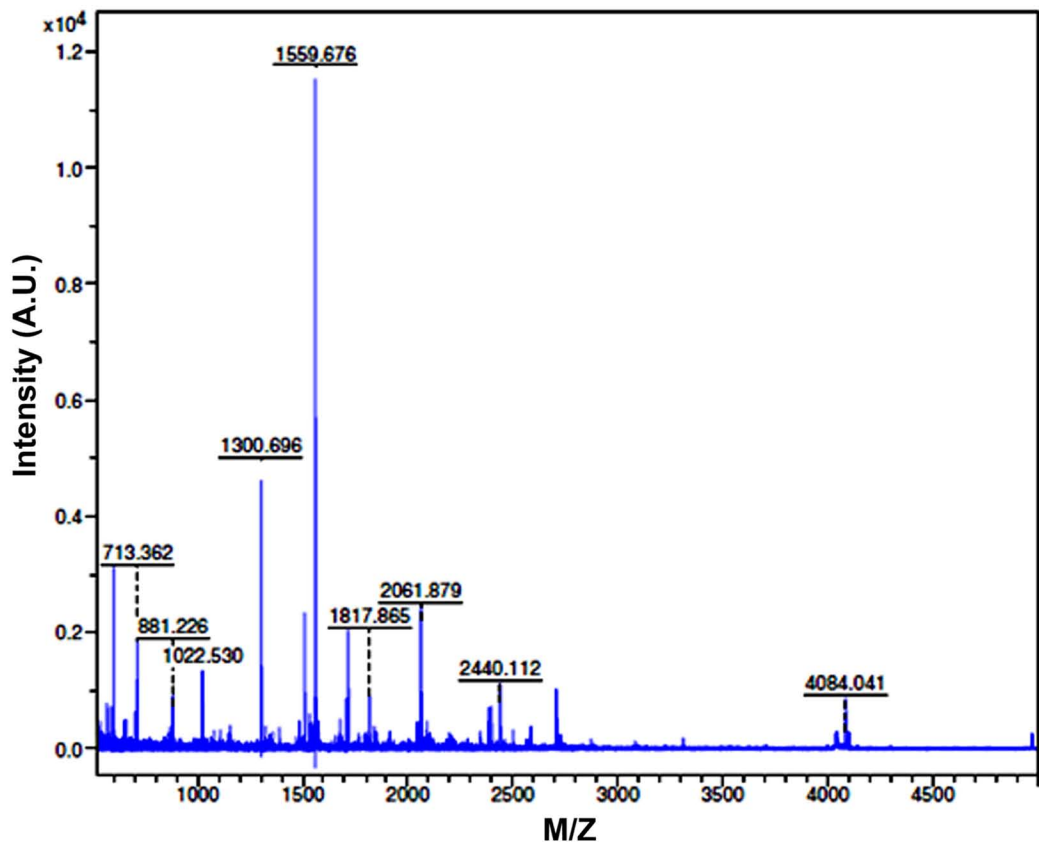


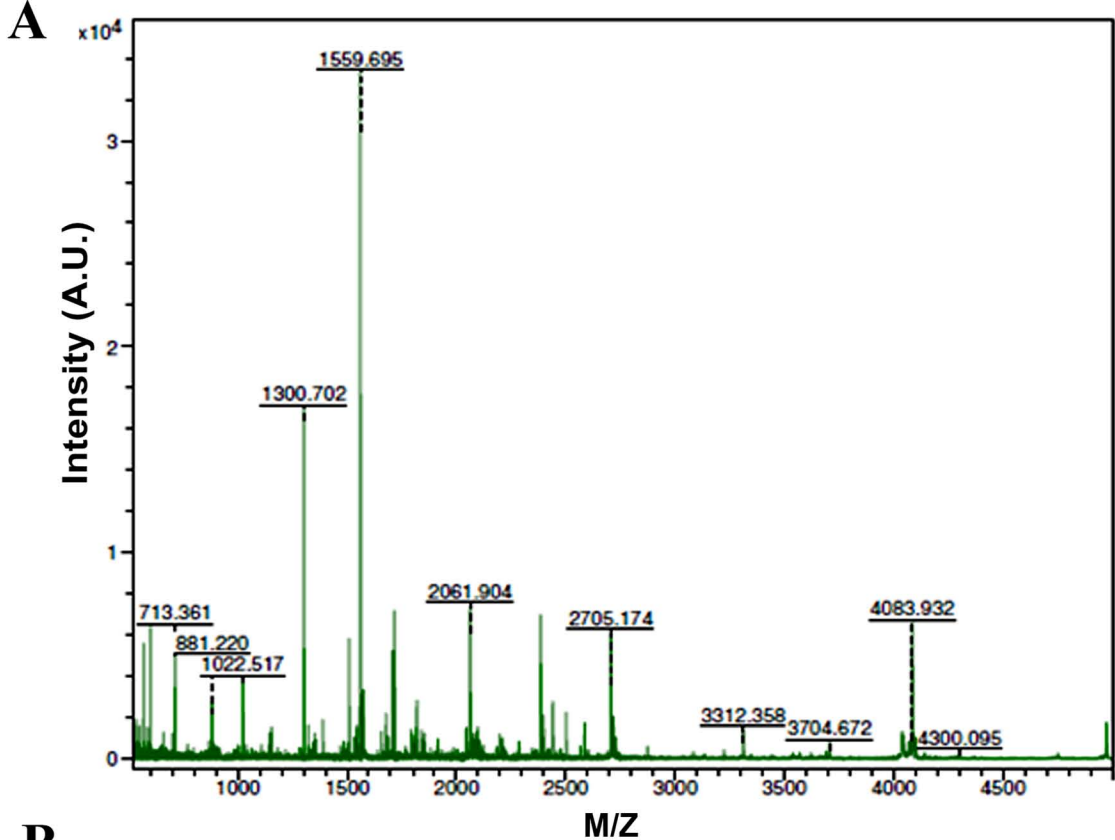
A



B

Sequence data:				
Interleukin - 10 <i>Labeo rohita</i>		Sequence Coverage MS:		48 %
Score: 96	pI (isoelectric point): 8.11		Mass: 21.314 kDa	
10	20	30	40	50
MFTGVILSS	LVMLLLSDSA	QCRRV <u>DC</u> KSD	<u>CCSFVEGFPV</u>	<u>RLKELRSAYR</u>
60	70	80	90	100
<u>EIQRFY</u> ESND	DMEPLL <u>N</u> ENV	QQNIN <u>SP</u> YGC	HVMNEIL <u>RF</u> Y	<u>LDTILPTAVQ</u>
110	120	130	140	150
<u>KSHLH</u> SKTPI	<u>DSIGNIFQDL</u>	<u>KRDMLKCKNY</u>	<u>FSCQNP</u> FELA	<u>SIKNSY</u> EKMK
160	170	180		
EKG <u>VSKAMGE</u>	<u>LDMLFKYIEQ</u>	<u>YLTSKR</u> VKHL		

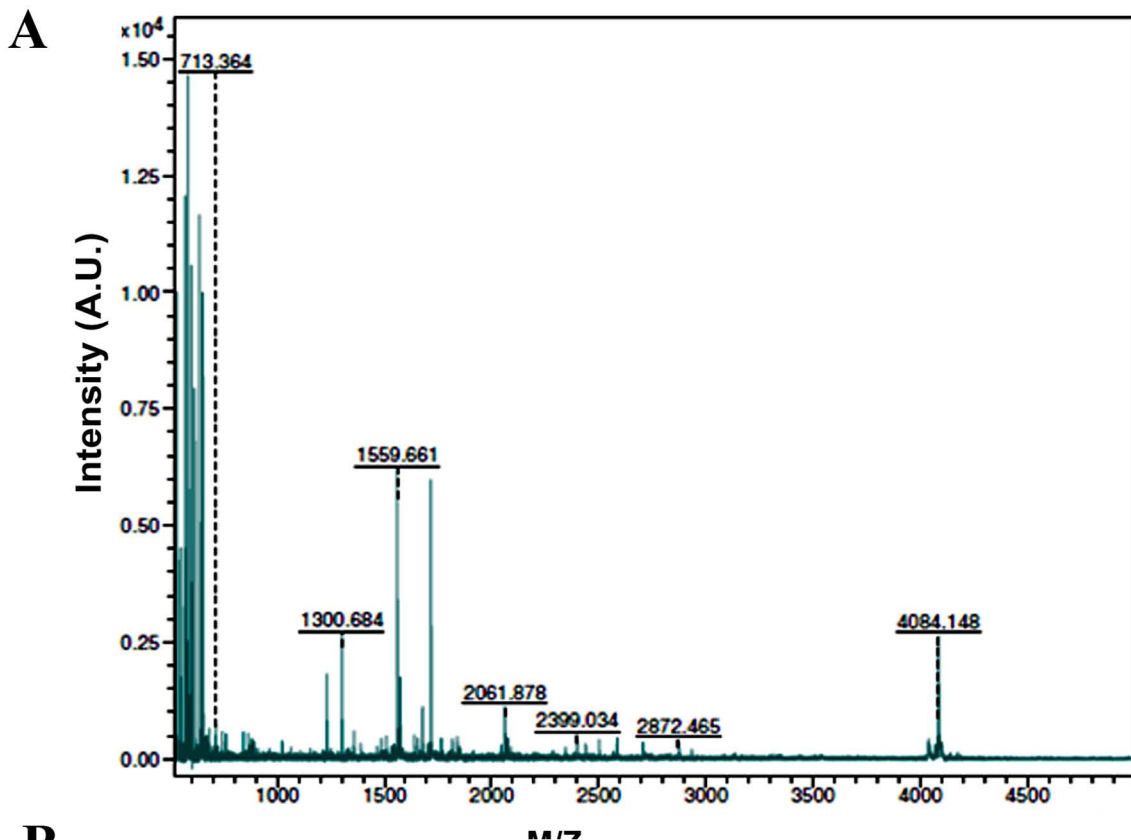
Fig. S 1(A) Mass spectrum analysis report of the tryptic digest of the spot 1 of the *rLr*IL-10 separated by 2D (shown in Fig. 2A). (B) The identified protein, score, amino acid sequence coverage and the number of identified peptides are shown. The matched peptide ions in the IL-10 sequence (shown in red) are shown in bold and underlined.



B

Sequence data:				
Interleukin - 10 <i>Labeo rohita</i>		Sequence Coverage MS:	64 %	
Score: 117	pI (isoelectric point): 8.11		Mass: 21.314 kDa	
10	20	30	40	50
<u>MIETGVILSS</u>	<u>LVMLLLSDSA</u>	<u>QCRRVDCCKSD</u>	<u>CCSFVTEGFPV</u>	<u>RLKELRSAYR</u>
60	70	80	90	100
<u>EIQRFYESND</u>	<u>DMEPLLNEV</u>	<u>QQNINSPYGC</u>	<u>HVMNEILRFY</u>	<u>LDTILPTAVQ</u>
110	120	130	140	150
<u>KSHLHSKTPI</u>	<u>DSIGNIFQDL</u>	<u>KRDMLKCKNY</u>	<u>FSCONPFELA</u>	<u>SIKNSYEKMK</u>
160	170	180		
<u>EKGVSKAMGE</u>	<u>LDMLFKYIEQ</u>	<u>YLTSKRVKHL</u>		

Fig. S2(A) Mass spectrum analysis report of the tryptic digest of the spot 2 of the rLrIL-10 separated by 2D (shown in Fig. 2A). (B) The identified protein, score, amino acid sequence coverage and the number of identified peptides are shown. The matched peptide ions in the IL-10 sequence (shown in red) are shown in bold and underlined.



B

Sequence data:				
Interleukin - 10 <i>Labeo rohita</i>		Sequence Coverage MS:	71 %	
Score: 100	pI (isoelectric point): 8.11	Mass: 21.314 kDa		
10	20	30	40	50
MIFTGVLSS	LVMLLLSDSA	<u>QCRRVDCKSD</u>	<u>CCSFVEGFPV</u>	<u>RLKELRSAYR</u>
60	70	80	90	100
<u>EIQRFYESND</u>	<u>DMEPLLNEV</u>	<u>OONINSPYGC</u>	<u>HVMNEILRFY</u>	<u>LDTILPTAVQ</u>
110	120	130	140	150
<u>KSHLHSKTPI</u>	<u>DSIGNIFQDL</u>	<u>KRDMLKCKNY</u>	<u>FSCQNPFELA</u>	<u>SIKNSYEKMK</u>
160	170	180		
<u>EKGVSKAMGE</u>	<u>LDMLFKYIEQ</u>	<u>YLTSKRVKHL</u>		

Fig. S3 (A) Mass spectrum analysis report of the tryptic digest of the spot 3 of the rLrIL-10 separated by 2D (shown in Fig. 2A). (B) The identified protein, score, amino acid sequence coverage and the number of identified peptides are shown. The matched peptide ions in the IL-10 sequence (shown in red) are shown in bold and underlined.

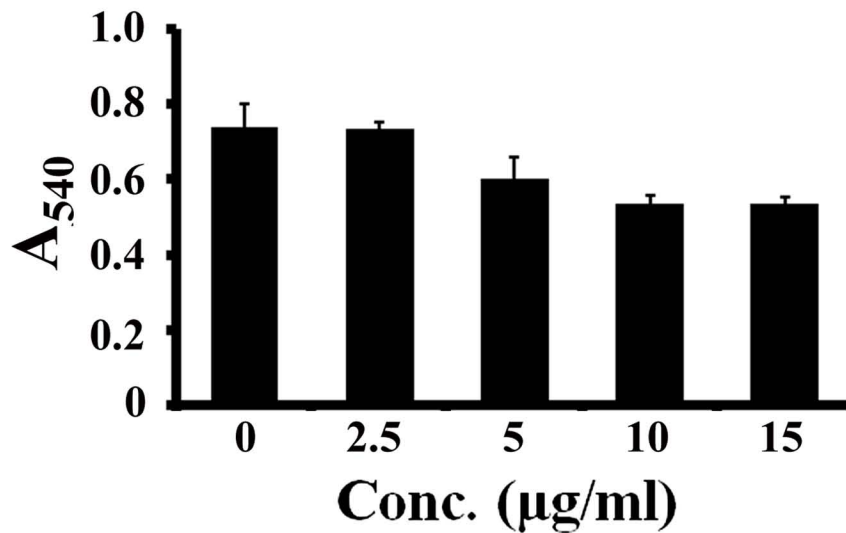


Fig. S4. To determine optimum concentration of rlrIL-10 required to induce NBT reduction, heparinized blood collected from five fish was pooled. It was then distributed into fifteen tubes containing 100 µl of blood in each tube. Three tubes were considered as negative control and were treated with corresponding volume of 1x PBS. To the remainder 12 tubes, four different concentrations of rLrIL-10 was added (three tubes each). The tubes were further incubated for 1 h at 25 °c. To each tube, NBT (0.2%, Sigma-Aldrich Chemicals Co., USA) was added in 1:1 ratio, mixed well and allowed to incubate further for 1 h at 25 °c. Further, 50 µl of this reaction mixture was transferred to glass centrifuge tube and 1 ml of dimethyl formamide (SRL, India) was added to it to solubilize the reduced formazan granule. The product was centrifuged at 2000 × g for 5 minutes and NBT reduction was measured in the supernatant of all samples at 540 nm. The data represent mean + S.D. for analysis conducted in triplicate.