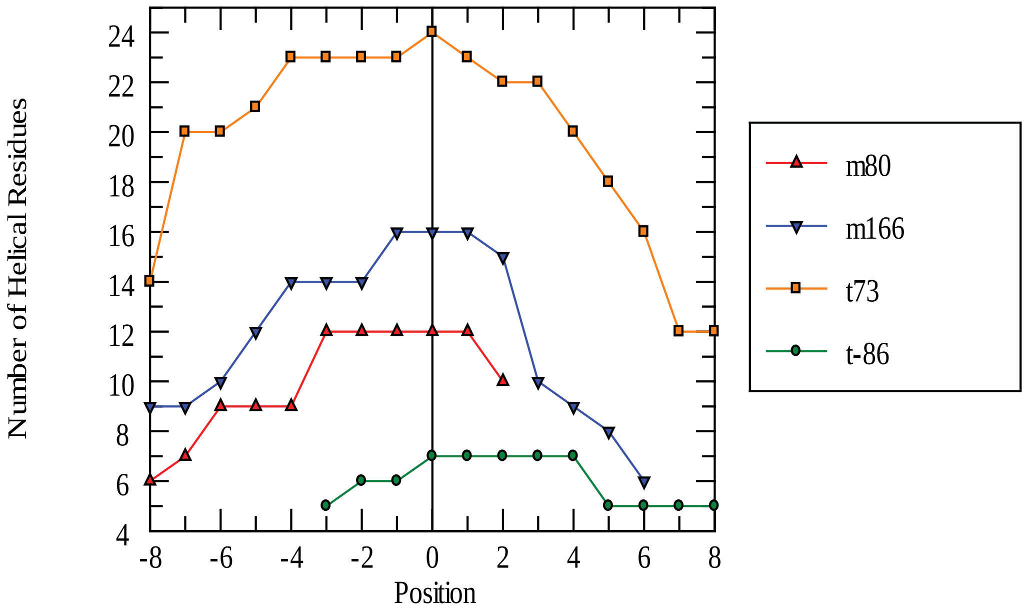
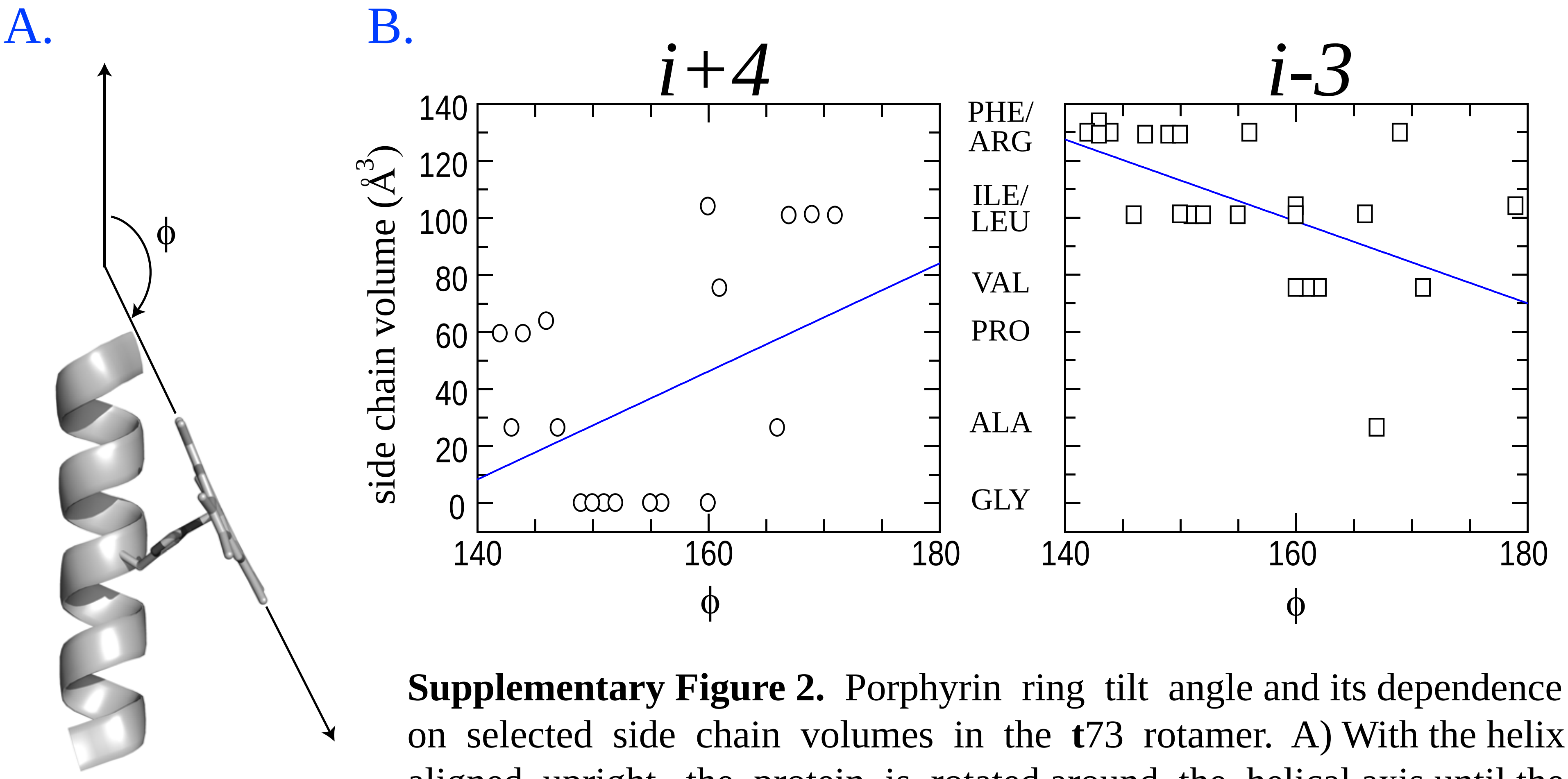
Supplementary Figure 1. The helical population of each rotamer by helical position.





Supplementary Figure 2. Porphyrin ring tilt angle and its dependence on selected side chain volumes in the **t**73 rotamer. A) With the helix aligned upright, the protein is rotated around the helical axis until the porphyrin macrocycle is normal to the observer. The tilt angle is defined as the angle formed between the helix vector and the porphyrin vector, which begins at the point of closest approach to the helix. B) Dependence of the tilt angle on side chain volumes at i+4 and i-3 in the database. Lines drawn are linear fits of the data. Side chain volumes taken from Hackel *et al* Biophysical Chemistry **82** *(1999) pp 35-50*

Supplementary Table 1. The non redundant dataset of heme proteins discussed in this paper, sorted by ligand histidine rotamer. Asterisk-labeled *b*-type proteins are the non cysteine containing side of a *c*-type heme.

PDB ID	Residue Number	Chain	Rotamer	Paired Rotamer	Paired Chain	Paired Residue Number	Heme Type	Position -3 for t73	Position 4 for t73	Position 8 for t73	Tilt Angle	Protein	Organism
1EZV	183	C	t73	t73	C	82	*b*-type	PHE	PRO	ALA	144	Cythochrome *b*	*Saccharomyces Cerevisiae*
1EZV	96	C	t73	t73	C	197	*b*-type	MET	GLY	Non helical	160	Cythochrome *b*	*Saccharomyces Cerevisiae*
1EZV	197	C	t73	t73	C	96	*b*-type	VAL	LEU	Non helical	171	Cythochrome *b*	*Saccharomyces Cerevisiae*
1EZV	82	C	t73	t73	C	183	*b*-type	ARG	ALA	PHE	147	Cythochrome *b*	*Saccharomyces Cerevisiae*
1GU2	95	A	t73				*b*-type *	PHE	ILE	Non helical	169	Cytochrome *c*'	*Methylophilus Mehtylotrophus*
1KQF	155	C	t73	t73	C	57	*b*-type	LEU	GLY	ILE	151	Formate Dehyrogenase, Cytochrome b_{556}(FDN) Subunit	*Drosophila Melanogaster*
1KQF	169	C	t73	t-86	C	18	*b*-type	ILE	ALA	Non helical	166	Formate Dehyrogenase, Cytochrome b_{556} (FDN) Subunit	*Drosophila Melanogaster*
1KQF	57	C	t73	t73	C	155	*b*-type	ARG	GLY	PHE	149	Formate Dehyrogenase, Cytochrome b_{556} (FDN) Subunit	*Drosophila Melanogaster*
1M56	419	A	t73				*a*-type	VAL	Non helical	Non helical	162	Cytochrome *c* Oxidase	*Rhodobacter Sphaeroides*

1NEN	71	D	t73	t73	C	84	*b*-type	ILE	GLY	VAL	150	Succinate Dehydrogenase Hydrophobic Membrane Anchor Protein	*Drosophila Melanogaster*
1NEN	84	C	t73	t73	D	71	*b*-type	LEU	GLY	MET	152	Succinate Dehydrogenase Cytochrome b_{556} subunit	*Drosophila Melanogaster*
1V54	376	A	t73				*a*-type	VAL	VAL	Non helical	161	Cytochrome *c* oxidase polypeptide I	*Bos Taurus*
1V54	61	A	t73	m80	A	378	*a*-type	VAL	MET	Non helical	160	Cytochrome *c* oxidase polypeptide I	*Bos Taurus*
1VF5	187	A	t73	t73	A	86	*b*-type	TYR	Non helical	Non helical	143	Cytochrome *b* 6F Complex	*Mastigocladus Laminosus*
1VF5	86	A	t73	t73	A	187	*b*-type	ARG	Non helical	Non helical	150	Cytochrome *b* 6F Complex	*Mastigocladus Laminosus*
1VF5	100	A	t73				*b*-type	MET	Non helical	Non helical	179	Cytochrome *b* 6F Complex	*Mastigocladus Laminosus*
1XME	72	A	t73				*b*-type	LEU	ASN	PHE	146	Cytochrome c oxidase polypeptide I	*Thermus Thermophilus*
1Y5N	187	C	t73	m80	C	66	*b*-type	PHE	GLY	PHE	156	Respiratory nitrate reductase 1 gamma chain	*Drosophila Melanogaster*
1ZOY	101	C	t73	t73	D	79	*b*-type	LEU	GLY	LEU	155	Large cytochrome binding protein	*Sus Scrofa*
1ZOY	79	D	t73	t73	C	101	*b*-type	Non helical	GLY	VAL	155	Small cytochrome binding protein	*Sus Scrofa*
2A06	97	C	t73	t73	C	196	*b*-type	LEU	GLY	Non helical	160	Cytochrome *bc*1 Complex with Stigmatellin Bound	*Bos Taurus*

2A06	182	C	t73	t73	C	83	*b*-type	PHE	PRO	MET	142	Cytochrome *bc*1 Complex with Stigmatellin Bound	*Bos Taurus*
2A06	83	C	t73	t73	C	182	*b*-type	ARG	ALA	PHE	143	Cytochrome *bc* 1 Complex with Stigmatellin Bound	*Bos Taurus*
2A06	196	C	t73	t73	C	97	*b*-type	ALA	LEU	Non helical	167	Cytochrome *bc*1 Complex with Stigmatellin Bound	*Bos Taurus*
1EW0	194	A	t-86				*b*-type				156	Cruzain	*Trypanosoma Cruzi*
1H29	159	B	t-86				*b*-type*				150	High-Molecular-Weight Cytochrome c	*Desulfovibrio Vulgaris*
1KQF	18	C	t-86	t73	C	169	*b*-type				150	Formate Dehyrogenase, Cytochrome b_{556} (FDN) Subunit	*Drosophila Melanogaster*
1MWB	46	A	t-86	m166	A	70	*b*-type				154	Putative Hemoglobin	*Synechocystis Sp*
1V9Y	77	A	t-86				*b*-type				155	Heme pas sensor protein	*Drosophila Melanogaster*
1WE1	17	A	t-86				*b*-type				152	Heme Oxygenase 1	*Synechocystis Sp*
2BK9	61	A	t-86				*b*-type				150	Hemoglobin	*Drosophila Melanogaster*
1BBH	125	A	m166				*c*-type				17	Na Cytochrome *c*	*Chromatium Vinosum*
1FGJ	279	A	m166				*b*-type*				35	Hydroxylamine Oxidoreductase	*Nitrosomonas Europaea*
1FT5	27	A	m166				*b*-type*				10	Cytochrome c_{554}	*Nitrosomonas Europaea*

1H29	516	B	m166				*b*-type*	169	High-Molecular-Weight Cytochrome *c*	*Desulfovibrio Vulgaris*
1H29	111	B	m166				*b*-type*	3	High-Molecular-Weight Cytochrome *c*	*Desulfovibrio Vulgaris*
1H29	222	B	m166				*b*-type*	18	High-Molecular-Weight Cytochrome *c*	*Desulfovibrio Vulgaris*
1H29	523	B	m166				*c*-type	22	High-Molecular-Weight Cytochrome *c*	*Desulfovibrio Vulgaris*
1H29	229	B	m166	m80	B	162	*c*-type	22	High-Molecular-Weight Cytochrome *c*	*Desulfovibrio Vulgaris*
1H29	353	B	m166	m80	B	301	*c*-type	23	High-Molecular-Weight Cytochrome *c*	*Desulfovibrio Vulgaris*
1H29	118	B	m166	m80	B	69	*c*-type	25	High-Molecular-Weight Cytochrome *c*	*Desulfovibrio Vulgaris*
1J0P	83	A	m166				*c*-type	23	Cythochrome c_3 Y43L	*Desulfovibrio Vulgaris*
1MWB	70	A	m166	t-86	A	46	*b*-type	160	Putative Hemoglobin	*Synechocystis Sp*
1OR6	123	A	m166				*b*-type	12	Heme-based aerotactic transducer hemAT	*Bacillus Subtilis*
256B	102	A	m166				*b*-type	12	NA Cytochrome b_{562}	*Drosophila Melanogaster*
2CCY	122	A	m166				*c*-type	156	Ferricytochrome *c*'	*Rhodospirillum Molischianum*
4VHB	85	A	m166				*b*-type	162	Hemoglobin	*Vitreoscilla Stercoraria*
1H29	162	B	m80				*b*-type*	156	High-Molecular-Weight Cytochrome *c*	*Desulfovibrio Vulgaris*

1H29	69	B	m80	m166	B	118	*b*-type*	154	High-Molecular-Weight Cytochrome *c*	*Desulfovibrio Vulgaris*
1H29	301	B	m80	m166	B	353	*b*-type*	157	High-Molecular-Weight Cytochrome *c*	*Desulfovibrio Vulgaris*
1IRD	87	A	m80				*b*-type	166	Hemoglobin Beta Chain	*Homo Sapiens*
1IRD	292	B	m80				*b*-type	169	Hemoglobin Beta Chain	*Homo Sapiens*
1IT2	103	A	m80				*b*-type	165	Hemoglobin	*Eptatretus Burgeri*
1ITH	94	B	m80				*b*-type	165	NA Hemoglobin (Cyano Met)	*Urechis Caupo*
1PBY	126	A	m80				*b*-type	172	Quinohemoprotein amine dehydrogenase 60 kDa subunit	*Paracoccus Denitrificans*
1V54	378	A	m80	t73	A	61	*a*-type	165	Cytochrome c oxidase polypeptide I	*Bos Taurus*
1Y5N	66	C	m80	t73	C	187	*b*-type	12	Respiratory nitrate reductase 1 gamma chain	*Drosophila Melanogaster*
1Y5N	56	C	m80				*b*-type	160	Respiratory nitrate reductase 1 gamma chain	*Drosophila Melanogaster*
3SDH	101	B	m80				*b*-type	165	Hemoglobin I (Homodimer) (Carbon-Monoxy)	*Scapharca Inaequivalvis*

Supplementary Table2. Heme Propensity

A. All Helices

ALA	1.1	0.5	0.9	1.3	0.3	0.9	1.2	1.6	0.0	1.3	0.8	1.1	1.9	0.4	0.3	0.0	0.7
ARG	0.0	0.8	0.9	1.6	0.7	2.1	1.0	0.3	0.0	0.3	1.1	0.9	0.0	0.4	1.9	0.6	1.4
ASN	0.0	0.9	1.4	0.6	0.0	1.3	0.9	0.6	0.0	0.5	2.9	0.7	0.9	0.0	1.0	3.3	0.0
ASP	0.0	0.0	0.0	1.3	0.3	0.0	0.9	0.0	0.0	1.1	2.0	0.5	0.0	0.0	0.0	0.0	1.1
CYS	0.0	0.0	0.0	0.0	17.9	0.0	0.0	11.8	0.0	3.5	0.0	4.9	0.0	0.0	10.2	0.0	0.0
GLU	0.0	0.0	1.1	0.0	0.2	0.2	0.8	0.0	0.0	0.7	1.2	0.6	0.3	1.2	0.5	0.0	0.5
GLN	0.0	0.0	1.4	0.9	0.0	0.3	0.4	0.4	0.0	0.9	0.8	0.5	0.0	1.2	0.0	1.6	0.0
GLY	2.2	2.9	0.0	1.1	1.2	0.0	2.0	0.4	0.0	1.3	3.9	1.7	7.5	3.3	1.9	0.0	0.0
HIS	0.0	2.9	0.0	2.1	0.0	1.6	0.7	0.0	1.0	0.0	2.9	0.7	0.0	2.6	1.2	6.9	0.0
ILE	2.6	3.1	0.4	0.9	2.4	1.1	0.9	1.3	0.0	0.5	0.2	0.9	2.1	3.4	2.9	2.2	0.6
LEU	0.6	1.2	0.8	0.9	1.1	0.8	0.5	1.2	0.0	0.8	0.2	1.1	0.7	0.6	0.0	0.6	0.3
LYS	0.7	0.5	3.2	0.9	1.1	1.6	0.7	1.4	0.0	1.2	1.2	0.3	0.0	1.0	0.0	0.0	0.6
MET	3.1	1.2	1.7	2.1	2.6	2.1	1.3	2.8	0.0	1.9	1.4	0.8	2.7	2.0	2.1	0.0	5.0
PHE	1.0	1.9	1.2	1.6	1.8	3.0	0.4	1.6	0.0	1.4	1.2	1.2	1.2	1.9	1.4	3.4	7.9
PRO	0.0	0.8	0.0	0.0	0.8	0.0	1.4	0.0	0.0	3.6	0.0	0.0	12.2	0.0	0.0	0.0	0.0
SER	0.7	0.0	0.5	0.6	1.2	1.2	2.7	0.8	0.0	0.9	0.0	0.5	0.0	1.9	1.8	0.0	0.0
THR	3.2	0.0	2.1	1.7	0.4	0.4	1.2	0.0	0.0	1.6	1.8	0.5	0.0	0.7	1.4	0.0	1.1
TRP	0.0	1.8	4.2	0.0	0.0	0.0	0.0	0.0	0.0	0.9	2.9	1.2	0.0	0.0	3.5	2.2	0.0
TYR	3.5	2.1	2.2	1.3	1.7	0.8	1.9	2.5	0.0	1.2	0.5	2.6	0.0	0.0	0.9	2.4	0.0
VAL	1.7	1.5	0.7	0.9	1.0	2.5	1.2	0.3	0.0	1.0	0.9	1.9	1.4	0.0	0.0	1.6	2.2
	P-8	P-7	P-6	P-5	P-4	P-3	P-2	P-1	P0	P1	P2	P3	P4	P5	P6	P7	P8

B.t73

ALA	0.0	0.5	0.5	0.7	0.7	0.4	1.1	1.5	0.0	1.9	0.7	0.8	1.4	0.4	0.5	0.0	0.7
ARG	0.0	0.0	1.0	2.6	0.0	3.4	0.8	0.0	0.0	0.7	0.0	0.6	0.0	0.0	1.9	0.0	0.0
ASN	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.6	1.4	1.9	0.0	0.0	0.0	0.0
ASP	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0
CYS	0.0	0.0	0.0	0.0	4.3	0.0	0.0	0.0	0.0	3.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
GLU	0.0	0.0	0.6	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
GLN	0.0	0.0	2.0	0.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.2	0.0
GLY	3.0	3.2	0.0	0.0	2.5	0.0	0.0	0.0	0.0	2.3	2.0	2.3	15.0	0.0	1.8	0.0	0.0
HIS	0.0	0.0	0.0	2.2	0.0	0.0	0.0	0.0	1.0	0.0	5.5	0.0	0.0	5.0	0.0	5.6	0.0
ILE	5.3	4.8	0.8	2.0	3.0	1.3	1.6	2.7	0.0	0.0	0.6	0.9	0.8	4.9	4.6	4.5	1.2
LEU	0.6	1.3	0.8	0.8	0.4	1.9	1.0	2.0	0.0	0.9	0.6	1.1	0.7	0.8	0.0	1.3	0.6
LYS	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	0.0	0.0	0.0	0.6	0.0	0.0	0.0	0.0	0.0
MET	3.2	2.2	1.8	4.5	3.8	3.3	3.1	7.0	0.0	3.4	1.8	1.5	1.8	3.9	2.1	0.0	5.0
PHE	2.0	2.3	2.5	3.5	2.6	4.7	0.9	1.0	0.0	2.8	2.0	2.4	0.0	3.8	2.7	3.4	11.3
PRO	0.0	1.5	0.0	0.0	1.8	0.0	0.0	0.0	0.0	4.8	0.0	0.0	24.4	0.0	0.0	0.0	0.0
SER	0.0	0.0	0.0	0.0	1.7	0.0	2.2	0.0	0.0	0.0	0.0	1.1	0.0	2.5	0.0	0.0	0.0
THR	4.0	0.0	2.2	1.2	0.0	0.0	2.9	0.0	0.0	1.1	0.0	0.0	0.0	0.0	1.3	0.0	0.0
TRP	0.0	0.0	8.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	7.4	2.5	0.0	0.0	6.7	0.0	0.0
TYR	2.4	3.8	3.0	1.4	3.8	1.8	3.4	2.5	0.0	1.0	1.2	2.6	0.0	0.0	1.7	0.0	0.0
VAL	1.1	1.4	1.5	0.7	1.4	2.6	1.2	0.7	0.0	1.9	1.8	2.3	0.6	0.0	0.0	1.6	2.9
	P-8	P-7	P-6	P-5	P-4	P-3	P-2	P-1	P0	P1	P2	P3	P4	P5	P6	P7	P8

C.t73 bis-histidine

ALA	0.0	0.6	0.6	1.0	0.5	0.6	1.7	0.6	0.0	2.3	1.0	1.1	1.4	0.0	0.7	0.0	0.8
ARG	0.0	0.0	1.3	3.6	0.0	5.2	0.0	0.0	0.0	1.1	0.0	0.9	0.0	0.0	2.5	0.0	0.0
ASN	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.5	2.0	0.0	0.0	0.0	0.0	0.0
ASP	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CYS	0.0	0.0	0.0	0.0	6.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
GLU	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
GLN	0.0	0.0	2.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.9	0.0
GLY	3.5	4.2	0.0	0.0	1.9	0.0	0.0	0.0	0.0	1.8	3.0	3.4	19.1	0.0	2.5	0.0	0.0
HIS	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	2.7	0.0	0.0	6.5	0.0	6.7	0.0
ILE	3.1	6.4	0.0	2.8	3.4	1.0	1.6	3.1	0.0	0.0	0.9	1.3	0.0	5.2	5.0	5.4	1.4
LEU	0.7	1.1	1.1	0.6	0.6	2.3	1.0	1.6	0.0	1.0	0.8	0.5	1.0	1.0	0.0	0.8	0.7
LYS	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	0.0	0.0	0.0	0.0	0.0
MET	3.7	0.0	2.3	6.4	2.9	2.5	4.7	10.7	0.0	2.6	2.7	0.0	0.0	2.5	2.7	0.0	6.0
PHE	2.4	3.1	3.4	3.3	3.9	3.6	1.4	1.5	0.0	1.4	1.5	3.5	0.0	3.2	1.8	4.1	8.2
PRO	0.0	2.0	0.0	0.0	2.7	0.0	0.0	0.0	0.0	7.3	0.0	0.0	34.9	0.0	0.0	0.0	0.0
SER	0.0	0.0	0.0	0.0	2.6	0.0	3.4	0.0	0.0	0.0	0.0	1.6	0.0	3.2	0.0	0.0	0.0
THR	4.7	0.0	2.9	1.7	0.0	0.0	0.0	0.0	0.0	1.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0
TRP	0.0	0.0	11.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	10.9	3.6	0.0	0.0	4.5	0.0	0.0
TYR	2.8	0.0	2.0	1.9	1.9	2.8	5.3	3.9	0.0	1.6	0.0	0.0	0.0	0.0	2.3	0.0	0.0
VAL	1.3	0.9	1.0	0.0	1.1	1.0	0.0	1.1	0.0	2.0	0.9	2.2	0.0	0.0	0.0	0.0	3.5
	P-8	P-7	P-6	P-5	P-4	P-3	P-2	P-1	P0	P1	P2	P3	P4	P5	P6	P7	P8

D.t-86

ALA	0.0	1.4	4.3	0.0	1.2	0.0	2.4	0.0	0.0	0.0	0.0	1.6
ARG	3.9	6.3	0.0	0.0	0.0	2.3	1.9	0.0	2.8	6.0	0.0	3.4
ASN	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	7.9	0.0
ASP	0.0	0.0	0.0	0.0	3.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CYS	0.0	0.0	12.7	0.0	0.0	0.0	0.0	0.0	0.0	15.8	0.0	0.0
GLU	0.0	0.0	0.0	0.0	0.0	2.5	0.0	1.9	0.0	0.0	0.0	0.0
GLN	3.7	0.0	0.0	0.0	2.6	0.0	0.0	0.0	4.3	0.0	0.0	0.0
GLY	0.0	0.0	0.0	0.0	0.0	12.7	0.0	0.0	0.0	0.0	0.0	0.0
HIS	0.0	0.0	0.0	1.0	0.0	0.0	4.4	0.0	0.0	7.5	0.0	0.0
ILE	0.0	0.0	0.0	0.0	0.0	0.0	0.0	4.7	5.9	0.0	0.0	0.0
LEU	0.0	0.0	1.3	0.0	0.0	0.0	0.0	1.0	1.4	0.0	0.0	0.0
LYS	8.8	3.3	0.0	0.0	0.0	2.4	0.0	0.0	0.0	0.0	0.0	0.0
MET	0.0	0.0	0.0	0.0	0.0	5.7	0.0	0.0	0.0	0.0	0.0	6.0
PHE	5.5	0.0	0.0	0.0	0.0	0.0	0.0	3.3	0.0	0.0	4.1	10.9
PRO	0.0	6.5	0.0	0.0	15.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0
SER	0.0	4.3	3.6	0.0	3.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0
THR	0.0	0.0	0.0	0.0	0.0	3.7	0.0	0.0	0.0	4.2	0.0	0.0
TRP	0.0	0.0	0.0	0.0	8.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
TYR	0.0	0.0	0.0	0.0	3.4	0.0	8.3	0.0	0.0	0.0	11.4	0.0
VAL	0.0	0.0	0.0	0.0	0.0	0.0	2.4	3.2	0.0	0.0	3.8	0.0
	P-3	P-2	P-1	P0	P1	P2	P3	P4	P5	P6	P7	P8

E.m166

ALA	2.7	1.0	1.8	1.2	0.0	1.8	2.4	1.6	0.0	1.1	0.5	0.8	4.3	0.0	0.0
ARG	0.0	1.7	2.0	1.5	1.2	1.4	0.0	0.0	0.0	0.0	2.1	1.4	0.0	0.0	0.0
ASN	0.0	0.0	2.9	2.4	0.0	2.6	0.0	0.0	0.0	2.0	2.7	0.0	0.0	0.0	5.2
ASP	0.0	0.0	0.0	0.0	1.2	0.0	0.0	0.0	0.0	1.4	3.9	0.0	0.0	0.0	0.0
CYS	0.0	0.0	0.0	0.0	49.7	0.0	0.0	33.3	0.0	4.5	0.0	21.9	0.0	0.0	39.5
GLU	0.0	0.0	1.1	0.0	0.0	0.7	1.0	0.0	0.0	1.7	3.4	0.0	0.0	5.5	0.0
GLN	0.0	0.0	2.0	1.7	0.0	0.0	0.0	0.0	0.0	2.3	3.2	0.0	0.0	0.0	0.0
GLY	0.0	4.7	0.0	0.0	0.0	0.0	7.9	0.0	0.0	1.7	0.0	0.0	0.0	9.7	0.0
HIS	0.0	11.8	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0
ILE	0.0	0.0	0.0	0.0	2.4	2.2	0.9	1.0	0.0	0.0	0.0	0.0	3.7	0.0	0.0
LEU	1.0	0.0	0.0	2.2	0.0	0.0	0.0	0.0	0.0	0.9	0.0	2.4	0.0	0.0	0.0
LYS	2.1	2.0	4.4	1.8	2.7	3.1	0.0	2.5	0.0	1.5	3.3	0.0	0.0	4.2	0.0
MET	0.0	0.0	0.0	0.0	3.1	2.7	0.0	0.0	0.0	2.4	0.0	0.0	8.1	0.0	5.5
PHE	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
PRO	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
SER	0.0	0.0	0.0	0.0	0.0	0.0	5.5	0.0	0.0	0.0	0.0	0.0	0.0	2.8	4.6
THR	2.1	0.0	4.4	2.1	0.0	1.4	0.0	0.0	0.0	3.1	1.7	2.4	0.0	0.0	0.0
TRP	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
TYR	7.4	0.0	0.0	2.4	0.0	0.0	0.0	5.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0
VAL	1.8	1.5	0.0	1.2	0.0	2.1	1.0	0.0	0.0	0.0	0.0	1.7	1.3	0.0	0.0
	P-8	P-7	P-6	P-5	P-4	P-3	P-2	P-1	P0	P1	P2	P3	P4	P5	P6

F.m80

ALA	1.4	0.0	1.0	1.6	0.0	1.4	0.0	0.7	0.0	0.7	1.5
ARG	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0
ASN	0.0	4.6	0.0	0.0	0.0	3.0	4.3	2.7	0.0	0.0	0.0
ASP	0.0	0.0	0.0	2.3	0.0	0.0	4.3	0.0	0.0	1.9	2.9
CYS	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.0	0.0
GLU	0.0	0.0	1.2	0.0	0.0	0.0	1.2	0.0	0.0	1.1	0.0
GLN	0.0	0.0	0.0	0.0	0.0	0.0	2.1	1.8	0.0	0.0	0.0
GLY	3.5	0.0	0.0	2.7	0.0	0.0	0.0	2.0	0.0	0.0	8.9
HIS	0.0	0.0	0.0	5.2	0.0	7.3	3.4	0.0	1.0	0.0	4.1
ILE	0.0	2.8	0.0	0.0	1.9	0.0	0.0	0.0	0.0	2.5	0.0
LEU	0.0	2.4	1.9	0.0	5.2	0.0	0.6	1.3	0.0	0.6	0.0
LYS	0.0	0.0	7.4	2.4	0.0	0.0	1.7	1.7	0.0	2.0	0.0
MET	7.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
PHE	0.0	3.3	0.0	0.0	3.3	2.3	0.0	5.7	0.0	1.8	2.2
PRO	0.0	0.0	0.0	0.0	0.0	0.0	3.3	0.0	0.0	0.0	0.0
SER	3.3	0.0	2.4	3.1	2.2	5.6	0.0	1.8	0.0	0.0	0.0
THR	3.1	0.0	0.0	2.8	0.0	0.0	0.0	0.0	0.0	2.1	5.2
TRP	0.0	9.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
TYR	0.0	0.0	3.4	0.0	0.0	0.0	2.2	0.0	0.0	2.0	0.0
VAL	2.7	2.0	0.0	1.6	1.8	2.5	2.3	0.0	0.0	1.2	1.3
	P-8	P-7	P-6	P-5	P-4	P-3	P-2	P-1	P0	P1	P2