with disorder regions L>=11	% in disorder region L>=11
Bacteria	Actinobacteria	Gly	9.00	2.31	10.03
		His	2.26	0.49	2.13
		Ile	4.27	0.45	1.94
		Leu	9.88	1.53	6.64
		Lys	2.53	0.74	3.20
		Met	1.99	0.42	1.84
		Phe	3.02	0.32	1.40
		Pro	5.70	2.03	8.83
		Ser	5.55	1.84	7.98
		Thr	6.08	1.52	6.63
		Trp	1.46	0.13	0.56
		Tyr	2.15	0.24	1.04
		Val	8.43	1.16	5.03
	Alphaproteobacteria	Ala	11.17	2.26	12.01
		Arg	6.44	1.59	8.45
		Asn	3.32	0.61	3.25
		Asp	5.59	1.18	6.28
		Cys	0.96	0.09	0.46
		Gln	3.20	0.81	4.31
		Glu	5.70	1.54	8.20
		Gly	8.03	1.47	7.83
		His	2.06	0.35	1.88
		Ile	6.03	0.57	3.01
		Leu	9.97	1.29	6.86
		Lys	4.39	1.17	6.20
		Met	2.47	0.46	2.43
		Phe	3.89	0.34	1.81
		Pro	4.82	1.35	7.18
		Ser	5.89	1.69	9.01
		Thr	5.26	1.06	5.62
		Trp	1.21	0.07	0.38
		Tyr	2.48	0.20	1.07
		Val	7.13	0.80	4.23
	Aquificae	Ala	5.89	0.70	4.39
		Arg	4.92	0.96	6.05
		Asn	3.60	0.48	3.02
		Asp	4.32	0.56	3.50
		Cys	0.79	0.06	0.39
		Gln	2.05	0.42	2.66
		Glu	9.65	2.86	17.93
		Gly	6.75	0.83	5.19
		His	1.55	0.19	1.18
		Ile	7.33	0.75	4.71
		Leu	10.58	1.42	8.90
		Lys	9.42	2.59	16.23
		Met	1.93	0.29	1.80
		Phe	5.15	0.41	2.56
		Pro	4.07	0.77	4.81
		Ser	4.80	0.95	5.93
		Thr	4.21	0.56	3.51
		Trp	0.93	0.05	0.34
		Tyr	4.14	0.33	2.10
		Val	7.94	0.86	5.41
	Bacteroidetes/Chloro	Ala	7.98	1.33	8.36
		Arg	5.37	1.14	7.16
		Asn	4.38	0.67	4.18
		Asp	5.57	1.02	6.42
		Cys	1.12	0.07	0.45
		Gln	3.43	0.72	4.52
		Glu	6.58	1.66	10.45
		Gly	7.19	1.13	7.09
		His	1.98	0.28	1.78
		Ile	6.39	0.50	3.13
		Leu	9.50	1.05	6.60
		Lys	5.60	1.24	7.78
		Met	2.61	0.39	2.44
		Phe	4.36	0.31	1.96
		Pro	4.15	0.94	5.93

Superkingdom	Phylum	AA	% in all proteins	% in proteins with disorder regions L>=11	% in disorder region L>=11
Bacteria	Bacteroidetes/Chloro	Ser	6.29	1.54	9.66
		Thr	5.68	0.99	6.22
		Trp	1.22	0.06	0.38
		Tyr	3.88	0.28	1.76
		Val	6.71	0.68	4.25
	Betaproteobacteria	Ala	12.75	2.91	14.85
		Arg	7.41	2.07	10.56
		Asn	2.79	0.51	2.59
		Asp	5.43	1.15	5.88
		Cys	0.99	0.12	0.60
		Gln	3.75	0.96	4.88
		Glu	5.39	1.41	7.17
		Gly	8.22	1.59	8.10
		His	2.33	0.46	2.34
		Ile	4.72	0.44	2.24
		Leu	10.43	1.38	7.04
		Lys	3.35	0.84	4.29
		Met	2.37	0.43	2.18
		Phe	3.56	0.31	1.60
		Pro	5.13	1.49	7.59
		Ser	5.28	1.53	7.79
		Thr	4.96	0.97	4.96
		Trp	1.34	0.08	0.40
		Tyr	2.46	0.20	1.01
		Val	7.35	0.85	4.33
	Chlamydiae/Verrucon	Ala	7.00	1.18	6.59
		Arg	4.53	0.95	5.30
		Asn	3.97	0.78	4.36
		Asp	4.55	0.87	4.84
		Cys	1.57	0.13	0.70
		Gln	4.22	1.03	5.73
		Glu	6.56	1.82	10.17
		Gly	6.11	0.93	5.19
		His	2.40	0.36	2.02
		Ile	7.02	0.70	3.88
		Leu	11.31	1.42	7.95
		Lys	6.25	1.73	9.67
		Met	2.01	0.34	1.88
		Phe	4.82	0.44	2.47
		Pro	4.32	1.01	5.65
		Ser	7.84	2.23	12.46
		Thr	5.24	1.08	6.01
		Trp	1.01	0.05	0.30
		Tyr	3.25	0.29	1.61
		Val	6.03	0.66	3.67
	Chloroflexi	Ala	8.59	1.28	8.74
		Arg	5.02	0.97	6.60
		Asn	3.92	0.60	4.10
		Asp	5.04	0.81	5.53
		Cys	1.36	0.11	0.74
		Gln	3.31	0.65	4.42
		Glu	6.49	1.57	10.72
		Gly	7.60	0.94	6.39
		His	1.84	0.23	1.57
		Ile	7.23	0.55	3.76
		Leu	10.32	1.09	7.43
		Lys	5.86	1.41	9.63
		Met	2.64	0.40	2.71
		Phe	3.83	0.26	1.78
		Pro	4.39	0.87	5.91
		Ser	6.34	1.44	9.82
		Thr	5.29	0.84	5.75
		Trp	1.05	0.04	0.27
		Tyr	3.16	0.22	1.47
		Val	6.72	0.55	3.74
	Cyanobacteria	Ala	8.93	1.51	8.40
		Arg	5.89	1.35	7.51

Superkingdom	Phylum	AA	% in all proteins	% in proteins with disorder regions L>=11	% in disorder region L>=11
Bacteria	Cyanobacteria	Asn	3.86	0.77	4.26
		Asp	5.04	1.00	5.56
		Cys	1.09	0.09	0.48
		Gln	4.98	1.23	6.85
		Glu	6.04	1.58	8.79
		Gly	7.28	1.15	6.38
		His	1.89	0.29	1.62
		Ile	6.09	0.60	3.32
		Leu	11.57	1.56	8.70
		Lys	4.24	1.11	6.15
		Met	1.87	0.33	1.85
		Phe	3.78	0.34	1.87
		Pro	5.02	1.31	7.28
		Ser	6.37	1.82	10.11
		Thr	5.24	1.03	5.75
		Trp	1.56	0.09	0.49
		Tyr	2.61	0.22	1.22
		Val	6.65	0.71	3.97
	Deinococcus-Thermu	Ala	11.81	2.85	12.18
		Arg	8.05	2.50	10.68
		Asn	1.89	0.35	1.49
		Asp	4.18	0.96	4.08
		Cys	0.49	0.09	0.39
		Gln	3.10	0.91	3.89
		Glu	7.49	2.57	10.95
		Gly	9.28	2.07	8.85
		His	1.96	0.39	1.67
		Ile	2.92	0.30	1.27
		Leu	13.37	2.54	10.86
		Lys	3.28	1.00	4.29
		Met	1.70	0.35	1.50
		Phe	3.53	0.40	1.72
		Pro	6.33	2.24	9.56
		Ser	4.09	1.29	5.53
		Thr	4.56	1.06	4.54
		Trp	1.34	0.12	0.53
		Tyr	2.65	0.29	1.24
		Val	7.98	1.19	5.10
	Deltaproteobacteria	Ala	9.83	1.83	10.49
		Arg	6.41	1.39	7.98
		Asn	3.18	0.54	3.10
		Asp	5.33	1.00	5.71
		Cys	1.32	0.14	0.78
		Gln	3.40	0.82	4.69
		Glu	6.30	1.66	9.54
		Gly	8.01	1.38	7.92
		His	2.15	0.36	2.04
		Ile	5.54	0.49	2.78
		Leu	10.28	1.21	6.94
		Lys	4.62	1.21	6.92
		Met	2.62	0.45	2.58
		Phe	4.02	0.32	1.86
		Pro	4.61	1.13	6.48
		Ser	5.81	1.55	8.90
		Thr	5.39	1.03	5.88
		Trp	1.11	0.06	0.33
		Tyr	2.71	0.22	1.24
		Val	7.38	0.77	4.39
	Epsilonproteobacteria	Ala	7.02	1.07	6.20
		Arg	3.61	0.68	3.95
		Asn	5.40	1.14	6.60
		Asp	5.02	0.95	5.51
		Cys	1.09	0.07	0.43
		Gln	3.37	0.86	4.97
		Glu	7.16	1.97	11.40
		Gly	5.96	0.82	4.73
		His	1.96	0.30	1.72
		Ile	8.03	0.83	4.82

Superkingdom	Phylum	AA	% in all proteins	% in proteins with disorder regions L>=11	% in disorder region L>=11
Bacteria	Epsilonproteobacteria	Leu	10.77	1.42	8.18
		Lys	8.45	2.33	13.44
		Met	2.38	0.38	2.20
		Phe	5.35	0.46	2.68
		Pro	3.11	0.62	3.59
		Ser	6.85	1.76	10.18
		Thr	4.40	0.85	4.91
		Trp	0.75	0.03	0.19
		Tyr	3.70	0.33	1.89
		Val	5.61	0.53	3.04
	Firmicutes	Ala	7.08	1.14	6.49
		Arg	3.94	0.81	4.58
		Asn	4.96	1.05	5.96
		Asp	5.28	1.06	6.02
		Cys	0.72	0.05	0.26
		Gln	3.81	0.96	5.43
		Glu	6.98	1.98	11.25
		Gly	6.51	0.97	5.48
		His	2.00	0.31	1.74
		Ile	7.96	0.76	4.28
		Leu	9.69	1.16	6.57
		Lys	7.39	2.19	12.41
		Met	2.59	0.42	2.38
		Phe	4.58	0.37	2.11
		Pro	3.44	0.71	4.05
		Ser	6.01	1.60	9.10
		Thr	5.58	1.08	6.13
		Trp	0.94	0.05	0.29
		Tyr	3.70	0.34	1.94
		Val	6.86	0.75	4.27
	Fusobacteria	Ala	5.47	0.77	4.52
		Arg	3.19	0.63	3.69
		Asn	6.38	1.32	7.77
		Asp	5.39	0.98	5.76
		Cys	0.77	0.04	0.26
		Gln	2.17	0.43	2.54
		Glu	7.89	2.25	13.23
		Gly	6.34	0.92	5.42
		His	1.18	0.15	0.88
		Ile	9.96	1.09	6.42
		Leu	9.34	1.15	6.79
		Lys	10.12	2.76	16.25
		Met	2.39	0.38	2.25
		Phe	4.90	0.42	2.47
		Pro	2.55	0.39	2.29
		Ser	5.97	1.45	8.53
		Thr	4.84	0.85	4.99
		Trp	0.62	0.03	0.19
		Tyr	4.42	0.44	2.59
		Val	6.09	0.65	3.80
	Gammaproteobacteria	Ala	9.74	1.67	10.17
		Arg	5.73	1.20	7.31
		Asn	3.81	0.67	4.09
		Asp	5.28	0.98	5.96
		Cys	1.07	0.08	0.46
		Gln	4.54	1.06	6.49
		Glu	5.74	1.41	8.58
		Gly	7.30	1.11	6.77
		His	2.30	0.36	2.17
		Ile	5.84	0.47	2.85
		Leu	10.85	1.25	7.65
		Lys	4.48	1.10	6.68
		Met	2.52	0.39	2.40
		Phe	3.86	0.28	1.69
		Pro	4.46	1.01	6.15
		Ser	6.06	1.58	9.66
		Thr	5.24	0.95	5.77
		Trp	1.40	0.07	0.40

Superkingdom	Phylum	AA	% in all proteins	% in proteins with disorder regions L>=11	% in disorder region L>=11
Bacteria	Gammaproteobacteri	Tyr	2.87	0.22	1.35
		Val	6.90	0.67	4.07
	Planctomycetes	Ala	9.26	2.37	8.92
		Arg	6.95	2.22	8.32
		Asn	3.37	0.98	3.68
		Asp	6.23	1.80	6.75
		Cys	1.27	0.22	0.82
		Gln	4.03	1.31	4.91
		Glu	6.02	2.12	7.96
		Gly	7.48	1.85	6.96
		His	2.31	0.56	2.10
		Ile	4.95	0.74	2.79
		Leu	9.33	1.77	6.63
		Lys	3.42	1.20	4.53
		Met	2.43	0.65	2.44
		Phe	3.70	0.56	2.09
		Pro	5.33	2.00	7.51
		Ser	7.38	3.03	11.39
		Thr	5.85	1.70	6.38
		Trp	1.54	0.16	0.60
		Tyr	2.10	0.27	1.03
		Val	7.05	1.16	4.36
	Spirochaetes	Ala	5.88	0.91	5.18
		Arg	4.40	0.87	4.96
		Asn	5.20	1.03	5.84
		Asp	4.88	0.95	5.39
		Cys	1.01	0.08	0.48
		Gln	3.08	0.71	4.03
		Glu	6.96	1.99	11.31
		Gly	6.25	0.96	5.46
		His	1.67	0.25	1.42
		Ile	8.30	0.90	5.12
		Leu	10.17	1.32	7.50
		Lys	8.04	2.23	12.65
		Met	2.06	0.34	1.95
		Phe	5.66	0.51	2.90
		Pro	3.58	0.77	4.37
		Ser	7.45	1.99	11.31
		Thr	4.91	0.92	5.21
		Trp	0.97	0.05	0.30
		Tyr	3.71	0.33	1.85
		Val	5.83	0.60	3.41
	Thermotogae	Ala	5.85	0.65	4.44
		Arg	5.54	1.05	7.20
		Asn	3.61	0.47	3.25
		Asp	4.96	0.69	4.73
		Cys	0.71	0.06	0.40
		Gln	2.01	0.39	2.70
		Glu	8.93	2.44	16.75
		Gly	6.91	0.78	5.38
		His	1.58	0.19	1.33
		Ile	7.18	0.68	4.67
		Leu	10.03	1.19	8.16
		Lys	7.62	1.86	12.74
		Met	2.40	0.37	2.53
		Phe	5.19	0.36	2.47
		Pro	3.99	0.67	4.60
		Ser	5.66	1.18	8.08
		Thr	4.53	0.59	4.07
		Trp	1.10	0.05	0.31
		Tyr	3.58	0.28	1.89
		Val	8.61	0.75	5.12