

Table S1: Table of sequences used in this study (sequences marked with an asterisk (*) were manually annotated).

Organism	Taxonomy	globin type	Abbreviation	Accession no.
<i>Dyadobacter fermentans</i> DSM 18053	Bacteria; Bacteroidetes; Cytophagia	FHb	Dyfe	YP_003086573.1
<i>Bacillus methanolicus</i> PB1	Bacteria; Firmicutes	FHb	Bame	ZP_10132293.1
<i>Brevibacillus brevis</i>	Bacteria; Firmicutes	FHb	Brbr	YP_002770625.1
<i>Macrococcus caseolyticus</i> JCSC5402	Bacteria; Firmicutes	FHb	Maca	YP_002560087.1
<i>Oceanobacillus iheyensis</i> HTE831	Bacteria; Firmicutes	FHb	Ocih	NP_691212.1
<i>Commensalibacter intestini</i> A911	Bacteria; Proteobacteria; Alphaproteobacteria	FHb	Coin	ZP_09012025.1
<i>Achromobacter arsenitoxydans</i> SY8	Bacteria; Proteobacteria; Betaproteobacteria	FHb	Acar	ZP_09299925.1
<i>Bordetella pertussis</i> Tohama I	Bacteria; Proteobacteria; Betaproteobacteria	FHb	Bope	NP_880857.1
<i>Burkholderia oklahomensis</i> C6786	Bacteria; Proteobacteria; Betaproteobacteria	FHb	Buok	ZP_02364016.1
<i>Enterobacter cloacae</i> EcWSU1	Bacteria; Proteobacteria; Gammaproteobacteria	FHb	Encl	YP_004953209.1
<i>Enterobacteriaceae bacterium</i> 9_2_54FAA	Bacteria; Proteobacteria; Gammaproteobacteria	FHb	Enba	ZP_07949282.1
<i>Escherichia coli</i> K-12	Bacteria; Proteobacteria; Gammaproteobacteria	FHb	Hmp	P24232.1
<i>Pasteurella multocida</i> 36950	Bacteria; Proteobacteria; Gammaproteobacteria	FHb	Pamu	YP_005177472.1
<i>Psychrobacter</i> sp. PRwf-1	Bacteria; Proteobacteria; Gammaproteobacteria	FHb	PsPR	YP_001279574.1
<i>Vibrio fischeri</i> ES114	Bacteria; Proteobacteria; Gammaproteobacteria	FHb	Vifi	YP_205699.1
<i>Dictyostelium discoideum</i>	Eukaryota; Amoebozoa; Mycetozoa	FHb	DidiA	XP_629622.1
<i>Dictyostelium discoideum</i>	Eukaryota; Amoebozoa; Mycetozoa	FHb	DidiB	XP_629623.1
<i>Dictyostelium fasciculatum</i>	Eukaryota; Amoebozoa; Mycetozoa	FHb	Difa	EGG20401.1*
<i>Dictyostelium purpureum</i>	Eukaryota; Amoebozoa; Mycetozoa	FHb	DipuA	XP_003293958.1
<i>Dictyostelium purpureum</i>	Eukaryota; Amoebozoa; Mycetozoa	FHb	DipuB	XP_003294272.1
<i>Physarum polycephalum</i>	Eukaryota; Amoebozoa; Mycetozoa	FHb	Phpo-1	*
<i>Physarum polycephalum</i>	Eukaryota; Amoebozoa; Mycetozoa	FHb	Phpo-2	*
<i>Physarum polycephalum</i>	Eukaryota; Amoebozoa; Mycetozoa	FHb	Phpo-3	*
<i>Polysphondylium pallidum</i>	Eukaryota; Amoebozoa; Mycetozoa	FHb	Popa	EFA85250.1
<i>Giardia lamblia</i>	Eukaryota; Fornicata; Diplomonadida	FHb	Gila	XP_001704478
<i>Aspergillus terreus</i> NIH2624	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Aste-2	XP_001216520.1

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<i>Aspergillus terreus</i> NIH2624	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Aste-1	XP_001211325.1
<i>Botryotinia fuckeliana</i>	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Bofu	CCD45135.1
<i>Exophiala dermatitidis</i>	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Exde	EHY55963.1
<i>Fusarium oxysporum</i> Fo5176	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Fuox-2	EGU87788.1
<i>Fusarium oxysporum</i> Fo5176	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Fuox-1	EGU83833.1
<i>Glomerella graminicola</i> M1.001	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Glgr-2	EFQ33070.1
<i>Glomerella graminicola</i> M1.001	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Glgr-1	EFQ33638.1
<i>Kazachstania africana</i> CBS 2517	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Kaaf	CCF56724.1
<i>Kluyveromyces marxianus</i>	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Klma	CCA89273.1
<i>Lachancea thermotolerans</i>	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Lath	XP_002554200.1
<i>Penicillium chrysogenum</i> Wisconsin 54-1255	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Pech-2	XP_002559620.1
<i>Penicillium chrysogenum</i> Wisconsin 54-1255	Eukaryota; Fungi; Dikarya; Ascomycota	FHb	Pech-1	XP_002561314.1
<i>Phytophthora sojae</i>	Eukaryota; Stramenopiles	FHb	Phso	EGZ15693.1
<i>Aeropyrum pernix</i> K1	Archaea; Crenarchaeota	Pgb	Aepe	NP_147118.1
<i>Methanosarcina acetivorans</i> C2A	Archaea; Euryarchaeota	Pgb	Meac	NP_617780.1
<i>Thermobifida fusca</i> YX	Bacteria; Actinobacteria	Pgb	Thfu	YP_288788.1
<i>Nitrosococcus oceani</i> ATCC 19707	Bacteria; Proteobacteria; Gammaproteobacteria	Pgb	Nioc	YP_343124.1
<i>Kitasatospora setae</i> KM-6054	Bacteria; Actinobacteria	SDFgb	Kise	YP_004905496.1
<i>Leptospirillum</i> sp. Group II 'C75'	Bacteria; Nitrospirae	SDFgb	Lell	EIJ75556.1
<i>Hartmannella vermiformis</i>	Eukaryota; Amoebozoa; Tubulinea	SDFgb	Have	HVL00000028
<i>Spathaspora passalidarum</i> NRRL Y-27907	Eukaryota; Fungi; Dikarya; Ascomycota	SDFgb	Sppa	EGW34978.1
<i>Verticillium albo-atrum</i> VaMs.102	Eukaryota; Fungi; Dikarya; Ascomycota	SDFgb	Veal	EEY23787.1
<i>Thermus thermophilus</i> HB8	Bacteria; Deinococcus- Thermus	SDSgb	Thth	YP_144735.1
<i>Mariprofundus ferrooxydans</i> PV-1	Bacteria; Proteobacteria; Zetaproteobacteria	SDSgb	Mafe	ZP_01453014.1
<i>Aspergillus fumigatus</i> Af293	Eukaryota; Fungi; Dikarya; Ascomycota	SDSgb	Asfu	XP_750111.1
<i>Gibberella zeae</i> PH-1	Eukaryota; Fungi; Dikarya; Ascomycota	SDSgb	Gize	XP_388101.1
<i>Haladaptatus paucihalophilus</i> DX253	Archaea; Euryarchaeota	trHbN	HapaN	ZP_08045356.1
<i>Halalkalicoccus jeotgali</i> B3	Archaea; Euryarchaeota	trHbN	HajeN	YP_003735235.1

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<i>Natrialba magadii</i> ATCC 43099	Archaea; Euryarchaeota	trHbN	NamaN	YP_003480147.1
<i>Arthrospira platensis</i> str. Paraca	Bacteria; Cyanobacteria	trHbN	ArpIN	ZP_06382595.1
<i>Cyanothece</i> sp. PCC 8801	Bacteria; Cyanobacteria	trHbN	CyPCN	YP_002370447.1
<i>Microcoleus chthonoplastes</i> PCC 7420	Bacteria; Cyanobacteria	trHbN	MichN	ZP_05025218.1
<i>Bacillus cellulosilyticus</i> DSM 2522	Bacteria; Firmicutes	trHbN	BaceN	YP_004093818.1
<i>Kyrpidia tusciae</i> DSM 2912	Bacteria; Firmicutes	trHbN	KytuN	YP_003589034.1
<i>Coralloccoccus coralloides</i> DSM 2259	Bacteria; Proteobacteria; Deltaproteobacteria	trHbN	CocoN	YP_005367733.1
<i>Methylococcus capsulatus</i> str. Bath	Bacteria; Proteobacteria; Gammaproteobacteria	trHbN	MecaN	YP_114918.1
<i>Methylomonas methanica</i> MC09	Bacteria; Proteobacteria; Gammaproteobacteria	trHbN	MemeN	YP_004514063.1
<i>Coraliomargarita akajimensis</i> DSM 45221	Bacteria; Verrucomicrobia	trHbN	CoakN	YP_003548557.1
<i>Ichthyophthirius multifiliis</i>	Eukaryota; Alveolata; Ciliophora	trHbN	IcmuN	EGR32641.1
<i>Tetrahymena pyriformis</i>	Eukaryota; Alveolata; Ciliophora	trHbN	TepyN	P17724.1
<i>Perkinsus marinus</i> ATCC 50983	Eukaryota; Alveolata; Perkinsea	trHbN	PemaN	XP_002782190.1
<i>Acanthamoeba castellanii</i>	Eukaryota; Amoebozoa; Centramoebida	trHbN	AccaN	*
<i>Batrachochytrium dendrobatidis</i> JAM81	Eukaryota; Opisthokonta; Fungi; Chytridiomycota	trHbN	BadeN	EGF79192.1
<i>Chlamydomonas moewusii</i>	Eukaryota; Viridiplantae; Chlorophyta	trHbN	ChmoN	Q08753.1
<i>Volvox carteri f. nagariensis</i>	Eukaryota; Viridiplantae; Chlorophyta	trHbN	VocaN	XP_002945683.1
<i>Ricinus communis</i>	Eukaryota; Viridiplantae; Streptophyta	trHbN	RicoN	XP_002539183.1
<i>Intrasporangium calvum</i> DSM 43043	Bacteria; Actinobacteria	trHbO	IncaO	YP_004098602.1
<i>Thermobifida fusca</i> YX	Bacteria; Actinobacteria	trHbO	ThfuO	YP_290271.1
<i>Turneriella parva</i> DSM 21527	Bacteria; Spirochaetes	trHbO	TupaO	YP_006440763.1
<i>Acanthamoeba castellanii</i>	Eukaryota; Amoebozoa; Centramoebida	trHbO	AccaO	*
<i>Thalassiosira pseudonana</i> CCMP1335	Eukaryota; Stramenopiles	trHbO	ThpsO	XP_002292446.1
<i>Chlorella variabilis</i>	Eukaryota; Viridiplantae; Chlorophyta	trHbO	ChvaO	EFN55622.1
<i>Ricinus communis</i>	Eukaryota; Viridiplantae; Streptophyta	trHbO	RicoO	XP_002516587.1
<i>Selaginella moellendorffii</i>	Eukaryota; Viridiplantae; Streptophyta	trHbO	SemoO	XP_002991488
<i>Mycobacterium avium</i> subsp. paratuberculosis K-10	Bacteria; Actinobacteria	trHbP	MyavP	AAS05726.1

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<i>Methylococcus capsulatus</i> str. Bath	Bacteria; Proteobacteria; Gammaproteobacteria	trHbP	MecaP	YP_114018.1

Table S2: Templates used for tertiary structure modeling employing Swiss-Model and SwissPDBViewer.

query	template	pdb	Identity (%)	e-value
<i>A. castellanii</i> trHbN	<i>Synechococcus</i> sp. PCC 7002 trHbN	2kscA	32.6	2E-45
	<i>Synechocystis</i> sp. PCC 6803 trHbN	1s69A	33.0	4E-44
	<i>Tetrahymena pyriformis</i> trHbN	3aq9A	29.6	6E-43
	<i>Mycobacterium tuberculosis</i> trHbN	1s61B	25.7	1E-42
	<i>Chlamydomonas moewusii</i> trHbN	1dlyA	27.9	1E-42
<i>A. castellanii</i> trHbO	<i>Bacillus subtilis</i> trHbO	1ux8A	18.7	1E-15
	<i>Thermobifida fusca</i> trHbO	2bmmA	13.9	2E-13
	<i>Geobacillus stearothermophilus</i> trHbO	2bkmB	19.1	3E-13
<i>P. polycephalum</i> FHb-3	<i>Escherichia coli</i> Hmp	1gvhA	41.3	1E-148
	<i>Cupriavidus necator</i> Hmp	1cqxB	48.0	1E-147
<i>D. purpureum</i> FHbA	<i>Escherichia coli</i> Hmp	1gvhA	38.2	1E-155
	<i>Cupriavidus necator</i> Hmp	1cqxB	42.7	1E-151
<i>D. discoideum</i> FHbB	<i>Escherichia coli</i> Hmp	1gvhA	33.5	1E-155
	<i>Cupriavidus necator</i> Hmp	1cqxB	37.0	1E-157
<i>D. fasciculatum</i> FHb	<i>Escherichia coli</i> Hmp	1gvhA	55.3	1E-166
	<i>Cupriavidus necator</i> Hmp	1cqxB	40.1	1E-153

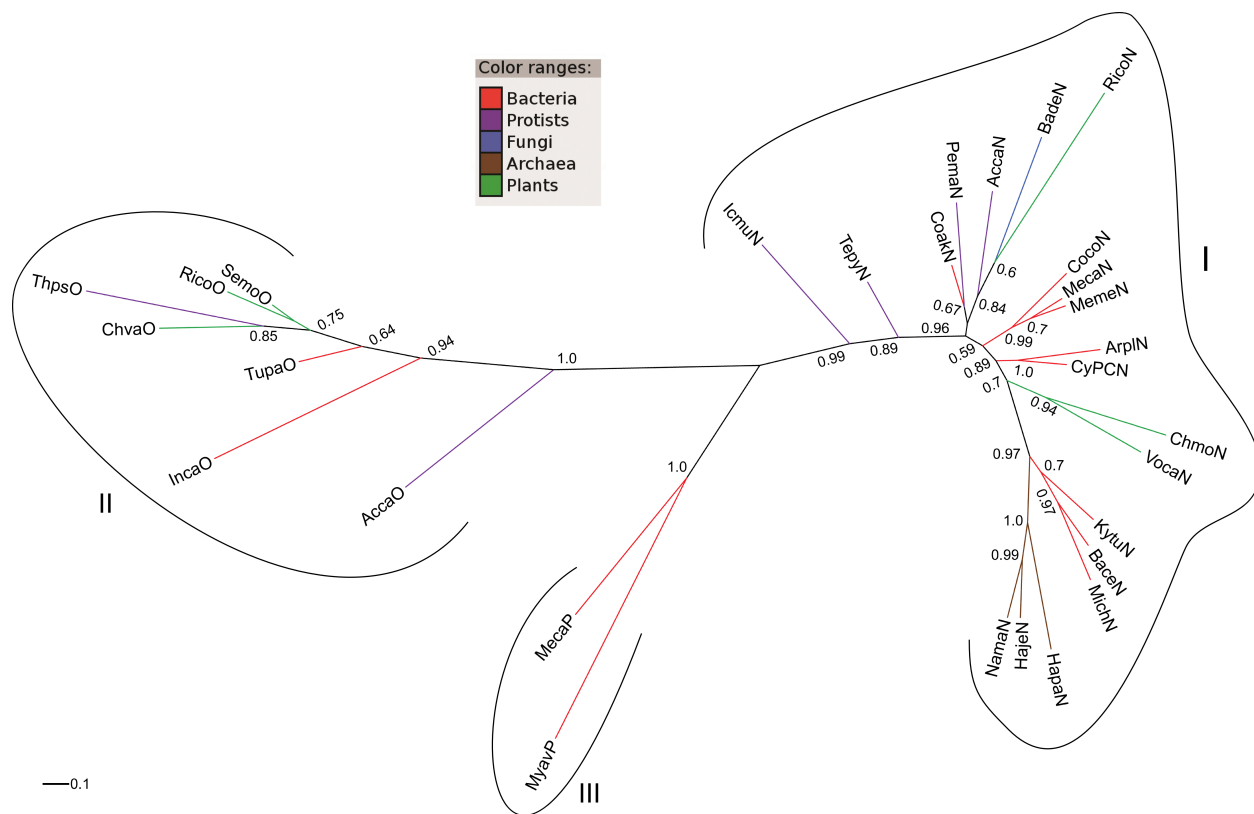


Figure S1: Bayesian tree of trHb proteins. The colors of branches correspond to the taxonomic classification of the used sequences. Posterior probability values equal or greater than 50 % are indicated. The trHb proteins cluster in accordance to their classification in three distinct clades. For a description of used abbreviations please refer to table S1.