Supplementary Information

Figure S1. Sequence alignment of Dph1 and orthologs. Archaeal PhDph2 (*P. horikoshii*), mammalian chinese hamster (*C. griseus*) CgDph2, human HsDph1 and HsDph2, and *S. cerevisiae* ScDph2 are included for comparison of conserved regions. The highest degree of conservation between the six sequences is marked in dark blue. The three conserved cysteine residues in PhDph2, which bind the iron-sulfur cluster (Cys59, Cys163 and Cys287) are marked with a red triangle [7,8]. The position of N-terminal truncations (N1-N4) as well as C-terminal truncations (C1-C4) of ScDph1 are highlighted. Sequence alignment was performed using Jalview.

		N1	N2
PhDph2/1-342	1		M LHE IPK SEILKELKR IGAKRV L 23
ScDph2/1-534	1	VLOPCYN SDELMOLTS	
CgDph2/1-489	1		
HsDph2/1-489			GVXELERVAGEVEDLGCERXA 51
ScDph1/1-425	1 M SG ST ESKKOPRERFIGEK SGN SNNDKLTTVA ENGNEI IHKOK SE IALGESVNH		
HsDph1/1-443	1MRRQ VM AA L		
1150 pt11/1-445	N3 N4	ter a real of a gaara ta ta	CONTRACTOR OF THE TYPE OF THE TO
PhDph2/1-342	24 IO SE EGERREA EELAGFLEENN IEVFLHGE IN YGAC DPADREAK LVGCDALIHLGH	SYMKLELEVPT	FVPAF-ARVSVVEALKEN IGE IKKL 115
ScDph2/1-534	67 LOFPDDL IKDSSLIVELLOSKFPHGKIKFWVLADTAYSACCVDEVAAEHVHAEVVVHFGD		
CgDph2/1-489	52 LO FF DO LLGDAGAVAVR LEEVTG SKM FILODTAYG SCCVDVLGA EQ AGA EA LVH FGP	ACT SPRASLLP IT F	LGORSVALELCAKAFEARNE DP 145
HsDph2/1-489	52 LO FF DO LLGDAVAVAAX LEE TTG SKM F ILOD TAYG SC CVDV LGA EQ AGXQA LIH FGP	ACLSPRX RPLPVAF	LSST FCGLGTLCOD LW GPXP RX 145
ScDph1/1-425	97 LOM PEGLL IYSL I ISD ILEO FCGVET LVM GDVSTGACC ID DFT ARALDC DF IVHYAH	SCLV-PIDVTKIKVLY	FVT IN TO EDH I IKT LOKN FR K 190
HsDph1/1-443	79 LON PEGELLEACT IVD ILER FTEAEVN VM GDVTYGACCVDDFTARALGADFLVHYGH		
		-	
PhDph2/1-342	116 GRK I IVTTTAOH INO KE-AKEFLESEGF-EVS IGRGD	SR ISW PGOVLGCNY	SV-AKVRGEGILFIGSGIFNPLGL 188
ScDph2/1-534	163 S SK IC LM ANAP F SKH SO LYN ILKGD LHYTN I IY SO VNT SAV EEK FYT ILDT FHVP EDVDO		
CgDph2/1-489	146 TAPVVLLSEPACAHALEALATLLEPKYODLLISSPAL-PLPVGSPSSOPEPLE		
HsDph2/1-489	146 Q SACGAAGEPACAHALEALAXLLRPRYLDLLVSSPAF-POPVGSLSPEPMPXEI	REGRREPLAPERRLE	EYGA FYVOG SKA SPDPD LD 231
ScDph1/1-425	191 G SR IATFGT IQ FN PAVH SVRDK	IXPLSRC EVLGCT SI	ER LDK EQ YDAN V F IC DGR FH LE SA 265
HsDph1/1-443	175 ATALALVST 10 FVST 10 AAAQ E LK A-EYRV SVP0	CKPLSPGEILGCTSI	RLSKE-VEAVVYLODGRFHLESV 244
	C4		C3
PhDph2/1-342	189 AVAT-RKKVLA IDPYTKAFSW IDPERFIRKEWAQ IAKAM DAKI	K FCV IV S IK KGO LR LA EAF	R IVKLLKKHGREARLIVMNDVNYHK 273
ScDph2/1-534	256 PO DPR LLY L ST V FO SVH IFD PALP GM VT GP FP SLM R YKYM HVART AG		
CgDph2/1-489	232 PD LSR LL	VVGLLAGTLGVAQHREAL	HERELT EAAGER SYV LALGR PT PAK 326
HsDph2/1-489	232 PDLSRLLLGWAPGOPFSSCCPDTGKTODEGARAGGLRARRYXVERARDAR	VVGLLAGTXGVAQHREAL	HERNLTO AAGKR SYV LALGRPT PAK 326
ScDph1/1-425	266 MINNELIPAFKYDPYNRKFTREGYDO KO LVEVRA EA IEVARKGKY	V FGL ILGALGROGNLNTV	NLEKNLIAACKTVVKIILSEVFPOK 353
HsDph1/1-443	245	SW G L ILGT LGROG SPK ILI	EHLESRLRALGLSFVRLLLSEIFPSK 332
	C2 C1		Contractive of the second of the prover of the second second second
PhDph2/1-342	274 LEG PP-FEAYWVV ACPRVPL-DDYGAWRKPVLTPKEVEILLGLREEY	EFDEILGGPS	ESDEPFGISIHSTR 342
ScDph2/1-534	348 LAN FED ID INC ILC SO SG I IVDO FNEFYKPI I TPYELNLALSEEV-TWTGKWVVDFR-DJ	A ID E IEO N LOGO DT ISA ST	T S D B P E F D V VR G 436
CgDph2/1-489	327 LAN PPEND IFV LLACP LGA LAPOP SGG F FR FILTP CELEAACNPA HPPPG LAPH LTH	Y A E L L P G S P F Y V P L P I	P E S E LW D T P D V S L 412
HsDph2/1-489	327 LAN PPEVOVFVLLACPLGALAPOLSGSPFOPILAPCELEAACNPA HPPPGLAPHLTH	YADL LPOSPFHVALPS	PESELWETPDVSL412
ScDph1/1-425	354 LAM POO IDV FVOVACPRLSI- DW GYAPNKPLLTPY EASVLLKKDVM FSEKYY		
HsDph1/1-443	333 LSLLPEVDVW VOVACPRLSIDWGTAPPKPLLTPYEAAVALRD ISMOOPY	PM D FYA C S SI	L G PW TVNH GQ D R R P H A P G R P A R G 413
PhDph2/1-342		· · · · · · · · · · · · · · · · · · ·	
ScDph2/1-534	437 R - YT ST S R P LRALTH LE LEAAD D D D S KO LTTRHTA SGAV IKGTV ST SA SA LO NR SW KG LG		
CgDph2/1-489	413 ISGDLRPPPSWKSSSDTGCSALTPRPQLELAESSPAASFLSSRSWQGLE		
HsDph2/1-489	413 ITGDLRPPPAWKSSNDHGSLALNPRPQLXLAESSPAVSFLSSRSWQGLE	PRLGQTPVTEAVSGI	R G IA IAY ED EG SG 489
ScDph1/1-425			
HsDph1/1-443	414 K VQ EG SA RPP SAVACEDC SCRDEKVAP LAP		443