

DOR Human [Homo sapiens] NP_067025
MFQRLSSLFFSTPSPEDPDCPRAFVSEEDEVDGWLIIIDL^DSYAAPPSPGAAPAPAGRP
PPAPSLMDESWFVTTPACFTAEGPGLGPARLQSSPLEDLLIEHPSMSVVTGSTIVLEPG
SPSPLPDAALPDGDL^SE^GLTPARREPRARAHRAPLPARAALLEKAGQVRRQLQRARQRAE
RHAlSAKAVQRQRNARESRPRSKNQSSFYQPCQRQFNY

TP53INP1 Human [Homo sapiens] NP_150601
MFQRLNKMVFGEVSSSNQEPEFNEKEDEWILVDF^IDTCTGFSAEEEEEEE^DISEESPT
EHPSVFSCLPASLECLADTSDFLQFESCPMEESWFITPPPCFTAGGLTTIKVETSPME
NLLIEHPSMSVYAVHNCPGLSEATRGTD^ELHSPSSPRVEAQNEMGQHIHCYVAALAAHT
TFLEQPKSFRPSQWIKEHSERQPLNRNSLRRQNLTRDCHPRQVKHNGWVHQPCPRQNY

DOR Opossum [Monodelphis domestica] XP_001371459
MFQRLTSLFFSTSPSEPPSPKA^FICPEEEVGWLIIIDL^DSFAAPPSPKPASPCLL
DESWFVTTPACFTAEGPELGP^AHLESSPLEDLLIEHPSMSVVTGSTIVLEPGPGPTLTP
PRSPPPP^RAGHREVMQFRRDPGPRHHTASMP^SR^TALLEKASQARWVQRARQRADRQRLSP
KVVQRQNVRERHP^RRSKHQGSFLHQPCQRQFNY

TP53INP1 Opossum [Monodelphis domestica] XP_001368955
MFQRLNSMFVFGEIKNSSKEPEFSEKEDEWILVDF^IDTNFSTEVEEEDVSEESP^TNHPP
VFSCLPASLECLADTS^ECFVQFEACPMEESWFITPPPCFTAGGLTTIKVETSPLENLLI
EHPSMSVYNSSRNLN^EAGC^TDEFHN^PSSPR^RLEVQNEMGQHVHCVYAALAAHSTFLEQTK
SFRPTQWIKEHSERHSLNRNSLRRQNLTRDCHSRQIKHNGWVHQPCQRQNY

DOR Lizard [Anolis carolinensis] Genomic profiling
MFQRLTSLFFSDSSA^PDEEPKPFISKEEEEDDWLII^DIT^GEKDSVCASCCHGSLPPT
SSLPLSPSDCISRSMPSQDPCLMDESWFVT^TPPPCFTAECSDPVSMESNP^MEDLLIEHPS
MSVYVTSSTIV^VETQ^TPEEHINRD^GE^EPERRLQRHAPHH^HSTS^LATAKAAILEKV^SQVHRIQ
RAKQLAEKHNF^SQKV^MQRQNRTREC^RPRAKHQGSFVYQPSQRQNY

TP53INP1 Lizard [Anolis carolinensis] Genomic profiling
MFQRLNNMFME^ENNL^PSQEPAF^EKEEE^EWIVVDF^IDT^CNNFSMVEEDEEEEEE^EDN
CNIHETSSVDHPVFSHLPNSLECLSDASESCFIQFDSCPMEESWFITPPPCFTAGGLAT
LK^VETSPLENLLIEHPSMSVYAVHNTHS^LNKTSG^DEEEEE^EEEKENRNATNP^QSEA
QSQM^GQHRCYIATLATHSTFLEQTKNLRPSQWTKEHHERQYLTRNCLRRQNLTRDCYSR
QLKNNGILVHQPCQRQNY

DOR Chicken [Gallus gallus] CN231263, XP_001232258 and
genomic profiling
MFQRLTSLFFSDSSA^PEGLEEPKPFVSEEEEDGWLI^IELG^AH^TGSSTPTLPS^PCLM^DES
WFVT^TPPPCFTA^EEPGP^DGVGSSPMEDLLIEHPSMSVY^VT^TST^LELDAEGPQDDAV^GEVPEP
RLERHVPHRSASLSVKA^AVLKVSQARRVQRAKQ^LAEPKWL^SQ^KALQRQDRARQR^PRR^A
RQRAGSFLHQPCQRHCNY

TP53INP1 Chicken [Gallus gallus] NP_001026117
MFQRLNNMF^GEIDGLSSQEPEFSEKEDEWILVDF^IADTCTNCTTEQDDIAETSPAGSS
PVFTCLPSPLEHLPEAGESCFIQFESCPMEESWFITPPPCFTAGGLTAIKVETSPMENLL
IEHPSMSVYAVHNACHS^LSDT^GC^DEEFCGP^GSP^RLEARNETGQRVHCFVAALPTRSSVL
EKNKSFRPTW^IKEHGERHYP^SRNGLRRQNLTRDCHSRH^IKHNGLFVHQPCQRQFNY

DOR Frog [Xenopus tropicalis] multiple ESTs short and long
MFQRLTRLFFSDV^PSSNTNEPK^ISEEEEDGWLI^ID^IP^ESYDLN^SSGDEV^AQEQE^DDAT
PSPLPHSLADRIGWTP⁵³INP¹PHPPQSM^DESWFVT^TPPPCFTAEPGQ^DELGTSPLEDLL
IEHPSMSVYITNGSIVVEEDT^REAPRDR^SPSKTRVERRTPHATSMSAKAAILGKV^GQAS
RIQRAKAHVDRRKISRKSLQRQN^LAREIQGRSMTRHRSFLCQPRQRQCNY

TP53INP1 Frog [Xenopus tropicalis] ensemble
ENSXETP00000014600 and ESTs
MFQMLNNMF^ARECSNALSQETKLSEKEDEWILVDF^IAQVDPGSRV^SEEAATFEVISHSD
ETSVLPHVSNTFERL^GTTSDFCIHFNLCPMEESWFVT^TPPPCFTAGELTSMAVK^TSPMEN
LLIEHPSMSVYAVHN^MCHK^PETSCESGF^PSPD^RTE^ELATENKKKGK^HIHC^SIAALAARMKG
LENTKIYLGDKLT^LHL^EKHPSRK^GFR^RQNLIRGCRSQQT^KHSRLLVHQPSPRQNY

GOR Medaca [*Oryzias latipes*] BJ721597 genomic profiling
MFQRLSNLFGVEEEVAELKGPNPCLTEADEEGWMLVNL^DPGSECNGNGRSREGSER
GCMDESWFVTPPPCFTA^EGATAEASP MEDLLIEHPSMSVYVSPNNTSMVTSDSLGVGE
CILSASSVSSRVSEPGVIPAARSTMTRVTRGGAAHPGALAKVTQVARVQRCKARI DRR
HLSRNHIQRQNRTREQVPCCHAHARNTFLHQPSKRNFCH

TP53INP1 Medaca [*Oryzias latipes*] genomic profiling and ESTS
(AM335308; AM316165; AM322529; AM306335)
MFQVFASALFRDGVEELSQCSRPGDDKREEEEDDEDWILVNLY^TDACSGDCGDGLSRM
SPEDEDEEEIDLVMIPSP^IASPAIRYPSCTS LNSVADTD^PDGGVDEDEFYVDDEGGFLRLD
ACSLEESWFVT^{PPP}CFTGRGSQPVLLETSPLENLLIEHPSMSVYAHHSPPRIMLNPLPQH
SLEGKLDLFLSSGSPDRKPSRGKEVRC SIEGSRH^RQDAAAQRRPMLHSPCYAATLSPNA
GFLQQQQRRPGSAAQRSQPLSRKGLRRRNLLRPPKTGTMHLLQQPIQRHLNF

GOR Elephant fish [*Callorhinus milius*] genomic profiling
MFHRFTSLFYGGSENTCIEGPDP SLTEKEDDGWLIVDFPV^EVKASTCVSPHLPDDHLPL
ASSSLESLHC GISSRPPRSKACTLEESWFVT^{PPP}CFTA^EGQEPGEVEISPLENLLIEHP
SMSVYAGSNTNISTMEDEPSEVPSS^RSARQPRAERLTAPS PAVAAGI QSSLVEKVSQVRR
LQRAKQRMERHQLSRNRIQRQNLTRECRLHRTKHGSFVYQPRQRHCNY

TP53INP1 Elephant fish [*Callorhinus milius*] genomic
profiling
MYQRFSMLFGEIDGAERESQELEISEKEDEEWILVDY^IDGM DRATSPNSAMFSSSTSSL
ELLGNSSDPCFLQLDSCALEESWFIT^{PPP}CFTAGGQAPVQVEMSPMENLLIEHPSMSVYT
VHN HSSLRENS^RVIPIVQYVPRRVSAFRIRDSVLEHTNHIFMQCALKYVERRKLCNH
LRRQRARKRYFAKEKHFGHKQPCQRNHKY

GOR Sea squirt [*Ciona intestinalis*] XP_002130814
MLNTIAYWAGFGNSDTPVVDDNLSFITKETGDWTLVDLENQN^DAQSNYPT^{PPPS}PRIEH
WLIT^{PPP}CFTA^EASMHV GALNARENLLIEHPMSFKPAEPSEEPKNTESRSVQRHK^{GAP}
TSLRSHRRASRQASCVISQMHSNQIKRDVARSNKAMQKMRQIVHQPRKRC

GOR Lancelet [*Branchiostoma floridae*] CF918976; BW697867;
CF9189763; BW698074;
MFSAVTNLLFGASEEVGACDLRTSTLDDWLV ELPAGMNIQQMEKETEAL TQS RPGDRP
STSSSPVP IPE NH PVEE SWFT^{PPP}CFTAGGQSPVAMETNP MENLLIEHPSMSVYVQQRS
SRNSGETTESSDSSGQHQQQRDVH RPPQ RAAIAARVGIVEQAKM KRHAQ RVQERHE
KKANSKTNLQRANLTSCRPIRASRHN RNRL MCKQ PGRVN KGR C

GOR Sea urchin [*Strongylocentrotus purpuratus*] XP_001177555
NCBI predicted plus genomic profiling and multiple ESTs
MLSGLSDYLF GSNNQAGDAMV TDDTQPQR DTPVKP VEIEMDG DWVLVDVT^{NDGSPS}
PLRS PTRSPSKDGFQSQPAVPEKPHRM ESWFT^{PPP}CFTAGGHS PHQLAT SP LEDLLI
EHPMSVYHHSQRGAPMAH RRQHL PRQKSS RTPKR THN RL VLN AKP PRRAAAIAARVG
IEQS ANQV GLQEQ RDT K RHQ RQ YSPG KIER HNKAYH HQSASS RRHYK QN SIS GRHSGA
IYKQPR

GOR Fly *Drosophila melanogaster*] NP_728991
MLSSLASYLFGSATSDSISQEA NPAQNR TNASNANSSSPGPTSDPAAGDVIEV TSSTPS
VAGSSRGAVRASNGKRGKNRRGKQ QRTNQQQRKQQPAITKL LT PSGEIV DEDF DEDE WYI
VEKE D EEDDSLPRSDSEEELSV VEVSPQRGGSN NASSPMVTVATGTA FNC RRRQ GVNSCS
LYSGP RPQQ QRNLYLQRSGRSV RPLS I STLSP PRS VPAL GAGDH DLT LQSL YV AS PGS DQG
QDHGQGANVLMEE S WYVTPP PCFT SIGP INMETSPF ENLLIEHP SMSV HSIR STQEG TD
SFVNLDLG VSTE VPQ QREE PEPEA EPQD QRQ ALQ EQQ RAPN ARFD SHAA VQL KQ QT LAR Q
SQKSKN KKEHQQLCRSAIKRANKVRDFQAKANP RRR SEMQHCKL VSGANN RSKCCY

GOR Sea slug [*Aplysia californica*] genomic profiling
MFNSVAKYLWG DANEVEQGYMEVSGQADTAGEQLDLAIHQ DDDDWL VVGQP^{GASDIELDE}
AASLRCSYNPLTGCS DSVQGALQDCTMNLNNFDLDSNYSSDGE SG DSGVRPSS PESVFS
VCSGRSHATYRPSGSSHD PWIVAPP PCFTGSG GLGEL PTI SSSP LE NLLIEHPSMSVYLSV
PPSSLPPSHPFH LAHL AGESAPAS SEPRD SGDDSGEP DALREDRTH QLPV GEQLPAA HR
AHREGLGRHWGFAAPA QVSPA QAVARL HAAQRVQSGK SNSKAVSRQK CRRENKVYEYKGCP
KGNTKRSKRSR PSSCKSGRM CQ RV

DOR Capitella [Capitella sp] EY564360 and genomic profiling
MLSGISSYLFGASSAAEDNLPQPTVDPPEVQDDLERLMTREGEEEWVLVDKAA**RSPRSP**
RCRFRGSADTPNGSSGHSTPVHILHPSLCESWLVTPPSCFT**AAGSARSDPLENNLIEHP**
SMSVYSLGQRGGGRGRSAGEESEESDVEEEAVRSQRLQASRPHPLAINTAIASRKVTQRSM
QKAVKKHEQQRLARNVMQRNNRVQKHNNSCRRPSSERMMQPSGRSNRSM LH

DOR Sea anemone [Nematostella vectensis] XP_001623518
MFSSLTSYIWGQTDDQVVPDCPLDVDSRTEEGWIMVLGSVVNPKD**VKKHEKAENAVPD**
SVEESWYVTTPPSCFESRD**NFSGVLESNPME**DLIEHPSMSVYGPRESSADASAGPSSRSAS
QAAEENQELEKKPPRTVQFQEKLIAQKRKVEAPQHGTIRPNKKNIKKQNLVQFHQS R
TRRTKKRDRMVGKHIGVHGKRG S

DOR Trichoplax [Trichoplax adherens] genomic profiling
MLWQSLSSYLWDQSSTEDASNHRVNVS LT EDDWILVVKKENKD**LEEVS NEDQLVKNRKE**
KESGWLLTPPPFCDFGHVME**ELSVSPFED**LLIEHPSMSIYRRIDSSASIRNNLDHDFAASL
ANSGDNNNTHE DTHEQSRSRSIELYMDRELNKKS DRFNYIRKARDLNVRSLTFSKANSRS
YSNSWSRRHCFTNFSYRR

DOR Sponge [Ephydatia muelleri] AM760558
NLIWGYPAAESREEPTDHITV EAEDWLLVQRS DKAQVCEGGSA PLDHGSQVTS DNES VCS
DASWVVA PAPRFRD SPETTNAGHPL ENLLIEHPSMSVY GQIQVGSDTIVPTADVQLVTTV
SEQAGQAPNRQR QVALHMDVPPKMP IAATQRVQFKHPKLSRASITRH NATVTKTRVPRM
RTRMSNSKKAGRRGC

DOR Rainbow trout [Oncorhynchus mykiss] CA358690
MFQALSSLFFGEVVEEVAEIKGPNCVTDADEEGWMVLVNLPEGATAETSPMEDLLIEHP
SMSVYSPSNLSMISNGNLSIVGEESITS LGSMSRVAEP AATS A VHNTM PTRVTRGAA
AQAGTLAKVTQVARVQRGKARTERRHLGRNRIQRQNRTREQVPRHA AHARNTY LHQPCQ
RNICH

DOR Salmon [Salmo salar] BG935547
MIGKIFAHFLGSTDDDFPTDDNETYEELIEFEEGGVV VNIQENNSLTPPEEDPLENLL
IEHPSMSVYQIRHQTSD EVADEEDASPRPVVKQHV SWRLAAWGSP L PCNVQL LAIQR
ARTHMECKELTR SALQRQNLAKVRFSPSDRRFGHKQPCQRL NY

Supplementary table 1