

	IRF3	IRF5	IRF7	IRF4	IRF6	IRF8	IRF9
IRF3	179 0	<b>28%</b> <b>44%</b>	<b>25%</b> <b>41%</b>	<b>23%</b> <b>40%</b>	<b>22%</b> <b>45%</b>	<b>22%</b> <b>41%</b>	<b>21%</b> <b>37%</b>
IRF5	<b>54</b> <b>85</b>	186 0	26% 46%	33% 51%	61% 79%	35% 52%	25% 40%
IRF7	<b>48</b> <b>79</b>	52 91	190 0	21% 39%	27% 44%	19% 37%	20% 37%
IRF4	<b>43</b> <b>74</b>	63 96	42 75	171 0	33% 50%	37% 53%	29% 45%
IRF6	<b>43</b> <b>86</b>	115 148	54 89	62 94	184 0	34% 52%	25% 40%
IRF8	<b>41</b> <b>76</b>	66 97	39 74	68 97	64 97	178 0	26% 45%
IRF9	<b>38</b> <b>68</b>	47 76	40 71	50 78	47 75	47 81	166 0

**Suppl. Fig. 2 Sequence similarity between human IRF3 IAD (190-369) and corresponding regions of other human IRF family members.** Full-length sequences for human IRF 3-9 were aligned by CLUSTALX and imported into multiple alignment annotation program GeneDoc. Similarity matrix has been generated for the region of alignment, aa 190-369 of the human IRF3. The percentage of identical and conserved residues for each pairwise comparison is shown in the upper-right half of the matrix, whereas their number is shown in the lower-left half of the matrix. The diagonal represents the length of aligned fragments.