Table S2 Sequences of SOD proteins from watermelon and other plant species

>ClFSD2

MASIAMLPSTKLHQNQLPRSSFRGTPLPPSAISSTSNKQKQHVSKTCLTK
ITAKFDLKPPPYPLDALEPHMSRSTLEYHWGKHHRAYVDNLNRQIEGTEL
EELSLEDIITKTYNKGDILPQFNNAAQIWNHDFLWESIKPGGGGKPSGEL
LELIERDFGSFEKFLEEFKSAATTQFGSGWAWLAYKDNTVDHPRPSEKDK
KLVILKSPNAVNPLVWDYAHAYYLDFQNRRPDYISTFVSNLISWEAADSR
LQKAKVEAAERAKEKEKKKEKKKAKGSDEEVYVDSSSSESDSDSD

>ClCSD3

MVKAVAVLGSSEGVSGTIFFSQEGDGPTTVTGNVSGLKPGLHGFHVHALG
DTTNGCMSTGPHFNPAGKQHGAPEDANRHAGDLGNITAGEDGKASFTITD
SQIPLCGHDSIIGRAVVVHGDPDDLGKGGHELSLSTGNAGARVACGIIGL
QG

>ClCSD5

MELARVEANFSGLSPGKHGWSINEFGDLTRGAASTGKIFGSADSGPSNEP
LGDLGTLDADEKGEAFFSGVKQKLRVSDLIGRSIAVYETEDKSDPGIAAA
VVARSAGVGENYKKLCTCDGTTIWESSNMDFVTSKV

>ClCSD4

MGALKAVALIAGGDSNIRGSIQFVQDSNGATRVNGRISGLSPGLHGFHIH
SLGDTTNGCNSTGPHFNPLKKDHGGPGDAERHAGDLGNICAGPDGVAEVS
ITDRLISLKGLHSILGRAVVVHADPDDLGKGGHELSKTTGNAGARVGCG

>ClCSD1

MVKAVAVLESNQGVSGTVFFSQNGNGSTTVTGNISGLKAGLHGFHVHALG
DTTNGCLSTGPHFNPEGKDHGAPNDENRHVGDLGNLVAGDDGTATFTIID

KQISLVGPNSVLGRAIVVHADADDLGRARTELSLTTGNAGERIGCGVIGV

QE

>ClCSD2

MQAVLAAMAAQSLLSASLSHYIALPPFSNSSPPPSLSSSFHGASLKLPRH

SLSLAASAAPKPLAVVAATKKAVAVLKGTSNVEGVVTLTQEDDGPTTVNV

RITGLTEGLHGFHLHEYGDTTNGCISTGAHFNPNKLTHGAPEDEIRHAGD

LGNIIANADGVAEATIVDTQIPLSGPNSVVGRALVVHELEDDLGKGGHEL

SLTTGNAGGRLACGMQT

>ClMSD

MALRILSRKNLTPTISGALGSGHFRGLQTFSLPDLPYDYGALEPVINAEI

MQLHHQKHHQAYITNYNKALEQLHEAINKGHTSTVVKLQSAIKFNGGGHI

NHSIFWNNLAPIHEGGGEPPKGSLGWAIDSQFGSLEALIQRVNAEGAALQ

GSGWVVWLALDKELKKLSVETTANQDPLVTKGSALVPLLGIDVWEHAYYLQ

YKNVRPDYLKNIWKVINWKYAGEIFAKEAPMVESR

>ClFSD1

MISCYNPLNVSYPLLVTNSSQELKSTKHPYLHQSKLHKRSSDVTTRGMKV

SAYYGLRTPPYELDALEPYMSRRTLEVHWGKHHRNYVEGLNKQLSQNDIL

YGHTLDELLKVTYNNGNPLPEFNNAAQVWNHDFFWESMQPGGGNMPKLGV

LQQIEKDFGSFINFRDKFIQASLSLFGSGWVVWLVLKRQEKRLTVITTSNA

ISPLLWDDIPIICLDMWEHAYYLDYKNDKKEYVNVFMDHLVSWNAALGRM

ARAECFVNLGEPKIPVA

>MtCSD1

MHLTMASHSLMSPSPLTSHSLLRSSFSGVSVKLSPQFSTLSRSTFKPLSVVAAAKKAVAVLKG
NSTVEGVVTLTQENEGPTTVNVRITGLTPGLHGFHLHEYGDTTNGCISTGPHFNPNQLTHGAP
EDEIRHAGDLGNIIADANGVAEATIVDNQIPLTGPNSVVGRALVVHELEDDLGKGGHELSLST
GNAGGRLACGVVGLTPV

>MtCSD2

MAFLRSIATTATAISTLAFSSLSSSFSHSHHSPNTDLSSNPKSNNSFRLVKTFATSPSPLLMDQNLSS
QTQTDHDVLPELLTEYMVDMKCEGCVNAVKNKLQTIHGIKNVEVDLSNQVVRILGSTPVKTMTE
ALEQTGKKARLIGQGVPEDFLISAAVSEFKGPEIFGVVRLAQVNMELARIEANFSGLSPGKHSWSI
NEFGDLTRGAASTGKVFNPLNEENTKEPLGDLGTLDVNEKGEAFFTGVKEKLRVSDLIGRAVVLY
ATEDKSEHGIAAAVVARSAAVGENYKKLCTCDGTTIWEASDADFVPSKF

>MtCSD3

MEGGKGTVKGVALIIGDNNVRGSLHFLQHPNGNYTHVTGKITGLSPGLHGFHIHALGDTTNGCNS
TGPHFNPLKKDHGAPTDDERHAGDLGNIVAGPDGVAEISIRDGKIPLSGVHSILGRAVVVHADPD
DLGRGGHELSKTTGNAGARVACGIIGLQSSV

>MtCSD4

MVKAVAVLGNSNDVSGTISFTQEGNGPTTVTGNLSGLKPGLHGFHIHALGDTTNGCLSTGPHFNP
NGKEHGAPEDETRHAGDLGNVTVGDDGTASFTITDNQIPLTGPNSIIGRAVVVHADPDDLGKGGH
ELSKTTGNAGGRVACGIIGLQG

>MtFSD1

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HDFFWESMKPGGGGKPSGELLKLIERDFGSFEKFVEQFKLAASTQFGSGWAWLAYKENRLDVGN
AVNPLATEEDKKLVVLKSPNAVNPLVWNHHHPLLTIDVWEHAYYLDYQNRRPEYISVFLDKLVS
WEAVSSRLEKAKASIAEREKEEERKRREEEEKSRTGEDTPAPEIFADSDTD

>MtFSD2

MASCYLNPIPTSSRLFSPDLSTKFKIPKLLHRKKRFGVLPRSSKVTAFYGLKTPPYEHDALEPYMSK
QTIDVHWGEHHRNFIEGLNKQLGKDDILYGYTLDELVKVTYNNGNPSPEFNNAAEVWNHDFFWE
SMQPGGGDIPILGLLQQIEKDFGSFTNFKEKFTEAALTLFGSGWVWLVLKREEKQLAIVKTSNSICP
IVWGDIPIINLDLWEHAYYLDYKNDRAKYVNVFLNHLVSWNAATERLTWGEAFVNLGEPKIPVA

>MtMSD

MAVRTLLSKKTLTTVLRNDPKPIGAAITQSRGLHVFTLPDLAYDYGALEPVISGEIMQIHHQKHHQ
TYITNYNKALEQLHDSVAKADSLTTVKLQNAIKFNGGGHINHSIFWKNLAPVREGGGEPPKEALG
WAIDTNFGSLEALIQKVNAEGAALQGSGWVWLALDKELKRLVVETTANQDPLVTKGTSLVPLLG
IDVWEHAYYLQYKNVRPDYLKNIWKVINWKYASEVYENAF

>AtCSD1

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DTTNGCMSTGPHFNPDGKTHGAPEDANRHAGDLGNITVGDDGTATFTITD
CQIPLTGPNSIVGRAVVVHADPDDLGKGGHELSLATGNAGGRVACGIIGL
QG

>AtCSD2
MAATNTILAFSSPSRLLIPPSSNPSTLRSSFRGVSLNNNNLHRLQSVSFA
VKAPSKALTVVSAAKKAVAVLKGTSDVEGVVTLTQDDSGPTTVNVRITGL
TPGPHGFHLHEFGDTTNGCISTGPHFNPNNMTHGAPEDECRHAGDLGNIN
ANADGVAETTIVDNQIPLTGPNSVVGRAFVVHELKDDLGKGGHELSLTTG
NAGGRLACGVIGLTPL

>AtCSD3
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EILIKDKHIPLSGQYSILGRAVVVHADPDDLGKGGHKLSKSTGNAGSRVG
CGIIGLQSSADAKL

>AtMSD1
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IMQIHHQKHHQAYVTNYNNALEQLDQAVNKGDASTVVKLQSAIKFNGGGH
VNHSIFWKNLAPSSEGGGEPPKGSLGSAIDAHFGSLEGLVKKMSAEGAAV
QGSGWVWLGLDKELKKLVVDTTANQDPLVTKGGSLVPLVGIDVWEHAYYL
QYKNVRPEYLKNVWKVINWKYASEVYEKENN

>AtMSD2
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NGGGHVNHAIFWKNLAPVHEGGGKPPHDPLASAIDAHFGSLEGLIQKMNA
EGAAVQGSGWVWFGLDRELKRLVVETTANQDPLVTKGSHLVPLIGIDVWE

HAYYPQYKNARAEYLKNIWTVINWKYAADVFEKHTRDLDIN

>AtFSD1

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KPSGELLALLERDFTSYEKFYEEFNAAAATQFGAGWAWLAYSNEKLKVVK
TPNAVNPLVLGSFPLLTIDVWEHAYYLDFQNRRPDYIKTFMTNLVSWEAV
SARLEAAKAASA

>AtFSD2

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LSLEEVVLLSYNKGNMLPAFNNAAQAWNHEFFWESIQPGGGGKPTGELLR
LIERDFGSFEEFLERFKSAAASNFGSGWTWLAYKANRLDVANAVNPLPKE
EDKKLVIVKTPNAVNPLVWDYSPLLTIDTWEHAYYLDFENRRAEYINTFM
EKLVSWETVSTRLESAIARAVQREQEGTETEDEENPDDEVPEVYLDSDID
VSEVD

>AtFSD3

MSSCVVTTSCFYTISDSSIRLKSPKLLNLSNQQRRRSLRSRGGLKVEAYY
GLKTPPYPLDALEPYMSRRTLEVHWGKHHRGYVDNLNKQLGKDDRLYGYT
MEELIKATYNNGNPLPEFNNAAQVYNHDFFWESMQPGGGDTPQKGVLEQI
DKDFGSFTNFREKFTNAALTQFGSGWVWLVLKREERRLEVVKTSNAINPL
VWDDIPIICVDVWEHSYYLDYKNDRAKYINTFLNHLVSWNAAMSRMARAE
AFVNLGEPNIPIA

>BdCSD1

MVKAVAVLSGSEGVKGTIFFTQEGDGPTTVTGSVSGLKEGLHGFHVHALGDTTNGCMSTGP
HFNPAGKEHGAPEDETRHAGDLGNV

TAGVDGVANINVVDTQIPLTGPHSIIGRAVVVHGDPDDLGKGGHELSKSTGNAGARVACGII
GLQG

>BdCSD2

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TNGCNSTGPHFNPHNKSHGAPIDD

ERHVGDLGNIQANNDGIAEVFIKDLQISLSGPQSILGRAVVVHADSDDLGRGGHELSKSTGNA
GARIGCGIIGIQPAV

>BdCSD3

MASVTAAAQTTLLSAATAPTSLFQAAPSSARPFHPLRLVSAGRRTLVVADATKKAVAVLKG
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GLTPGLHGFHLHEFGDTTNGCISTGPHFNPNGLTHGAPGDEVRHAGDLGNIVANAEGIAETTI
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TGNAGGRLACGVVGLTPL

>BdMSD

MALRTLTSKKTLALALGGVRPLVARGVATFTLPDLPYDYGALEPAISGEIMRLHHQKHHATY
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>BdFSD1

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ANVATDVEVDQVADAEGDTTDAPDSLNPDDVASVAWIK

QQPLPYPTDALEPYISKETVEQHWGVHQHKHVERLNGMIDGSEWQGMSLGKMMLSSFNEG
REPPQAPFFHAAQIWNHDFYWRSMKPGGGGKPPERLLKFI

SRDFGSYDGMIQQFMDAALTQFGSGWVWLSYKGSKLPHVNSKSPIPSDNVGRLVISKTPNAV
NPLVWGHSPLLAIDVWEHAYYLDYENRRAEYVSAILEK

LVSWEMVESRLRKAVVRAIERDGHPNMKQRRKQLVSQAKTRHGDASTSGQARRRPRSQDQ
QHASGSLSMAGEAVRN

>BdFSD2

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SPFYGYTLEELVKEAYNNGNPLPEYNNAAQVWNHHFFWESMQPDGGGSPEGGVLRQIEKDF
GSFFNFREEFVRSALSLLGSGWVVWLVLKRNEKKLAVVRT

RNAISPLAAGDIPIISLDLWEHAYYLDYKDDRRAYVSNFMDHLVSWNSVTLRMMRAEAFVN
LGEPNIPEF

>CsFSD1

MISCCNSLNVNSPFLLTNYSQQLKSTRHPYLHQSKLQKRNSDGTTRGMKVVAYYGLKTPPYE
LVWNHDFFWESMQPGGGDMPKLGVLQQIEKDFGSFTNFREKFILASLSHFGSGWVWLVLKR
QEKRLAVITTSNALSPILWDDIPIVCLDLWEHAYYLDYKNDKIEYVNVFMDHLVSWNAALG
RMARAECFVNLGEPKIPVA

>CsCSD1

MVKAVAVLGSSEGVSGTIFFTQEGDGPTTVTGNVSGLKPGLHGFHVHALGDTTNGCMSTGP
HFNPAGKQHGAPEDENRHAGDLGNIIVGEDGKANFTITDCQIPLCGHESIIGRAVVVHGDPDD
LGKGGHELSSSTGNAGARVACGIIGLQG

>CsMSD

MALRILGRKNLIPTISGGLGSGHLRGLQTFSLPDLPYDYGALEPVINAEIMQLHHQKHHQAYI
TNYNKPTSPTTTRLLSNFTRPSTKATPPPSSHSIGKSFDARLCHINHSIFWNNLEEVSEGGGEPP
KGSLGWAIDSEFGSLEALIQRVNAEGTALQGSGWVVWLALNKELKKLSVETTANQDPLVTKG
SALVPLLGIDVWEHAYYLQYKNVRPDYLKNIWKVINWKYAGDIFAKEAPLVESR

>CsCSD2

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NPEGKDHGAPDDENRHVGDLGNVVAGDDGTATFSIIDKQISLVGPNSVLGRSIVVHADPDDL
GRGGTELSLTTGNAGERIGCGVIGLQE

>CsCSD3

MAFLRSTATTTSFAIAAASALPAAFIFTGPSSSSLPFHFPQSFKPISLSLYSSQFPTSNSFGFVRNF
APPPSAVRMETPTSESISSSQNNVDLPELLTEYMVDMKCEGCVSAVKNKLQGVDGVKSVDV
DLSNQVVRILGATPVKIMTEALEQTGRKARLIGQGVPEDFLISAAVAEFKGPNIFGVVRLAQV
NMELTRVEANFSGLSPGKHGWSINEFGDLTKGAASTGKIFGSADSDPSNEPLGDLGTLDVNE

KGEAFFSGVKQKLRVSDVIGRSIAVYETEDKSVPGITAAVVARSAGVGENYKQLCTCDGTTI
WESSDRDFVTSKV

>CsFSD2

MQEQTHSDTSKTDMAASIALPPSTKLHQNQLHHSSFRGSPLPPSATPCTSIKQGGDEVKKLDD
KKHGNGYETLKQHGSKTYLTKISAKFELKPPPYPLDALEPHMSRSTLEYHWGKHHRAYVDN
LNRQIEGTELEELSLEDIIMKTYKKGNILQQFNNAAQIWNHDFLWESIKPGGGGKPTGELLELI
ERDFGSFEKFLEEFKSAAATQFGSGWAWLAYKDNTVDHPRPSEKDKKLVILKSPNAVNPLV
WDYAPLLTIDVWEHAYYLDFQNRRPDYISTFVSNLISWEAADLRLQKAKIEAAERVKEKEKK
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>CsCSD4

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GPHFNPLKKDHGSPGDSERHVGDLGNIYAGPDGVAEVSISDRLISLKGPHSVIGRAVVVHADP
DDLGKGGHELSKTTGNAGARIGCGLFVEGCMNHDRKVIPTPKDAQFGYCWTSNHFAYKRK
KSVKVMMGITLKTKGGEVVYKECFGDQQMRSYLKD

>CsCSD5

MAAQSLLSVSLSNYVALPPFSNSSSSSSLSLTSSFHGASLKLPRHSLSLAASVAPKPLAIVAAT
KKAVAVLKGTSAVEGVVTLTQEDDGPTSVNVRITGLTPGLHGFHLHEFGDTTNGCISTGAHF
NPNKLTHGAPEDEIRHAGDLGNITANADGVAEAIIVDNQIPLSGPYSVVGRAFVVHELEDDLG
KGGHELSLTTGNAGGRLACGVVGLTPV

>CsFSD3

MLRVGDLQRSIDFYTNVLGMRLLRTSENPEYKYSLAFVGYGPESEEAVIELTYNWGVDSYEL
GTAYGHIALEVDNAAEACEPCITAGIAFDGTQAHSALYDTERTAELFCEIVNRWKRLGGWPL
PMGDEADLQSLFDQLLQFAALIHFNQNITAANQFTVNPQLWEGLLATYKTIRRVAMSFELPA
LPYAKDALAPHISAETLEYHYGKHHQTYVTNLNNLIKGTDFEGKTLEEIVRSSDGGVFNNAA
QVWNHTFYWHCLAPNAGKTSTGTAWLQMQAENLPMSWPQRLNFKAKFTDAAVKNFGSG
WTWLVKEADGKLAIVSTSNAGTPLTTSATPLMTVDVWEHAYYIDYRNARPNYLEHFWALV
NWEFVAKNFAA

>SlSOD1

MVKAVAVLNSSEGVSGTILFTQDGDAPTTVNGNISGLKPGLHGFHVHALGDTTNGCMSTGP
HYNPAGKEHGAPEDEVRHAGD

LGNITVGEDGTASFTITDKQIPLTGPQSIIGRAVVVHADPDDLGKGGHELSKSTGNAGGRIAC
GIIGLQG

>SlSOD2

MGNLKAVAVISGNDSVQGSLQFIQQSNGVTHVRGRIIGLAPGLHAFHIHALGDTTNGCNSTG
PHFNPLKKDHGAPMDEVRHA

GDLGNIVAGPNGVAEISISDMQIPLSGVHSILGRAVVVHADPDDLGRGGHELSKTTGNAGAR
VGCGVIGLQSSV*

>SlSOD3

MAAHSIFTTTSTTNSFLYPISSSSSSPNINSSFHGVSLNVKSKFGQSLTLYAVTTPKPLTVFAAT
KKAVAVLKGNSNVEGVV

TLSQDDDGPTTVNVRITGLAPGLHGFHLHEYGDTTNGCMSTGAHFNPNKLTHGAPGDEIRHA
GDLGNIVANADGVAEVTLVDNQIPLTGPNSVVGRALVV

HELEDDLGKGGHELSLTTGNAGGRLACGVVGLTPI*

>SlSOD4

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PPSALHMETHSSNHQT

SSDNGVVLPELLTEFMVDMSCQGCVSAVKSKLQTVEGVKNVDVDLDNQVVRILGSSPVKTM
TEALEQTGRKARLIGQGVPDDFLISAAVAEFKGPDIFGV

VRLAQVNMELTRIEANFSGLSPGKHAWSINEFGDLTRGAASTGKLYSLPLGDLGTLDVDEKG
EAFYSGPKEKLRVADLIGRAIAVYATEDKSDPGLTAAV

IARSAGVGENYKKLCTCDGTTIWEATSKI*

>SlSOD5

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HMSSRTFEFHWGKHHRAYV

DNLNKQIDGTELDGKTLEDIILVTYNNGAPLPAFNNAAQAWNHQFFWESMKPNGGGEPSGE
LLELINRDFGSYDTFVKEFKAAAATQFGSGWAWLAYKPE

DKKLALVKTPNAENPLVLGYTPLLTIDVWEHAYYLDFQNRRPDYISIFMEKLVSWEAVSIRL
KAASA*

>SlSOD6

MAAATASATLFSPFLPSPGFHESCRSLNWRTHKKQIASKAGTVKVTAKFELNPPPYPMNALE
PHMSRTTFEYHWGKHHRAYV

DNLNKQIVGTELDELTLEDIILVTYNQGNLLPPFNNAAQAWNHQFFWESMKPGGGGQPSGEL
LKLINRDFGSFEAFVKEFKAAAATQFGSGWAWLAYKAN

RLDVGNASNPHPSDEDKKLVIVKTPNAINPLVWDYSPLLTIDVWEHAYYLDFRNRRPDYISIF
MEKLVSWEAVSSRLEAAQAQAAEREKEEERKKREEEE

EYQDGNEVREMYVETTDSEAD*

>SlSOD7

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IHWGEHHRGYVESLNKQIENN

DIFYGCTMEQLIKLTYNNGNPLPEFSDAAQVWNHDFFWESMQPGGGDMPKLGFLHQIDKDF
GSFTNFKDKFIEAALTLFGSGWIWLVLSREEKRLAIIKT

SNAVNPLVWNDIPLIGLDLWEHAYYLDYKNDKAKYVNVFMNHLVSWDAALGRMARAQAF
VNLGEPKIPVA*

>SlSOD8

MANFGKHHRSYDDNLNKKIHGTELHGKTLQDLILVTYNNGSLLPAFNNDAQMKPNGGRESS
GELLQLINRDFGSYDTFVKEF

KAAAATQFGSGWSWLAYKPEDKKLALVKTPNAENPLVLGYTDAYYLDFQNCPPDYISLFME
KLISWEAVSSRLKAATA*

>SlSOD9

MALRTLVSRRTLAAGLGFRQQLRGVQTFSLPDLPYDYGALEPAISGDIMQLHHQKHHQTYIT
NYNKALEQLHDAISKGDAPA

VAKLHSALKFNGGGHINHSIFWNNLAPVSEGGGEPPKGSLGWAIDTNFGSLEALVKKMNAE
GAALQGSGWVWLGVDKELKRLVVETTANQDPLVSKGANL

VPLLGIDVWEHAYYLQYKNVRPDYLKNIWKVINWKYANDVYENECP*

>SbSOD1

MAGKAGGLKGVALIGGGANSTVAGALHFFEDPSTRYTEVRGKVTGLTPGRHGFHIHVFGDT
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FDKERHAGDLGNIVANEDGVAEVFIRDLQISLSGPHSILGRAVVVHADPDDLGRGGHELSKST
GNAGARIGCGIIGIQSSV

>SbSOD2

MNFIPLGFWWQITEKMVKGVAVLAGPDVKGTIFFSQEGDGPTTVTGSISGLKPGLHGFHVHA
LGDTTNGCMSTGPHFNPAGK

EHGAPEDENRHAGDLGNVTAGEDGVVNVNITDSQIPLTGPHSIIGRAVVVHADPDDLGKGGH
ELSKSTGNAGGRVACGIIGLQG

>SbSOD3

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RDARLIGQGNPNDFLVSAAVAEFKGPVIFGVVRLAQVNMELARVEATFSGLSPGKHGWSINQ
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EAHFSGPKEKLRVVDLIGRSIALYATEDRSDPGIAAAVIARSAGVGENYKKLCTCDGVTIWES
S

>SbSOD4

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VNVRITGLTPGLHGFHLHEFGDTTNGCISTGPHFNPNNLTHGAPEDEVRHAGDLGNIVANAE
GVAEATIVDTQIPLSGPNSVVGRAFVVHELEDDLGKGG

HELSLSTGNAGGRLACGVVGLTPL

>SbSOD5

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HYNPASKEHGAPEDENRHAGD

LGNVTAGADGVANISVTDSQIPLTGPNSIIGRAVVVHADPDDLGKGGHELSKSTGNAGGRVA
CGIIGLQG

>SbSOD6

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ATYVANYNKALEQLDAAVAK

SDASAVVQLQGAIKFNGGGHVNHSIFWKNLKPISEGGGEPPHGKLGWAIDEDFGSFEALVKK
MNAEGAALQGSGWVWLALDKEAKKLSVETTANQDPLVT

KDASLVPLLGIDVWEHAYYLQYKNVRPDYLNNIWKVMNWKYAGEVYENVLA

>SbSOD7

MASTALVAVAVGGGLCPGLVASCSVASCSLRAGGGDSPRLGRRLVLLQRGGGAEGERKRIR
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GDATDDEEDLEAAADDAIDADVDTEDELDSSLPEDVEWIKQQPLPYPLDALEPYISKETVGQ
HWGVHQQIHVDRLNGMIGGSEWEGMSLGQMMLASFNEG

REQPHPPFFHAAQVWNHDFYWRSMKPGGGGKPPERLLKFINRDFGSYEGMIRQFMDAALTQ
FGSGWVWLSYKGSGLPYVKSRSPIASDNYGRLVISKTPN

AINPLVWGHSPLLGIDVWEHAYYLDYEDRRADYVSAILENLVSWEIVESRLTKAVVRAVER
DEDLRRRIQRKQHLSQANGQSRARPRTRQGRPTGWQGDQ

EVARSSPVEA

>SbSOD8

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DGLNKQLATSPLYGYTLEDLIKEAYNNGNPLPEYNNAAQVWNHHFFWESMQPEGGGVPVG
GVLQQIEKDFGSFTNFREEFIRSALQLLGSGWVWLVLKRN

ERKLSVVHTRNAISPLAFGDIPIISLDLWEHAYYLDYKDDRLAYITNFMDHLISWDTVTLRMM
RAESFVNLGEPTIPEA

>cCuZn-SOD1

MVKAVVVLGSSEIVKGTIHFVQEGDGPTTVTGSVSGLKPGLHGF

HIHALGDTTNGCISTGPHYNPAGKEHGAPEDETRHAGDLGNVTAGEDGVANIHVVDSQ

IPLTGPNSIIGRAVVVHADPDDLGKGGHELSKTTGNAGGRVACGIIGLQG

>cCuZn-SOD2

MVKAVAVLASSEGVKGTIFFSQEGDGPTSVTGSVSGLKPGLHGF

HVHALGDTTNGCMSTGPHFNPTGKEHGAPQDENRHAGDLGNITAGADGVANVNVSDSQ

IPLTGAHSIIGRAVVVHADPDDLGKGGHELSKTTGNAGGRVACGIIGLQG

>CuZn-SOD-L

MAGKAGGLKGVALIGGAGGNSAVAGALHFFQDPSTGYTEVRGRVTGLAPGLHGFHIHSFG

DTTNGCNSTGPHFNPHNKSHGAPSDDERHVGDLGNIVANKDGVADIFIKDLQISLSGPHS

ILGRAVVVHADSDDLGRGGHELSKTTGNAGARIGCGIIGLRSAV

>pCuZn-SOD

MQAILAAAMAAQTLLFSATAPPASLFQSPSSARPFHSLRLAAGPAGAAAARALVVADATKK
AVAVLKGTSQVEGVVTLTQDDQGPTTVNVRVTGLTPGLHGFHLHEFGDTTNGCISTGPHFNP
NNLTHGAPEDEVRHAGDLGNIVANAEGVAEATIVDKQIPLSGPNSVVGRAFVVHELEDDLG
KGGHELSLSTGNAGGRLACGVVGLTPL

>CuZn-SOD-CCh

MVGFLRALTAASAVPAAAAVAAVALSTNSSSSSRLRLPSPASLPSLSSAYAAAPASGSAR

KPNAVPPMAAAAATADLSAAADKGAALPELMTEFMVDMKCDGCVTAVKNKFQTLEGIKNI

EVDLNNQVVRVLGSLPVNTMLDTLHQTGRDARLIGQGNPNDFLVSAAVAEFKGPVIFGVV

RLAQVNMELAIVEATFSGLSPGKHGWSINEFGDLTRGAESTGKVYNPSDYRSNKPLGDLG

TLEAGEKGEAQFSASKEKLKVVDLIGRSIALYATEDRSDPGIAAAVIARSAGVGENYKKL

CTCDGVTIWESS*

>Mn-SOD1

MALRTLASRKTLAAAALPLAAAAAARGVTTVALPDLPYDYGALE

PAISGEIMRLHHQKHHATYVANYNKALEQLDAAVAKGDAPAIVHLQSAIKFNGGGHVN

HSIFWNNLKPISEGGGDPPHAKLGWAIDEDFGSFEALVKKMSAEGAALQGSGWVWLAL

DKEAKKLSVETTANQDPLVTKGANLVPLLGIDVWEHAYYLQYKNVRPDYLSNIWKVMN

WKYAGEVIENATA

>Fe-SOD3

MAAFASALRVLPSPPAAVPRRLRSREQRQGCRSRRYSKVVAYYA

LTTPPYKLDALEPYISKRTVELHWGKHQQDYVDSLNKQLATSMFYGYTLEELIKEAYN

NGNPLPEYNNAAQVWNHHFFWESMQPEGGGSPGRGVLQQIEKDFGSFTNFREEFIRSA

LSLLGSGWVLLVLKRKERKLSVVHTQNAISPLALGDIPLINLDLWEHAYYLDYKDDRR

MYVTNFIDHLVSWDTVTLRMMRAEAFVNLGEPNIPVA

>Fe-SOD2

MAFATLVGVGGLSPALFSPSRPLSCSSSTSVSAPFILRAGGGGD

ARRHGLRRLVTPLRGSACRGESTNSRVLQCANEANVVTEDDIVNDGIDDETASDAEMD

EDAEANGDESSGTDEDASVSWIEQQPLPYPSDALEPYISKETVEQHWGVHQNIHVERL

NGMIGGSEWEGMSLGQMMLSSFNEGREAPHPPFFHAAQIWNHDFYWRSMQPGGGGKPP

ERLLKFINRDFGSYDGMIRQFMDAASTQFGSGWVWLCYKTSKLPHVKSRSPIPSDNYG

RLVISKSPNAINPLVWGHSPLLAIDLWEHAYYLDYEDRRSDYVSTFLEKLVSWETVES

RLKKAVQRAVERDEYVSTKHIRKQLLARAKSQIRAMPQQVNGDAREQTSGQEKSLGV