## (A) Amino acid sequence of human ZAR2 protein

MERFVRVPYGLYQGYGSTVPLGQPGLSGHKQPD
WRQNMGPPTFLARPGLLVPANAPDYCIDPYKRA
QLKAILSQMNPSLSPRLCKPNTKEVGVQVSPRV
DKAVQCSLGPRTLSSCSPWDGRDPQEPLPACGV
TSPATGRRGLIRLRRDGDEAESKALPGPAEASQ
PQPPSRRSGADRQEEPGQLEESGEKDAPCPQET
KSKQVPGDAASEPLRRPNFQFLEPKYGYFHCKD
CKTRWESAYVWCISGTNKVYFKQLCCKCQKSFN
PYRVEAIQCQTCSKSHCSCPQKKRHIDLRRPHR
QELCGRCKDKRFSCGNIYSFKYVM

## (B) Alignment between ZAR1 and ZAR2 protein amino acid sequences

| hZar1 | MAALGDEVLDGYVFPACPPCSYRYPYPAATKGKGAAGGSWQQRGRGCLPASSPCSAGAAS   | 60  |
|-------|--|-----|
| hZar2 | merfvrvpygly <mark>g</mark> gygs <mark>t</mark> vpl <mark>go</mark> pglsghkopdwronmgpptflarpg  | 48  |
| hZar1 | LSFPGCGRLTAAEYFDSYQRERLMALLAQVGPGLGPRARRAGSCDVAVQVSPRIDAAVQC   | 120 |
| hZar2 | LLVPAN <mark>A</mark> PDYC <mark>IDPYKRAQLKAILSQM</mark> NPSLSPRLC <mark>K</mark> PN <mark>TKE</mark> VGVQVSPR <mark>V</mark> DKAVQC | 105 |
| hZar1 | SLGRRTLQRRARDPESPAGPGAEGTTGGGSFSQQPSRRGLEQGSPQNGAPRPMRFPRTVA   | 180 |
| hZar2 | SLGPRTLSSCSPWDGRDPQEPLP-ACG  | 131 |
| hZar1 | VYSPLALRRLTAFLEGPGPAAGEQRSGASDGERGPPPARLQGPEEGEVWTKKAPRRPQSD   | 240 |
| hZar2 | VTSPATGRRGLIRLRRDGDEAESKALPGPAEASQPQPPSRRSGA   | 175 |
| hZar1 | DDGEAQAAVRASWEQPADGPELPPREAQEGEAAPRSALRSPGQPPSAGRARDGGDGREAA   | 300 |
| hZar2 | DRQEEPGQLEESGEKDAPCPQETKSKQVPGDAASEPLRRPZinc Finger #1   | 215 |
| hZar1 | VAGEGPSPRSPELGKERLRFQFLEQKYGYYHCKDCNIRWESAYVWCVQGTNKVYFKQFCR   | 360 |
| hZar2 | nfqflepkygyfh <mark>c</mark> kd <mark>ck</mark> trwesayvwc <mark>i</mark> sgtnkvyfkq <mark>lc</mark> c                               | 257 |
|       | Zinc Finger #2   |     |
| hZar1 | TCQKSYNPYRVEDITCQSCKQTRCSCPVKLRHVDPKRPHRQDLCGRCKGKRLSCDSTFSF   | 420 |
| hZar2 | KCQKSFNPYRVEAIQCQTCSKSHCSCPQKKRHIDLRRPHRQELCGRCKDKRFSCGNIYSF   | 317 |
| h7aw1 | WUIT 424   |     |

321