

Supplemental data Figure 1. Clustal W alignment of 142 ferrochelatase primary sequences retrieved from the public database.

CLUSTAL W (1.83) multiple sequence alignment

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sp|P42043|HEMH1_ARATH      MQATAL-SSGFN-----PLTKRKDHRFPRSCSQRNLSLSLIQCD----- 37
sp|P42044|HEMH_CUCSA      MDAASS-SLALSNIKLGSTNTLNSDQRISSLCSLPKSRVTFSCKTSGNL 49
sp|P42045|HEMH_HORVU      MECVRSGALDLGR-----SGNFLGKSGSTTSCGKVR CSTNLAGSTKCEQ 44
sp|O04921|HEMH2_ARATH     -----MNC PAMTAS P S S S S S S S S Y S T F R P P P P L L P Q L S N 33
sp|O22101|HEMH_ORYSA     -----N S S R V N L S R T Y A I K S C S V S S R T G - L C L G Q C Y H 31
sp|Q8YQR8|HEMH_ANASP     -----
sp|P54225|HEMH_SYNY3     -----
sp|Q8DGU6|HEMH_SYNEL     -----
sp|Q7VD58|HEMH_PROMA     -----
sp|Q7V2F5|HEMH_PROMP     -----
sp|Q7V6C6|HEMH_PROMM     -----
sp|Q7U5G0|HEMH_SYN PX     -----
sp|Q7NMC7|HEMH_GLOVI     -----
sp|Q9ZC84|HEMH_RICPR     -----
sp|Q68VM9|HEMH_RICTY     -----
sp|Q92FV4|HEMH_RICCN     -----
sp|Q73FY6|HEMH_WOLPM     -----
sp|P57777|HEMH_CAUCR     -----
sp|O67083|HEMH_AQUAE     -----
sp|P22830|HEMH_HUMAN     -----M 1
sp|P22315|HEMH_MOUSE     -----M 1
sp|P22600|HEMH_BOVIN     -----
sp|O42479|HEMH_CHICK     -----
sp|O57478|HEMH_XENLA     -----
sp|Q9V9S8|HEMH_DROME     -----
sp|O59786|HEMH_SCHPO     -----
sp|P16622|HEMH_YEAST     -----
sp|Q6APB0|HEMH_DESPS     -----
sp|Q747F5|HEMH_GEOSL     -----
sp|Q9ZKD4|HEMH_HELPJ     -----
sp|P56107|HEMH_HELPY     -----
sp|Q7M7P9|HEMH_WOLSU     -----
sp|Q7VHH1|HEMH_HELHP     -----
sp|Q9PI08|HEMH_CAMJE     -----
sp|Q8DFM2|HEMH_VIBVU     -----
sp|Q7MMR4|HEMH_VIBVY     -----
sp|Q9KTB6|HEMH_VIBCH     -----
sp|Q87RH3|HEMH_VIBPA     -----
sp|Q6LTE0|HEMH_PHOPR     -----
sp|Q8EFF4|HEMH1_SHEON     -----
sp|Q8XD39|HEMH_ECO57     -----
sp|P23871|HEMH_ECOLI     -----
sp|Q8FK83|HEMH_ECOL6     -----
sp|Q83SE5|HEMH_SHIFL     -----
sp|Q8Z8T2|HEMH_SALTI     -----
sp|P37408|HEMH_SALTY     -----
sp|Q8ZC98|HEMH_YERPE     -----
sp|Q05338|HEMH_YERPS     -----
sp|P43413|HEMH_YEREN     -----
sp|Q6D7Z4|HEMH_ERWCT     -----
sp|Q7N0P6|HEMH_PHOLL     -----
sp|P43868|HEMH_HAEIN     -----
sp|P57874|HEMH_PASMU     -----
sp|Q65SV7|HEMH_MANSM     -----
sp|Q8CWW4|HEMH_STRMU     -----
sp|Q8D226|HEMH_WIGBR     -----
sp|Q8EBZ7|HEMH2_SHEON     -----

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sp	Q7W515	HEMH_BORPA	-----
sp	Q7VVX8	HEMH_BORPE	-----
sp	Q62HD1	HEMH_BURMA	-----
sp	Q63R43	HEMH_BURPS	-----
sp	Q8XW32	HEMH_RALSO	-----
sp	Q7NV65	HEMH_CHRVO	-----
sp	Q82UK8	HEMH_NITEU	-----
sp	Q9JVA5	HEMH_NEIMA	-----
sp	Q9K097	HEMH_NEIMB	-----
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sp	Q8P3H6	HEMH_XANCP	-----
sp	Q9PFU1	HEMH_XYLFA	-----
sp	Q87B82	HEMH_XYLFT	-----
sp	Q607T4	HEMH_METCA	-----
sp	Q8U9F7	HEMH_AGRT5	-----
sp	Q92M52	HEMH_RHIME	-----
sp	Q93TG2	HEMH_BRUME	-----
sp	Q98H61	HEMH_RHILO	-----
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sp	Q9PJQ6	HEMH_CHLMU	-----
sp	O84492	HEMH_CHLTR	-----
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sp	Q81U22	HEMH1_BACAN	-----
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sp	Q81GN7	HEMH2_BACCR	-----
sp	Q9KDK9	HEMH_BACHD	-----

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sp	Q72L32	HEMH_THET2	-----
sp	Q9RV98	HEMH_DEIRA	-----
sp	Q97R30	HEMH_STRPN	-----
sp	Q8DQ04	HEMH_STRR6	-----
sp	Q8FTB1	HEMH_COREF	-----
sp	Q8NQA1	HEMH_CORGL	-----
sp	Q6NH66	HEMH_CORDI	-----
sp	Q740Y1	HEMH_MYCPA	-----
sp	P71765	HEMH_MYCTU	-----
sp	Q9CBM2	HEMH_MYCLE	-----
sp	Q5YU18	HEMH_NOCFA	-----
sp	O07401	HEMH_MYCAV	-----
sp	Q83H94	HEMH_TROW8	-----
sp	Q83FJ2	HEMH_TROWT	-----
sp	Q6AHF2	HEMH_LEIXX	-----
sp	Q82KJ6	HEMH_STRAW	-----
sp	O50533	HEMH_STRCO	-----
sp	Q7UFZ7	HEMH_RHOBA	-----
sp	P72183	HEMH_PROFR	-----
sp	Q9HLB8	HEMH_THEAC	-----
sp	Q978U9	HEMH_THEVO	-----

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sp	P42045	HEMH_HORVU	NLHGKAKPLLLSASGKARG--TSGLVHRSPVLKHQHHLRSTSTDVCT	91
sp	O04921	HEMH2_ARATH	DSQRSVVMHCTRLPFEAFAATSSNRLGKHSPLRAALVTSNPLNISSSS	83
sp	O22101	HEMH_ORYSA	K--KSSACRCK-----LGWSSQPLSSLRHHLRVHSSASEA	64
sp	Q8YQR8	HEMH_ANASP	-----	
sp	P54225	HEMH_SYNY3	-----	
sp	Q8DGU6	HEMH_SYNEL	-----	
sp	Q7VD58	HEMH_PROMA	-----	
sp	Q7V2F5	HEMH_PROMP	-----	
sp	Q7V6C6	HEMH_PROMM	-----	
sp	Q7U5G0	HEMH_SYNPX	-----	
sp	Q7NMC7	HEMH_GLOVI	-----	
sp	Q9ZC84	HEMH_RICPR	-----	
sp	Q68VM9	HEMH_RICTY	-----	
sp	Q92FV4	HEMH_RICCN	-----	
sp	Q73FY6	HEMH_WOLPM	-----	
sp	P57777	HEMH_CAUCR	-----	
sp	O67083	HEMH_AQUAE	-----	
sp	P22830	HEMH_HUMAN	RSLGANMAAALRAAGVLLRDPLASSSWRVCQPWRWKSAAAAAVTTETAQ	51
sp	P22315	HEMH_MOUSE	LSASANMAAALRAAGALLREPLVHGSSRACQPWRCQSG-AAVAATTEKVH	50
sp	P22600	HEMH_BOVIN	-----MAAALRSAGVLLRDRLLYGGSRACQPRRCQSGAATAAAATETAQ	44
sp	O42479	HEMH_CHICK	-----MAAAGRAA----RPLVAGGRQLRVPLRWRGQVAAAAPS-----	34
sp	O57478	HEMH_XENLA	-----MAAFRAAHRLLGHILRNESSAGLVTQRWSSSAAVASVP-----	38
sp	Q9V9S8	HEMH_DROME	-----MFLHNTKFC--RLASGLAGGVRN-----	21
sp	O59786	HEMH_SCHPO	-----MSVSSYSSDASSTVMDESPPNGVTKS-----	26
sp	P16622	HEMH_YEAST	-----MLSRITIRTQGSFLRRSQLTITRSFVSFTFN-----	29
sp	Q6APB0	HEMH_DESPS	-----	
sp	Q747F5	HEMH_GEOSL	-----	
sp	Q9ZKD4	HEMH_HELPJ	-----MNL	3
sp	P56107	HEMH_HELPY	-----MDL	3
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sp	Q7VHH1	HEMH_HELHP	-----	
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sp	Q8DFM2	HEMH_VIBVU	-----	
sp	Q7MMR4	HEMH_VIBVY	-----	
sp	Q9KTB6	HEMH_VIBCH	-----	
sp	Q87RH3	HEMH_VIBPA	-----	
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sp	Q8EFF4	HEMH1_SHEON	-----MLAC	4
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sp	Q63R43	HEMH_BURPS	-----MSFDSVPRHALSMRFDLEP	19
sp	Q8XW32	HEMH_RALSO	-----MPFLPEP	7
sp	Q7NV65	HEMH_CHRVO	-----MAMPRYLTEP	10
sp	Q82UK8	HEMH_NITEU	-----MTRMLPEP	8
sp	Q9JVA5	HEMH_NEIMA	-----MLPFLPEP	8
sp	Q9K097	HEMH_NEIMB	-----MLPFFPEP	8
sp	Q8PEX0	HEMH_XANAC	-----	
sp	Q8P3H6	HEMH_XANCP	-----	
sp	Q9PFU1	HEMH_XYLFA	-----	
sp	Q87B82	HEMH_XYLFT	-----	
sp	Q607T4	HEMH_METCA	-----	
sp	Q8U9F7	HEMH_AGRT5	-----MATELSALP	9
sp	Q92M52	HEMH_RHIME	-----MDAN-	4
sp	Q93TG2	HEMH_BRUME	-----MSGTDKVRVNVSQTAQT	17
sp	Q98H61	HEMH_RHILO	-----MTSAIAVDPKAAKPVGVT	18
sp	P28602	HEMH_BRAJA	-----MSTAAPNETT	10
sp	Q6NBF3	HEMH_RHOPA	-----MSVIVPIHGP	10
sp	Q59735	HEMH_RHOCA	-----MTIANRILPHAP	12
sp	P57779	HEMH_ZYMMO	-----MTD	3
sp	Q833G5	HEMH_ENTFA	-----	
sp	Q9CFB4	HEMH_LACLA	-----	
sp	Q67T48	HEMH_SYMTH	-----	
sp	Q88XC3	HEMH_LACPL	-----	
sp	P57778	HEMH_PSEFL	-----	
sp	Q888A2	HEMH_PSESM	-----	
sp	Q88PV4	HEMH_PSEPK	-----	
sp	Q9HVD7	HEMH_PSEAE	-----	
sp	Q6MHT3	HEMH_BDEBA	-----	
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sp	Q8GCV0	HEMH_LEPBI	-----	
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sp	Q8CNS1	HEMH_STAEP	-----	
sp	Q81TU9	HEMH2_BACAN	-----	
sp	Q6HM28	HEMH2_BACHK	-----	
sp	Q63EK7	HEMH2_BACCZ	-----	
sp	Q73C08	HEMH2_BACC1	-----	
sp	Q81GN7	HEMH2_BACCR	-----	
sp	Q9KDK9	HEMH_BACHD	-----	
sp	Q5WHT1	HEMH_BACSK	-----	
sp	Q72L32	HEMH_THET2	-----	
sp	Q9RV98	HEMH_DEIRA	-----	
sp	Q97R30	HEMH_STRPN	-----	
sp	Q8DQ04	HEMH_STRR6	-----	
sp	Q8FTB1	HEMH_COREF	-----	
sp	Q8NQA1	HEMH_CORGL	-----	
sp	Q6NH66	HEMH_CORDI	-----	
sp	Q740Y1	HEMH_MYCPA	-----	
sp	P71765	HEMH_MYCTU	-----	
sp	Q9CBM2	HEMH_MYCLE	-----	
sp	Q5YU18	HEMH_NOCFA	-----	
sp	O07401	HEMH_MYCAV	-----	
sp	Q83H94	HEMH_TROW8	-----MIRRSAVSRVVAE	13
sp	Q83FJ2	HEMH_TROWT	-----MIRRSAVSRVVAE	13
sp	Q6AHF2	HEMH_LEIXX	-----MLGATPAAAGVAE	13
sp	Q82KJ6	HEMH_STRAW	-----MPEALDAS	8
sp	O50533	HEMH_STRCO	-----MPDVLDAS	8
sp	Q7UFZ7	HEMH_RHOBA	-----MSELP	5
sp	P72183	HEMH_PROFR	-----	
sp	Q9HLB8	HEMH_THEAC	-----	
sp	Q978U9	HEMH_THEVO	-----	

sp	P42043	HEMH1_ARATH	YDETSAKARSHVVAEDKIGVLLLNLLGGPE--TLNDVQPFLYNLFADPDII	120
sp	P42044	HEMH_CUCSA	VGEFALESQSQAV-DDKVGVLLLNLLGGPE--TLDDVQPFLYNLFADPDII	145
sp	P42045	HEMH_HORVU	TFDEDVKGVSSHAVEEKVGVLLLNLLGGPE--TLNDVQPFLYNLFADPDII	139
sp	O04921	HEMH2_ARATH	VISDAISSSSVITDDAKIGVLLLNLLGGPE--TLDDVQPFLYNLFADPDII	131
sp	O22101	HEMH_ORYSA	VLTSQSDFTKLLVGNKIGVLLLNLLGGPE--TLDDVQPFLYNLFADPDII	112
sp	Q8YQR8	HEMH_ANASP	-----MGRVGVLLLNLLGGPD--KLEDVAPFLYNLFSDPEII	34
sp	P54225	HEMH_SYNY3	-----MGRVGVLLLNLLGGPE--KLEDVRPFLYNLFADPEII	34
sp	Q8DGU6	HEMH_SYNEL	-----MASQTGVLLLNLLGGPD--RPEDVRPFLYNLFSDPEII	35
sp	Q7VD58	HEMH_PROMA	-----MTRVGVLLMNLGGPE--RIKDVGPFLYNLFSDPEII	34
sp	Q7V2F5	HEMH_PROMP	-----MEKVGVLMLNLLGGPE--RITDVGPFYLNLFSDPEII	34
sp	Q7V6C6	HEMH_PROMM	-----MARVGVLLMNLGGPE--RIQDVGPFLFNIFADPEII	34
sp	Q7U5G0	HEMH_SYNPX	-----MSRVGVLLLNLLGGPE--RIQDVGPFLYNLFADPEII	34
sp	Q7NMC7	HEMH_GLOVI	-----MAEVGVLLLNLLGGPD--KQEDVRPFLYNLFADPEII	34
sp	Q9ZC84	HEMH_RICPR	-----MKNKRIAIIVLFNLGGPE--DIEYVKPFLFNLFYDKAII	35
sp	Q68VM9	HEMH_RICTY	-----MKNKRIAIIVLFNLGGPE--DIEYVKPFLFNLFYDKAII	35
sp	Q92FV4	HEMH_RICCN	-----MKNKRIAIIVLFNLGGPK--NLKSVKPFYLNLFYDKAII	35
sp	Q73FY6	HEMH_WOLPM	-----MKK--AVILFNLGGPD--SLNAVRPFLFNLFYDRRII	33
sp	P57777	HEMH_CAUCR	-----MTQKLAVVLFNLGGPD--GPDVAVRPFYLNLFYDRPAII	35
sp	O67083	HEMH_AQUAE	-----MKK--GVILINLLGGPD--SLEAVEPFLYNLFSDPDIF	33
sp	P22830	HEMH_HUMAN	HAQGAKPQVQPQRKPKTGILMLNMGGPE--TLGDVHDFLLRFLDQDLM	99
sp	P22315	HEMH_MOUSE	HAKTTKPAQAPERRKPKTGILMLNMGGPE--TLGEVQDFLQRLFLDRDLM	98

sp	P22600	HEMH_BOVIN	RARSPKQAQPGNRKPRGTGILMLNMGGPE--TVEEVQDFLQRLFLDQDLM	92
sp	Q42479	HEMH_CHICK	----TKPQAEPETRKPKTGILMLNMGGPE--RLDDVHDFLLRLFLDRDLM	78
sp	O57478	HEMH_XENLA	KSSDPKPHAQPDKRKPKTGILMLNMGGPE--TLDDVHGFLRLFLDKDLM	86
sp	Q9V9S8	HEMH_ROME	-----LSGQKPKTAI LMLNMGGPT--HTDQVHDYLLRIMTDRDMI	59
sp	O59786	HEMH_SCHPO	-----VSGKGP-TAVVMMNMGGPS--NLDEVGPFLLERLFTDGDII	63
sp	P16622	HEMH_YEAST	-----MQNAQKRSPTGIVLMMNMGGPS--KVEETYDFLYQLFADNDLI	69
sp	Q6APP0	HEMH_DESPS	-----MQNIPTGVILLNMGGPT--QTKDVRPFLLYNLFSREII	36
sp	Q747F5	HEMH_GEOSL	-----MSDK-TAVLLLQMGGPD--SLDAVEPFLNLFSDRDI	35
sp	Q9ZKD4	HEMH_HELPJ	INEKLNLENSATKSPKEAVVLLNMGGPN--SLYEVGVFLKNMFDDPFIL	51
sp	P56107	HEMH_HELPY	INEKLNLENNATKSPKEAVILLNMGGPN--SLYEVGVFLKNMFDDPFIL	51
sp	Q7M7P9	HEMH_WOLSU	-----MKAIVILLNMGGPS--SLLEVDMFLKNMFNDPRIL	33
sp	Q7VHH1	HEMH_HELHP	-----MGSPN--SLFEVESFLKNMFNDPLIL	24
sp	Q9PI08	HEMH_CAMJE	-----MKLVFLNMGGAT--NLQDCEVFLKNMFNDPYIL	32
sp	Q8DFM2	HEMH_VIBVU	-----MNNTKKRGVLLVNLGTPPEATAPAVKRFLSQFLHDQRVV	39
sp	Q7MMR4	HEMH_VIBVY	-----MNNTKKRGVLLVNLGTPPEATAPAVKRFLSQFLHDQRVV	39
sp	Q9KTB6	HEMH_VIBCH	-----MNNHKKLGILLANLGTDPQAPTSQAVKAFLSQFLHDQRVV	39
sp	Q87RH3	HEMH_VIBPA	-----MQTKNKQGVLLVNLGTPDEPTAPAVKRFLSQFLHDHRVV	39
sp	Q6LTE0	HEMH_PHOPR	-----MKNNN-YGVLLVNLGTPDEASPAAIKRFLSEFLSDRRVV	38
sp	Q8EFF4	HEMH1_SHEON	RGIWLIKGSTLTSPSPAFVLLVNLGTPDEPTPKAVKRFLKQFLSDRRVV	54
sp	Q8XD39	HEMH_ECO57	-----MRQTKTGILLANLGTDPAPTPEAVKRYLKQFLSDRRVV	38
sp	P23871	HEMH_ECOLI	-----MRQTKTGILLANLGTDPAPTPEAVKRYLKQFLSDRRVV	38
sp	Q8FK83	HEMH_ECOL6	-----MRQTKTGILLANLGTDPAPTPEAVKRYLKQFLSDRRVV	38
sp	Q83SE5	HEMH_SHIFL	-----MRQTKTGILLANLGTDPAPTPEAVKRYLKQFLSDRRVV	38
sp	Q8Z8T2	HEMH_SALTI	-----MRQTKTGILLANLGTDPAPTPEAVKRYLKQFLSDRRVV	38
sp	P37408	HEMH_SALTY	-----MRQTKTGILLANLGTDPAPTPEAVKRYLKQFLSDRRVV	38
sp	Q8ZC98	HEMH_YERPE	-----MMQSKPGVLMVNLGTPDAPTSKAIKRYLAEFLSDRRVV	38
sp	Q05338	HEMH_YERPS	-----MMQSKPGVLMVNLGTPDAPTSKAIKRYLAEFLSDRRVV	38
sp	P43413	HEMH_YEREN	-----MKQSKLGVLMVNLGTPDAPTPQAVKRYLAEFLSDRRVV	38
sp	Q6D7Z4	HEMH_ERWCT	-----MKQEKYGVLMVNLGTPDAPTPQAVRRYLAEFLSDRRVV	38
sp	Q7N0P6	HEMH_PHOLL	-----MNNGKFGVLLVNLGTPDKPTTAAIRRYLAEFLSDKRVV	38
sp	P43868	HEMH_HAEIN	-----MTKPAKIGVLLANLGTDPDSPTPKSISRYLWQFLTDPRVV	39
sp	P57874	HEMH_PASMU	-----MNK-AKTGVLLVNLGTPESPTPKAISRYLWQFLTDPRVV	38
sp	Q65SV7	HEMH_MANSM	-----MKSSKTGILLANLGTDPDTPSPKAI SRYLKEFLSDPRVV	38
sp	Q8CWW4	HEMH_STRMU	-----MSQQKIGVLLVNLGTPPEHTAPAIRKFLKPFPLADSRVI	38
sp	Q8D226	HEMH_WIGBR	-----MKNNIGI I I SNVGT PSHPNKKS VKKYLSEFLSDKRVV	37
sp	Q8EBZ7	HEMH2_SHEON	-MGHAA-----RGKVGVLLNLGTPDAPTASAVRRYLAEFLSDPRVV	41
sp	Q6F7N0	HEMH_ACIAD	-MPIFP-----KPKVTVILANLGTDPDVTASAVRAFLKQFLSDQRVI	41
sp	Q7WGI0	HEMH_BORBR	PAQDPFDENPPPCGPRGVLLVNLGTPDEPTRGAI RRYLGEFLSDPRVI	68
sp	Q7W515	HEMH_BORPA	PAQDPFDENPPPCGPRGVLLVNLGTPDEPTRGAI RRYLGEFLSDPRVI	68
sp	Q7VVX8	HEMH_BORPE	PAQDPFDENPPPCGPRGVLLVNLGTPDEPTRGAI RRYLGEFLSDPRVI	68
sp	Q62HD1	HEMH_BURMA	PSHASA-----AHRVAVLLVNLGTPDAPT PRAVRRYLAQFLSDPRVV	61
sp	Q63R43	HEMH_BURPS	PSHASA-----AHRVAVLLVNLGTPDAPT PRAVRRYLAQFLSDPRVV	61
sp	Q8XW32	HEMH_RALSO	LFQHGQ-----PDRTA ILLVNLGTPDGTSPREVGRYLRQFLSDPRVV	49
sp	Q7NV65	HEMH_CHRVO	AFRHDY-----APKTGVLLINLGTDPAPTAQALRPYLKQFLSDPRVI	52
sp	Q82UK8	HEMH_NITEU	AYRHGS-----VGKIGVLLINLGTDPAPTAKALRAYLKQFLSEPRIV	50
sp	Q9JVA5	HEMH_NEIMA	SLSYDQ-----QNRTAVLLNLGTPDAPTAQAVRPYLKSFLLTDRRVV	50
sp	Q9K097	HEMH_NEIMB	SLSYDQ-----QNRTAVLLNLGTPDAPTAQAVRPYLKSFLLTDRRVV	50
sp	Q8PEX0	HEMH_XANAC	-MN-----TTPDTALLVNLGTPESPTAPAVRRYLAEFLSDRRVV	39
sp	Q8P3H6	HEMH_XANCP	-MN-----TSDTALLVNLGTPESPTVPAVRRYLAEFLSDRRVV	39
sp	Q9PFU1	HEMH_XYLFA	-MN-----HTSDTALLIVNLGTPPEAPTAAAVRRYLGEFLSDRRVV	39
sp	Q87B82	HEMH_XYLFT	-MN-----HTSDTALLIVNLGTPPEAPTAAAVRRYLGEFLSDRRVV	39
sp	Q607T4	HEMH_METCA	-MHP-----TAARTGVLLINLGTPEAPT PKAVRRYLREFLSDPRVV	40
sp	Q8U9F7	HEMH_AGRT5	ANHPRV-----TFGKVGVLLVNLGTPDGTDYWPMRRYLAEFLSDKRVV	52
sp	Q92M52	HEMH_RHIME	TEHPAV-----GYKLGVLLVNLGTPDGT DVTSMRRYLREFLSDRVV	47
sp	Q93TG2	HEMH_BRUME	PLHTSA-----KLPKVGVLLVNLGTPDGT SYGPMRRYLAEFLSDRVV	60
sp	Q98H61	HEMH_RHILO	AGHAPA-----GAGKVGVLLVNLGTPDGT EFKPMRRYLREFLSDRVV	61
sp	P28602	HEMH_BRAJA	QPTVQS-----GQKRVGVLLVNLGTPDTADAPGVRVYLKEFLSDARVI	53
sp	Q6NBF3	HEMH_RHOPA	AIAPAP-----APERVGVLLVNLGTPDSCDTKGVRIYLREFLSDRVV	53
sp	Q59735	HEMH_RHOCA	ADHPPV-----PVPRVGVLLANLGTDPATDYWSMRRYLNEFLSDRVV	55
sp	P57779	HEMH_ZYMMO	SNNPLP-----ISEKIGVLLVNLGTPDAPNAKALRRYLQFLSVQRVI	46
sp	Q833G5	HEMH_ENTFA	-----MKRTGILLVNLGTPKDSKTEVRKYLKTFLLSDRVV	36
sp	Q9CFB4	HEMH_LACLA	-----MDKKKGI LLVALGT PRSCEADDVRDYLKEFLGDPLVI	37
sp	Q67T48	HEMH_SYMTH	-----MEKTAVLLVNLGTPSAPEPDAVRPYLAEFLGDWVVI	36

sp	Q88XC3	HEMH_LACPL	-----MHPGLLLVNLGSPASPRTKDVKAYLQEFLLSDPSVI	35
sp	P57778	HEMH_PSEFL	-----MTDH-----ALLLVNLGSPASTSVADVRSYLNQFLMDPYVI	36
sp	Q888A2	HEMH_PSESM	-----MTDH-----ALLLVNLGSPASTQVADVRSYLNQFLMDPYVI	36
sp	Q88PV4	HEMH_PSEPK	-----MTDH-----ALLLVNLGSPASTSVADVRRYLNQFLMDPYVI	36
sp	Q9HVD7	HEMH_PSEAE	-----MTEN-----ALLLVNLGSPDSTRVEDVRRYLDQFLMDPYVV	36
sp	Q6MHT3	HEMH_BDEBA	-----MGKK-----GLLLINIGSPKSYQVNDVKKYLSEFLMDEDVI	36
sp	Q83FA4	HEMH_COXBU	-----MAVKNNNKIGVLLINLGTPEPSVPAVRRYLRQFLSDPKVI	41
sp	Q6MAW8	HEMH_PARUW	-----MNQR-----TGILLVNLGTPKTPRPKDVYRYLNEFLTDGRVI	37
sp	Q7MXP4	HEMH_PORGI	---MADRRRTDDNKGAREVVLNIGSPDSPEEKDVARYLNSFLTDRRII	47
sp	Q824K8	HEMH_CHLCV	-----MVS--AYLLANFGGPR--HSNDIEVFLTSLTDRDVT	33
sp	Q9Z7V1	HEMH_CHLPN	-----MTPPAYLLANFGGPR--HAKDLQEFLLISLLTDRDVT	34
sp	Q9PJQ6	HEMH_CHLMU	-----MTV--YLLANFGGPR--ISQEI PPSFLHALLTDQDVT	32
sp	O84492	HEMH_CHLTR	-----MVT--YLLANFGGPR--TSQEI VSFLLQALLTDRDVT	32
sp	Q8GCV0	HEMH_LEPBI	-----MITNKVKTLLVNLGGPR--TPSEIEVFLRDLFSDPFVF	37
sp	Q81U22	HEMH1_BACAN	-----MKKKIGLLVMAYGTPY--KEEDIERYTH-----	27
sp	Q6HM97	HEMH1_BACHK	-----MKKKIGLLVMAYGTPY--KEEDIERYTH-----	27
sp	Q63ES4	HEMH1_BACCZ	-----MKKKIGLLVMAYGTPY--KEEDIERYTH-----	27
sp	Q73C98	HEMH1_BACC1	-----MKKKIGLLVMAYGTPY--KEEDIERYTH-----	27
sp	Q81GW5	HEMH1_BACCR	-----MKKKIGLLVMAYGTPY--KEEDIERYTH-----	27
sp	P32396	HEMH_BACSU	-----MSRKKMGLLVMA YGTPY--KEEDIERYTH-----	28
sp	Q8ERX9	HEMH_OCEIH	-----MEKKKIGLLVMAYGTPY--KEEDIERYTH-----	28
sp	Q71XF4	HEMH_LISMF	-----MTKKVGLLVMA YGTPY--KDEDIERYTH-----	27
sp	Q8Y565	HEMH_LISMO	-----MTKKVGLLVMA YGTPY--KDEDIERYTH-----	27
sp	Q929G2	HEMH_LISIN	-----MTKKVGLLVMA YGTPY--KDEDIERYTH-----	27
sp	P64124	HEMH_STAAM	-----MTKKMGLLVMA YGTPY--KESDIEPYTH-----	27
sp	P64125	HEMH_STAAN	-----MTKKMGLLVMA YGTPY--KESDIEPYTH-----	27
sp	Q6G8A3	HEMH_STAAS	-----MTKKMGLLVMA YGTPY--KESDIEPYTH-----	27
sp	P64126	HEMH_STA AW	-----MTKKMGLLVMA YGTPY--KESDIEPYTH-----	27
sp	Q6GFM4	HEMH_STAAR	-----MTKKMGLLVMA YGTPY--KESDIEPYTH-----	27
sp	Q8CNS1	HEMH_STAEP	-----MTKTIGLLVMA YGTPY--KESDIEPYTH-----	27
sp	Q81TU9	HEMH2_BACAN	-----MKKKIGLLVMA YGTPD--SLDEVEAYTH-----	28
sp	Q6HM28	HEMH2_BACHK	-----MKKKIGLLVMA YGTPD--SLDEVEAYTH-----	28
sp	Q63EK7	HEMH2_BACCZ	-----MKKKIGLLVMA YGTPD--SLEDVEAYTH-----	28
sp	Q73C08	HEMH2_BACC1	-----MAKKKIGLLVMA YGTPD--SLEDVEAYTH-----	28
sp	Q81GN7	HEMH2_BACCR	-----MKKKIGLLVMA YGTPD--SLDDVEAYTH-----	28
sp	Q9KDK9	HEMH_BACHD	-----MTKKKIGLLVMA YGTPR--TKEEIEPYTH-----	28
sp	Q5WHT1	HEMH_BACSK	-----MEKKKIGLLVMA YGTPR--KKEEIEPYTH-----	28
sp	Q72L32	HEMH_THET2	-----MNVLLMAYGTPY--APEEVEPYTH-----	23
sp	Q9RV98	HEMH_DEIRA	-----MTTLTNQKPLGVLFMAYGGPE--NLGEMPGYLAD--	32
sp	Q97R30	HEMH_STRPN	-----MKKAILMMTFGSPEE IIFEGVADFFTN-----	27
sp	Q8DQ04	HEMH_STRR6	-----MKKAILMMTFGSPEE IIFEGVADFFTN-----	27
sp	Q8FTB1	HEMH_COREF	---MNARTPDTKSDSYDALLVLSFGGPE--GPEEVRPFLEN-----	36
sp	Q8NQA1	HEMH_CORGL	---MNERT---SDAFDALLVLSFGGPE--GHEEVRPFLEN-----	32
sp	Q6NH66	HEMH_CORDI	---MLPLPTWTLSD--VDAILVLSFGGPE--GQDVIPFLEN-----	35
sp	Q740Y1	HEMH_MYCPA	-----MDFDAVLLLSFGGPE--GPEQVRPFLEN-----	26
sp	P71765	HEMH_MYCTU	-----MQFDAVLLLSFGGPE--GPEQVRPFLEN-----	26
sp	Q9CBM2	HEMH_MYCLE	-----MLFDAALLLSFGGPD--GPEQVRPFLEN-----	26
sp	Q5YU18	HEMH_NOCFA	-----MAVEALLLSFGGPE--RPEDVMPFLEN-----	26
sp	O07401	HEMH_MYCAV	-----MDFDAVLLLSFGGPE--GPSRFGRSWRTSPG-----	29
sp	Q83H94	HEMH_TROW8	GSAIASDSGFALGASQYDAVLLSFGGPE--GPEDVVPFLKK-----	53
sp	Q83FJ2	HEMH_TROWT	GSAIASDSGFALGASQYDAVLLSFGGPE--GPEDVVPFLKK-----	53
sp	Q6AHF2	HEMH_LEIXX	HVTEP-----VAYDAILLAGFGGPE--GQDDVIPFLRN-----	44
sp	Q82KJ6	HEMH_STRAW	-----PYDALLLSFGGPE--GPDDVVPFLEN-----	33
sp	O50533	HEMH_STRCO	-----PYDALLLSFGGPE--GPDDVVPFLEN-----	33
sp	Q7UFZ7	HEMH_RHOBA	-----PYDSFLLVSFGGPE--GQDDVMPFLEN-----	30
sp	P72183	HEMH_PROFR	-----MTSFDALLVAGFGGPE--SMAEVPDFLQR-----	27
sp	Q9HLB8	HEMH_THEAC	-----MKSALLLSYGSPE--RIEDLDEYLKN-----	25
sp	Q978U9	HEMH_THEVO	-----MKTAVLLLSYGSPE--KMSDIDEYLSK-----	25

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sp	P42043	HEMH1_ARATH	RLPRPFQFLQGTIAKFISVVRAPKSKEGYAAIGGGS-----PLRKITDE	164
sp	P42044	HEMH_CUUSA	RLPRLFRFLQEPKALLISTYRAPKSKEGYASIGGGS-----PLRKITDE	189
sp	P42045	HEMH_HORVU	RLPRLFRFLQRPLAKLISTFRAPKSNEGYASIGGGS-----PLRKITDE	183

sp	O04921	HEMH2_ARATH	RLPPVFQFLQKPLAQFISVARAPKSKEGYASIGGGG-----PLRHITDA	175
sp	O22101	HEMH_ORYSA	RLPRLFRFLQKPLAQFISVVRAPKSKEGYASIGGGG-----PLRQITDA	156
sp	Q8YQR8	HEMH_ANASP	RLP--FRWLQKPLAWFIASRRTKTSQENYKQIGGGG-----PLRRITEA	76
sp	P54225	HEMH_SYNY3	RLP--FPWLQKPLAWLISTLRAKKSQANYAEIGGGG-----PLLQITEA	76
sp	Q8DGU6	HEMH_SYNEL	RLP--FRWLQKPLAWFIISTSRARRSQANYAQIGGGG-----PLRRITEQ	77
sp	Q7VD58	HEMH_PROMA	RLP--LPFQKPLAWFISTLRSSKSQKAYQAIGGGG-----PLRRITEQ	76
sp	Q7V2F5	HEMH_PROMP	RLP--VPAFQKPLAWLISTLRSTTSQQAYLSIGGGG-----PIRRITEQ	76
sp	Q7V6C6	HEMH_PROMM	RLP--NPALQRPLAWLISTLRSSKSEQAYRSIGGGG-----PLRRITEQ	76
sp	Q7U5G0	HEMH_SYNPX	RLP--SPALQKPLAWLISTLRSGKSQEAYRSIGGGG-----PLRRITEQ	76
sp	Q7NMC7	HEMH_GLOVI	RIP--VPPLQKPLAWLISTLRAPKSRKNYQAIGGGG-----PLRAITNQ	76
sp	Q9ZC84	HEMH_RICPR	NLPN---PLRYIIAKIISITREKKSQKIYSLIGGKS-----YLIQETEK	76
sp	Q68VM9	HEMH_RICTY	NLPN---PLRYVIAKIIISIVREKKSQKIYSLIGRKS-----YLIQETEK	76
sp	Q92FV4	HEMH_RICCN	NLPN---PLRYIIAKIISITREKKSQKIYSLIGGKS-----SLLQETEE	76
sp	Q73FY6	HEMH_WOLPM	NLPN---PFRFLLAKFISAKRENTARKIYEEIGGKS-----PILENTKM	74
sp	P57777	HEMH_CAUCR	GAPA---LIRYPLAALISTTREKSAKANYAIMGGGG-----PLLPETEK	76
sp	O67083	HEMH_AQUAE	SLP-----FQKVLAKIIAKLRKAKTRHYELMGGKS-----PQYEQTLE	72
sp	P22830	HEMH_HUMAN	TLP-----IQNKLAPFIAKRRTPKIQEQYRRIGGGG-----PIKIWTSK	138
sp	P22315	HEMH_MOUSE	TLP-----IQNKLAPFIAKRRTPKIQEQYRRIGGGG-----PIKMWTSK	135
sp	P22600	HEMH_BOVIN	TLP-----VQDKLGFPIAKRRTPKIQEQYRRIGGGG-----PIKMWTSK	131
sp	O42479	HEMH_CHICK	TLP-----AQNKLAPFIAKRRTPRIQEQYSRIGGGG-----PIKKWTAV	117
sp	O57478	HEMH_XENLA	TLP-----AQSKLAPFIAKRRTPKIQEQYSKIGGGG-----PIKKWTEQ	125
sp	Q9V9S8	HEMH_DROME	QLP-----VQSRLGPWIAQRRTPEVQKQYKEIGGGG-----PILKWTEL	98
sp	O59786	HEMH_SCHPO	PLGY----FQNSLGKFIKRRTPKVQNHYSIDIGGGG-----PILHWTRI	103
sp	P16622	HEMH_YEAST	PISA---KYQKTIAKYIAKFRTPKIEKQYREIGGGG-----PIRKWSEY	110
sp	Q6APB0	HEMH_DESPS	PLGP--RLMQLPLAWLIAKRRAPKSAATYERIGGGG-----PLKQITEA	78
sp	Q747F5	HEMH_GEOSL	RIGP--AFLQPFIIARLIAKRSPGVERKYEEIGGKS-----PIRELTES	77
sp	Q9ZKD4	HEMH_HELPJ	TIKN--NFMRMVGMKMIVNSRIEKSKKIYEKLGGS-----PLTPITFA	93
sp	P56107	HEMH_HELPY	TIKN--NFMRMVGMKMIVNSRIEKSKKIYEKLGGS-----PLTPITFA	93
sp	Q7M7P9	HEMH_WOLSU	PIKS--PFRSLVASFIANRRSETAKANYRKIGGGG-----PLIGHTFN	75
sp	Q7VHH1	HEMH_HELHP	GIKN--TFARKMLASFIHRSVEETKKNYQAIGGGG-----PLTAHTLN	66
sp	Q9PI08	HEMH_CAMJE	GIKN--RFLRKFVAWIIITKARVKAMQENYKMGGS-----PLNELTQS	74
sp	Q8DFM2	HEMH_VIBVU	D--MTRWLWCPILHGIILPIRSPKVAKLYQTVWMKE----GSPLMVYSKR	83
sp	Q7MMR4	HEMH_VIBVY	D--MTRWLWCPILHGIILPIRSPKVAKLYQTVWMKE----GSPLMVYSKR	83
sp	Q9KT6	HEMH_VIBCH	D--MSRWLWCPILLHGIILPTRSPKVAKLYQSIWMDE----GSPLMVYSRR	83
sp	Q87RH3	HEMH_VIBPA	D--MTRWLWCPILHGVILPIRSPKVAKLYESVWMEE----GSPLMVYSKR	83
sp	Q6LTE0	HEMH_PHOPR	D--MTRWLWCPILHGVILPIRSPKVAKLYQSVWMED----GSPLMVYSQR	82
sp	Q8EFF4	HEMH1_SHEON	D--LSPWLWQPILOGIILNTRPKKVAKLYQSVWTEQ----GSPLMVISQC	98
sp	Q8XD39	HEMH_ECO57	D--TSRLLWWPLLRGVILPLRSRPAKLYASVWMMEG----GSPLMVYSRQ	82
sp	P23871	HEMH_ECOLI	D--TSRLLWWPLLRGVILPLRSRPAKLYASVWMMEG----GSPLMVYSRQ	82
sp	Q8FK83	HEMH_ECOL6	D--TSRLLWWPLLRGVILPLRSRPAKLYASVWMMEG----GSPLMVYSRQ	82
sp	Q83SE5	HEMH_SHIFL	D--TSRLLWWPLLRGVILPLRSRPAKLYASVWMED----GSPLMVYSRQ	82
sp	Q8Z8T2	HEMH_SALTI	D--TPRLLWWPLLRGVILPLRSRPAKLYQSIWMDG----GSPLMVYSRE	82
sp	P37408	HEMH_SALTY	D--TPRLLWWPLLRGVILPLRSRPAKLYQSIWMDG----GSPLMVYSRE	82
sp	Q8ZC98	HEMH_YERPE	D--TSPLLWWPLLHGVILPLRSRPAKLYQSVWMEE----GSPLLVSRR	82
sp	Q05338	HEMH_YERPS	D--TSPLLWWPLLHGVILPLRSRPAKLYQSVWMEE----GSPLLVSRR	82
sp	P43413	HEMH_YEREN	D--TSPWLWWPLLRGVILPIRSPRPAKLYQSVWMDE----GSPLLVSRR	82
sp	Q6D7Z4	HEMH_ERWCT	D--TPRLLWWPLLRGVILPIRSPRPAKLYQSVWMEG----GSPLLVSRR	82
sp	Q7N0P6	HEMH_PHOLL	D--LSRFLWKPILYGFVLPFRSSRPAKLYQKIWTDE----GSPLLVSRR	82
sp	P43868	HEMH_HAEIN	D--LPRCKWYPLLKAIILPLRSKRIAKNYQAIWTEQ----GSPLLAISRQ	83
sp	P57874	HEMH_PASMU	D--LPRYKWFPLLKGIILPLRAKRVAKNYASIWTEQ----GSPLLTITRE	82
sp	Q65SV7	HEMH_MANSM	D--LPRWKWLPLNGIILPIRSRRIAKNYGAIWTEQ----GSPLFAITQK	82
sp	Q8CWW4	HEMH_STRMU	D--YPKFLWKPILYGFVLPFRPRKVKPLYQHVWTNE----GSPLYANAIG	82
sp	Q8D226	HEMH_WIGBR	D--ISRFFWIPYLHLHYFLPLKSYKSVNLYKKIWEKD----GSPLMINSLN	81
sp	Q8EBZ7	HEMH2_SHEON	E--IPKLLWMLILYGVILRVPAKSAALYQKVWTEAG----SPLMDISLR	85
sp	Q6F7N0	HEMH_ACIAAD	E--IPKLLWMLILYGFVLPFRPKRVAHAYASVWGQD----SPMREILFA	84
sp	Q7WGI0	HEMH_BORBR	E--IPRYLWMPILHGLVLAAMRPKLLAPRYAGIWMEE----GSPLLVSQR	112
sp	Q7W515	HEMH_BORPA	E--IPRYLWMPILHGLVLAAMRPKLLAPRYAGIWMEE----GSPLLVSQR	112
sp	Q7VXX8	HEMH_BORPE	E--IPRYLWMPILHGLVLAAMRPKLLAPRYAGIWMEE----GSPLLVSQR	112
sp	Q62HD1	HEMH_BURMA	E--IPQLVWQVILCTLILPLRGRASAKKYAAVWLPE----GSPLRVYTER	105
sp	Q63R43	HEMH_BURPS	E--IPQLVWQVILRTLILPLRGRASAKKYAAVWLPE----GSPLRVYTER	105
sp	Q8XW32	HEMH_RALSO	E--IPRAAWWFILNVLILPLRSRASAKKYETVWLREANMTGSPLLVSER	97
sp	Q7NV65	HEMH_CHRVO	E--IPRLPWWLILNGIILNTRPKQSAKKYASIWTEQ----GSPLLLHTRS	96
sp	Q82UK8	HEMH_NITEU	E--FPRWLWWFILNGIILNVRPAKSAKKYEQIWTSE----GSPLRVHTAR	94

sp	Q9JVA5	HEMH_NEIMA	E--LPKWLWYPILHGLVLTLPKKS AHAYEKIWFKE ----GSPLEVYTAR	94
sp	Q9K097	HEMH_NEIMB	E--LPKWLWYPILHGLVLTLPKKS AHAYEKIWFKE ----GSPLEVYTAR	94
sp	Q8PEX0	HEMH_XANAC	A--IPPLFWKPLLYGVILPIRGPKSAEKYAKVWLPE ----GSPLAVYTRR	83
sp	Q8P3H6	HEMH_XANCP	A--IPPLFWKPLLYGVILPIRGPKSAEKYAKVWLPE ----GSPLAVYTRR	83
sp	Q9PFU1	HEMH_XYLFA	S--IPPLFWKPLLHMVILPIRGPRSASKYAKVWLQE ----GSPLSVYTRR	83
sp	Q87B82	HEMH_XYLFT	S--IPPLFWKPLLHMVILPIRGPRSASKYAKVWLQE ----GSPLSVYTRR	83
sp	Q607T4	HEMH_METCA	E--IPRVLWVWPILNLVVLTRSRKSAHAYRTIWTER ----GSPLLAYTQD	84
sp	Q8U9F7	HEMH_AGRT5	E--WSRLYWYPILYGIVLNKRPQKVGKAYEEIWNHERN --ESYLRTYTRS	98
sp	Q92M52	HEMH_RHIME	E--WSRLFWYPILYGIVLNTRPRKVGKAYELIWNKDLN --ESWLRTYTRN	93
sp	Q93TG2	HEMH_BRUME	E--WSRLIWYPILYGIVLNTRPRRSGRLYDRIWNHENN --ESPLRTYTRA	106
sp	Q98H61	HEMH_RHILO	E--LNKAIWYPILYGLVILTRPKKSGANYARIWNQERN --ESPLRTYTRA	107
sp	P28602	HEMH_BRAJA	E--DQGLVWVVLNGIILRSRPTKALDYQKIWNNEKN --ESPLKTI TRS	99
sp	Q6NBF3	HEMH_RHOPA	E--NQGLFWKLALNGIILNTRPARKAKDYQKIWNHEKN --ESPLKTI TRS	99
sp	Q59735	HEMH_RHOCA	D--YPIWKWQPLLQLIILSKRPFTSGNNYRSIWNEERD --ESPLMTITRD	101
sp	P57779	HEMH_ZYMMO	E--LPAVFWQIILRGIILPFRAPRSARAYQKIWTNE ----GSPLAATTK	90
sp	Q833G5	HEMH_ENTFA	K--IHPIIWKPIILNGIILNIRPKKSAKLYQKICTEN ----GFPLLEYTEK	80
sp	Q9CFB4	HEMH_LACLA	Q--KPRWLWLPILNGIILKVRPQKSAEMYKKIWTDE ----GSPLMIYTV	81
sp	Q67T48	HEMH_SYMTH	D--KPRWQWPLILHGIILRPPRVAKIYQKIWLPE ----GSPLHYTRR	80
sp	Q88XC3	HEMH_LACPL	E--MPAALWQPLL RGIILPTRSWRSATFYQDSWLPQ ----GSPLIVYSA	79
sp	P57778	HEMH_PSEFL	D--LPWPVRRLLVSLILIKRPA-QSAHAYASIWWE ----GSPLVLSRR	79
sp	Q888A2	HEMH_PSESM	D--IPWPLRLLVSLILIKRPE-QSAHAYASIWWE ----GSPLVLSKR	79
sp	Q88PV4	HEMH_PSEPK	D--LPWPVRRLLVSLVILIKRPE-QSAHAYASIWWE ----GSPLVLTTR	79
sp	Q9HVD7	HEMH_PSEAE	D--LPWPLRLLVSLILIKRPA-ESAHAYSSIWWE ----GSPLIVLSRR	79
sp	Q6MHT3	HEMH_BDEBA	T--LPYVLRWPLVNLIVPRRAFSAENYKVVWME ----GSPiAVYTRR	80
sp	Q83FA4	HEMH_COXBU	D--VPSLVRWIIVHLCILPFRPKRSKLYQKIWMPE ----GSPLLVYSEM	85
sp	Q6MAW8	HEMH_PARUW	D--LPWLKRQLLVRCIIVPFYKQSSMLYQKLWTAE ----GSPLLVHGIA	81
sp	Q7MXP4	HEMH_PORGI	T--LPFLLRQLLV RGIITPFRRKSSAQKYRTVWDES ----TRSFPLISHT	91
sp	Q824K8	HEMH_CHLCV	GGFLPSFIHKRLFS-FIAKKRALKVLQPQYNCI --GG----FSPiYQDTEL	76
sp	Q927V1	HEMH_CHLPN	GTFLPRVLRHRLFT-FIAKKRVPKVLPQYQSL --QN----WSPiYFDTET	77
sp	Q9PJQ6	HEMH_CHLMU	GGRIPPWLHRPLFS-YIAKRRHRVAEQYAYL --GG----RSPiFQDTEK	75
sp	Q84492	HEMH_CHLTR	GGMIPSM LHRPLFS-YIAKRRAPHVARQYAYL --GG----GSPiFDTER	75
sp	Q8GCV0	HEMH_LEPBI	DLPLPEFLRLRLAR-FIAKKRAPKVQKSYESMGFGG ----GSPiVEETAK	82
sp	Q81U22	HEMH1_BACAN	-----IRRGRKPSEEMLEDLTERYRAIGGIS -----PLATITTE	61
sp	Q6HM97	HEMH1_BACHK	-----IRRGRKPSEEMLEDLTERYRAIGGIS -----PLATITTE	61
sp	Q63ES4	HEMH1_BACCZ	-----IRRGRKPSEEMLEDLTERYRAIGGIS -----PLATITTE	61
sp	Q73C98	HEMH1_BACC1	-----IRRGRKPSEEMLEDLTERYRAIGGIS -----PLATITTE	61
sp	Q81GW5	HEMH1_BACCR	-----IRRGRKPSEEMLEDLTERYRAIGGIS -----PLATITTE	61
sp	P32396	HEMH_BACSU	-----IRHGRKPEPEMLQDLKDRYEAIGGIS -----PLAQITEQ	62
sp	Q8ERX9	HEMH_OCEIH	-----IRHGRKPDPEALQDLKERYEAIGGIS -----PLAKITTE	62
sp	Q71XF4	HEMH_LISMF	-----IRHGKHPSEEMIADLRGRYHAIGGLS -----PLAKITEA	61
sp	Q8Y565	HEMH_LISMO	-----IRHGKHPSEEMIADLRGRYHAIGGLS -----PLAKITEA	61
sp	Q929G2	HEMH_LISIN	-----IRHGKHPSEEMIADLRGRYHAIGGLS -----PLAKITEA	61
sp	P64124	HEMH_STAAM	-----IRHGKRPSEELQDLKDRYEFIGGLS -----PLAGTTDD	61
sp	P64125	HEMH_STAAN	-----IRHGKRPSEELQDLKDRYEFIGGLS -----PLAGTTDD	61
sp	Q6G8A3	HEMH_STAAS	-----IRHGKRPSEELQDLKDRYEFIGGLS -----PLAGTTDD	61
sp	P64126	HEMH_STAAN	-----IRHGKRPSEELQDLKDRYEFIGGLS -----PLAGTTDD	61
sp	Q6GFM4	HEMH_STAAR	-----IRHGKRPSEELQDLKDRYEFIGGLS -----PLAGTTDD	61
sp	Q8CNS1	HEMH_STAEP	-----IRRGGKPTSEELQDLKDRYEFIGGLS -----PLAGTTDR	61
sp	Q81TU9	HEMH2_BACAN	-----IRHGRKPSEELQDLIGRYKAIGGIS -----PLAKITKE	62
sp	Q6HM28	HEMH2_BACHK	-----IRHGRKPSEELQDLIGRYKAIGGIS -----PLAKITKE	62
sp	Q63EK7	HEMH2_BACCZ	-----IRHGRKPSEELQDLIGRYKAIGGIS -----PLAKITKE	62
sp	Q73C08	HEMH2_BACC1	-----IRHGRKPSEELQDLIGRYKAIGGIS -----PLAKITKE	62
sp	Q81GN7	HEMH2_BACCR	-----IRHGRKPSEELQDLIGRYKAIGGIS -----PLAKITKE	62
sp	Q9KDK9	HEMH_BACHD	-----IRHGRKPSQELLDLTERYEAIGGVS -----PLAKITDD	62
sp	Q5WHT1	HEMH_BACSK	-----IRHGRKPSEELADLQERYEAIGGTS -----PLARITDE	62
sp	Q72L32	HEMH_THET2	-----IRRGRRPSEELKELAERYEAIG-KS -----PLNEITLA	56
sp	Q9RV98	HEMH_DEIRA	-----IRAGRVTSQAILDEITNNYRLIGGKS -----PLPEFTRA	66
sp	Q97R30	HEMH_STRPN	-----IRRGVRPQDHEIQTLYDNYVRIG-GT -----PLQKITRQ	60
sp	Q8DQ04	HEMH_STRR6	-----IRRGVRPQDHEIQTLYDNYVRIG-GT -----PLQKITRQ	60
sp	Q8FTB1	HEMH_COREF	-----VTRGRGIPPERLDEVGAHYHFFGGVS -----PLNRLNKE	70
sp	Q8NQA1	HEMH_CORGL	-----VTHGRGIPPERLDEVAVHYHFFGGIS -----PINALNRE	66
sp	Q6NH66	HEMH_CORDI	-----VTRGRGIPPERLEEVAVHYRHFFGGIS -----PLNALNRE	69
sp	Q740Y1	HEMH_MYCPA	-----VTRGRGVPPERLDHVAEHYLHFFGGVS -----PINGINRA	60

sp	P71765	HEMH_MYCTU	-----VTRGRGVPAERLDAVAEHYLHFGGVS-----	PINGINRT	60
sp	Q9CBM2	HEMH_MYCLE	-----VTRGCNVPPERLDEVTKHYLHFGGVS-----	PINGINLA	60
sp	Q5YU18	HEMH_NOCA	-----VTRGRGVPRARLEEVAQHYLHFGGVS-----	PINALNRD	60
sp	O07401	HEMH_MYCAV	-----AAACRGTSRPRRRTLPAFRRGVADQR-----	HQPRADRA	63
sp	Q83H94	HEMH_TROW8	-----VTSGRGVPPERLYEVAEHYNHFGSGIS-----	PINDCNRR	87
sp	Q83FJ2	HEMH_TROWT	-----VTSGRGVPPERLYEVAEHYNHFGSGIS-----	PINDCNRR	87
sp	Q6AHF2	HEMH_LEIXX	-----VTRGRGILDERLEEVAQHYRHFGGVS-----	PINDQNRA	78
sp	Q82KJ6	HEMH_STRAW	-----VTRGRGIPRERLKEVQHYFLFGGIS-----	PINDQNRA	67
sp	O50533	HEMH_STRCO	-----VTRGRGIPKERLKEVQHYFLFGGVS-----	PINDQNRA	67
sp	Q7UFZ7	HEMH_RHOBA	-----VLRGKNVPRERMLEVAEHYKHFGGVS-----	PINEQNRQ	64
sp	P72183	HEMH_PROFR	-----VSGG-HIPDRLAEVEHHYARFGGVS-----	PSNAQHRA	60
sp	Q9HLB8	HEMH_THEAC	-----IFNGKPVPEVREENLRKYEMFGGRS-----	PSNRIIES	59
sp	Q978U9	HEMH_THEVO	-----IFGGKPVPKGVAAEENYRKYEMFGGLS-----	PSNRIIQS	59

sp	P42043	HEMH1_ARATH	QADAIKMSLQA-----	KNIAANVYVGMRYWYPFTEEA	197
sp	P42044	HEMH_CUCSA	QAQALKMALAE-----	KNMSTNVYVGMRYWYPFTEEA	222
sp	P42045	HEMH_HORVU	QANALKVALKS-----	KNLEADIYVGMRYWYPFTEEA	216
sp	O04921	HEMH2_ARATH	QAEELRKCLWE-----	KNVPAKVYVGMRYWHPFTEEA	208
sp	O22101	HEMH_ORYSA	QAEALRKALCD-----	KDIPAKVYVGMRYWHPFTEEA	189
sp	Q8YQR8	HEMH_ANASP	QGEALKEQLHY-----	LGQEQANIYVGMRYWHPYTEEA	109
sp	P54225	HEMH_SYNY3	QASALTTTLER-----	LGQDAKVYIGMRYWHPFTEEA	109
sp	Q8DGU6	HEMH_SYNEL	QARALKDALEG-----	IGIEANLYIGMRYWHPFTEEA	110
sp	Q7VD58	HEMH_PROMA	QARELQSALRN-----	RGINATSYVAMRYWHPFTEEA	109
sp	Q7V2F5	HEMH_PROMP	QARELQSKLRD-----	KGLNVTTYIAMRYWHPFTEEA	109
sp	Q7V6C6	HEMH_PROMM	QARELQSLLRQ-----	RGIDATSYVAMRYWHPFTEEA	109
sp	Q7U5G0	HEMH_SYNPX	QARELQSLLRQ-----	RLDATTYVAMRYWHPFTEEA	109
sp	Q7NMC7	HEMH_GLOVI	QGRVLKALAA-----	RLDIEVYVGMRYWHPFTEEA	109
sp	Q9ZC84	HEMH_RICPR	QKLAITKELKEFI-----	K-EDFIIFINMRYSTPFAKEVI	110
sp	Q68VM9	HEMH_RICTY	QKLAITKKLKEIL-----	K-EDFIIFISMRYSTPFAKEVI	110
sp	Q92FV4	HEMH_RICCN	QKLALTEKLKQLI-----	K-EDFAIFINMRYSAFFAKEVI	110
sp	Q73FY6	HEMH_WOLPM	QANASELKNENR-----	N-HVHKVFIAMRYWHPFADEVI	108
sp	P57777	HEMH_CAUCR	QARALEAALALAM-----	PGVEAKCFIAMRYWHPPLTDETA	111
sp	O67083	HEMH_AQUAE	QAKALQERLG-----	EDYKVVVGMRYWKPYIKDAL	102
sp	P22830	HEMH_HUMAN	QGEGMVKLLDELSP-----	NTAPHKYYIGFRYVHPLTEEA	174
sp	P22315	HEMH_MOUSE	QGEGMVKLLDELSP-----	ATAPHKYYIGFRYVHPLTEEA	171
sp	P22600	HEMH_BOVIN	QGEGMVKLLDELSP-----	HTAPHKYYIGFRYVHPLTEEA	167
sp	O42479	HEMH_CHICK	QGEGMVKLLDSMSP-----	QTAPHKYYIGFRYVHPLTEEA	153
sp	O57478	HEMH_XENLA	QGEGMVKLLDELSP-----	ATAPHKYYIGFRYVHPLTEEA	161
sp	Q9V9S8	HEMH_DROME	QGQLMCEQLDRISP-----	ETAPHKHYVGFYVHPLTENTL	134
sp	O59786	HEMH_SCHPO	QGSEMCKILDKKCP-----	ESAPHLPFVAFRYAPPLTEDML	139
sp	P16622	HEMH_YEAST	QATEVCKILDKTCP-----	ETAPHKPYVAFRYAKPLTAETY	146
sp	Q6APB0	HEMH_DESPS	QAEALEKSLQAHG-----	NFTVTYAMRYWPPYCYDEAL	110
sp	Q747F5	HEMH_GEOSL	QARALEVDLGDG-----	YRCFVAMRYWKPSTMEAL	107
sp	Q9ZKD4	HEMH_HELPH	LTERLNELDPS-----	RFYTYAMRYTPPYASML	122
sp	P56107	HEMH_HELPY	LTERLNELDPS-----	RFYTYAMRYTPPYASML	122
sp	Q7M7P9	HEMH_WOLSU	LIQKLQSLDPS-----	RFYTYAMRYTPPMTDMAV	104
sp	Q7VHH1	HEMH_HELPH	LTNKLNELDCK-----	RFYTYAMRYTPPFAYQVL	95
sp	Q9PI08	HEMH_CAMJE	LCDKLNKQDE-----	FKFDFVNLVPPFATEIL	103
sp	Q8DFM2	HEMH_VIBVU	QQVELQAKL-----	NCPVEIGMTYGTSPVLDGV	111
sp	Q7MMR4	HEMH_VIBVY	QQVELQAKL-----	NCPVEIGMTYGTSPVLDGV	111
sp	Q9KTB6	HEMH_VIBCH	QRDKLAELS-----	QRPVELGMTYGEPSLLEGV	111
sp	Q87RH3	HEMH_VIBPA	QAKKLAQHL-----	DMPVELGMTYGNPSLQSGF	111
sp	Q6LTE0	HEMH_PHOPR	QRQALEKQL-----	NVPVALGMTYGTSPSIATGL	110
sp	Q8EFF4	HEMH1_SHEON	QAQKLATDLSATF-----	NQTIPVELGMSYGNPSIESGF	132
sp	Q8XD39	HEMH_ECO57	QQQALAQLRP-----	ETPVALGMSYGNPSLES	111
sp	P23871	HEMH_ECOLI	QQQALAQLRP-----	EMPVALGMSYGNPSLES	111
sp	Q8FK83	HEMH_ECOL6	QQQALAQLRP-----	ETPVALGMSYGNPSLES	111
sp	Q83SE5	HEMH_SHIFL	QQQALAQLRP-----	DTPVALGMSYGNPSLES	111
sp	Q8Z8T2	HEMH_SALTI	QQQALAARLP-----	DTPVALGMSYGNPSLES	111
sp	P37408	HEMH_SALTY	QQQALAARLP-----	DTPVALGMSYGNPSLES	111
sp	Q8ZC98	HEMH_YERPE	QQKALAARMP-----	DIPVELGMSYGNPSLEAI	111
sp	Q05338	HEMH_YERPS	QQKALAARMP-----	DIPVELGMSYGNPSLEAI	111

sp	P43413	HEMH_YEREN	QQKALAERMP-----EIPVELGMSYSGSPNLPDAI	111
sp	Q6D7Z4	HEMH_ERWCT	QHQALAAAMP-----DTPVELGMSYSGSPSLRSAL	111
sp	Q7N0P6	HEMH_PHOLL	QQKLLAERLA-----GIPVELGMNYGSPSLEQAI	111
sp	P43868	HEMH_HAEIN	QKDALQAYLDNQ-----NIDTQVEIAMTYGNPSMQSAV	116
sp	P57874	HEMH_PASMU	QQHALQTYFKQQ-----EKNIVVEVAMTYGEPKSIKSAI	115
sp	Q65SV7	HEMH_MANSM	QKALLTEFFQQR-----QQNVIIEIGMTYGNPSMQYAI	115
sp	Q8CWW4	HEMH_STRMU	QEKALQAHFDQS-----EHGVLVRATMAYSKPSISDVV	115
sp	Q8D226	HEMH_WIGBR	QRNYLINKFP-----NFKIELGMRYGDPSICVAI	110
sp	Q8EBZ7	HEMH2_SHEON	QTAKLSDKLTADG-----HQVSVHLA--MRYGNPSVASTL	118
sp	Q6F7N0	HEMH_ACIAD	QTDALKRQLISHY-----PQLDLNIVPAMTYGNPVGQHL	119
sp	Q7WGI0	HEMH_BORBR	QAAGVRQGLAARG-----VHAEVELAMRYGKPSIPAAI	145
sp	Q7W515	HEMH_BORPA	QAAGVRQGLAARG-----VHAEVELAMRYGKPSIPAAI	145
sp	Q7VVX8	HEMH_BORPE	QAAGVRQGLAARG-----VHAEVELAMRYGKPSIPAAI	145
sp	Q62HD1	HEMH_BURMA	QVESVKPLFAANG-----YRVIVDYAMRYGTPSIADVL	138
sp	Q63R43	HEMH_BURPS	QVESVKPLFAANG-----YRVIVDYAMRYGTPSIADVL	138
sp	Q8XW32	HEMH_RALSO	QAHALQQQLLDAQG-----HDVVVACAMRYGNPSIP SVM	130
sp	Q7NV65	HEMH_CHRVO	QAKLLKGQLGEMG-----L-HNLAVDYAMRYGNPSIESVI	130
sp	Q82UK8	HEMH_NITEU	QTALVAALLEQQA-----D-SSLVVEYAMIIGNPSIAEKL	128
sp	Q9JVA5	HEMH_NEIMA	QAAALAKRMP-----DLIVRHAMTYGNPSVADVL	123
sp	Q9K097	HEMH_NEIMB	QAAALAKRMP-----DLIVRHAMTYGNPSVADVL	123
sp	Q8PEX0	HEMH_XANAC	LAGGLQAVMP-----DWHVEWAMRYGEPALRRTL	112
sp	Q8P3H6	HEMH_XANCP	LTEGLQQVMP-----DWHVTWAMRYGAPALRRL	112
sp	Q9PFU1	HEMH_XYLFA	IAEGLTQHLP-----DWRVAVAMRYGAPALTKAL	112
sp	Q87B82	HEMH_XYLFT	IAEGLTQHLP-----DWRVAVAMRYGAPALTKAL	112
sp	Q607T4	HEMH_METCA	LRDRLAADGR-----FAAVEIAMRYGNPSVRLKL	113
sp	Q8U9F7	HEMH_AGR5	QGELMAAALKDFP-----NVVVDWAMRYGQPSIASRI	130
sp	Q92M52	HEMH_RHIME	QAALMAEAFGGQP-----QVVVDWAMRYGQPSIASRI	125
sp	Q93TG2	HEMH_BRUME	QGEKLAKALSDQP-----NVVVDWAMRYGQPSIESIT	138
sp	Q98H61	HEMH_RHILO	QSEKLAELGDLDP-----DVTVDWAMRYGNPSTASVA	139
sp	P28602	HEMH_BRAJA	QSDKLAALSDRD-----HVVVDWAMRYGNPSIKSGI	131
sp	Q6NBF3	HEMH_RHOPA	QAEKLSASLGDRG-----HLIVDWAMRYGNPSLRDRI	131
sp	Q59735	HEMH_RHOCA	QVRKLRAAVETRY-----GAGNVVDFCMRYGNPSTRDVL	136
sp	P57779	HEMH_ZYMMO	QAQGLQKRMP-----NITVDYAMRYGTPSISSRL	119
sp	Q833G5	HEMH_ENTFA	QMENLKN--ICP-----EVEVTIGMSYSEPSIETAL	109
sp	Q9CFB4	HEMH_LACLA	QAKQLQD--MRE-----DFDVRFAMTYGEPRIDKVI	110
sp	Q67T48	HEMH_SYMTH	QQAALQQRLEPE-----GIRVALGMTYGQPSVKSAI	111
sp	Q88XC3	HEMH_LACPL	ICQQVQAALP-----DWNVRLAMTYGQPDIGATL	108
sp	P57778	HEMH_PSEFL	LQQQMTAQWTQG-----PVELAMRYGEPSESIVL	108
sp	Q888A2	HEMH_PSESM	LQQAMKKEWSHG-----PVELAMRYGEPSEIVL	108
sp	Q88PV4	HEMH_PSEPK	LQAAMAEHWPHG-----PVEIAMRYGQPALPDVL	108
sp	Q9HVD7	HEMH_PSEAE	LQEAMKPHWPHG-----PVELAMRYGQPAIEKVL	108
sp	Q6MHT3	HEMH_BDEBA	FAALLQEELKDQF-----VVKVGLQYSEPSVESAL	110
sp	Q83FA4	HEMH_COXBU	LRERVGETLGDDF-----CVALGMRYGKPSIETAL	115
sp	Q6MAW8	HEMH_PARUW	VQTKLQMILGESF-----QVELAMRYGNPSIEEGL	111
sp	Q7MXP4	HEMH_PORGI	KAIARALAHTR-----EVHVAMRYGKPAVADVL	120
sp	Q824K8	HEMH_CHLCV	LAETLSSHLDAP-----VITFHRYLPDTHPHTIQQI	107
sp	Q9Z7V1	HEMH_CHLPN	LAKTLSEILRAP-----VIPFHRYLPSTHEKTLAL	108
sp	Q9PJQ6	HEMH_CHLMU	LAQNLSQELQAP-----VISFHRYLTETHQDTLAL	106
sp	Q84492	HEMH_CHLTR	LAQNLSQELQAS-----VIPFHRYLPETHRETLQAL	106
sp	Q8GCV0	HEMH_LEPBI	QAHALELALNERS-----SEQWNVKAMACGYPNMRDIE	116
sp	Q81U22	HEMH1_BACAN	QAKKLEKRLNEVD-----EVEYHMYLGLKHIEPFIEDAV	96
sp	Q6HM97	HEMH1_BACHK	QAKKLEKRLNEVD-----EVEYHMYLGLKHIEPFIEDAV	96
sp	Q63ES4	HEMH1_BACCZ	QAKKLEKRLNEVD-----EVEYHMYLGLKHIEPFIEDAV	96
sp	Q73C98	HEMH1_BACC1	QAKKLEKRLNEVD-----EVEYHMYLGLKHIEPFIEDAV	96
sp	Q81GW5	HEMH1_BACCR	QAKKLEKRLNEVD-----EVEYHMYLGLKHIEPFIEDAV	96
sp	P32396	HEMH_BACSU	QAHNLEQHLNEIQD-----EITFKAYIGLKHIEPFIEDAV	97
sp	Q8ERX9	HEMH_OCEIH	QTKALEKKLANQD-----QYEFKAYIGLKHIEPFIEDT	97
sp	Q71XF4	HEMH_LISMF	QAYGLEKALNSQD-----EVEFKAYIGLKHIEPFIEDAV	96
sp	Q8Y565	HEMH_LISMO	QAYGLEKALNSQD-----EVEFKAYIGLKHIEPFIEDAV	96
sp	Q929G2	HEMH_LISIN	QAYGLEKALNSQD-----EVEFKAYIGLKHIEPFIEDAV	96
sp	P64124	HEMH_STAAM	QADALVSALNKAYA-----DVEFKLYLGLKHISPFIEDAV	96
sp	P64125	HEMH_STAAN	QADALVSALNKAYA-----DVEFKLYLGLKHISPFIEDAV	96
sp	Q6G8A3	HEMH_STAAS	QADALVSALNKAYA-----DVEFKLYLGLKHISPFIEDAV	96

sp	P64126	HEMH_STA AW	QADALVSALNKAYA-----DVEFKLYLGLKHISPFIEDAV	96
sp	Q6GFM4	HEMH_STAAR	QADALVSALNKAYA-----DVEFKLYLGLKHISPFIEDAV	96
sp	Q8CNS1	HEMH_STAEP	QAEALLEALNKEQD-----DVNFKLYIGLKHISPYIEEAV	96
sp	Q81TU9	HEMH2_BACAN	QAHKLTDSMNNMFT-----EYEFNCYLGLKHTAPFIEDAV	97
sp	Q6HM28	HEMH2_BACHK	QAHKLTDSMNNMFT-----EYEFNCYLGLKHTAPFIEDAV	97
sp	Q63EK7	HEMH2_BACCZ	QAHKLTDSMNNMFT-----EYEFNCYLGLKHTAPFIEDAV	97
sp	Q73C08	HEMH2_BACC1	QAHKLTDSMNNIFT-----EYEFNCYLGLKHIAPFIEDAV	97
sp	Q81GN7	HEMH2_BACCR	QAHKLTDSMNNIFT-----EYEFTCYLGLKHTAPFIEDAV	97
sp	Q9KDK9	HEMH_BACHD	QAIALEQKLNELYD-----DIEFKSYLGLKHIDPFIEDAV	97
sp	Q5WHT1	HEMH_BACSK	QANGLAAVLNEQQE-----DIVFVPLYLGLKHIDPFIEDAV	97
sp	Q72L32	HEMH_THET2	QAVRLQALLNLEAPPYKRLGLGPFPPRAPHGPARVYVGTKHWHPISIGEAV	106
sp	Q9RV98	HEMH_DEIRA	QVEATMEQLASTGR-----PLKAYIGMRNHWSPWIEDAV	99
sp	Q97R30	HEMH_STRPN	EVALVEARLGSEYS-----VYFANKFSSPFIPDVI	90
sp	Q8DQ04	HEMH_STRR6	EVTTLVEARLGNEYS-----VYFANKFSSPFIPDVI	90
sp	Q8FTB1	HEMH_COREF	IIANVKAEALARGY-----DIPVYFGNRNWKPFIDNEAA	103
sp	Q8NQA1	HEMH_CORGL	IIANVEKELASRDH-----KLPVYFGNRNWKPFIDNEAA	99
sp	Q6NH66	HEMH_CORDI	IIGNIEVLSSRGL-----EIPVYFGNRNWHPFVNDTA	102
sp	Q740Y1	HEMH_MYCPA	LIEQLR-----AAQ-----DLPVYFGNRNWEPYVEDTV	88
sp	P71765	HEMH_MYCTU	LIAELE-----AQQ-----ELPVYFGNRNWEPYVEDTV	88
sp	Q9CBM2	HEMH_MYCLE	LVNELQ-----VEL-----DLPVYFGNRNWEPYIEDSV	88
sp	Q5YU18	HEMH_NOCFA	IIAGVERELDEAGI-----DLPVYFGNRNWHPMVEDTV	93
sp	007401	HEMH_MYCAV	AAGRPE---PARLL-----RQPQLGALRRRH---GEGH	90
sp	Q83H94	HEMH_TROW8	LRGALEKELFSRGI-----RIPVLWANRNWQPQLEEV	120
sp	Q83FJ2	HEMH_TROWT	LRGALEKELFSRGI-----RIPVLWANRNWQPQLEEV	120
sp	Q6AHF2	HEMH_LEIXX	LKAALEAELASRGI-----DLPVLWGNRNWDPYLADAL	111
sp	Q82KJ6	HEMH_STRAW	LLDALRKDFAEHGL-----NLPVYWGNRNWAPYLTDTL	100
sp	050533	HEMH_STRCO	LLDALRKDFAEHGL-----DLPVYWGNRNWAPYLTDTL	100
sp	Q7UFZ7	HEMH_RHOBA	LIAALQKRFDANGI-----DLPIYWGNRNWDPYFADTL	97
sp	P72183	HEMH_PROFR	LAAALGEALVARGI-----DVP IANANRHSMPYMDQAL	93
sp	Q9HLB8	HEMH_THEAC	IARKLH-EKIG--D-----DMDVILAYKHWNPISIEEAV	89
sp	Q978U9	HEMH_THEVO	IRDRLQ-KRFDQSG-----DVDVFTAFKHWYPSIGEVV	91

sp	P42043	HEMH1_ARATH	QQIKKD-KITRLVVLPLYPQYSISTTGSSIRVLQDLFR--KDPYLAGVPV	244
sp	P42044	HEMH_CUCSA	QQIKRD-GITRLVVLPLYPQYSISTTGSSIRVLQKMF--EDAYLSSLPV	269
sp	P42045	HEMH_HORVU	DQIKKD-KITKLVVLPLYPQYSISTSGSSIRVLQNIWK--EDPYFAGLPI	263
sp	004921	HEMH2_ARATH	EQIKRD-GITKLVVLPLYPQFSISTSGSSLRLLERIFR--EDEYLVNMQH	255
sp	022101	HEMH_ORYSA	EQIKRD-GITKLVVLPLYPQFSISTSGSSLRLLLEGIFR--EDEYLVNMQH	236
sp	Q8YQR8	HEMH_ANASP	ALLTQD-NLDNLVILPLYPQFSISTSGSSFRLLELWQ--EDPKLQRLLEY	156
sp	P54225	HEMH_SYNY3	EKIKGD-RLQRLVILPLYPHFSISTSGSSFRVLEEMWH--NDPSLRQLDY	156
sp	Q8DGU6	HEMH_SYNEL	AQIKAD-QIRELVILPLYPQFSISTSGSSFRLLESLEWN--QDPELQKIRY	157
sp	Q7VD58	HEMH_PROMA	EDIKAD-NINEVVVLPLYPHFSISTSGSSFRELRLRE--VDKEFQKLSI	156
sp	Q7V2F5	HEMH_PROMP	ADMKAD-GVDQIVVLPLYPHFSISTSGSSFRELKLRD--SDSEFQKIPM	156
sp	Q7V6C6	HEMH_PROMM	ADIKAD-GIDQVVVLPLYPHFSISTSGSSFRELQRLRQ--TDESFRKLPI	156
sp	Q7U5G0	HEMH_SYNPX	ADMKAD-GMDEVVVLPLYPHFSISTSGSSFRELQRLRQ--SDAEFQKLP	156
sp	Q7NMC7	HEMH_GLOVI	RKIKAD-GIRRLVLLPLYPQYSISTSGSSFKLLDQIWA--RDPSLKAIER	156
sp	Q9ZC84	HEMH_RICPR	GQIKEY-NPSEIILLPLYPQFSSTTTGSSVKNFLQNLID-----IDIPI	152
sp	Q68VM9	HEMH_RICTY	CQIKEY-NPSEIILLPLYPQFSSTTTGSSVKNFLQNLID-----IDIPI	152
sp	Q92FV4	HEMH_RICCN	GQIKKY-NPSEIILLPLYSQFSSTTTGSSVKNFLQNLID-----IDIPI	152
sp	Q73FY6	HEMH_WOLPM	ESVKQF-DPDEVILLPLYPQYSTTTTLSSIENWQKNAK--RY--GLKCNT	153
sp	P57777	HEMH_CAUCR	RQVAAF-APDQVLLPLYPQFSTTTTGSLLKAWKTYK-----GSGVQ	153
sp	067083	HEMH_AQUAE	SELLKE-GINEVILLPLYPQYKSTTTTGSFAFNEFERSK--ALK-ADHIKV	148
sp	P22830	HEMH_HUMAN	EEMERD-GLERAIIFTQYPQYSCSTTGSSLNAIYRYN--QVGRKPTMKW	221
sp	P22315	HEMH_MOUSE	EEMERD-GLERAIIFTQYPQYSCSTTGSSLNAIYRYN--EVGQKPTMKW	218
sp	P22600	HEMH_BOVIN	EEMERD-GLERAVIFTQYPQYSCSTTGSSLNAIYRYN--EVGRKPTMKW	214
sp	042479	HEMH_CHICK	EEMEDD-GIERAIIFTQYPQYSCSTTGSSLNAIYRYN--KKGKPKMKW	200
sp	057478	HEMH_XENLA	EEMERD-GVERAIIFTQYPQYSCSTTGSSLNAIYRYN--AKGTQPKMKW	208
sp	Q9V9S8	HEMH_DROME	AEIEKD-KPERVILFSQYPQYSCATSGSSFNSIFTHYR--SNNLPSDIKW	181
sp	059786	HEMH_SCHPO	DELKKA-NVSRVAFSQQYQWSCATSGASLNELRRKLI--EKGMEKDFEW	186
sp	P16622	HEMH_YEAST	KQMLKD-GVKKAVAFSQQYPHFSYSTTGSSINELWRQIK--ALDSERSISW	193
sp	Q6APB0	HEMH_DESPS	DYLLSK-GVERLVALSLYPHYSKATTGSSLTQLHKTLC--KKN--ISLPL	155
sp	Q747F5	HEMH_GEOSL	AAIRRE-GISRVIALSYPHYSRATTGSSVNELKRVLS--QSG--VQFQM	152
sp	Q9ZKD4	HEMH_HELPJ	QDLALK-EIESLVFFSMYPQYSSTTTLSSFNDAFNALK--SLET-PRPKV	168

sp	P56107	HEMH_HELPHY	QDLALK-EVESLVFFSMYPQYSSTTTLSSFNDAFNALK--SLET-FRPKV	168
sp	Q7M7P9	HEMH_WOLSU	RELAQK-EIEEVTLFSLYPQYSTTTTLSSI-EEFHKQC--ALLS-YFPKT	149
sp	Q7VHH1	HEMH_HELHP	EDIKTQ-GIQSVVLFSLYPQFSYSTIASSLIDAKAALQ--KLA--FTPTL	140
sp	Q9PI08	HEMH_CAMJE	QKYTLN-ASDEIILFPLYPHHSCTTTSLEVLQNEIS--KQK--IQAKV	148
sp	Q8DFM2	HEMH_VIBVU	NKLQAQ-GVDEICVPLPLYPQYSGTTTGAAYDALAHALR--KVAV--VPSI	156
sp	Q7MMR4	HEMH_VIBVY	NKLQAQ-GVDEICVPLPLYPQYSGTTTGAAYDALAHALR--KVAV--VPSI	156
sp	Q9KTB6	HEMH_VIBCH	RKLQQQ-GVEQIVVLPLYPQYSATTTAAVFDGLAKALR--QLPV--VPEL	156
sp	Q87RH3	HEMH_VIBPA	EALIAQ-GVEEVIVLPLYPQYSGTTTAAVSDGITKAFK--QLPV--MPAF	156
sp	Q6LTE0	HEMH_PHOPR	AELKQQ-GCNKVLVPLPLYPQYSGTTTAAVFDRIAKELK--QOPH--IPEL	155
sp	Q8EFF4	HEMH1_SHEON	AKLKAQ-GAERIVVLPLYPQYSCSTVASVFDVAHYLT--RVRD--IPEL	177
sp	Q8XD39	HEMH_ECO57	DELLAE-HVDHIVVLPLYPQFSCSTVGAVWDELARILA--RKRS--IPGI	156
sp	P23871	HEMH_ECOLI	DELLAE-HVDHIVVLPLYPQFSCSTVGAVWDELARILA--RKRS--IPGI	156
sp	Q8FK83	HEMH_ECOL6	DELLAE-HVDHIVVLPLYPQYSCSTVGAVWDELARILA--RKRS--IPGI	156
sp	Q83SE5	HEMH_SHIFL	DELLAE-HVDHIVVLPLYPQFSCSTVGAVWDELARILA--RKRS--IPGI	156
sp	Q8Z8T2	HEMH_SALTI	DELLAS-DVDHIVVLPLYPQYSCSTVGAVWDELGRILA--RKRR--IPGI	156
sp	P37408	HEMH_SALTY	DELLAS-DVDHIVVLPLYPQYSCSTVGAVWDELGRILA--RKRR--IPGI	156
sp	Q8ZC98	HEMH_YERPE	EKLLAQ-GVTNLVILPLYPQYSCSTSAAVWDAVARVLK--GYRR--LPSI	156
sp	Q05338	HEMH_YERPS	EKLLAQ-GVTNLVILPLYPQYSCSTSAAVWDAVARVLK--GYRR--LPSI	156
sp	P43413	HEMH_YEREN	DKLLAQ-GVTKLVPLPLYPQYSCSTSAAVWDAVARILK--GYRR--LPSI	156
sp	Q6D7Z4	HEMH_ERWCT	DKLLAQ-GVTQLVPLMPYPQYSCSTTAAVWDGLAAQLR--DNRQ--LPAI	156
sp	Q7N0P6	HEMH_PHOLL	DNLLKQ-NVEQLIVLPLYPQYSGSSAAVFDGVSLLVQ--KYRT--IPGM	156
sp	P43868	HEMH_HAEIN	KNLLKN-QVERIIVLPLYPQYSSSTTGAVFDAFANALK--EERG--LLPF	161
sp	P57874	HEMH_PASMU	QRLSTQ-QVDNLIVFPLYPQYSSSTTGAVFDFAAQVLK--TQRG--VLPF	160
sp	Q65SV7	HEMH_MANSM	DNLIEQ-KVDKIIVLPLYPQYSSTTTAPVFDVFAQALK--RHRH--IVPF	160
sp	Q8CW44	HEMH_STRMU	DEFLKE-KVAKMIVLPLFPQYSSSTTAAIFDAFAQSLK--KKKD--IPPF	160
sp	Q8D226	HEMH_WIGBR	KKMKIYNVNKLIILMPYPQYSCSTTASVLDVCEVIK--KYRN--IPSI	156
sp	Q8EBZ7	HEMH2_SHEON	REMHKQ-GIDKLVPLPLYPQYAAPTGTSAFDAIAKELS--QWRY--LPSL	163
sp	Q6F7N0	HEMH_ACIAD	KDLAAS-PQEHVILLPLFPQYSATSTAPLYDAFANWIP--KQRH--LPGL	164
sp	Q7WG10	HEMH_BORBR	TALRER-GCDHILAVPLYPQYAASSTATVVDVAVTRHAG--RLRD--QPAL	190
sp	Q7W515	HEMH_BORPA	TALRER-GCDHILAVPLYPQYAASSTATVVDVAVTRHAG--RLRD--QPAL	190
sp	Q7VVX8	HEMH_BORPE	TALRER-GCDHILAVPLYPQYAASSTATVVDVAVTRHAG--RLRD--QPAL	190
sp	Q62HD1	HEMH_BURMA	AQLKRA-GAERVLLLPLFPQYSSSTTATAFDAFAALG--RMRN--QPEV	183
sp	Q63R43	HEMH_BURPS	AQLKRA-GAERVLLLPLFPQYSSSTTATAFDAFAALG--RMRN--QPEV	183
sp	Q8XW32	HEMH_RALSO	QTLRKQ-GVERILVPLMPYPQYSGTTTATAFDEVFRVMG--QMRN--QPEL	175
sp	Q7NV65	HEMH_CHRVO	GKMREQ-GVERLLLLPLYPQYAASSSATALDEAFRVLS--RLRN--MPEV	175
sp	Q82UK8	HEMH_NITEU	QQMKVQ-GCDRILVPLFPQYAASSTGCVLDGVFSELR--KMRN--IPDI	173
sp	Q9JVA5	HEMH_NEIMA	SELKAQ-GAGRLLVIPMPYPQYAASSGAADVCKVCEQLL--LQRN--QMSV	168
sp	Q9K097	HEMH_NEIMB	SELKAQ-GAGRLLVIPMPYPQYAASSGAADVCKVCEQLL--LQRN--QMSV	168
sp	Q8PEX0	HEMH_XANAC	DRLRAR-GIKRIVVLPLYPQYSTTTTASIQD-VVDAWR--TSAP--EIAV	156
sp	Q8P3H6	HEMH_XANCP	DGLRAR-GIKRIVVLPLYPQYSTTTTASIQD-VVDAWR--PSAP--EIAV	156
sp	Q9PFU1	HEMH_XYLFA	DALQAQ-QVRRIVILPLYPQYSTTTTASVQD-VVEAWC--KRTP--QVQV	156
sp	Q87B82	HEMH_XYLFT	DALQAQ-QVRRIVILPLYPQYSTTTTASVQD-VVEAWC--KRTP--QVQV	156
sp	Q607T4	HEMH_METCA	EELRNR--VETIVVLPLYPQYSAATTGSADFVCDTLK--TWRH--IPSL	157
sp	Q8U9F7	HEMH_AGR75	DALKEQ-GCEKILLFPLYPQYAASSTATVNDKAFEHLM--KLRW--QPAI	175
sp	Q92M52	HEMH_RHIME	EALQKA-GCERILVPLYPQYAASSTATVNDKAFEALL--KMRW--QPAL	170
sp	Q93TG2	HEMH_BRUME	DRLQQQ-GCERIVIFPLYPQYSATTTATVNDKFFEALM--KKRF--MPAI	183
sp	Q98H61	HEMH_RHILO	ERLVAQ-GCDRILSFPLYPQYSATTTATANDQLFRALM--KLRR--APAI	184
sp	P28602	HEMH_BRAJA	DALIAE-GCDRILAVPLYPQYSASTSATVCDDEVFRVLA--RLRA--QPTL	176
sp	Q6NBF3	HEMH_RHOPA	EALVAK-GCTRLVPLYPQYSAATSATVCDQAFRVLR--ELRA--QPTL	176
sp	Q59735	HEMH_RHOCA	DDMLAQ-GCERILFPLYPQYAGATSATANDQFFRALM--QVKR--QPAA	181
sp	P57779	HEMH_ZYMMO	EKLIAF-RCRILLAPLYPQYSAASTATVQDEAYRYLQ--KIRW--QPNL	164
sp	Q833G5	HEMH_ENTFA	DTLLSK-EIEELNVIPLYPQYSGTTVGSVFDVSMNYFI--KSDR--IVDI	154
sp	Q9CFB4	HEMH_LACLA	AEMKES-GVEEITVPLPLYPQYSLTTVEPVIQQVKKIDD--K-----I	149
sp	Q67T48	HEMH_SYMTH	EELRGW-GVRRLLVPLFPQYSSTTTAAVWSKVQKALD--GWRD--LPEQ	156
sp	Q88XC3	HEMH_LACPL	KAMVAD-GCEKPIILPLFPQYQTQSTHGGIHRQVEATGL--P-----H	147
sp	P57778	HEMH_PSEFL	TRLAQG-GISKVTLAPLYPQFADSTVTTVIEEARRVVR--DKQL--DLQF	153
sp	Q888A2	HEMH_PSESM	TRLSEQ-GFKKVTLAPLYPQFADSTVTTVIEEAKRVVR--AKSL--KMQF	153
sp	Q88PV4	HEMH_PSEPK	ARLAAQ-GVRKVTLAPLYPQFADSTVTTVIEQAKQTVS--EHQL--PLQM	153
sp	Q9HVD7	HEMH_PSEAE	LDLARR-GIRRVTLAPLYPQFADSTTTTAEQEVRRVIA--AHRL--GLEV	153
sp	Q6MHT3	HEMH_BDEBA	KDLQQA-GVDEILVAPMPFQYAEATNGSSFKLAERMAK--KLHL--TAPL	155
sp	Q83FA4	HEMH_COXBU	KKLQEA-QCRQLIVLPLFPQYSTSTTASALEEVR-----AKNS--FKEM	156
sp	Q6MAW8	HEMH_PARUW	ERLKLA-NVKEIVIFPLFPQYASATTGSVHQEVMKHLQ--QWQN--IPTL	156
sp	Q7MXP4	HEMH_PORGI	KELPHG---RSLVVLPLFPHYAMSSYETAVEHCKAEIR--RLCP--NLSF	163

sp	Q824K8	HEMH_CHLCV	KTLGDF----	PIVGVPLFPHFYAVTGSIVRFIHNQLP--LLNI--S---	146
sp	Q9Z7V1	HEMH_CHLPN	RTLHTR----	HVIGIPLFPHFYTSVTGSIVRFFMKHVP--EIPi--S---	147
sp	Q9PJQ6	HEMH_CHLMU	RESAG----	DIIGIPLFPHFYFAVTGSIIRFFLERIP--EKPM--A---	144
sp	Q84492	HEMH_CHLTR	QESQG----	SIVGIPLFPHFYFAVTGSIIRFFLQHLF--EKPI--S---	144
sp	Q8GCV0	HEMH_LEPBI	FGKPNQ----	DTVYLPPLYPQFSRSTVLSLAILLETKFG--ECPV--GS-G	157
sp	Q81U22	HEMH1_BACAN	KEMHND-GIQDAIALVLAPHYSTFSVKSIVGRAQEEAE----	KLGN-LTI	140
sp	Q6HM97	HEMH1_BACHK	KEMHND-GIQDAIALVLAPHYSTFSVKSIVGRAQEEAE----	KLGN-LTI	140
sp	Q63ES4	HEMH1_BACCZ	KEMHND-GIQDAIALVLAPHYSTFSVKSIVGRAQEEAE----	KLGN-LTI	140
sp	Q73C98	HEMH1_BACC1	KDMHND-GIQDAIALVLAPHYSTFSVKSIVGRAQEEAE----	KLGN-LTI	140
sp	Q81GW5	HEMH1_BACCR	KDMHND-GIQDAIALVLAPHYSTFSVKSIVGRAQEEAE----	KLGN-LTI	140
sp	P32396	HEMH_BACSU	AEMHKD-GITEAVSIVLAPHFSTFVSQSYNKRakeEAE----	KLGG-LTI	141
sp	Q8ERX9	HEMH_OCEIH	EEMAKD-GIKEAISLVLAPHYSTFSVKSYNKRANETAE----	KYG--IQL	140
sp	Q71XF4	HEMH_LISMF	EAMHKD-GIEEASIVLAPHYSSFSVEAYNKRAKDAAD----	KLGG-LRI	140
sp	Q8Y565	HEMH_LISMO	EAMHKD-GIEEASIVLAPHYSSFSVEAYNKRAKEAAD----	KLGG-PRI	140
sp	Q929G2	HEMH_LISIN	EAMHKD-GIEEASIVLAPHYSSFSVEAYNKRAKDAAD----	KLGG-IHI	140
sp	P64124	HEMH_STAAM	EQMHND-GITEAITVVLAPHYSSFSVGSYDKRADEEAA----	KYG--IQL	139
sp	P64125	HEMH_STAAN	EQMHND-GITEAITVVLAPHYSSFSVGSYDKRADEEAA----	KYG--IQL	139
sp	Q6G8A3	HEMH_STAAS	EQMHND-GITEAITVVLAPHYSSFSVGSYDKRADEEAA----	KYG--IQL	139
sp	P64126	HEMH_STAAW	EQMHND-GITEAITVVLAPHYSSFSVGSYDKRADEEAA----	KYG--IQL	139
sp	Q6GFM4	HEMH_STAAR	EQMHND-GITEAITVVLAPHYSSFSVGSYDKRADEEAA----	KYG--IQL	139
sp	Q8CNS1	HEMH_STAEP	EQMHND-GIKEAVTVLAPHYSSFSVGSYDQRAQEKAD----	EYG--IQL	139
sp	Q81TU9	HEMH2_BACAN	EEMKRD-GIEQAISIVLAPHYSTFSIKAYNERAIRLSE----	EIGG-PVI	141
sp	Q6HM28	HEMH2_BACHK	EEMKRD-GIEQAISIVLAPHYSTFSIKAYNERAIRLSE----	EIGG-PVI	141
sp	Q63EK7	HEMH2_BACCZ	EEMKRD-GIEQAISIVLAPHYSTFSIKAYNERAIRLSE----	EIGG-PVI	141
sp	Q73C08	HEMH2_BACC1	EEMKRD-GIEQAISIVLAPHYSTFSIKAYNDRAIRLSE----	EIGG-PVI	141
sp	Q81GN7	HEMH2_BACCR	EEMKRN-GIEQTISIVLAPHYSTFSIKAYNDRAIRLSK----	EIGG-PVI	141
sp	Q9KDK9	HEMH_BACHD	EQMKED-GVQEAVSIVLAPHFSTFVSVKSIVNGRAHEESK----	KIGG-PRI	141
sp	Q5WHT1	HEMH_BACSK	QKMKND-GIETAVSIVLAPHFSTFVSQSYNKRakeEAD----	RIGG-PTI	141
sp	Q72L32	HEMH_THET2	AAMHED-GVRRVAIVAAAPHYSLRSVAEYREKVDLSALK----	TLPEPIDF	151
sp	Q9RV98	HEMH_DEIRA	REMLDD-GIEQAIAIVLAPQYSSLSVAKYQKKIKAALE----	MNHGHIDF	144
sp	Q97R30	HEMH_STRPN	GQMEAD-GIEQCICLILEPHYSFYVMGYEKFLSKQ-----	IQF	129
sp	Q8DQ04	HEMH_STRR6	GQMEAD-GIEQCICLILEPHYSFYVMGYEKFLSKQ-----	IQF	129
sp	Q8FTB1	HEMH_COREF	EQMAAD-GIRNALVFATSAGGYSGCRQYHEDIQGMRAHLEEIGAPEVTF		152
sp	Q8NQA1	HEMH_CORGL	EQMADD-GVKNALVLATSAGGYSGCRQYQEDIQGMIKHLESQGG--SITF		147
sp	Q6NH66	HEMH_CORDI	EKMVRD-GVRNVAVFATSAGGYSGCRQYDEDIVRMNHHEEKELPTLNC		151
sp	Q740Y1	HEMH_MYCPA	KVMRDN-GIRRAAVFTTSAWGSYSSCTQYVEDIARAR---	TAAGTGAPEL	134
sp	P71765	HEMH_MYCTU	TAMRDN-GVRRAAVFATSAGGYSYSSCTQYVEDIARAR---	RAAGRDAPEL	134
sp	Q9CBM2	HEMH_MYCLE	VTMRDD-GIRCAAVFITSAWGSYSSCTRYVEAIARAR---	RRAGTGAPNL	134
sp	Q5YU18	HEMH_NOCFA	AEMARD-GVTGALVFPPTSAWGSYSGCRQYHEDIERAR---	AAVGAAPHL	139
sp	O07401	HEMH_MYCAV	TRQRDS-ACRGVHHLRLERLQLHAVRRGHRPGAHG-----	RAGRART	133
sp	Q83H94	HEMH_TROW8	REAYDR-GFRAFLTLFTSAYSCYSSCRQYREDIAHAVERAGLSGR--IIV		167
sp	Q83FJ2	HEMH_TROWT	REAYDR-GFRAFLTLFTSAYSCYSSCRQYREDIAHAVERAGLSGR--IIV		167
sp	Q6AHF2	HEMH_LEIXX	TEADQR-GFTKLIAVATSAYSSYSSCRQYREDFARALRETGLEGR--IQI		158
sp	Q82KJ6	HEMH_STRAW	REMAAD-GRRRILVLATSAYASYSGCRQYRENLAGALATLEAEGLEVPRV		149
sp	O50533	HEMH_STRCO	REMVGD-GRRRILVLATSAYASYSGCRQYRENLAGALALESEGLPLPKI		149
sp	Q7UFZ7	HEMH_RHOBA	RQMKAD-GKKRSLAFFTSMFSCYSGCRQYRENIIQAR---	EEVGEAPLV	143
sp	P72183	HEMH_PROFR	ADLQSR-GIRRVLTLPVTPYASYSGCRAYRELLAGTR--IDDEGRPALQV		141
sp	Q9HLB8	HEMH_THEAC	KGLG---SYDNIVAIPLFSFYSONVKDSYLNPLESALR----	RYGFSPLR	132
sp	Q978U9	HEMH_THEVO	PDLK---GYDNIVSIPLFSFFSENKASYKPLAEALE----	KNDIRTKM	134

sp	P42043	HEMH1_ARATH	AIKSWYQRRGYVNSMADLIEKELQTFSDPK-----	EVMI	279
sp	P42044	HEMH_CUCSA	SIIKSWYQREGYIKSMADLMQAEKLNKFNANPQ-----	EVMI	304
sp	P42045	HEMH_HORVU	SIIESWYQREGYVKSADLIEKELSVFSNPE-----	EVMI	298
sp	O04921	HEMH2_ARATH	TVIPSWYQREGYIKAMANLIQSELGKFGSPN-----	QVVI	290
sp	O22101	HEMH_ORYSA	TVIPSWYQREGYIKAMATLIEKELRTFSEPO-----	KVMI	271
sp	Q8YQR8	HEMH_ANASP	TVIPSWYKEPGYLQAMAEIRQEIEQFPHPD-----	QVHV	191
sp	P54225	HEMH_SYNY3	SLIPSWYDHPGYLQAMADLIAQELKKFPNPD-----	QAHV	191
sp	Q8DGU6	HEMH_SYNEL	TLIPSWYNHPGYVAAMADLIRQELDRCPNPD-----	EAVI	192
sp	Q7VD58	HEMH_PROMA	RCIRSWFDNTGYIASMAELIEQEISSCESPN-----	AAHI	191
sp	Q7V2F5	HEMH_PROMP	RCVRSWFSQSGYLKSMVELISEQISLCESPD-----	SAHI	191
sp	Q7V6C6	HEMH_PROMM	RCIRSWYDHPGYVRAMAEIAEQVRLSDVPE-----	EAQV	191
sp	Q7U5G0	HEMH_SYNPX	RCIRSWFDHPGYIKAMAEIAEVRNSDDPE-----	KAHV	191

sp	Q7NMC7	HEMH_GLOVI	ITINSWYSRPGYIRAMGERVREGLDKFDNPD-----GVHI	191
sp	Q9ZC84	HEMH_RICPR	KTICCCYIEEDFIKAHVSLIKE--KLYDKN-----FRI	183
sp	Q68VM9	HEMH_RICTY	KTICCCYIEEDFIKAHVSLIKE--KLYDKN-----FRI	183
sp	Q92FV4	HEMH_RICCN	KTICCCYPLEKDFIKAHVSLIKE--KLYDKN-----FRI	183
sp	Q73FY6	HEMH_WOLPM	KMIHRYDNDQDFIEAHTNLIKAKYYKLARKIG-----KPRV	188
sp	P57777	HEMH_CAUCR	TTVGCYPTTEGGLIEAHARMIRESWEKAGSPT-----NIRL	188
sp	O67083	HEMH_AQUAE	KKIEHFYDHPYLIKAWAEQIKQS---VEKPE-----EYHF	180
sp	P22830	HEMH_HUMAN	STIDRWPTHLLIQCFFADHILKELDHFPLEKR-----SEVVI	258
sp	P22315	HEMH_MOUSE	STIDRWPTHPLLIQCFFADHILKELNHFPEEKR-----SEVVI	255
sp	P22600	HEMH_BOVIN	STIDRWPTHPLLIQCFFADHILKELDHFPEEKR-----REVVI	251
sp	O42479	HEMH_CHICK	SIIDRWPTHPLLIQCFFADHIQKELDLFPPDKR-----KDVVI	237
sp	O57478	HEMH_XENLA	SVIDRWPTHPLLIQCFFADHIQKELNMFADKR-----GEVVI	245
sp	Q9V9S8	HEMH_DROME	SIIDRWGTHPLLIKTFAQRIRDELAKFVETKR-----NDVVI	218
sp	O59786	HEMH_SCHPO	SIVDRWPLQOGLINAFANIETLKTYPEDVR-----DDVVI	223
sp	P16622	HEMH_YEAST	SVIDRWPTNEGLIKAFSENI TKKLQEFQPVR-----DKVVL	230
sp	Q6APB0	HEMH_DESPS	TEIPSWPKQRDYIAAIAANIKKGLATFHG-----EKTEI	189
sp	Q747F5	HEMH_GEOSL	MYVDRFFDHPYIIDLAEKIREGLDDFHPL-----AEVQV	187
sp	Q9ZKD4	HEMH_HELPLJ	RVIERFYASKKLNELIILNTILSALNNCKSQD-----FVL	202
sp	P56107	HEMH_HELPY	RVIERFYASKKLNELIILNTILNLRKNSQD-----FVL	202
sp	Q7M7P9	HEMH_WOLSU	KEIDRYFEDSNYNEAIIIDRILEALGGDNPEE-----FTL	183
sp	Q7VHH1	HEMH_HELHP	YEISSYHTHPDYISCIIERIKESLGADNPNE-----FVL	174
sp	Q9PI08	HEMH_CAMJE	KTIDIFYKNELYNEMIVSHILAKKSKFPAK-----IL	180
sp	Q8DFM2	HEMH_VIBVU	QFIRDYHDHPYIKALAESVRQSWQVQGK-----GDYL	189
sp	Q7MMR4	HEMH_VIBVY	QFIRDYHDHPYIKALAESVRQSWQAQGK-----GDYL	189
sp	Q9KTB6	HEMH_VIBCH	HFIRDYHDHPYIQAALAKSVRASWQQHGQ-----GDLL	189
sp	Q87RH3	HEMH_VIBPA	SFIRDYHDHPYIEALAHSVRQYWEHGK-----GDYL	189
sp	Q6LTE0	HEMH_PHOPR	RFINHYFDHPDYIDALALSVTDFWAENGE-----PDYL	188
sp	Q8EFF4	HEMH1_SHEON	RFNKQYFAHEAYIAALAHSVKRHWKTHGQ-----AEKL	210
sp	Q8XD39	HEMH_ECO57	SFIRDYADNHDYINALANSVRASFAGHGE-----PDL	189
sp	P23871	HEMH_ECOLI	SFIRDYADNHDYINALANSVRASFAGHGE-----PDL	189
sp	Q8FK83	HEMH_ECOL6	SFIRDYADNHDYINALANSVRASFAGHGE-----PDL	189
sp	Q83SE5	HEMH_SHIFL	SFIRDYADNHDYINALANSVRASFAGHGE-----PDL	189
sp	Q8Z8T2	HEMH_SALTI	SFIRDYADDGAYIDALAKSARESFARHGE-----PDL	189
sp	P37408	HEMH_SALTY	SFIRDYADDGAYIDALAKSARESFARHGE-----PDVL	189
sp	Q8ZC98	HEMH_YERPE	SFIRDYAEHPAYISALKQSVERSFAEHGQ-----PDL	189
sp	Q05338	HEMH_YERPS	SFIRDYAEHPAYISALKQSVERSFAEHGQ-----PDL	189
sp	P43413	HEMH_YEREN	SFIRDYAEHPAYISALKQSVENSFVQHKG-----PDL	189
sp	Q6D7Z4	HEMH_ERWCT	RFIRDYAEHPAYIAALKHRVEQSFAGHGE-----PDL	189
sp	Q7N0P6	HEMH_PHOLL	HFIRSYADHPAYIAALKHRTIEQSFDKHGQ-----PDL	189
sp	P43868	HEMH_HAEIN	DFIHSYHIDENYINALADSIKVRKLS-----EFL	191
sp	P57874	HEMH_PASMU	DFIHSYHTNEDYIAALVTTIQEHFQPD-----EFL	190
sp	Q65SV7	HEMH_MANSM	EFIHSYHLDENYIEALVKSIVKRLKND-----EFL	190
sp	Q8CWW4	HEMH_STRMU	DFIHHYERPSYIQALAQTI--HLQEN-----EHL	188
sp	Q8D226	HEMH_WIGBR	IFIRDYADNINYNAINITNSIKKSFNKNGI-----PEML	189
sp	Q8EBZ7	HEMH2_SHEON	HFINTYHDNPDYIINALVNSIRDDDFDKHGK-----PQKL	196
sp	Q6F7N0	HEMH_ACIAD	TIIDKYRHPVFIQALVSSVQRFOQQHGK-----PQKL	197
sp	Q7WGI0	HEMH_BORBR	RFVKRFHNDPAYVEAQAGRIAEFWQAHGR-----PQKL	223
sp	Q7W515	HEMH_BORPA	RFVKRFHNDPAYVEAQAGRIAEFWQAHGR-----PQKL	223
sp	Q7VVX8	HEMH_BORPE	RFVKRFHNDPAYVEAQAGRIAEFWQAHGR-----PQKL	223
sp	Q62HD1	HEMH_BURMA	RTVRYADHPAYIHALAEQVRQYWAHGRPA-----FDAGDKL	221
sp	Q63R43	HEMH_BURPS	RTVRYADHPAYIHALAEQVRQYWAHGRPA-----FDAGDKL	221
sp	Q8XW32	HEMH_RALSO	RLVKHFHDHPAYINALHQVQAYWAQHAGPD-----FARGDKL	213
sp	Q7NV65	HEMH_CHRVO	RTVRHFHDDPGYIAALAAQIRKHWQYGGQR-----PDKL	208
sp	Q82UK8	HEMH_NITEU	RTVRHYHDDPGYIAALQNVRDYWEKHGQ-----PDKL	206
sp	Q9JVA5	HEMH_NEIMA	RTVSRFYDDTGYIDAMKNHILRYWAEHGR-----GKKL	201
sp	Q9K097	HEMH_NEIMB	RTVSRFYDDTGYIDAMKNHILRYWAEHGR-----GKKL	201
sp	Q8PEX0	HEMH_XANAC	EVIQDYCEDTGWVAIAIESIRAHWQVHGR-----SEKL	189
sp	Q8P3H6	HEMH_XANCP	EVIQDYCEDAGWVAIAIADSIRTHWQVHGR-----SEKL	189
sp	Q9PFU1	HEMH_XYLFA	ECIQDYAEDSAWVAVAASIRRHWAHGR-----SEKL	189
sp	Q87B82	HEMH_XYLFT	ECIQDYAEDPAWVAVAASIRRHWAHGR-----SEKL	189
sp	Q607T4	HEMH_METCA	HFIGDYHRSPKYLEAVAASIRSFWEHGR-----PERL	190
sp	Q8U9F7	HEMH_AGR5	RTVPPYHDDPAYIEGLAASVKNHLATLDWE-----PEML	209
sp	Q92M52	HEMH_RHIME	RTVPPYHDDPVYIDALATSINKHLATLDWE-----PELV	204

sp	Q93TG2	HEMH_BRUME	RTVPSYEAEPVYIDALARSVEKHLATLSFK-----PEVI	217
sp	Q98H61	HEMH_RHILO	RSVPPYYAEPVYIEALASSIERHLATLDLFE-----PEVV	218
sp	P28602	HEMH_BRAJA	RVTTPPYEDEAYIEALAVSIETHLATLPFK-----PELI	210
sp	Q6NBF3	HEMH_RHOPA	RVTTPPYRDSAYIDALATSIKSHLASLTFE-----PELI	210
sp	Q59735	HEMH_RHOCA	RTVPEYFARPSYIEALASSVERVYATLDTR-----PDVL	215
sp	P57779	HEMH_ZYMMO	RSLEPYYPHAYIQTLLKNIEDQIKALDFK-----PDSL	198
sp	Q833G5	HEMH_ENTFA	KFIRSFYNNPQYIDYFSKINEALNESP-----IDAI	186
sp	Q9CFB4	HEMH_LACLA	KVIRDFHKVESYSDLLAESIREKWQAND-----YDKL	181
sp	Q67T48	HEMH_SYMTH	IFIRDFPHTPKYLAFLTERISGYIAEKGR-----PDAL	189
sp	Q88XC3	HEMH_LACPL	TFIDSFYDQPTYIHLLATKVWQSYQAHHY-----DAV	179
sp	P57778	HEMH_PSEFL	SILQPFYDQPEYLDLAVASARPHLQOD-----YDHL	184
sp	Q888A2	HEMH_PSESM	SVLQPFYDQPEYVSALVESVRPHLEQP-----YDHL	184
sp	Q88PV4	HEMH_PSEPK	RVLQPFYEHAYIEALASARPYLEQG-----YDHL	184
sp	Q9HVD7	HEMH_PSEAE	STLPPFYDQPVYLDALVESVRPYLQQP-----HDHL	184
sp	Q6MHT3	HEMH_BDEBA	RRLPAFFDDASVFGTSSVKLVEETLQDKE-----VDHY	187
sp	Q83FA4	HEMH_COXBU	TVIDRFFEEPHYIDSMTTLIHENLNEFQ-----PDYF	188
sp	Q6MAW8	HEMH_PARUW	TFINSYDPHPLVGFACERAKQYDLSI-----YDYF	187
sp	Q7MXP4	HEMH_PORGI	RVVQPFYAHAYIRVLDNIRPYLTKP-----FDKL	194
sp	Q824K8	HEMH_CHLCV	-WVSHFGNHPEFISCMMDHILKFLQSHD-----ISTHDCL	181
sp	Q9Z7V1	HEMH_CHLPN	-WIPQFGSDSKFVSLITCHIRDFLQKLG-----ILEKECCF	182
sp	Q9PJQ6	HEMH_CHLMU	-WITHFGVHPQFISCMREHIQDCLIAQG-----IVAEDCFF	179
sp	O84492	HEMH_CHLTR	-WITQFVGHPEFVSCMQQHIRDCLAAQQ-----IAVEDCYF	179
sp	Q8GCV0	HEMH_LEPBI	GYVPHFGLDPNFHISISAKFIYEFFTNQLPKDQYLHYPEEKPNCDWRNLDL	207
sp	Q81U22	HEMH1_BACAN	HGIDSWYKEPKFIQYVWDAVKSIYSGMSDAER-----EKAVL	177
sp	Q6HM97	HEMH1_BACHK	HGIDSWYKEPKFIQYVWDAVKGIYSGMSDAER-----EKAVL	177
sp	Q63ES4	HEMH1_BACCZ	HGIDSWYKEPKFIQYVWDAVKGIYNGMSDAER-----EKAVL	177
sp	Q73C98	HEMH1_BACC1	HGIDSWYKEPKFIQYVWDAVKGIYNGMSDAER-----EKAVL	177
sp	Q81GW5	HEMH1_BACCR	HGIDSWYKEPKFIQYVWDAVKGIYNGMSDAER-----EKAVL	177
sp	P32396	HEMH_BACSU	TSVESWYDEPKFVTVYVWDRVKETYASMPEDER-----ENAML	178
sp	Q8ERX9	HEMH_OCEIH	DSVEDWYTEPGFIKFWADGIKATYAEMTEEER-----NNSVL	177
sp	Q71XF4	HEMH_LISMF	KAINDWYKQPKFIQMWADRINETAKQIPADEL-----LDTVL	177
sp	Q8Y565	HEMH_LISMO	NAINDWYKQPKFIQMWADRINETAKQIPADEL-----LDTVL	177
sp	Q929G2	HEMH_LISIN	QAINDWYKQPKFIQMWADRINETAKQIPAEEL-----IDTVL	177
sp	P64124	HEMH_STAAM	THVKHYEQPKFIEYWTNKVNETLAQIPEEEH-----KDTVL	176
sp	P64125	HEMH_STAAN	THVKHYEQPKFIEYWTNKVNETLAQIPEEEH-----KDTVL	176
sp	Q6G8A3	HEMH_STAAS	THVKHYEQPKFIEYWTNKVNETLAQIPEEEH-----KDTVL	176
sp	P64126	HEMH_STAAW	THVKHYEQPKFIEYWTNKVNETLAQIPEEEH-----KDTVL	176
sp	Q6GFM4	HEMH_STAAR	THVKHYEQPKFIEYWTNKVNETLAQIPEEEH-----KDTVL	176
sp	Q8CNS1	HEMH_STAEP	THIKHYEQPKFIKYWTEKINETLEQIPNQEHE-----DETVL	176
sp	Q81TU9	HEMH2_BACAN	KPIDQWYDEPKFISYWADQIKETFTKIEDKE-----KAVV	176
sp	Q6HM28	HEMH2_BACHK	EPIDQWYDEPKFISYWADQIKETFTKIEDNE-----KAVV	176
sp	Q63EK7	HEMH2_BACCZ	EPIDQWYDEPKFISYWADQIKETFTKIEDKE-----KAVV	176
sp	Q73C08	HEMH2_BACC1	EPIEQWYDEPKFISYWADQIKETFTKIEDKE-----KAVV	176
sp	Q81GN7	HEMH2_BACCR	ESIEQWYDEPKFISYWADQIKETFTTEIDDKE-----KAVV	176
sp	Q9KDK9	HEMH_BACHD	QSVESWYDEPLFIQYVWVNDTMAKIEDKD-----KACV	176
sp	Q5WHT1	HEMH_BACSK	YTIESWYKEPGFLQFWKEQIENEMKKADSID-----DLCV	176
sp	Q72L32	HEMH_THET2	VWVESYEAHPGLIAAYARRLEEVIWRLKNPG-----KAAY	186
sp	Q9RV98	HEMH_DEIRA	AYIDNYHTPEGYITALADRVRIGIQEFPEDER-----DDVHV	181
sp	Q97R30	HEMH_STRPN	LVIKDWYQEEALLNYWADEIAKILKEEVKQD-----SFKV	164
sp	Q8DQ04	HEMH_STRR6	LVIKDWYQEEALLNYWADEIAKILKEEVKQD-----SFKV	164
sp	Q8FTB1	HEMH_COREF	TKLRQFYDHPFRVTRTMAQYVRESFDKL-----P-----EDLRDEARL	189
sp	Q8NQA1	HEMH_CORGL	TKLRQFYDHPFRVSTMAQLVQDSYAKL-----P-----DELDRDEARL	184
sp	Q6NH66	HEMH_CORDI	LKLRQFFDHPFLFIEEMSSVVFQAARELGISA-L-----DELQLHQKV	192
sp	Q740Y1	HEMH_MYCPA	VKLRPYFDHPFLFVEMFAGAIADAAAKVPA-----GARL	167
sp	P71765	HEMH_MYCTU	VKLRPYFDHPFLFVEMFADAITAAAATVRG-----DARL	167
sp	Q9CBM2	HEMH_MYCLE	VKLRPYFDHPFLFVEMFVDAITAAAASLPAA-----LRSEARL	171
sp	Q5YU18	HEMH_NOCPA	TKLRQFYFDHPFLFIEAFADAIRAALERLPAD-----RRDRARL	176
sp	O07401	HEMH_MYCAV	GQAAAVFRPSAVRGDVRRRDADAAAKVPAG-----ARL	166
sp	Q83H94	HEMH_TROW8	DKLRQFFDHPGFVLPFIEGIQDCLEQVKERG-----FKVSRTAI	206
sp	Q83FJ2	HEMH_TROWT	DKLRQFFDHPGFVLPFIEGIQDCLEQVKERG-----FKVSRTAI	206
sp	Q6AHF2	HEMH_LEIXX	DKVRQFFDHPGFVEPFIEGVKNAVEELRERAPE-----IHPATGURI	200
sp	Q82KJ6	HEMH_STRAW	DKLRHYFNHPGFVEPMTGEVLRSLAELP-----EDVRPGAHI	186
sp	O50533	HEMH_STRCO	DKLRHYFNHPGFVEPMVDGVRSLAELP-----AEVRDGAHI	186

sp	Q7UFZ7	HEMH_RHOBA	EKVRMGFNHPGFIAAMADNVSKAAQTIG-----ASPAR-TKV	179
sp	P72183	HEMH_PROFR	VKLDPYADLPALVTAQVQLLRAALADHP-----DAHL	173
sp	Q9HLB8	HEMH_THEAC	EFVNGLANSDLFLPMWANIISEDASEDS-----FY	162
sp	Q978U9	HEMH_THEVO	EFVNGISNYDLFIPMWHLIEEKEKGDS-----FY	164

sp	P42043	HEMH1_ARATH	FFSAHGVPVSYVENAG-----DPYQKQMEECI	306
sp	P42044	HEMH_CUCSA	FFSAHGVPVSYVENAG-----DPYKQDMEECI	331
sp	P42045	HEMH_HORVU	FFSAHGVPPLTYVKDAG-----DPYRDQMEDCI	325
sp	O04921	HEMH2_ARATH	FFSAHGVPVSYVENAG-----DPYKAEEMEECV	317
sp	O22101	HEMH_ORYSA	FFSAHGVPVSYVENAG-----DPYKAEEMEECV	298
sp	Q8YQR8	HEMH_ANASP	FFSAHGVPKSYVEEAG-----DPYQOEIEECT	218
sp	P54225	HEMH_SYNY3	FFSAHGVPQSYVDEAG-----DPYQAEIEACT	218
sp	Q8DGU6	HEMH_SYNEL	FFSAHGVPKSYVTEAG-----DPYQEEIEACV	219
sp	Q7VD58	HEMH_PROMA	CFTAHGVPKSYVEEAG-----DPYKDEIQDCA	218
sp	Q7V2F5	HEMH_PROMP	FFTAHGVPKSYVEEAG-----DPYKEQIEDCS	218
sp	Q7V6C6	HEMH_PROMM	FFSAHGVPKSYVEQAG-----DPYQKEIEACT	218
sp	Q7U5G0	HEMH_SYNPX	FFSAHGVPKSYVEEAG-----DPYQQQIEACT	218
sp	Q7NMC7	HEMH_GLOVI	LFSAHGVPRTYVDQDG-----DPYQRQTEETV	218
sp	Q9ZC84	HEMH_RICPR	LFSAHGLPKRIIK-AG-----DPYSFQIKETV	209
sp	Q68VM9	HEMH_RICTY	LFSAHGLPKRIIK-AG-----DPYSFQIKETV	209
sp	Q92FV4	HEMH_RICCN	LFSAHGLPEKIIK-AG-----DPYSFQIKETV	209
sp	Q73FY6	HEMH_WOLPM	LFSAHSLPLSIIK-KG-----DPYASQVERSV	214
sp	P57777	HEMH_CAUCR	LFSAHGLPEKVIL-AG-----DPYQKQVEATA	214
sp	O67083	HEMH_AQUAE	LFSAHSLPKKLIIE-EG-----DPYQEQTETV	206
sp	P22830	HEMH_HUMAN	LFSAHSLPMSVVN-RG-----DPYPQEVSATV	284
sp	P22315	HEMH_MOUSE	LFSAHSLPMSVVN-RG-----DPYPQEVGATV	281
sp	P22600	HEMH_BOVIN	LFSAHSLPMSVVN-RG-----DPYPQEVGATV	277
sp	O42479	HEMH_CHICK	LFSAHSLPMSVVN-RG-----DPYPQEVGATV	263
sp	O57478	HEMH_XENLA	LFSAHSLPMSVVN-RG-----DPYPQEVGATV	271
sp	Q9V9S8	HEMH_DROME	LFTAHSPLPKAVN-RG-----DAYPSEIGASV	244
sp	O59786	HEMH_SCHPO	VFSAHSLPMSQVA-KG-----DPYVYIEAATS	249
sp	P16622	HEMH_YEAST	LFSAHSLPMDVVN-TG-----DAYPAEVAATV	256
sp	Q6APB0	HEMH_DESPS	VYSAHSLPTSFIIE-AG-----DPYVEHTKQSI	215
sp	Q747F5	HEMH_GEOSL	LFSAHSLPQSFID-EG-----DPYLDHIRETV	213
sp	Q9ZKD4	HEMH_HELPJ	IFSVHGLPKSVID-AG-----DTYQQECEHHV	228
sp	P56107	HEMH_HELPY	IFSVHGLPKSVID-AG-----DTYQQECEHHV	228
sp	Q7M7P9	HEMH_WOLSU	IFSAHGLPQSVID-AG-----DPYKEVHANI	209
sp	Q7VHH1	HEMH_HELHP	LLSAHSLPQSRID-EG-----DPYQKQCEENK	200
sp	Q9PI08	HEMH_CAMJE	IFSAHSLPQSIID-KG-----DLYEKHVNDHV	206
sp	Q8DFM2	HEMH_VIBVU	LCSYHGIPQRYADNG-----DVYPLHCEMTT	215
sp	Q7MMR4	HEMH_VIBVY	LCSYHGIPQRYADNG-----DIYPLHCEMTT	215
sp	Q9KTB6	HEMH_VIBCH	LCSYHGIPKRYAQN-----DIYPEHCLKTT	215
sp	Q87RH3	HEMH_VIBPA	LCSYHGIPKRYADNG-----DIYPQHCEATT	215
sp	Q6LTE0	HEMH_PHOPR	LCSYHGIPKRYADNG-----DDYPQRCHAT	214
sp	Q8EFF4	HEMH1_SHEON	ILSFHGIPLRATEG-----DPYPEQCRTTA	236
sp	Q8XD39	HEMH_ECO57	LLSYHGIPQRYADEG-----DDYPQRCRTTT	215
sp	P23871	HEMH_ECOLI	LLSYHGIPQRYADEG-----DDYPQRCRTTT	215
sp	Q8FK83	HEMH_ECOL6	LLSYHGIPQRYADEG-----DDYPQRCRTTT	215
sp	Q83SE5	HEMH_SHIFL	LLSYHGIPQRYADEG-----DDYPQRCRTTT	215
sp	Q8Z8T2	HEMH_SALTI	LLSYHGIPQRYADEG-----DDYPQRCRDTT	215
sp	P37408	HEMH_SALTY	LLSYHGIPQRYADEG-----DDYPQRCRDTT	215
sp	Q8ZC98	HEMH_YERPE	VMSFHGIPKRYAQLG-----DDYPIRCEDTS	215
sp	Q05338	HEMH_YERPS	VMSFHGIPKRYAQLG-----DDYPIRCEDTS	215
sp	P43413	HEMH_YEREN	VLSFHGIPKRYAQLG-----DDYPQRCEDTS	215
sp	Q6D7Z4	HEMH_ERWCT	VISYHGIPVRYANEG-----DDYPQRCRATT	215
sp	Q7N0P6	HEMH_PHOLL	LLSYHGIPQRFVDTG-----DIYAEQCKLTT	215
sp	P43868	HEMH_HAEIN	LFSYHGIPLRYEKMG-----DYYREHCKQTT	217
sp	P57874	HEMH_PASMU	LFSFHGIPVRYENMG-----DYYREHCKQTV	216
sp	Q65SV7	HEMH_MANSM	LFSFHGIPKRYEQEG-----DFYRPQCEQTA	216
sp	Q8CWW4	HEMH_STRMU	LFSFHGIPQRYVIEG-----DYYTEHCQQTA	214
sp	Q8D226	HEMH_WIGBR	IMSFHGIPKRYIKDG-----DDYLKRCNVTK	215
sp	Q8EBZ7	HEMH2_SHEON	VLSYHGMPERNLHLG-----DPYCFMCKTT	222

sp	Q6F7N0	HEMH_ACIAD	LMSFHGIPQPYADKG-----DPYADRCRETA	223
sp	Q7WG10	HEMH_BORBR	VMSFHGLPRYSIELG-----DPYRDCLDTA	249
sp	Q7W515	HEMH_BORPA	VMSFHGLPRYSIELG-----DPYRDCLDTA	249
sp	Q7VVX8	HEMH_BORPE	VMSFHGLPRYSIELG-----DPYRDCLDTA	249
sp	Q62HD1	HEMH_BURMA	VLSFHGVPKRTLDLG-----DPYHDQCQQT	247
sp	Q63R43	HEMH_BURPS	VLSFHGVPKRTLDLG-----DPYHDQCQQT	247
sp	Q8XW32	HEMH_RALSO	LLSFHGVPRRTLELG-----DPYHCACLKTG	239
sp	Q7NV65	HEMH_CHRVO	VMSFHGVPRFTRDKG-----DPYHCECQKTG	234
sp	Q82UK8	HEMH_NITEU	IISFHGVPKRTLEMG-----DPYHCECQKTG	232
sp	Q9JVA5	HEMH_NEIMA	MLSFHGVPQKHYDLG-----DPYPDECRTA	227
sp	Q9K097	HEMH_NEIMB	MLSFHGVPQKHHDLG-----DPYPDECRTA	227
sp	Q8PEX0	HEMH_XANAC	MFSFHGLPQRVADAG-----DPYPQQCERSA	215
sp	Q8P3H6	HEMH_XANCP	MFSFHGLPQRVANAG-----DPYPQQCERSA	215
sp	Q9PFU1	HEMH_XYLFA	MFSFHGLPQRVANNG-----DPYPQRCQVSA	215
sp	Q87B82	HEMH_XYLFT	MFSFHGLPQRVANNG-----DPYPQRCQVSA	215
sp	Q607T4	HEMH_METCA	VFSFHGLPKCCIDRG-----DPYASQCQATA	216
sp	Q8U9F7	HEMH_AGR5	ITSFHGIPQSYFKKG-----DPYCHCQKTA	235
sp	Q92M52	HEMH_RHIME	LASFHGLPQKSYFEKG-----DPYQCQKTA	230
sp	Q93TG2	HEMH_BRUME	LTSYHGIPKSYSDKG-----DPYRQCLETT	243
sp	Q98H61	HEMH_RHILO	ITSYHGIPKPYSDKG-----DPYQAHCLETT	244
sp	P28602	HEMH_BRAJA	VASFHGMPPKSYVDKG-----DPYQEHCIATT	236
sp	Q6NBF3	HEMH_RHOPA	VASFHGMPPQAYIDKG-----DPYQAQCQVATV	236
sp	Q59735	HEMH_RHOCA	VASYHGMPPKRYHREG-----DPYHCQCQKTS	241
sp	P57779	HEMH_ZYMMO	LLSYHGMPVKTRELG-----DPYFQCQATS	224
sp	Q833G5	HEMH_ENTFA	VFSYHGIPMSYVKDG-----DNPYKECTKTT	212
sp	Q9CFB4	HEMH_LACLA	VLSYHGIPLSYVTKKK-----DAYEEQCKETT	208
sp	Q67T48	HEMH_SYMTH	VLSYHSIPQAYTASG-----DDYAAQCESTT	215
sp	Q88XC3	HEMH_LACPL	IFSYSIPTAMVRHG-----DPYQRECEATT	205
sp	P57778	HEMH_PSEFL	LFSFHGLPERHLNKLNPGHSLG--GSGDCCANASPEVRTTCYRGQCFVA	232
sp	Q888A2	HEMH_PSESM	LLSFHGLPERHLHKRDPKTKHC--LKDDCCMTAPAQVVATCYRAQCQLQSA	232
sp	Q88PV4	HEMH_PSEPK	LLSFHGLPERHLKLFKPKGVKHDLRADCCGHGATAEVSSVCYRGQCLATA	234
sp	Q9HVD7	HEMH_PSEAE	LLSFHGLPERHIRKLVKDPADH--LLAENSRNVSPALALCYRQCCLRTA	232
sp	Q6MHT3	HEMH_BDEBA	LFSFHGLPESHVRKIP--GCLT---TEDCCFEKNACAKN-CYRAQCFATA	231
sp	Q83FA4	HEMH_COXBU	LFSYHGLPERHLVKSQCQLAICN--RKNNCSPISSNEN-CYRAQCFETS	235
sp	Q6MAW8	HEMH_PARUW	LFSFHGLPERQIRKGDSTGKCL---TENCCQVICSDNAFCYKAQCQYRTA	233
sp	Q7MXP4	HEMH_PORGI	ILSYHGIPRDHLDKTTTRQALNLR--HPEGCCTEEDPTANVCYRYQTYRRT	242
sp	Q824K8	HEMH_CHLCV	LFSAHGLPMRHVNKG-----DPYNMQCEKSF	207
sp	Q927V1	HEMH_CHLPN	LFSVHGLPVRYISQG-----DPYKQCYESF	208
sp	Q9PJQ6	HEMH_CHLMU	LFSVHGLPMRHIRLG-----DPYAKQCQDSF	205
sp	O84492	HEMH_CHLTR	LFSVHGLPQRHIRLG-----DPYAKQCQASAF	205
sp	Q8GCV0	HEMH_LEPBI	VFSAHGVPMRLIHKG-----DRYMEEVELSV	233
sp	Q81U22	HEMH1_BACAN	IVSAHSLPEKIIA-MGDP-----YPDQLNETA	203
sp	Q6HM97	HEMH1_BACHK	IVSAHSLPEKIIA-MGDP-----YPDQLNETA	203
sp	Q63ES4	HEMH1_BACCZ	IVSAHSLPEKIIA-MGDP-----YPDQLNETA	203
sp	Q73C98	HEMH1_BACCL	IVSAHSLPEKIIA-MGDP-----YPEQLHETA	203
sp	Q81GW5	HEMH1_BACCR	IVSAHSLPEKIIA-MGDP-----YPDQLNETA	203
sp	P32396	HEMH_BACSU	IVSAHSLPEKIKE-FGDP-----YPDQLHESA	204
sp	Q8ERX9	HEMH_OCEIH	IVSAHSLPEKILK-DGDP-----YKHQLEHTA	203
sp	Q71XF4	HEMH_LISMF	IVSAHSLPEKIKQ-HNDP-----YPDQLQETA	203
sp	Q8Y565	HEMH_LISMO	IVSAHSLPEKIKQ-HNDP-----YPNQLQETA	203
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sp	P64124	HEMH_STAAM	VVSAHSLPKGLIEKNNDP-----YPQLEHTA	203
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sp	Q6G8A3	HEMH_STAAS	VVSAHSLPKGLIEKNNDP-----YPQLEHTA	203
sp	P64126	HEMH_STAAN	VVSAHSLPKGLIEKNNDP-----YPQLEHTA	203
sp	Q6GFM4	HEMH_STAAR	VVSAHSLPKGLIEKNNDP-----YPQLEHTA	203
sp	Q8CNS1	HEMH_STAEP	VVSAHSLPKGLIERNDP-----YPHELHETA	203
sp	Q81TU9	HEMH2_BACAN	IVSAHSLPEKIIA-AGDP-----YVEQLQHTA	202
sp	Q6HM28	HEMH2_BACHK	IVSAHSLPEKIIA-AGDP-----YVEQLQHTA	202
sp	Q63EK7	HEMH2_BACCZ	IVSAHSLPEKIIA-AGDP-----YVEQLQHTA	202
sp	Q73C08	HEMH2_BACCL	IVSAHSLPEKIIA-AGDP-----YVQQLQHTA	202
sp	Q81GN7	HEMH2_BACCR	IVSAHSLPEKIIA-AGDP-----YVEQLKHTA	202
sp	Q9KDK9	HEMH_BACHD	IVSAHSLPEKIVD-YGDP-----YPQQLKHTA	202

sp	Q5WHT1	HEMH_BACSK	IFSAHSLPEKIIQ-ANDP-----YPEQLRETA	202
sp	Q72L32	HEMH_THET2	VFTAHSIPLSAVE-KGDP-----YPRQVEKTA	212
sp	Q9RV98	HEMH_DEIRA	ILSAHSLPVRIIK-EGDP-----YADQLHETA	207
sp	Q97R30	HEMH_STRPN	IFSAHSVPFALD-FGDP-----YIDQIFENS	190
sp	Q8DQ04	HEMH_STRR6	IFSAHSVPFALD-FGDP-----YIDQIFENS	190
sp	Q8FTB1	HEMH_COREF	VFTAHSIPLNSKDADGNPIDG-----SIYSRQVEESS	221
sp	Q8NQA1	HEMH_CORGL	VFTAHSIPLTADNAAGTPEDG-----SLYSTQVKEAS	216
sp	Q6NH66	HEMH_CORDI	VFTAHSIPEVANENSGRKEG-----PLYSRQVYEA	224
sp	Q740Y1	HEMH_MYCPA	VFTAHSVPAADERLGP-----RLYSRQVAYAA	195
sp	P71765	HEMH_MYCTU	VFTAHSIPTAADRRCGP-----NLYSRQVAYAT	195
sp	Q9CBM2	HEMH_MYCLE	VFTAHSVPVATDRRCGP-----ALYSRQVYAA	199
sp	Q5YU18	HEMH_NOCFA	VFTAHSVPAADAAAGPPADGG-----ELYSRQVADAA	209
sp	O07401	HEMH_MYCAV	VFTAHSVPAADERLGP-----RLYSRQVAYAA	194
sp	Q83H94	HEMH_TROW8	LFSTHSIPELDAAFSGPED-----AHFGKYGAYVSQHKAVV	242
sp	Q83FJ2	HEMH_TROWT	LFSTHSIPELDAAFSGPED-----AHFGKYGAYVSQHKAVV	242
sp	Q6AHF2	HEMH_LEIXX	LFSTHSIPSTDAGKSGPSGRPDS-----GEPWEGEGAYAAQHLAVA	241
sp	Q82KJ6	HEMH_STRAW	AFTTHSIPTAAADTSGPVE-----EHGDGGAYVQKHLDA	221
sp	O50533	HEMH_STRCO	AFCTHSIPTSAADTSGPVE-----EHGDGGAYVQKHLDA	221
sp	Q7UFZ7	HEMH_RHOBA	LFTAHSIPMGADN-----CDYEKQLRESC	204
sp	P72183	HEMH_PROFR	VFTTHSIPTAMAETSGPHG-----NAYIPQHLALI	203
sp	Q9HLB8	HEMH_THEAC	LFDAHSLPAPDREED-----YLFWLRYST	186
sp	Q978U9	HEMH_THEVO	LFDAHSLPHPENEE-----YLFWLRYST	188

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sp	P42043	HEMH1_ARATH	DLIMEELKAR-G---VLNDHKLAYQSRVGPVQWLKPYTDEVLVDLGKSG-	351
sp	P42044	HEMH_CUCSA	CLIMQELKAR-G---IGNEHTLAYQSRVGPVQWLKPYTDEVLVELGQKG-	376
sp	P42045	HEMH_HORVU	ALIMEELKSR-G---TLNDHTLAYQSRVGPVQWLKPYTDEVLVELGQKG-	370
sp	O04921	HEMH2_ARATH	DLIMEELDKR-K---ITNAYTLAYQSRVGPVEWLKPYTEEAITELGKKG-	362
sp	O22101	HEMH_ORYSA	DLIMEELEKR-G---ITNACTLAYQSRVGPVEWLRPYTDETIIELGQKG-	343
sp	Q8YQR8	HEMH_ANASP	ALIMQTLNR-----PNPHTLAYQSRVGPVEWLQPYTEDALKELGAQG-	260
sp	P54225	HEMH_SYNY3	RLIMRTLDR-----PNQYTLAYQSRVGPVEWLKPYTEBALQKLAGEG-	260
sp	Q8DGU6	HEMH_SYNEL	RLIIMAALNR-----PNAHVLAYQSRVGPVEWLQPYTEDVILELAAQG-	261
sp	Q7VD58	HEMH_PROMA	LLIIDKVEKSLG---FNSNYTSLYQSRVGPEEWLKPYTEEVLEELGANG-	264
sp	Q7V2F5	HEMH_PROMP	LLIIDELEKYLK---HTNPYTLAYQSRVGPVEWLKPYTEEVLTDLGKAK-	264
sp	Q7V6C6	HEMH_PROMM	TLIMAELENLLG---YGNPHSLAYQSRVGPPEEWIQQPYTDQVIEQLGEAG-	264
sp	Q7U5G0	HEMH_SYNPX	DLIMKSLAEHMG---HSPNHTLAYQSRVGPVEWLKPYTEEALEQLGEAK-	264
sp	Q7NMC7	HEMH_GLOVI	DLVMQSLGR-----PNAHSLAYQSRVGPVEWLKPYTEDTINELAQKG-	260
sp	Q9ZC84	HEMH_RICPR	NKIVKELNKR-----DLDYKITYQSRVGPVEWLKPNTEDEIE-LAGKL-	251
sp	Q68VM9	HEMH_RICTY	NKIVKELNIK-----DLDYKITYQSRVGPVEWLKPNTEDEIE-LAGKL-	251
sp	Q92FV4	HEMH_RICCN	QAIVKELNIK-----DLDYKITYQSRVGPVEWLKPNTEDEIE-LAGKL-	251
sp	Q73FY6	HEMH_WOLPM	ELIVEKLAIN-----NLDWSICYQSKIGPVKWLPESTSESELL-RAKAD-	256
sp	P57777	HEMH_CAUCR	AAVAHLPP-----QIEWTVCYQSRVGPLKWIGPSTDEIR-RAGE-	255
sp	O67083	HEMH_AQUAE	KLIMENFPE-----VEYTLAYQSKVGFQKWLPESTDEVIRNLIKKE-	247
sp	P22830	HEMH_HUMAN	QKVMERLEYCN-----PYRLVWQSKVGPMPWLGQPTDESIKGLCERG-	326
sp	P22315	HEMH_MOUSE	HKVMKELGYPN-----PYRLVWQSKVGPMPWLGQPTDEAIKGLCERG-	323
sp	P22600	HEMH_BOVIN	QRVMDKLGYSN-----PYRLVWQSKVGPMPWLGQPTDEAIKGLCKRG-	319
sp	O42479	HEMH_CHICK	QRVMEKLNHSN-----PYRLVWQSKVGPMPWLVQPTDETIKGLCQRG-	305
sp	O57478	HEMH_XENLA	QKVMERLGFNSN-----PYRLVWQSKVGPMAWLGPQPTDESIKGLCQRG-	313
sp	Q9V9S8	HEMH_DROME	HMVMQELGQTN-----PYSLAWQSKVGPLPWLAPATDDAIKGYVQKG-	286
sp	O59786	HEMH_SCHPO	QAVMKRLNYKN-----KFVNAWQSKVGPLPVMSPATDFVIEQLGNRG-	291
sp	P16622	HEMH_YEAST	YNIMQKLFKN-----PYRLVWQSQVGPMPWLGQPTDEIAEFLGPK--	297
sp	Q6APB0	HEMH_DESPS	G-AIEEITGK-----RGRLCFQSKSGPVEWLEPSTPDVLIQLAQEG-	255
sp	Q747F5	HEMH_GEOSL	RLVMERFEGV-----THHLAFQSRAGPVKWLPESTDEMLEHLAAHQ-	254
sp	Q9ZKD4	HEMH_HELPI	SLLKELMQQKNI---PFKEVLLSYQSKLGPMPKWLPESTEEELIE---KHR-	271
sp	P56107	HEMH_HELPY	SLLKELMQQKNT---PFKEVLLSYQSKLGPMPKWLPESTEEELIE---KHR-	271
sp	Q7M7P9	HEMH_WOLSU	QALTKLLEERGI---TFKKITHAYQSKVGPMPKWLPESTLDEVLK---LHA-	252
sp	Q7VHH1	HEMH_HELHP	EVIQKALESEGI---VFKKIALAYQSKVGRMKWIGPSTKETIT---KYK-	243
sp	Q9PI08	HEMH_CAMJE	EILKEKLDH-----FDEFILAYQSKLGPVVKWLEPNTSDVLA---NLN-	246
sp	Q8DFM2	HEMH_VIBVU	E-LLRLELGL-----DKSQIGTTYQSRFGREEWLQPYTDKTLLESLPAKG-	258
sp	Q7MMR4	HEMH_VIBVY	E-LLRLELGL-----DKSQIGTTYQSRFGREEWLQPYTDKTLLESLPAKG-	258
sp	Q9KTB6	HEMH_VIBCH	E-LLAQALGL-----PQDKVMTTYQSQFGKEEWLQPYTDKTMALPRQG-	258
sp	Q87RH3	HEMH_VIBPA	R-LLGEALGL-----SSDQIGMAYQSRFGREEWLQPYTDKTLLETITSKG-	258
sp	Q6LTE0	HEMH_PHOPR	E-KLAERLAM-----PREKMSMSYQSIFGREEWLQPYTEVTIEALAQKG-	257

sp	Q8EFF4	HEMH1_SHEON	K-LLAQALGL-----TDGQWQVCFQSRFGKEEWLTPYADELLADLPRQG-	279
sp	Q8XD39	HEMH_ECO57	R-ELASALGM-----APEKVMMTFQSRFGREPWLMPYTDDETLKMLGEKG-	258
sp	P23871	HEMH_ECOLI	R-ELASALGM-----APEKVMMTFQSRFGREPWLMPYTDDETLKMLGEKG-	258
sp	Q8FK83	HEMH_ECOL6	R-ELASALEM-----APEKVMMTFQSRFGREPWLMPYTDDETLKMLGEKG-	258
sp	Q83SE5	HEMH_SHIFL	R-ELASALGM-----VPEKVMMTFQSRFGREPWLMPYTDDETLKMLGEKG-	258
sp	Q8Z8T2	HEMH_SALTI	R-ELVSALGL-----PPEKVMMTFQSRFGREPWLTPYTDDETLKMLGEKG-	258
sp	P37408	HEMH_SALTY	R-ELVSALGL-----PPEKVMMTFQSRFGREPWLTPYTDDETLKMLGEKG-	258
sp	Q8ZC98	HEMH_YERPE	R-ALRAALPL-----PAEKIIMTYQSRFGREPWLTPYTDDETLKSLPSQG-	258
sp	Q05338	HEMH_YERPS	R-ALRAALPL-----PAEKIIMTYQSRFGREPWLTPYTDDETLKSLPSQG-	258
sp	P43413	HEMH_YEREN	R-ALRAEIAL-----PAEQIMMITYQSRFGREPWLTPYTDDETLKSLPSQG-	258
sp	Q6D7Z4	HEMH_ERWCT	E-ALIAALGL-----PEGKIMMITYQSRFGREPWLTPYTDDETMQGLPAQG-	258
sp	Q7N0P6	HEMH_PHOLL	R-LLKQALNY-----VPEKVMMTFQSRFGREPWLTPYVDQTMKTLNPGQ-	258
sp	P43868	HEMH_HAEIN	I-AVVNKLGL-----TENQWRMTFQSRFGREEWLQPYTDKFLSAAAQN-	260
sp	P57874	HEMH_PASMU	L-AVIDRLGL-----TENQWGLSFQSRFGKEEWLQPYTDQFLAQAPSON-	259
sp	Q65SV7	HEMH_MANSM	Q-AVVQKLGL-----KKEQWRLCFQSRFGSEPWLQPYTDKFLSAAAQN-	259
sp	Q8CWW4	HEMH_STRMU	Q-LIAVAAGL-----SEEQWQVSYQSRFGPEEWTRPYTDDETLIQLPKQG-	257
sp	Q8D226	HEMH_WIGBR	K-LVLSKLNLF-----SRKKVIMSFQSKFGNIPWITPITSEVISFLPKKG-	258
sp	Q8EBZ7	HEMH2_SHEON	R-LVAEQLGL-----SKDEFAITFQSRFGKAKWLQPYTDATMQLPSQG-	265
sp	Q6F7N0	HEMH_ACIAAD	R-LVAKQLGL-----TPDDWAI SFQSRFGKQEWKPYTDDELLTTWAANG-	266
sp	Q7WGI0	HEMH_BORBR	R-LLRERLGL-----REDEVEVTFQSRFGSARWLEPYTEPTLAELARQG-	292
sp	Q7W515	HEMH_BORPA	R-LLRERLGL-----REDEVEVTFQSRFGSARWLEPYTEPTLAELARQG-	292
sp	Q7VVX8	HEMH_BORPE	R-LLRERLGL-----REDEVEVTFQSRFGSARWLEPYTEPTLAELARQG-	292
sp	Q62HD1	HEMH_BURMA	A-LLMSALGL-----TTFECRVTFQSRFGKAEWLQPYTAPTLLKELGAAG-	290
sp	Q63R43	HEMH_BURPS	A-LLMSALGL-----TTFECRVTFQSRFGKAEWLQPYTAPTLLKELGAAG-	290
sp	Q8XW32	HEMH_RALSO	R-LLGEALGL-----PQGQYLVTFQSRFGRAEWLQPYTAPTLEELGRVG-	282
sp	Q7NV65	HEMH_CHRVO	R-LLAEALQL-----RPDQYVVSFQSRFGRTTEWLKPYTSEVLEALGKAK-	277
sp	Q82UK8	HEMH_NITEU	R-LLAEALEL-----ADDRYQICFQSRFGFAQWLGPYTAELAEALGKQK-	275
sp	Q9JVA5	HEMH_NEIMA	K-LLAEALEL-----TEDQYVVSFQSQFGRKAWVTPSTQDLFGKLPKQG-	270
sp	Q9K097	HEMH_NEIMB	K-LLAEALEL-----TEDQYVVSFQSQFGRKAWVTPSTQDLFGKLPKQG-	270
sp	Q8PEX0	HEMH_XANAC	Q-AIVALGL-----GADEWQMGYQSRFGAERWLQPYAEPTLWLKLAEGG-	258
sp	Q8P3H6	HEMH_XANCP	Q-AIVALGL-----GPDAWQMGYQSRFGAERWLQPYAEPTLWALAEGG-	258
sp	Q9PFU1	HEMH_XYLFA	S-LIAAALDL-----NESEWVLGYQSRFGAERWLQPYAEPTLWALAESG-	258
sp	Q87B82	HEMH_XYLFT	S-LIAAALNL-----NESEWVLGYQSRFGAERWLQPYAEPTLWALAESG-	258
sp	Q607T4	HEMH_METCA	Q-GIARLLEL-----SDDEWLLTYQSRFGRAEWLQPYCIDTLRELPSQG-	259
sp	Q8U9F7	HEMH_AGRT5	R-LLREALGR-----TEKNFMITFQSRFGPEEWLQPYTDKTVKLASEG-	278
sp	Q92M52	HEMH_RHIME	R-LLREKLGW-----PQDRLQVTFQSRFGPEEWLQPYTDATVERLAKEG-	273
sp	Q93TG2	HEMH_BRUME	R-LLRERLGL-----GEDEMRAITFQSRFGPEEWLQPYTDDETVKELAKNG-	286
sp	Q98H61	HEMH_RHILO	R-LLREKLGW-----DEKLLITTFQSRFGAQEWLQPYTDKTVKELGKDG-	287
sp	P28602	HEMH_BRAJA	E-ALRRRLGV-----DASKLLLTFQSRFGNDEWLQPYTDKTMERLAKEG-	279
sp	Q6NBF3	HEMH_RHOPA	E-ALRRRMGV-----ADDKLLLTFQSRFGFDQWLQPYTDKTI EALARKG-	279
sp	Q59735	HEMH_RHOCA	R-LLRERLGL-----GPDSIDTTFQSVFGTEEWLQPYTVEHVVLAEAG-	284
sp	P57779	HEMH_ZYMMO	Q-ALSSLLDI-----P---VITSFQSRFGSQKWFPTPATDMLKELPSKN-	264
sp	Q833G5	HEMH_ENTFA	K-LIMDKLG-----DIRYQTYQSKFGPSEWLKPATDDTLKKLPSKG-	253
sp	Q9CFB4	HEMH_LACLA	R-LVVS KLGL-----REEEYHTYQSKFGPEKWLQPYTIDRVAELPKEN-	251
sp	Q67T48	HEMH_SYMTH	D-AVRDRFP-----DLKIVMGYQSKFGNDPWLQPYTDVLELVRTG-	256
sp	Q88XC3	HEMH_LACPL	KAVLAERPEL-----PADKVITAYQSKFGPMPWLKPYLKNELMQLVELG-	249
sp	P57778	HEMH_PSEFL	R-DFAARMGL-----PDDKWSVAFQSRFGRAEWLQPYTETEARLEALAQQG-	275
sp	Q888A2	HEMH_PSESM	A-AFAKRMGI-----PDGKWSVAFQSRFGRAEWLQPYTETEARLEALAQQG-	275
sp	Q88PV4	HEMH_PSEPK	K-AFAQSMGI-----PDGKWSVAFQSRFGRAEWLQPYTETEARLEALAQQG-	277
sp	Q9HVD7	HEMH_PSEAE	E-AFAERAGL-----EQGRWSVAFQSRFGRAEWLQPYTETEARLEALAQQG-	275
sp	Q6MHT3	HEMH_BDEBA	T-AIAESLNL-----APSHWSVAFQSRFGRAEWLQPYTETEARLEALAQQG-	274
sp	Q83FA4	HEMH_COXBU	R-LIAKLNGL-----TDQYGVAFQSRFGRAEWLQPYTETEARLEALAQQG-	278
sp	Q6MAW8	HEMH_PARUW	K-AIASKLRI-----KLEQYTVCFQSRFGKGTWIPYTSDDLKDKLAKN-	276
sp	Q7MXP4	HEMH_PORGI	A-LIREALGL-----AEEQVEQVQSRFGHTTEWLQPYTETEARLEALAQQG-	285
sp	Q824K8	HEMH_CHLCV	R-AISERL-----PNLETHLCYQSKFGPGKWLSPSTKDLKATLTKTDK-	248
sp	Q9Z7V1	HEMH_CHLPN	S-AITTNF-----KQSENFLCFQSKFGPGKWLSPSTKDLKATLTKTDK-	249
sp	Q9PJQ6	HEMH_CHLMU	N-ALIG-----ESEGVL SFQSKFGIGEWLQPYTETEARLEALAQQG-	243
sp	Q84492	HEMH_CHLTR	E-ALRG-----ELGKIAFQSKFGIGKWLDPSTQEVCSLRTKK-	243
sp	Q8GCV0	HEMH_LEPBI	K-GIADELSKFG---FNGGVHISYQSKVGPAPKWTPESTIQMISSLAKQG-	278
sp	Q81U22	HEMH1_BACAN	DYIARGAEVAN-----YAVGW--QSAGNTPDPWIGPDVQDLTRELNEKYG	246
sp	Q6HM97	HEMH1_BACHK	DYIARGAEVAN-----YAVGW--QSAGNTPDPWIGPDVQDLTRELNEKYG	246
sp	Q63ES4	HEMH1_BACCZ	DYIARGAEVAN-----YAVGW--QSAGNTPDPWIGPDVQDLTRELNEKYG	246
sp	Q73C98	HEMH1_BACCI	DYIARGAEVAN-----YAVGW--QSAGNTPDPWIGPDVQDLTRELNEKYG	246

sp	Q81GW5	HEMH1_BACCR	DYIARGAEVAN-----YAVGW--QSAGNTPDPWIGPDVQDLTRELNEKHG	246
sp	P32396	HEMH_BACSU	KLIAEGAGVSE-----YAVGW--QSEGNTDPWLGPDVQDLTRDLFEQKG	247
sp	Q8ERX9	HEMH_OCEIH	KLIVEEADVKN-----YAVGW--QSEGNTDPWLGPDVQDLTRELYESEG	246
sp	Q71XF4	HEMH_LISMF	DFIFEKVVVPH-----YALGW--QSEGKTGEPWLGPDVQDLTRELYGREK	246
sp	Q8Y565	HEMH_LISMO	DFIFEKVVVPH-----YALGW--QSEGKTGEPWLGPDVQDLTRELYGREK	246
sp	Q929G2	HEMH_LISIN	DLIFDKVAVPH-----YALGW--QSEGKTGEPWLGPDVQDLTRELYGREK	246
sp	P64124	HEMH_STAAM	LLIIEQSNIEH-----IAIGW--QSEGNTGTPWLGPDVQDLTRDLYEKHQ	246
sp	P64125	HEMH_STAAN	LLIIEQSNIEH-----IAIGW--QSEGNTGTPWLGPDVQDLTRDLYEKHQ	246
sp	Q6G8A3	HEMH_STAAS	LLIIEQSNIEH-----IAIGW--QSEGNTGTPWLGPDVQDLTRDLYEKHQ	246
sp	P64126	HEMH_STAAW	LLIIEQSNIEH-----IAIGW--QSEGNTGTPWLGPDVQDLTRDLYEKHQ	246
sp	Q6GFM4	HEMH_STAAR	LLIIEQSNIEH-----IAIGW--QSEGNTGTPWLGPDVQDLTRDLYEKHQ	246
sp	Q8CNS1	HEMH_STAEP	EILKQESNIIH-----VAEGW--QSEGNTGTPWLGPDVQDLTRDLYEKHQ	246
sp	Q81TU9	HEMH2_BACAN	DLIAAAANIQN-----YTIGW--QSAGNTPDPWIGPDVQDLTRDLFEFYR	245
sp	Q6HM28	HEMH2_BACHK	DLIAAAANIQN-----YTIGW--QSAGNTSDSWIGPDVQDLTRDLFEHR	245
sp	Q63EK7	HEMH2_BACCZ	DLIAAAANIQN-----YTIGW--QSAGNTSDPWIGPDVQDLTRELFEHR	245
sp	Q73C08	HEMH2_BACC1	DLIAAAANIQN-----YTIGW--QSAGNTPDPWIGPDVQDLTRDLFEHR	245
sp	Q81GN7	HEMH2_BACCR	DLIAEAANIQN-----YTIGW--QSAGNTPDPWIGPDVQDLTKDLYEEHG	245
sp	Q9KDK9	HEMH_BACHD	DLIAKAGAITN-----YAVGW--QSEGNTPEPWLGPDVQDLTRDLYETHG	245
sp	Q5WHT1	HEMH_BACSK	DLIADMANVPN-----YAVGW--QSEGNTPEPWLGPDVQDLTRDLYETHG	245
sp	Q72L32	HEMH_THET2	ELIAKKLALPR-----FHVAY--QSAGRTPEPWLGPDINELLRTLKEE-G	254
sp	Q9RV98	HEMH_DEIRA	RLVAAQAGLTD-----EQWSWSYQSAGRSPEPWLGPDVQDLDEHLRDLNEQ-G	251
sp	Q97R30	HEMH_STRPN	KLVAEKLGLSS-----EQYNTWQSESDIGIPWIKPDVLEYLREQTEH--	233
sp	Q8DQ04	HEMH_STRR6	KLVAEKLGLSS-----EQYNTWQSESDIGIPWIKPDVLEYLREQTEH--	233
sp	Q8FTB1	HEMH_COREF	ALIAAREAGIDD-----FDVVW-QSRSGSPHPWLEPDIVDHAVELNENNG	265
sp	Q8NQA1	HEMH_CORGL	ALIAEAVGVSD-----FDVVW-QSRSGSPHTPWLEPDIVDHAVELNEK-G	259
sp	Q6NH66	HEMH_CORDI	SLVAKHLGISQE---RYDVVW-QSASGNGQIPWLEPDILDYAKCQHDE-G	269
sp	Q740Y1	HEMH_MYCPA	RLVAAAAGYAE-----HDLVW-QSRSGPPQVRWLEPDVADHLRALAES-G	238
sp	P71765	HEMH_MYCTU	RLVAAAAGYCD-----FDLAW-QSRSGPPQVPWLEPDVTDQTLGLAGA-G	238
sp	Q9CBM2	HEMH_MYCLE	RLVAAAGYAD-----YDLTW-QSRSGPPYVPWLAPDVGDLMTLASA-G	242
sp	Q5YU18	HEMH_NOCAF	RLCAAATGFAD-----HDLVW-QSRSGPPQVPWLEPDIVDHLEDLAGR-G	252
sp	O07401	HEMH_MYCAV	RLVAAAAGYAE-----HDLVW-QSRSGPPQVRWLEPDVADHLRALAES-G	237
sp	Q83H94	HEMH_TROW8	EVIMSRRLVTDPDQLQNYQLVY-QSRSGDPSTPWLEPDINDAIRVL--RG-	288
sp	Q83FJ2	HEMH_TROWT	EVIMSRRLVTDPDQLQNYQLVY-QSRSGDPSTPWLEPDINDAIRVL--RG-	288
sp	Q6AHF2	HEMH_LEIXX	EIVS--HEATGGTIG-WDLVY-QSRSGPPSMPWLEPDINDRIAELPELG-	286
sp	Q82KJ6	HEMH_STRAW	RLIADAVREETGIDHPWQLVY-QSRSGAPHIPWLEPDICDHLQELHGAG-	269
sp	O50533	HEMH_STRCO	RLIADAVREERTGVDHPWQLVY-QSRSGAPHIPWLEPDICDHLLEERQAAG-	269
sp	Q7UFZ7	HEMH_RHOBA	RLVADACGAVD-----WDLVY-QSRSGPPSQPWLEPDVLDIAIEMDDAKK	248
sp	P72183	HEMH_PROFR	DAVMAELAALG-LRPSWELAY-QSRSGSPRTPWLEPDINDVITRLAGEG-	250
sp	Q9HLB8	HEMH_THEAC	YKISQILGLSR-----SDFGF-QGG----HLGWLGPSIYNVYRKAKEK--	224
sp	Q978U9	HEMH_THEVO	YKITQIMGLRS-----SDFGF-QGG----HEGWLGPSIYNVYRKAKEK--	226

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sp	P42043	HEMH1_ARATH	VKSL LAVPVSFVSEHIETLEEIDMEYREL-ALESGVENWGRVPALGLTPS	400
sp	P42044	HEMH_CUCSA	IKSL LAVPVSFVSEHIETLEEIDMEYKHL-ALESGIQNWGRVPALNCNSS	425
sp	P42045	HEMH_HORVU	VKSL LAVPVSFVSEHIETLEEIDMEYREL-ALESGIENWGRVPALGCTSS	419
sp	O04921	HEMH2_ARATH	VENLLAVPISFVSEHIETLEEIDVEYKEL-ALKSGIKNWGRVPALGTPEM	411
sp	O22101	HEMH_ORYSA	VKSL LAVPISFVSEHIETLEEIDVEYKEL-ALESGIKHWGRVPALGCEPT	392
sp	Q8YQR8	HEMH_ANASP	VKDLVVVPISFVSEHIETLQEIDIEYREI-AEEAGIHNFRVPALNTHPV	309
sp	P54225	HEMH_SYNY3	IDDLVVVPISFVSEHIETLQEIDIEYREI-AEEAGIDNFRVPALNTHPV	309
sp	Q8DGU6	HEMH_SYNEL	VKTLVVVPISFVSEHIETLQEIDIEYREI-AEEAGIEVFRVPALNDHNG	310
sp	Q7VD58	HEMH_PROMA	VKELIVVPISFVSEHIETLQEIDIEYKLI-ALNNGIINFRVKALDITYPL	313
sp	Q7V2F5	HEMH_PROMP	VNDLIVVPISFVSEHIETLQEIDIEYKEI-AEKAGIVNFRVKALNTHPT	313
sp	Q7V6C6	HEMH_PROMM	TRDLVVVPISFVSEHIETLAEIDIEYREL-ATEAGIVHFRVPALDITYPT	313
sp	Q7U5G0	HEMH_SYNPX	TNDLVVVPISFVSEHIETLEEIDIEYREL-ATEAGVFNFRVRALDITYPP	313
sp	Q7NMC7	HEMH_GLOVI	VRSL LAVPVSFISEHIETLQEIEIEYREV-AEAAGIHFRRAKALNVNKT	309
sp	Q9ZC84	HEMH_RICPR	KKDIIIVPISFVSEHVETLVELDIEYKLI-ADKYKI-QYTRIPTLGTNKI	299
sp	Q68VM9	HEMH_RICTY	KKDIIIVPISFVSEHVETLVELDIEYKFI-ADKYNI-QYTRIPTLGTNKI	299
sp	Q92FV4	HEMH_RICCN	KKDIIIVPISFVSEHVETLVELDIEYKLI-ADKYEI-QYTRIPTLGTNKI	299
sp	Q73FY6	HEMH_WOLPM	GVPVVLSPISFVSEHSETLVELDIEYKAI-IKDG---YFRVPTLSTDPL	302
sp	P57777	HEMH_CAUCR	DKGVMITPIAFVSEHVETLVELDHEYAEI-AEEVGAAPYLRVSALGTAPE	304
sp	O67083	HEMH_AQUAE	VKKLLVIPISFVSEHSETLYELDKQYREL-AQELGYEEFVRVPTLRNTPY	296
sp	P22830	HEMH_HUMAN	RKNILLVPIAFTSDHIETLYELDIEYSQVLAKECGVENIRRAESLNGNPL	376
sp	P22315	HEMH_MOUSE	RKNILLVPIAFTSDHIETLYELDIEYSQVLAQKCGAENIRRAESLNGNPL	373

sp	P22600	HEMH_BOVIN	RKNILLVPIAFTSDHIETLYELDIEYSQVLASECGLENIRRAESLNGNPL	369
sp	Q42479	HEMH_CHICK	KKNMLLVPIAFTSDHIETLYELDIEYAQVLANECGVENIRRAESLNGNPL	355
sp	O57478	HEMH_XENLA	KKNILLVPIAFTSDHIETLYELDIEYAQVLAKECGVENIRRSESLNGNPL	363
sp	Q9V9S8	HEMH_DROME	LKNFILVPIAFVNEHIETLHIELDIEYCDLAKEVGVVEEIRRAATPNHDPL	336
sp	O59786	HEMH_SCHPO	QKNMILVPIAFTSDHIETLTKEL--EDYIEDAKQKGITGVKRVSSINGSMT	339
sp	P16622	HEMH_YEAST	VDGLMFIPIAFTSDHIETLHEIDLGVIGESEYK---DKFKRCESLNGNQT	344
sp	Q6APP0	HEMH_DESPS	VKNILMVPISFVSDHVVETLYEIDILYKKQ-AKCLG-MRLTSCPSLNTQEQ	303
sp	Q747F5	HEMH_GEOSL	VKNLLIVPLSFVSDHIETLHEIDIEYAQE-AHKLGYSRFRSPSLNTSPT	303
sp	Q9ZKD4	HEMH_HELPJ	KSNI I IYPLAFTIDNSETLYELDMQYRLM-AERLAVKEYLVCPCLNDSIE	320
sp	P56107	HEMH_HELPY	KSHI I IYPLAFTIDNSETLYELDMQYRLM-AERLAVKEYLVCPCLNDSIE	320
sp	Q7M7P9	HEMH_WOLSU	KEKILLYPIAFTLDNSETDFELRIEYQEK-ATHLGITDYRVASCLNDSTR	301
sp	Q7VHH1	HEMH_HELHP	KHKMIFPLSFTLDNSETYELKILYASL-AKELNVPQYRVSCFNDRNER	292
sp	Q9PI08	HEMH_CAMJE	-DKALIYPIISFCIDCSETIFELGMEY-----KHLKYNVDLISCPNDSDE	290
sp	Q8DFM2	HEMH_VIBVU	IKSLDVI TPAFVSDCLETLEEISEQQQES-FLHAGGEQYRFIPCLNDAPS	307
sp	Q7MMR4	HEMH_VIBVY	IKSLDVI TPAFVSDCLETLEEISEQQQES-FLHAGGEQYRFIPCLNDAPS	307
sp	Q9KTB6	HEMH_VIBCH	IKKLDVICPAFVSDCLETLEEIAEQNQEI-FLHSGGEAFHYVPCLNDSQS	307
sp	Q87RH3	HEMH_VIBPA	VKKIDIMTPAFSSDCLETLEEIAGENKEI-FMEAGGEQFHYIPCLNDDDM	307
sp	Q6LTE0	HEMH_PHOPR	IKRLDVMCPAFVSDCLETLEEIAEQCKET-FIKAGGDVFNLIIPCLNDNEA	306
sp	Q8EFF4	HEMH1_SHEON	VKSVDVICPAFATDCLETLEEISIGAKET-FLHAGGEAYHFIPCLNDEL	328
sp	Q8XD39	HEMH_ECO57	VGHIQVMCPGFAADCLETLEEIAEQNREV-FLGAGGKKEYEYIPALNATPE	307
sp	P23871	HEMH_ECOLI	VGHIQVMCPGFAADCLETLEEIAEQNREV-FLGAGGKKEYEYIPALNATPE	307
sp	Q8FK83	HEMH_ECOL6	VGHIQVMCPGFAADCLETLEEIAEQNREV-FLGAGGKKEYEYIPALNATPE	307
sp	Q83SE5	HEMH_SHIFL	VGHIQVMCPGFAADCLETLEEIAEQNREV-FLGAGGKKEYEYIPALNATPE	307
sp	Q8Z8T2	HEMH_SALTI	TGHIQVMCPGFAADCLETLEEIAEQNREI-FLEAGGKKEYEYIPALNATPE	307
sp	P37408	HEMH_SALTY	TGHIQVMCPGFAADCLETLEEIAEQNREI-FLEAGGKKEYEYIPALNATPE	307
sp	Q8ZC98	HEMH_YERPE	VKHIQLICPGFSADLETLEEIKEQNREF-FLHAGGEKFEYIPALNDDEG	307
sp	Q05338	HEMH_YERPS	VKHIQLICPGFSADLETLEEIKEQNREF-FLHAGGEKFEYIPALNDDEG	307
sp	P43413	HEMH_YEREN	VKHIQLICPGFSADLETLEEIKEQNREF-FIHAGGEKFEYIPALNDDEG	307
sp	Q6D7Z4	HEMH_ERWCT	IKHIQIMCPGFAADCLETLEEIQEQNREI-FLHAGGEAFHYIPALNDDDL	307
sp	Q7N0P6	HEMH_PHOLL	IKHIQVLCPGFSSDCLETLEEIKQLNKEM-FLNAGGEKFEYIPALNDNAS	307
sp	P43868	HEMH_HAEIN	IQKIAVICPGFVSDCLETLEEIDEENREN-FLNNGGQSYQYIPALNVEHA	309
sp	P57874	HEMH_PASMU	IQKMAVICPGFAADCLETLEEIEEENKEI-FLANGGISYRYIPALNARPE	308
sp	Q65SV7	HEMH_MANSM	ITKLAVICPGFSADLETLEEIKEENKRI-FLAYGGESYHYIPALNDSPE	308
sp	Q8CWW4	HEMH_STRMU	KKKLAVICPGFAADCLETLEEIDITNRKH-FMAAGGQAYRYIPALNASPA	306
sp	Q8D226	HEMH_WIGBR	IKNIQVICPGFSSDCLETLEEIKIQNKKI-FKDNGGKFFHYIPALNYSKI	307
sp	Q8EBZ7	HEMH2_SHEON	VRDVAIVCPAFSADLETLEEIVGENGHI-FTHAGGEKFRYIPALNDNDD	314
sp	Q6F7N0	HEMH_ACIAD	IKSVQILSPAFAADLETLEELEIQNAEL-FLEAGGTSYQYIPALNTSVE	315
sp	Q7WGI0	HEMH_BORBR	VTEVDVVC PGFVADLETLEEISQECRDA-FVAAGGRQFRYIPALNDCPP	341
sp	Q7W515	HEMH_BORPA	VTEVDVVC PGFVADLETLEEISQECRDA-FVAAGGRQFRYIPALNDCPP	341
sp	Q7VVX8	HEMH_BORPE	VTEVDVVC PGFVADLETLEEISQECRDA-FVAAGGRQFRYIPALNDCPP	341
sp	Q62HD1	HEMH_BURMA	VRRADVFCPGFTADLETLEEIGIEVRDE-FVHGGGKEFHRIPCLNASPA	339
sp	Q63R43	HEMH_BURPS	VRRADVFCPGFTADLETLEEIGIEVRDE-FVHGGGKEFHRIPCLNASPA	339
sp	Q8XW32	HEMH_RALSO	TGRVDVFCPGFPADLETLEEIAMEGQST-FRVAGGKDFHYIPCLNDSEP	331
sp	Q7NV65	HEMH_CHRVO	TARVDVVC PGFVGDLETLEEIAMEGKET-FLSHGGGEFHYIPCLNEDPQ	326
sp	Q82UK8	HEMH_NITEU	TGRVDVVC PGFVSDCLETLEEIALEGKAI-FTEAGGGEFHYIPCLNDSH	324
sp	Q9JVA5	HEMH_NEIMA	VTELDVFCPGFLADLETMEEIALMGREQ-FYEAGGKSRYRYIPCLNDNPD	319
sp	Q9K097	HEMH_NEIMB	VTELDVFCPGFLADLETMEEIALMGREQ-FYEAGGKSRYRYIPCLNDNPD	319
sp	Q8PEX0	HEMH_XANAC	VRSFDLVC PGFATDCLETLEEVALG-FSE-TLAERGATLSYIPCLNASDA	306
sp	Q8P3H6	HEMH_XANCP	VRSFDLVC PGFATDCLETLEEVALG-FAE-TLAERGATLSYIPCLNDSTT	306
sp	Q9PFU1	HEMH_XYLFA	IRRFDLVC PGFVSDCLETLEEVALG-FSE-TLAARGATMRYIPCLNDDEPA	306
sp	Q87B82	HEMH_XYLFT	IRRFDLVC PGFVSDCLETLEEVALG-FSE-TLAARGATMRYIPCLNDDEPA	306
sp	Q607T4	HEMH_METCA	IRHVDVVC PGFVADLETLEEIAIANRNE-FLGAGGKNRYRYIPALNASPA	308
sp	Q8U9F7	HEMH_AGR5	IKRIAVMNP GFVSDCLETLEEIAGEAGEI-FLHNGGKEFTHIPCLNDSTE	327
sp	Q92M52	HEMH_RHIME	VKRIAVINP GFVSDCLETLEEIAGQAAES-FHHNGGKEFAHIPCLNDSPE	322
sp	Q93TG2	HEMH_BRUME	VKSAVAVLNP GFVADLETVEIGNEAAEE-FLENGGENFSHIPCLNDSEE	335
sp	Q98H61	HEMH_RHILO	VKSIAIVNPGFVSDCIETLDEIGREAAET-FHHAGGKNFAHIPCLNDSAE	336
sp	P28602	HEMH_BRAJA	VRIAVVTPGFAADCLETLEEIAQENAEI-FKHNGGEQFSAIPCLNDSEP	328
sp	Q6NBF3	HEMH_RHOPA	VKNLAVMNP GFVSDCLETLEEIAQENAEI-FMEHGGEFTAIIPCLNDSDA	328
sp	Q59735	HEMH_RHOCA	KKNIAVISP AFVSDCIETLEEINGEIREA-FEHAGGESFTYVPCLNDDDL	333
sp	P57779	HEMH_ZYMMO	IRNLAVAMP GFVSDCLETLEEIALQKST-FLEAGGENFAALRCLNDSEE	313
sp	Q833G5	HEMH_ENTFA	IKNILIVAP GFVVDLETLEELEHENRNY-FLENGGEVYKYVHPFNGDIE	302
sp	Q9CFB4	HEMH_LACLA	AKKVLICSPAFVADLETLEFELEIENKEV-FVENGGETFDFVHPFNDSLD	300
sp	Q67T48	HEMH_SYMTH	HRHVAVMAPGFAADCIETLHELEVEYAEF-FVKAGGERYDYLPAANDHPL	305

sp	Q88XC3	HEMH_LACPL	KRNVLVVTPSFVVDCLLETLEEDYVQNYQT-FRASGGDRFDLVPMPNKDTG	298
sp	P57778	HEMH_PSEFL	VKKLLVMCPAFVADCIETLEEIGDRGLEQ-FREAGGEELVLPCLNDDPQ	324
sp	Q888A2	HEMH_PSESM	VKKLLVMCPAFVADCIETLEEIGDRGAEQ-FKEAGGEELILVPCLNDDPN	324
sp	Q88PV4	HEMH_PSEPK	VKKLLVMCPAFVADCIETLEEIGMRGSEQ-FVEAGGQELVLPCLNDHPE	326
sp	Q9HVD7	HEMH_PSEAE	VKRLLMCPAFVADCIETLEEIGMRGREQ-FISAGGEDLVLPCLNDHPA	324
sp	Q6MHT3	HEMH_BDEBA	KKNIAVICPSFVADCIETLEEIGIGGQET-FHEHGGDQYLLVPCVNDNPK	323
sp	Q83FA4	HEMH_COXBU	IKKLMVVCPSFPVDCLETLEEIGIRAQSQ-WORLDGETLKLIPSLNAHPQ	327
sp	Q6MAW8	HEMH_PARUW	RKKILVFCPAFVDCLETTEEVSIEYAE-EFKHLGGDTLHLVEGLNSHPV	325
sp	Q7MXP4	HEMH_PORGI	TKRILIACPSFVDCLESLLEEVADHGQSI-FKKAGGADFTYIPCLNSGAN	334
sp	Q824K8	HEMH_CHLCV	-KHLVIVPFGFTSDHIETLYEIEKEYIAV-LIDKG-YQALRVPAIYQSSP	295
sp	Q9Z7V1	HEMH_CHLPN	-PNVIVVPFGFISDHLETLYEIERDYLP-LRSRG-YRALRIPAIYSSPL	296
sp	Q9PJQ6	HEMH_CHLMU	-RYIVVVPFGFVSDHIETLYEIDHLYVPM-LLQRG-YRVVRIPAINSTR	290
sp	O84492	HEMH_CHLTR	-RYIVIVPFGFVSDHIETLHEIDHLYVPI-LLQKG-YRVVRIPAINASSR	290
sp	Q8GCV0	HEMH_LEPBI	-KHIAVYIPISFVSDHIETLEEIGEQFKDL-TWEMGGKSFVRIPALGIYPS	326
sp	Q81U22	HEMH1_BACAN	YTSFVYAPVGFVAEHLEVLVDNDFECKVV--TDEIGAKYYRPEMPNASDA	294
sp	Q6HM97	HEMH1_BACHK	YTSFVYAPVGFVAEHLEVLVDNDFECKVV--TDEIGAKYYRPEMPNASDA	294
sp	Q63ES4	HEMH1_BACCZ	YTSFVYAPVGFVAEHLEVLVDNDFECKVV--TDEIGAKYYRPEMPNASDA	294
sp	Q73C98	HEMH1_BACC1	YTSFVYAPVGFVAEHLEVLVDNDFECKVV--TDEIGAKYYRPEMPNASDA	294
sp	Q81GW5	HEMH1_BACCR	YTSFVYAPVGFVAEHLEVLVDNDFECKVV--TDEIGAKYYRPEMPNASDA	294
sp	P32396	HEMH_BACSU	YQAFVYVPGFVADHLEVLVDNDFECKVV--TDDIGASYRPEMPNAKPE	295
sp	Q8ERX9	HEMH_OCEIH	YKAFIYTPVGFVADHLEVLVDNDFECKVV--CDEIGASYRDPMPNVHPE	294
sp	Q71XF4	HEMH_LISMF	YKHFYIYTPVGFVAEHLEVLVDNDFECKVV--TDEVGATYHRPPMPNSDPE	294
sp	Q8Y565	HEMH_LISMO	YKHFYIYTPVGFVAEHLEVLVDNDFECKVV--TDEVGAAHYRPPMPNSDPE	294
sp	Q929G2	HEMH_LISIN	YKHFYIYTPVGFVAEHLEVLVDNDFECKVV--TDEVGAAHYRPPMPNADPE	294
sp	P64124	HEMH_STAAM	YKNFIYTPVGFVCEHLEVLVDNDFECKVV--CDDIGANYRPKMPNTHPL	294
sp	P64125	HEMH_STAAN	YKNFIYTPVGFVCEHLEVLVDNDFECKVV--CDDIGANYRPKMPNTHPL	294
sp	Q6G8A3	HEMH_STAAS	YKNFIYTPVGFVCEHLEVLVDNDFECKVV--CDDIGANYRPKMPNTHPL	294
sp	P64126	HEMH_STAAN	YKNFIYTPVGFVCEHLEVLVDNDFECKVV--CDDIGANYRPKMPNTHPL	294
sp	Q6GFM4	HEMH_STAAR	YKNFIYTPVGFVCEHLEVLVDNDFECKVV--CDDIGANYRPKMPNTHPL	294
sp	Q8CNS1	HEMH_STAEP	FKHFYIYTPVGFVCEHLEVLVDNDFECKVV--CDDIGVNYRPEMPNTHPL	294
sp	Q81TU9	HEMH2_BACAN	YESFIYCPVGFVAEHLEVLVDNDFECKVV--TDELNAAYFRPNMPNAQST	293
sp	Q6HM28	HEMH2_BACHK	YESFIYCPVGFVAEHLEVLVDNDFECKVV--TDELNAAYFRPNMPNAQST	293
sp	Q63EK7	HEMH2_BACCZ	YEAFIYCPVGFVAEHLEVLVDNDFECKVV--TDELNAAYFRPNMPNAQST	293
sp	Q73C08	HEMH2_BACC1	YESFIYCPVGFVAEHLEVLVDNDFECKVV--TDEINAAYFRPNMPNSQSI	293
sp	Q81GN7	HEMH2_BACCR	YESFIYCPVGFVAEHLEVLVDNDFECKVV--TDELNAKYFRPNMPNAQSA	293
sp	Q9KDK9	HEMH_BACHD	YTSMIYCPVGFVADHLEVLVDNDFECKVV--TDELGIDYRPEMPNAKPE	293
sp	Q5WHT1	HEMH_BACSK	YKTFMYCPVGFVAEHLEVLVDNDFECKLV--TDELGVRYLRRPMPNADTR	293
sp	Q72L32	HEMH_THET2	YEEVAVQAVGFVADHLEVLVDNDFECKLV--ARELGLRLLRARSLNADLD	302
sp	Q9RV98	HEMH_DEIRA	IKKVVSIAGFVSDHVEILFDIDIAAQEV--AHELGMTLVRPPALNTDPL	299
sp	Q97R30	HEMH_STRPN	PDHYIFVPISEHIEVLFVDFNDVECYDL--CQEFVNYHRPPMPNTDSR	281
sp	Q8DQ04	HEMH_STRR6	PDHYIFVPISEHIEVLFVDFNDVECYDL--CQEFVNYHRPPMPNTDSR	281
sp	Q8FTB1	HEMH_COREF	QKALVVCVGFISDHMEVWDLDELMDE--ATRRGMVIERVATVGPSTDE	313
sp	Q8NQA1	HEMH_CORGL	QKALVVCVGFISDHMEVWDLDELMDE--AEKRMVVERVATVGPSTDE	307
sp	Q6NH66	HEMH_CORDI	VSELVVPVIGFISDHMEVWDLDELMDE--ASDLGMSISRAATVGHSTDS	317
sp	Q740Y1	HEMH_MYCPA	TRAVIVCPVGFVADHIEVWDLDEELRAQ--AESAGMLMARASTPNAQPR	286
sp	P71765	HEMH_MYCTU	INAVIVCPVGFVADHIEVWDLDEELRLQ--AEAAGIAYARASTPNADPR	286
sp	Q9CBM2	HEMH_MYCLE	TKAVIVCPVGFVADHIEVWDLDEELRSQ--ADAAGVAFARAATPNADRR	290
sp	Q5YU18	HEMH_NOCHA	VDAVVVCPVGFVSDHLEVLVDNDFECKVV--AAELGMFAFARASTPGTDP	300
sp	O07401	HEMH_MYCAV	TRAVIVCPVGFVADHIEVWDLDEELRAQ--AESAGMLMARASTPNAQPR	285
sp	Q83H94	HEMH_TROW8	CEAVLIVPLGFISDHMEVWDLDELMDE--ARECGLFAIRTPPTPGTHPL	336
sp	Q83FJ2	HEMH_TROWT	CEAVLIVPLGFISDHMEVWDLDELMDE--ARECGLFAIRTPPTPGTHPL	336
sp	Q6AHF2	HEMH_LEIXX	VKAIIVPLGFVSDHMEVWDLDELMDE--SEENGLLAVRVPPTPGTHAK	334
sp	Q82KJ6	HEMH_STRAW	VPAVVMAPVGFVSDHMEVWDLDELMDE--AEELGLPVRRSATVGDAR	317
sp	O50533	HEMH_STRCO	VPAVVMAPVGFVSDHMEVWDLDELMDE--AEELGLPVRRSATVGDAR	317
sp	Q7UFZ7	HEMH_RHOBA	LESVLVPLVIGFVSDHMEVWDLDELMDE--CRERGIKMARASAAGTHPD	296
sp	P72183	HEMH_PROFR	VRDVICSPVGFVSDHMEVWDLDELMDE--AAEHSMAFTRVATVGTLPV	298
sp	Q9HLB8	HEMH_THEAC	--KITVPIPSFLYDHLIYLDLDFEYFRKA--VEAKGMHYRRVMPNDSAM	270
sp	Q978U9	HEMH_THEVO	--KIIAVPIPSFLYDHLIYLDLDFEYFRKA--IEEDGYSYERVPMPNDSAM	272

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sp	P42043	HEMH1_ARATH	FITDLADAVIESLPSA-----EAMSNPNAVVDSESE--	432
sp	P42044	HEMH_CUUSA	FISDLADAVIEALPSA-----TALAPHTSSTDDADD----	455
sp	P42045	HEMH_HORVU	FISDLADAVVEALPSA-----SAMATRKKVKTDSDD----	449

sp	O04921	HEMH2_ARATH	FISDLADAVVESLPYVGAMAVSNLEARQSLVPLGVSVEELLATYDSQRREL	461
sp	O22101	HEMH_ORYSA	FITDLADAVIESLPYVGAMAVSNLEARQLVPLGVSVEELLAAYDSKRDEL	442
sp	Q8YQR8	HEMH_ANASP	FIRALADLVIDALNKP-----SFKLSQAAQIKKMVKMYPPE-----	346
sp	P54225	HEMH_SYNY3	FIDALAQMVMSLNDP-----PCTFETVPHPKKNMKMYPQER---	346
sp	Q8DGU6	HEMH_SYNEL	FISALAQLVKEALAAP-----PRTFAEVNQSRKRKVKLYPQER---	347
sp	Q7VD58	HEMH_PROMA	FINGLADLVASCLSGP-----EISLDEAAKLPEKVKLYPQEK---	350
sp	Q7V2F5	HEMH_PROMP	FIDGLSELVVSCLEGP-----IINIEKASELPEKVKLYPQEK---	350
sp	Q7V6C6	HEMH_PROMM	FIEGLADLVGSSLEGP-----EINLDEAAKLAGRVKVFYPQER---	350
sp	Q7U5G0	HEMH_SYNPX	FIEGLADLVTTSLGEP-----EVSLDAAAELPTKVKLYPQEK---	350
sp	Q7NMC7	HEMH_GLOVI	FIDDLAEMVIENLG-----VYSR-----	327
sp	Q9ZC84	HEMH_RICPR	FINSLTNILLRFIN-----	313
sp	Q68VM9	HEMH_RICTY	FINSLTNILLRFIN-----	313
sp	Q92FV4	HEMH_RICCN	FINSLTNILLRFIN-----	313
sp	Q73FY6	HEMH_WOLPM	FIKCLADLCINLP-----	315
sp	P57777	HEMH_CAUCR	FIDGLAKAVRDSVG-----	318
sp	O67083	HEMH_AQUAE	FISALEDLVKNEV-----	309
sp	P22830	HEMH_HUMAN	FSKALADLVHSHIQSNEL---	394
sp	P22315	HEMH_MOUSE	FSKALADLVHSHIQSNKL-----	391
sp	P22600	HEMH_BOVIN	FSKALADLVHSHLQSKER-----	387
sp	O42479	HEMH_CHICK	FSKALADLVCSHIQSNEI-----	373
sp	O57478	HEMH_XENLA	FSKALADLVLSHMKSSEI-----	381
sp	Q9V9S8	HEMH_DROME	FIDALTNVVADHLKSQQA-----	354
sp	O59786	HEMH_SCHPO	AIQGMADLVAEHLKAKVP-----	357
sp	P16622	HEMH_YEAST	FIEGMADLVKSHLQSNQL---	362
sp	Q6APB0	HEMH_DESPS	FITGLRQLVLESSVNSD-----	320
sp	Q747F5	HEMH_GEOSL	FISCLADLVRR--VEG-----	317
sp	Q9ZKD4	HEMH_HELPJ	FAKFIIELVKN---LKSE-----	335
sp	P56107	HEMH_HELPY	FAQFIIERVKN---LKE-----	334
sp	Q7M7P9	HEMH_WOLSU	FAHAI IKLISQ---GEIS-----	316
sp	Q7VHH1	HEMH_HELHP	FAKSIMNILEEHLRGKAEV-----	311
sp	Q9PI08	HEMH_CAMJE	FMEFILKYLSD---LN-----	303
sp	Q8DFM2	HEMH_VIBVU	HIEMMARLVTER-----	319
sp	Q7MMR4	HEMH_VIBVY	HIEMMARLVTER-----	319
sp	Q9KT6	HEMH_VIBCH	HIELMAALVKVDC-----	320
sp	Q87RH3	HEMH_VIBPA	HIDMMAELVRSKL-----	320
sp	Q6LTE0	HEMH_PHOPR	HIRMMKNLVTQHSQGW-----	322
sp	Q8EFF4	HEMH1_SHEON	HIELLRLLVQEQTQSWISAE-----	348
sp	Q8XD39	HEMH_ECO57	HIEMMANLVAAYR-----	320
sp	P23871	HEMH_ECOLI	HIEMMANLVAAYR-----	320
sp	Q8FK83	HEMH_ECOL6	HIEMMANLVAAYR-----	320
sp	Q83SE5	HEMH_SHIFL	HIEMMANLVAAYR-----	320
sp	Q8Z8T2	HEMH_SALTI	HIDMILKLTAPYR-----	320
sp	P37408	HEMH_SALTY	HIDMMLKLTAPYR-----	320
sp	Q8ZC98	HEMH_YERPE	HIALLEQLIRHNI-----	320
sp	Q05338	HEMH_YERPS	HIALLEQLIRHNI-----	320
sp	P43413	HEMH_YEREN	HIDLLEQLVRDHLSC-----	322
sp	Q6D7Z4	HEMH_ERWCT	HIDLLEQLVGKVE-----	320
sp	Q7N0P6	HEMH_PHOLL	HILLLEELVNGFVRNRDE-----	325
sp	P43868	HEMH_HAEIN	HIEMMGKILILEKLT-----	323
sp	P57874	HEMH_PASMU	HIQMMANLILNKLNTQTSK---	326
sp	Q65SV7	HEMH_MANSM	HIACLGNNLLKRMITI-----	323
sp	Q8CWW4	HEMH_STRMU	HIQLLAELISERL-----	319
sp	Q8D226	HEMH_WIGBR	HIECLANIIRTHLK-----	321
sp	Q8EBZ7	HEMH2_SHEON	HIAMMANLVKPYL-----	327
sp	Q6F7N0	HEMH_ACIAAD	HLELLRQLLQAHLDALNYSLAYSAAH-----	340
sp	Q7WGI0	HEMH_BORBR	WIEGLTDLVERQLRGWPTGNP-----	362
sp	Q7W515	HEMH_BORPA	WIEGLTDLVERQLRGWPTGNP---	362
sp	Q7VVX8	HEMH_BORPE	WIEGLTDLVERQLRGWPTGNP-----	362
sp	Q62HD1	HEMH_BURMA	WIAALGEIAAENLQGW-----VRVAMAPEAVS-----	367
sp	Q63R43	HEMH_BURPS	WIAALGEIAAENLQGW-----VRVAMAPEAVS-----	367
sp	Q8XW32	HEMH_RALSO	WIAGLADIAQAHLQGWPLALPHPHVLEASRTAQSKGAAA-----	371
sp	Q7NV65	HEMH_CHRVO	WISSLAGIVRNNLAGWTEIR-AEDSQQR-AALAHDMGASA-----	364
sp	Q82UK8	HEMH_NITEU	WIEAIGNIIQTHLTGWADRRRLSEEAERSRKRALALGARE-----	364

sp	Q9JVA5	HEMH_NEIMA	WIDALVALAEENLGGWR-----	336
sp	Q9K097	HEMH_NEIMB	WIDALVALAEENLGSWR-----	336
sp	Q8PEX0	HEMH_XANAC	HAHALAAMARRA-----	318
sp	Q8P3H6	HEMH_XANCP	HAQALAAVARRA-----	318
sp	Q9PFU1	HEMH_XYLFA	HVQALAGLAQRALL-----	320
sp	Q87B82	HEMH_XYLFT	HVQALAGLAQRALP-----	320
sp	Q607T4	HEMH_METCA	HADILIGLLEPYLALTA-----	325
sp	Q8U9F7	HEMH_AGRT5	GMNVLEKVVRRRELQGWV-----	344
sp	Q92M52	HEMH_RHIME	GMAVLNHVVRRELEGWL-----	339
sp	Q93TG2	HEMH_BRUME	GMKVIETLVRRELLGWV-----	352
sp	Q98H61	HEMH_RHILO	GMTVIEAMVRRELSGWV-----	353
sp	P28602	HEMH_BRAJA	GMDVIRTLVLRRELQGWI-----	345
sp	Q6NBF3	HEMH_RHOPA	GVQVIRQLVLRRELQGWL-----	345
sp	Q59735	HEMH_RHOCA	HIAALLEVVEENLAGWID-----	351
sp	P57779	HEMH_ZYMMO	SLAMLEILVNQGLYGWLKSWE-----	334
sp	Q833G5	HEMH_ENTFA	FAKLVKDIISL-----	313
sp	Q9CFB4	HEMH_LACLA	FTRVLSEVVDQNRL-----	314
sp	Q67T48	HEMH_SYMTH	FIDCLEDLVRRHLPR-----	320
sp	Q88XC3	HEMH_LACPL	FSQFLADLAIQKQEASNHAITSSSKS-----	324
sp	P57778	HEMH_PSEFL	WAVALNTLCERAPVSL-----	340
sp	Q888A2	HEMH_PSESM	WAKELNRLCERAPLML-----	340
sp	Q88PV4	HEMH_PSEPK	WVRVLADMCEKA-----	338
sp	Q9HVD7	HEMH_PSEAE	WVGALAEMSGRLARPL-----	340
sp	Q6MHT3	HEMH_BDEBA	WVQGFADLVKSI-----	335
sp	Q83FA4	HEMH_COXBU	WVNIAIAKMAKKSLLQLF-----	343
sp	Q6MAW8	HEMH_PARUW	WIEAIKTIIQEHLPHPHSQFSR-----	347
sp	Q7MXP4	HEMH_PORGI	WIDALRNILEE-----	345
sp	Q824K8	HEMH_CHLCV	WVESLATIIQSTPHVEKKSLIKS-----	318
sp	Q927V1	HEMH_CHLPN	WVSTLVDIVKENSTVVAEELIKSGKKHTGIR-----	327
sp	Q9PJQ6	HEMH_CHLMU	WVSALASIVKSSPHETILEPLLMKRR-----	317
sp	O84492	HEMH_CHLTR	WVSSLAAIVRSSPQETSLEPLLM-----	314
sp	Q8GCV0	HEMH_LEPBI	FIQFLAEKVMHSDRKHQHCICREKGGESLQHCRFKD-----	362
sp	Q81U22	HEMH1_BACAN	FIDCLTDVVVKKKESVM-----	311
sp	Q6HM97	HEMH1_BACHK	FIDCLTDVVVKKKESVM-----	311
sp	Q63ES4	HEMH1_BACCZ	FIDSLTDVVVKKKESVM-----	311
sp	Q73C98	HEMH1_BACC1	FIDCLTDVVLKKKESVL-----	311
sp	Q81GW5	HEMH1_BACCR	FIDCLTDVVLKKKESVL-----	311
sp	P32396	HEMH_BACSU	FIDALATVVLKKLGR-----	310
sp	Q8ERX9	HEMH_OCEIH	FIETLANVVMKKAKSEVR-----	312
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sp	Q6G8A3	HEMH_STAAS	FIGAIVDEIKSIF-----	307
sp	P64126	HEMH_STAAW	FIGAIVDEIKSIF-----	307
sp	Q6GFM4	HEMH_STAAR	FIGAIVDEIKSIF-----	307
sp	Q8CNS1	HEMH_STAEP	FIGAIVDEIQSHI-----	307
sp	Q81TU9	HEMH2_BACAN	FIDCLATIVSRKMKEIVDKELILNNN-----	319
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sp	Q9RV98	HEMH_DEIRA	FIGTLASVIERKAAEVA-----	316
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sp	Q73FY6	HEMH_WOLPM	-----	
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sp	O67083	HEMH_AQUAE	-----	
sp	P22830	HEMH_HUMAN	-----CSKQLTLSCPLCV-NPVCRETKSFFTSQQL-----	423
sp	P22315	HEMH_MOUSE	-----CSTQLSLNCPCLCV-NPVCRTKTSFFTSQQL-----	420
sp	P22600	HEMH_BOVIN	-----CSTQLTLSCPLCV-NPTCRETKSFFTSQQL-----	416
sp	O42479	HEMH_CHICK	-----CSKQLTLCCPLCV-NPVCRETKAFFTNQQL-----	402
sp	O57478	HEMH_XENLA	-----CSKQLSLRCPMCV-NPVCGEAKSFFTKQQQ-----	411
sp	Q9V9S8	HEMH_DROME	-----VNPKFLMRCPMCS-NPKCRESKSWYRQLCSN-----	384
sp	O59786	HEMH_SCHPO	-----YSRQFTQRCPGCT-SESCAERINFFQDF-----	384
sp	P16622	HEMH_YEAST	-----YSNQLPLDFALGKSNPDKDLSLVFGNHEST-----	393
sp	Q6APB0	HEMH_DESPS	-----	
sp	Q747F5	HEMH_GEOSL	-----	
sp	Q9ZKD4	HEMH_HELPJ	-----	
sp	P56107	HEMH_HELPY	-----	
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sp	Q7VHH1	HEMH_HELHP	-----	
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sp	Q7MMR4	HEMH_VIBVY	-----	
sp	Q9KT6	HEMH_VIBCH	-----	
sp	Q87RH3	HEMH_VIBPA	-----	
sp	Q6LTE0	HEMH_PHOPR	-----	
sp	Q8EFF4	HEMH1_SHEON	-----	
sp	Q8XD39	HEMH_ECO57	-----	
sp	P23871	HEMH_ECOLI	-----	
sp	Q8FK83	HEMH_ECOL6	-----	
sp	Q83SE5	HEMH_SHIFL	-----	
sp	Q8Z8T2	HEMH_SALTI	-----	
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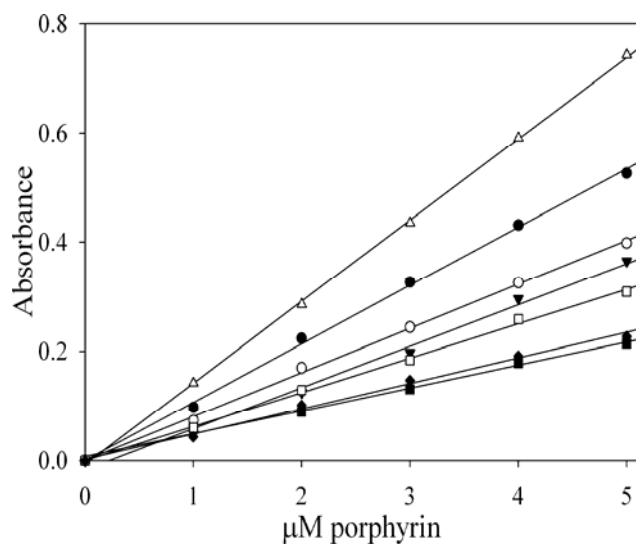
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sp	Q7NV65	HEMH_CHRVO	-----
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sp	Q88PV4	HEMH_PSEPK	-----
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sp	Q9RV98	HEMH_DEIRA	-----	
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sp	Q9CBM2	HEMH_MYCLE	-----	
sp	Q5YU18	HEMH_NOCFA	AA-----AGR-----	352
sp	O07401	HEMH_MYCAV	-----	
sp	Q83H94	HEMH_TROW8	FKPAYGGVAP-----	391
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sp	Q6AHF2	HEMH_LEIXX	FKPAVAGLTP-----	389
sp	Q82KJ6	HEMH_STRAW	-KPAAGADSPYA-----	375
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sp	Q7UFZ7	HEMH_RHOBA	-RPPVAGGRPVQAN-----	351
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sp	Q97R30	HEMH_STRPN	-----
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Supplemental data Figure 2. Standard curves for determination of apparent extinction coefficients of protoporphyrin IX and metallated porphyrins in ferrochelatase reaction buffer. The apparent extinction coefficients were: zinc protoporphyrin IX (triangles); 149,000 L/(mol·cm) at 417 nm, protoporphyrin IX (filled circles); 107,000 L/(mol·cm) at 407 nm, protoporphyrin IX (circles); 80,500 L/(mol·cm) at 417 nm, cobalt protoporphyrin IX (filled triangles); 75,400 L/(mol·cm) at 407 nm, copper protoporphyrin IX (squares); 62,600 L/(mol·cm) at 417 nm, iron protoporphyrin IX (filled triangles); 41,500 L/(mol·cm) at 407 nm, and nickel protoporphyrin IX (filled squares); 41,900 L/(mol·cm) at 417 nm. Data were collected at 30°C.

Supplemental data Figure 3. Spectral characterization of transition metal ion insertion into protoporphyrin IX catalyzed by ferrochelatase. 0.1 μM yeast ferrochelatase was incubated with 5 μM protoporphyrin IX and 10 μM of the indicated divalent transition metal (as the chloride salt) at 30°C in ferrochelatase reaction buffer. Spectra were recorded at regular intervals until the reaction reached completion. Arrows indicate the direction of spectral changes during the transformation of protoporphyrin IX into each of the various metalloporphyrins.

