

S2 Table: Domain function descriptions, species names, and Genbank accession numbers of proteins with known functions within the NTF2-like super-family. These protein sequences were used for phylogenetics analysis with conserved domains to identify the most closely related characterized homolog of 71cR.

Domains	Species	Accession number
Ca ²⁺ /calmodulin-dependent protein kinase	<i>Talaromyces islandicus</i>	CRG91577.1
Ca ²⁺ /calmodulin-dependent protein kinase	<i>Aureobasidium namibiae</i> CBS 147.97	KEQ70053.1
Ca ²⁺ /calmodulin-dependent protein kinase	<i>Pseudocercospora fijiensis</i> CIRAD86	EME78224.1
Ca ²⁺ /calmodulin-dependent protein kinase	<i>Zymoseptoria tritici</i> IPO323	EGP92285.1
Limonene-1, 2-epoxide hydrolase	<i>Cycloclasticus zancles</i> 7-ME	AGS39004.1
Limonene-1, 2-epoxide hydrolase	<i>Neorhizobium galegae</i>	WP_046627776.1
Limonene-1, 2-epoxide hydrolase	<i>Burkholderia pseudomallei</i>	KKI72085.1
Limonene-1, 2-epoxide hydrolase	<i>Mycobacterium</i> sp. UM_NZ2	WP_046283582.1
Lumazine-binding domain	<i>Bacillus azotoformans</i> MEV2011	KEF37658.1
Lumazine-binding domain	<i>Streptococcus pneumoniae</i>	CKF20303.1
Lumazine-binding domain protein	<i>Clostridium botulinum</i> 202F	AIY78946.1
Lumazine-binding domain protein	<i>Mycobacterium lentiflavum</i>	CQD24850.1
Putative lumazine-binding	<i>Burkholderia pseudomallei</i>	CPH87736.1
MBA1-like protein	<i>Aspergillus parasiticus</i> SU-1	KJK67754.1
MBA1-like protein	<i>Candida tenuis</i> ATCC 10573	EGV65914.1
MBA1-like protein	<i>Saccharomyces kudriavzevii</i> IFO 1802	EJT42540.1
NTF2-like N-terminal transpeptidase	<i>Chryseobacterium taiwanense</i>	KIC61686.1
NTF2-like N-terminal transpeptidase	<i>Riemerella anatipestifer</i> RA-GD	ADZ12144.1
NTF2-like N-terminal transpeptidase	<i>Enterococcus faecium</i> TX1330	EEI60277.1
Nuclear pore RNA shuttling protein Mtr2	<i>Saccharomyces cerevisiae</i>	CAA82029.1
Nuclear pore RNA shuttling protein Mtr2	<i>Snodgrassella alvi</i> SCGC AB-598-O11	KES10753.1
Nuclear pore RNA shuttling protein Mtr2	<i>Candida albicans</i>	P84148.1
Nuclear transport factor 2	<i>Rattus norvegicus</i>	NP_001007630.1
Nuclear transport factor 2	<i>Penicillium roqueforti</i> FM164	CDM28803.1
Nuclear transport factor 2	<i>Drosophila melanogaster</i>	AAS98195.1
Phenazine biosynthesis protein A/B	<i>Nocardiopsis dassonvillei</i>	ADH70409.1
Phenazine biosynthesis protein A/B	<i>Pseudomonas</i> sp. GM17	EJM14221.1
Phenazine biosynthesis protein A/B	<i>Streptomyces pratensis</i> ATCC 33331	ADW02923.1
Phenazine biosynthesis protein A/B	<i>Burkholderia lata</i>	ABB11682.1
Ring hydroxylating beta subunit	<i>Pseudomonas</i> sp. HMSC05H02	KJJ11284.1
Ring hydroxylating beta subunit	<i>Corynebacterium ammoniagenes</i> DSM 20306	EFG82184.1
ring hydroxylating beta subunit	<i>Bordetella bronchiseptica</i> B20-10725633	KDB66946.1
Scytalone dehydratase	<i>Colletotrichum lagenaria</i>	BAA13009.1
Scytalone dehydratase	<i>Talaromyces islandicus</i>	CRG86684.1
Scytalone dehydratase	<i>Aspergillus flavus</i> AF70	KJJ30121.1
Scytalone dehydratase	<i>Marssonina brunnea</i> f. sp. 'multigermtubi'	XP_007296032.1

SnoaL-like polyketide cyclase	<i>Saccharomonospora azurea NA-128</i>	EHY91179.1
SnoaL-like polyketide cyclase	<i>Bradyrhizobium sp. WSM471</i>	EHR01507.1
SnoaL-like polyketide cyclase	<i>Bacillus thuringiensis MC28</i>	AFU13283.1
SnoaL-like polyketide cyclase	<i>Methylobacterium album BG8</i>	EIC29135.1
Snoa2-A Putative Hydroxylase	<i>Streptomyces Nogalater</i>	2GEX
Snoa3 -Ketosteroid Isomerase	<i>Shewanella Frigidimarina</i>	3BB9
Tim44-like domain	<i>Roseburia intestinalis XB6B4</i>	CBL12234.1
Tim44-like domain	<i>Clostridium sp. CAG:492</i>	WP_022091013.1
Tim44-like domain	<i>Ostreococcus tauri</i>	CEF99583.1
Tim44-like domain	<i>Enterococcus sp. 7L76</i>	CBL31786.1
VirB8 protein (plasmid)	<i>Aeromonas caviae</i>	YP_067832.1
VirB8 protein	<i>Ehrlichia ruminantium str. Welgevonden</i>	CAI26955.1
VirB8 protein	<i>Bartonella tribocorum CIP 105476</i>	CAK02009.1
VirB8 protein (plasmid)	<i>Pseudomonas putida</i>	YP_008994866.1
VirB8 protein (plasmid)	<i>Xanthomonas axonopodis pv. citri str. 306</i>	AAM39286.1
Wound-induced protein WI12	<i>Mesembryanthemum crystallinum</i>	AAD23999.1
Wound-induced protein WI12	<i>Burkholderia mallei</i>	KGC14241.1
Wound-induced protein WI12	<i>Zea mays</i>	ACG48358.1