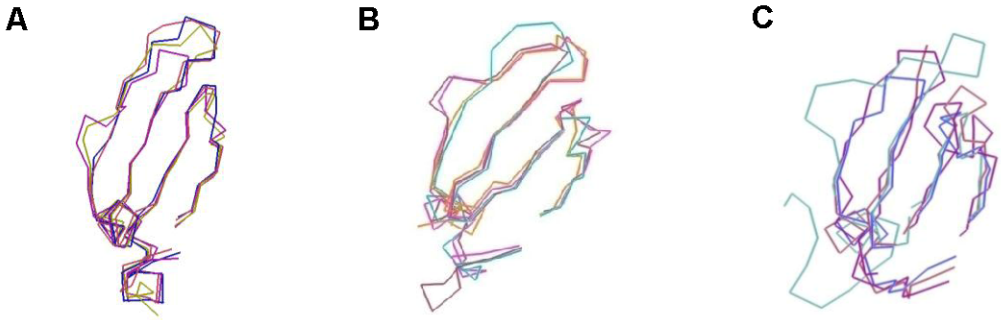
Figure S2



D

```
LS-24_I      7 NAAFRSSKNNEAYFFINDKYVLLDYAPGSSADKVLYGPTPVRDGFKSLNQTIFGSYGI 64
LS-24_II    65 DCSFD.TENNEAFIFYENFCALIDYAPHSKKDKIILGPKKIADVFPFFEGTVFES.GI 120
LS-24_III  121 DAAYRSTRGKEVYLFKGDQYARIDYGSNSMVNAEI...KSISSGYPCFRNTIFESGA. 174
LS-24_IV   175 DAAFASHKTNEVYFFKDDHYARVKVTPGGKL.AIMDGVREIVDYWPSLKDIVPL.... 227
               :.::   . :*.::*  :  . :.  . .     :     : . :  :. :
```

E

```
1GEN_I     476 DGIAQI..R.GEIFFFKDRFIWRTVT..PRDK.PM..GPLLVATF.W.PEL..PEKI. 520
1GEN_II    521 DAVYEAPQ.EEKAVFFAGNEYWIYS...A.S.TLERGYPKPLTSL..GLP.PDVQRV. 568
1GEN_III   569 DAAFNWS.KNKKTYIFAGDKFWRYNEVKK.K..MDPGFPKLIADAW.N.AI..PDNL. 617
1GEN_IV    618 DAVVDLQG.GGHSYFFKGAYYLKLENQS..LKSVK..F.GSIKSDWLG.........C 660
               *.  :      .  :* .                       :
```

F

```
1QHU_I      34 DATTLDD.N......GTMLFFKD.EFVWKS.....HR.GI.R..ELISERWK....NFIGPV. 74
1QHU_II     75 DAAFRH.G......HTSVYLIKG.DKVWVYTS.........P..KSLQDEFP....GIPFPL. 113
1QHU_III   121 DAAVEC.HRGECQD.EGILFFQGNRKWFWDL.TTG..T.KK...E.RS....WP.A.V.GNC. 165
1QHU_IV    166 TSALRWLG........RYYCFQGNQFLRFNPV..S.GE.VP.PGYPL.....D.VRD.....Y 204
               ::                  ::.
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Figure S2. Comparison of the blades within LS-24 and other hemopexins. A to C, Superimpositions of the four blades of LS-24 (A), the hemopexin domain of gelatinase A (PDB: 1GEN) (B), and the N-terminal domain of mammalian serum hemopexin (PDB: 1QHU) (C). D to F, Structure-based multiple sequence alignments of the individual blades from hemopexin domains of LS-24 (D), gelatinase A (E) and N-terminal domain of mammalian serum hemopexin (F). The sequences have been named as I, II, III and IV from N to C-terminus along with the PDB code. Sequences highlighted with yellow and turquoise, demarcate β-sheet and α-helix respectively.