

Supplementary Table S2. List of the 45 sequences found to be similar to LOXs from *P. arenysensis* or *F. cylindrus*. Sequences have been divided in six groups according to their cofactor coordination residues pattern and their placement in the phylogenetic tree (Figure 1 in the manuscript). Particularly, the same background color presents in each line of the same group corresponds to the clustering of these sequences under the same branch in the tree; color highlighting each NCBI Entry code corresponds to the color label present for these sequences in the tree, that is related to a similar residues' composition of the iron coordination pattern.

Entry NCBI	Entry UniProt	Organism of origin	Sequence type	Sequence length	Iron coordination pattern
GROUP I					
CAD9618313	A0A7S2LXV6	<i>Skeletonema marinoi</i>	protein	599	Hlgkth – HaavN
CAE1959045		<i>Skeletonema costatum</i>	protein	955	Hlgkth – HaavN
HBOY01017335		<i>Skeletonema dohrnii</i>	RNA	566	HlgntH – HaavN
HBLG01015303		<i>Skeletonema grethae</i>	RNA	637	HlgntH – HaavN
CAE2245853	A0A7S4J0G1	<i>Odontella aurita</i>	protein	219	HlgntH
HBLJ01006463		<i>Skeletonema japonicum</i>	RNA	515	HlgntH – HaavN
HBQM01026246		<i>Minidiscus sp.</i>	RNA	491	HlgetH – HaavN
CAE4882500		<i>Ditylum brightwellii</i>	protein	752	HlgntH – HaavN
HBJS01002470		<i>Detonula confervacea</i>	RNA	553	HlgdtH – HaavN
HBPL01043054		<i>Thalassiosira antarctica</i>	RNA	559	HlgdtH – HaavN
CAG1089053		<i>Aulacoseira subarctica</i>	protein	724	HlgrtH – HaavN
GROUP II					
HBGY01034511		<i>Leptocylindrus danicus</i>	RNA	612	HlantH – HagvN
CAE0708802	A0A7S4EF52	<i>Pseudo-nitzschia australis</i>	protein	698	HlgmtH – HaaiN
QWC64745	A0A8E8LBZ9	<i>Pseudo-nitzschia arenysensis</i>	protein	704	HlgmtH – HaavN
CAE4404401		<i>Chaetoceros affinis</i>	protein	519	HlamtH – HcavN

CAE3781055		<i>Stauroneis constricta</i>	protein	761	HlgktH – HaavN
GJGQ01026673		<i>Craspedostauros australis</i>	RNA	506	HlgktH – HaavN
CAD8937191	A0A7S1D4P1	<i>Cyclophora tenuis</i>	protein	778	HlgntH – HaavN
CAE2664940		<i>Astrosyne radiata</i>	protein	359	HlgrtH – HaavN
CAE5663449		<i>Fragilariopsis kerguelensis</i>	protein	712	HlaktH – HaavN
GROUP III					
XP_002180840	B7G1E2	<i>Phaeodactylum tricornutum</i>	protein	596	HswvH – HstdH
HBME01023157		<i>Synedropsis cf. recta</i>	RNA	588	HswvH – HstdH
CAD8884873	A0A7S1BET1	<i>Corethron hystrix</i>	protein	569	HatiH and HgatI
GROUP IV					
CAD9818490	A0A7S2UJH2	<i>Attheya septentrionalis</i>	protein	1378	HlvnvH – HelvgQ
GHBX01011490		<i>Nitzschia palea</i>	RNA	448	HlvnvH – HelvgQ
CAD8595700	A0A7S0KYY3	<i>Asterionellopsis glacialis</i>	protein	767	HlghcH – HehvgQ
OEU18547	A0A1E7FK81	<i>Fragilariopsis cylindrus</i>	protein	742	HlleIH – HnlvaN
HBQV01033768		<i>Synedra</i>	RNA	716	HllevH – HnvvaN
HBSF01004517		<i>uncultured Nitzschia</i>	RNA	360	HlleIH – HnlvaN
CAE3758544		<i>Chaetoceros cf. neogracilis</i>	protein	735	HlsveH – HssigN
GROUP V					
GJWO01009215		<i>Bellerochea sp.</i>	RNA	558	HlfnaH – HehvgS
HBQT01021118		<i>Navicula sp.</i>	RNA	511	HlynIH – HeqvgS
HBRE01028634		<i>Pleurosigma sp.</i>	RNA	585	HllwcH – HdlvgS
CAE4385921		<i>Chaetoceros affinis</i>	protein	555	HlvwsH – HelvgA
HBOX01063848		<i>Proboscia alata</i>	RNA	306	HlvwsH – HeimgH
HBPD01019733		<i>Thalassionema nitzschioides</i>	RNA	582	HliwtH – HelvgH

HBPJ01045426		<i>Thalassiosira minuscula</i>	RNA	358	HlcqtH – HelvgH
CAE0460244	A0A7S3V6L4	<i>Chaetoceros debilis</i>	protein	633	HlaqtH – Heiigh
GFH44228		<i>Chaetoceros tenuissimus</i>	protein	624	HlaqsH – Heligh
CAB9509299		<i>Seminavis robusta</i>	protein	576	HltwsH – HelvgN
GROUP VI					
CAD8419348	A0A7S0CCN1	<i>Proboscia inermis</i>	protein	336	HfvysH – HhswN
CAD8307630	A0A7R9VXA5	<i>Pseudictyota dubia</i>	protein	554	HfietH – HhvmN
CAE3007537		<i>Stephanopyxis turris</i>	protein	1179	HaltcH – HaavN
CAF33213		<i>Phaeodactylum tricornutum</i>	protein	937	Hfsrch – HaavN