Probe name	5’-3’ sequence
Probe b	CATGGCTTAATCTTTGAGAC
Probe c	GACTCTCCATCTCTTGTCTTCTTG
Probe d	TGTTACCTCTGGGCCC
Probe e	TTTCGCTGCGTTCTTCATC
Probe f	GGCCAGCAATTTCAAGTTA
Probe g	GAACATTGTTCGCCTAGA
Probe h	CTCCGCTTATTGATATGC
Probe 5S	GGTCACCCACTACACTACTCGG

Supplementary Table S1. Oligonucleotides used as probes for RNA analysis.

	ChErb1$_{435-801}$/ChYtm1	ChErb1$_{432-801}$/ChYtm1	ChErb1[R486E]$_{435-801}$/ChYtm1
Data collection			
Space group	P 6_5 2 2	P 2_1 2_1 2	P 6_5 2 2
Cell dimensions			
a, *b*, *c* (Å)	169.11, 169.11, 154.04	86.443, 108.149, 108.618	170.75, 170.75, 155.66
α, β, γ (°)	90, 90, 120	90, 90, 90	90, 90, 120
Resolution (Å)	48.82 - 3.1 (3.31 - 3.1)*	48.53 - 2.1 (2.175 - 2.1)*	85.38-3.0 (3.18-3.0)*
R_{merge}	0.282 (2.838)	0.05838 (0.924)	0.176 (1.862
I / σI	17 (2.5)	18.69 (2.18	13.5 (1.6)
Completeness (%)	100.00 (100.00)	99.90 (99.97)	100.00 (100.00)
Redundancy	39.1 (40.2)	6.5 (6.5)	12.2 (12.7)
Refinement			
Resolution (Å)	48.82 - 3.1 (3.31 - 3.1)	48.53 - 2.1 (2.175 - 2.1)	85.38-3.0 (3.18-3.0)
No. reflections	24180 (4313)	60041 (5923)	27367 (4333)
R_{work} / R_{free}	0.1936 (0.2940)/ 0.2390 (0.3557)	0.1639 (0.2386)/ 0.2132 (0.2703)	0.2016 (0.3153)/ 0.2621 (0.3914)
No. atoms	6170	6631	6182
Protein	6168	6279	6177
Ligand/ion	2[a]	26[b]	5[c]
Water	0	326	0
B-factors	102.40	63.20	89.70
Protein	102.40	63.40	89.70
Ligand/ion	96.10	76.70	84.70
Water		57.80	
R.m.s. deviations			
Bond lengths (Å)	0.006	0.008	0.006
Bond angles (°)	1.26	1.18	1.35

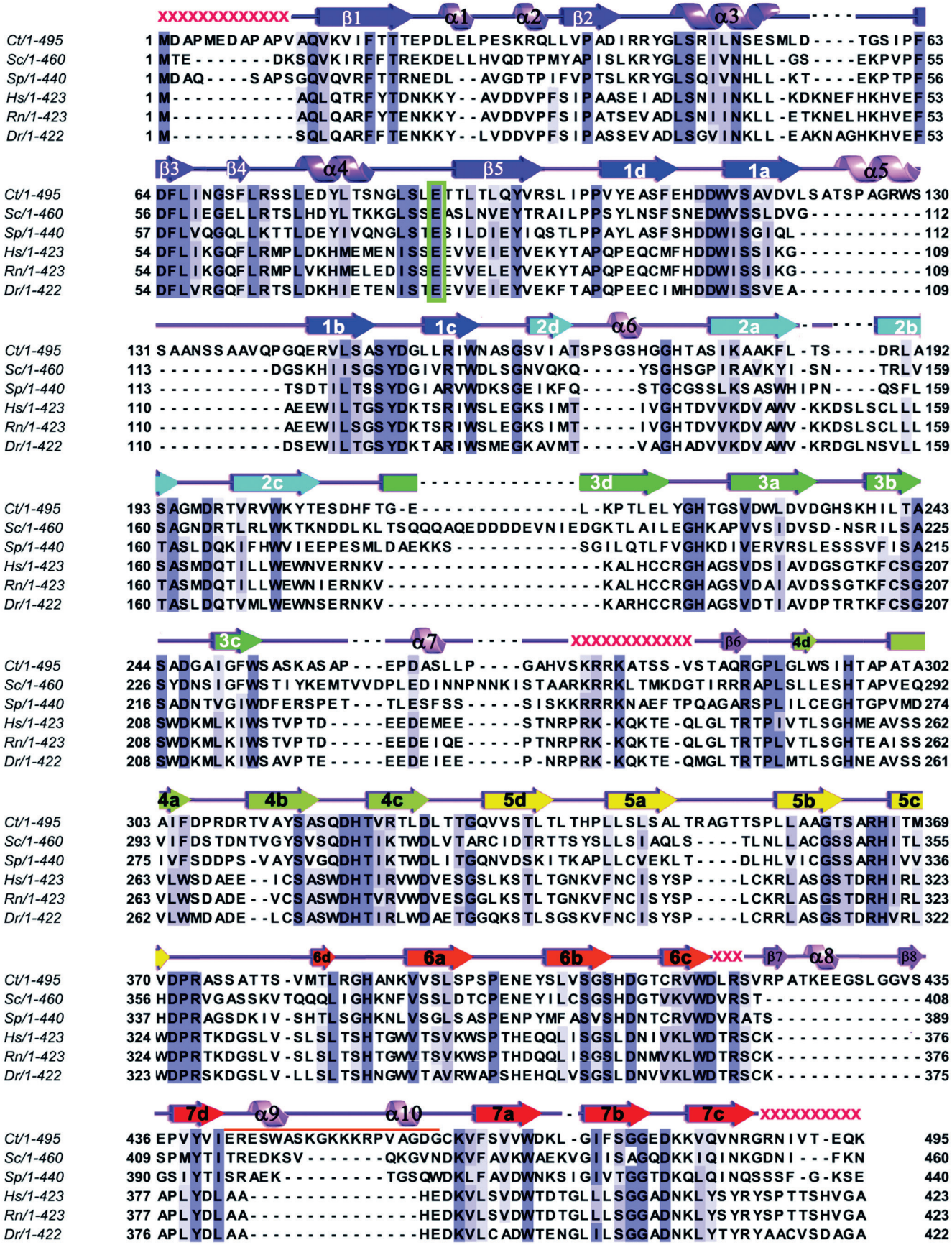
Supplementary table S2. Data collection and refinement statistics

*Values in parentheses are for highest-resolution shell.

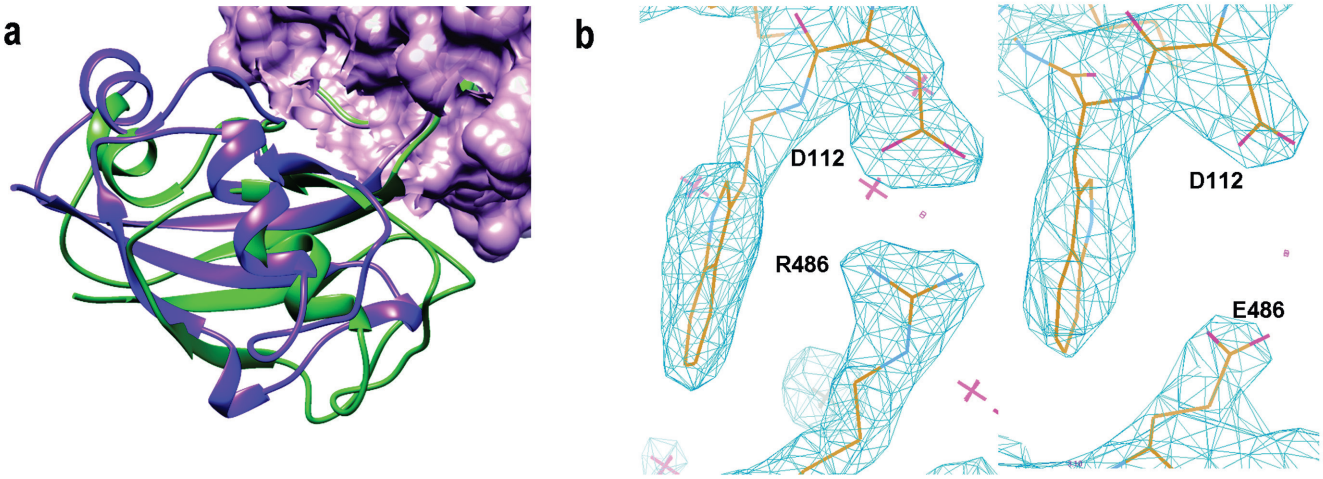
[a]) Ligands: chloride ion

[b]) Ligands: chloride ion, sodium ion, glycerol, ethylene glycol

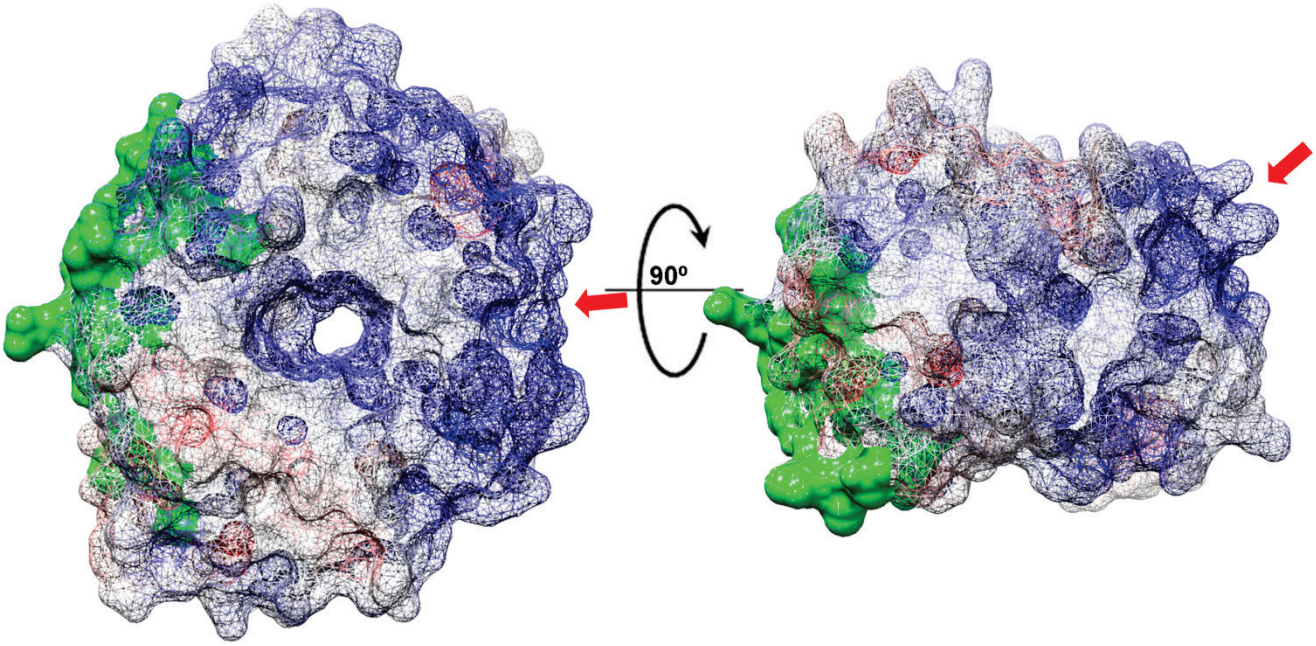
[c]) Ligands: chloride ion. Data were collected from one crystal for each dataset.


XXXXXXXXXXXXX β1 α1 α2 β2 α3
Ct/1-495 1 MDAPMEDAPAPVAQVKVIFTTTEPDLELPESKRQLLVPADIRRYGLSRILNSESMLD----TGSIPF 63
Sc/1-460 1 MTE-------DKSQVKIRFFTREKDELLHVQDTPMYAPISLKRYGLSEIVNHLL-GS----EKPVPF 55
Sp/1-440 1 MDAQ----SAPSGQVQVRFTTRNEDL--AVGDTPIFVPTSLKRYGLSQIVNHLL-KT----EKPTPF 56
Hs/1-423 1 M----------AQLQTRFYTDNKKY--AVDDVPFSIPAASEIADLSNIINKLL-KDKNEFHKHVEF 53
Rn/1-423 1 M----------AQLQARFYTENKKY--AVDDVPFSIPATSEVADLSNIINKLL-ETKNELHKHVEF 53
Dr/1-422 1 M----------SQLQARFFTENKKY--LVDDVPFSIPASSEVADLSGVINKLL-EAKNAGHKHVEF 53
β3 β4 α4 β5 1d 1a α5
Ct/1-495 64 DFLINGSFLRSSLEDYLTSNGLSLETTLTLQYVRSLIPPVYEASFEHDDWVSAVDVLSATSPAGRWS 130
Sc/1-460 56 DFLIEGELLRTSLHDYLTKKGLSSEASLNVEYTRAILPPSYLNSFSNEDWVSSLDVG----------112
Sp/1-440 57 DFLVQGQLLKTTLDEYIVQNGLSTESILDIEYIQSTLPPAYLASFSHDDWISGIQL----------112
Hs/1-423 54 DFLIKGQFLRMPLDKHMEMENISSEEVVEIEYVEKYTAPQPEQCMFHDDWISSIKG----------109
Rn/1-423 54 DFLIKGQFLRMPLVKHMELEDISSEEVVELEYVEKYTAPQPEQCMFHDDWISSIKG----------109
Dr/1-422 54 DFLVRGQFLRTSLDKHIETENISTEEVVEIEYVEKFTAPQPEECIMHDDWISSVEA----------109
1b 1c 2d α6 2a 2b
Ct/1-495 131 SAANSSAAVQPGQERVLSASYDGLLRIWNASGSVIATSPSGSHGGHTASIKAAKFL-TS----DRLA192
Sc/1-460 113 ----------DGSKHIISGSYDGIVRTWDLSGNVQKQ-----YSGHSGPIRAVKYI-SN----TRLV159
Sp/1-440 113 ----------TSDTILTSSYDGIARVWDKSGEIKFQ-----STGCGSSLKSASWHIPN----QSFL159
Hs/1-423 110 ----------AEEWILTGSYDKTSRIWSLEGKSIMT-----IVGHTDVVKDVAWV-KKDSLSCLLL159
Rn/1-423 110 ----------AEEWILSGSYDKTSRIWSLEGKSIMT-----IVGHTDVVKDVAWV-KKDSLSCLLL159
Dr/1-422 110 ----------DSEWILTGSYDKTARIWSMEGKAVMT-----VAGHADVVKDVAWV-KRDGLNSVLL159
2c 3d 3a 3b
Ct/1-495 193 SAGMDRTVRVWKYTESDHFTG-E--------------L-KPTLELYGHTGSVDWLDVDGHSKHILTA243
Sc/1-460 160 SAGNDRTLRLWKTKNDDLKLTSQQQAQEDDDDEVNIEDGKTLAILEGHKAPVVSIDVSD-NSRILSA225
Sp/1-440 160 TASLDQKIFHWVIEEPESMLDAEKKS----------SGILQTLFVGHKDIVERVRSLESSSVFISA215
Hs/1-423 160 SASMDQTILLWEWNVERNKV-----------------KALHCCRGHAGSVDSIAVDGSGTKFCSG207
Rn/1-423 160 TASMDQTILLWEWNIERNKV-----------------KALHCCRGHAGSVDAIAVDSSGTKFCSG207
Dr/1-422 160 TASLDQTVMLWEWNSERNKV-----------------KARHCCRGHAGSVDTIAVDPTRTKFCSG207
3c α7 XXXXXXXXXXXX β6 4d
Ct/1-495 244 SADGAIGFWSASKASAP---EPDASLLP----GAHVSKRRKATSS-VSTAQRGPLGLWSIHTAPATA302
Sc/1-460 226 SYDNSIGFWSTIYKEMTVVDPLEDINNPNNKISTAARKRRKLTMKDGTIRRRAPLSLLESHTAPVEQ292
Sp/1-440 216 SADNTVGIWDFERSPET---TLESFSS-----SISKKRRRKNAEFTPQAGARSPLILCEGHTGPVMD274
Hs/1-423 208 SWDKMLKIWSTVPTD-----EEDEMEE-----STNRPRK-KQKTE-QLGLTRTPIVTLSGHMEAVSS262
Rn/1-423 208 SWDKMLKIWSTVPTD-----EEDEIQE-----PTNRPRK-KQKTE-QLGLTRTPLVTLSGHTEAISS262
Dr/1-422 208 SWDKMLKIWSAVPTE-----EEDEIEE-----P-NRPRK-KQKTE-QMGLTRTPLMTLSGHNEAVSS261
4a 4b 4c 5d 5a 5b 5c
Ct/1-495 303 AIFDPRDRTVAYSASQDHTVRTLDLTTGQVVSTLTLTHPLLSLSALTRAGTTSPLLAAGTSARHITM369
Sc/1-460 293 VIFDSTDNTVGYSVSQDHTIKTWDLVTARCIDTRTTSYSLLSIAQLS----TLNLLACGSSARHITL355
Sp/1-440 275 IVFSDDPS-VAYSVGQDHTIKTWDLITGQNVDSKITKAPLLCVEKLT----DLHLVICGSSARHIVV336
Hs/1-423 263 VLWSDAEE--ICSASWDHTIRVWDVESGSLKSTLTGNKVFNCISYSP----LCKRLASGSTDRHIRL323
Rn/1-423 263 VLWSDADE--VCSASWDHTVRVWDVESGGLKSTLTGNKVFNCISYSP----LCKRLASGSTDRHIRL323
Dr/1-422 262 VLWMDADE--LCSASWDHTIRLWDAETGGQKSTLSGSKVFNCISYSP----LCRRLASGSTDRHVRL322
6d 6a 6b 6c XXX β7 α8 β8
Ct/1-495 370 VDPRASSATTS-VMTLRGHANKVVSLSPSPENEYSLVSGSHDGTCRVWDLRSVRPATKEEGSLGGVS435
Sc/1-460 356 HDPRVGASSKVTQQQLIGHKNFVSSLDTCPENEYILCSGSHDGTVKVWDVRST----------------408
Sp/1-440 337 HDPRAGSDKIV-SHTLSGHKNLVSGLSASPENPYMFASVSHDNTCRVWDVRATS---------------389
Hs/1-423 324 WDPRTKDGSLV-SLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDTRSCK---------------376
Rn/1-423 324 WDPRTKDGSLV-SLSLTSHTGWVTSVKWSPTHDQQLISGSLDNMVKLWDTRSCK---------------376
Dr/1-422 323 WDPRSKDGSLV-LLSLTSHNGWVTAVRWAPSHEHQLVSGSLDNVVKLWDTRSCK---------------375
7d α9 α10 7a 7b 7c XXXXXXXXXX
Ct/1-495 436 EPVYVIERESWASKGKKKRPVAGDGCKVFSVVWDKL-GIFSGGEDKKVQVNRGRNIVT-EQK 495
Sc/1-460 409 SPMYTITREDKSV-------QKGVNDKVFAVKWAEKVGIISAGQDKKIQINKGDNI---FKN 460
Sp/1-440 390 GSIYTISRAEK---------TGSQWDKLFAVDWNKSIGIVTGGTDKQLQINQSSSF-G-KSE 440
Hs/1-423 377 APLYDLAA----------------HEDKVLSVDWTDTGLLLSGGADNKLYSYRYSPTTSHVGA 423
Rn/1-423 377 APLYDLAA----------------HEDKVLSVDWTDTGLLLSGGADNKLYSYRYSPTTSHVGA 423
Dr/1-422 376 APLYDLAA----------------HEDKVLCADWTENGLILSGGADNKLYTYRYAACVSDAGA 422

Supplementary Figure S1. Multiple sequence aligment of Ytm1 orthologues. Sequences corresponding to Ytm1 (or WDR12) proteins from *Chaetomium thermophilum* (Ct), *Saccharomyces cerevisiae* (Sc), *Schizosaccharomyces pombe* (Sp), *Homo sapiens* (Hs), *Rattus norvegicus* (Rn) and *Danio rerio* (Dr) were aligned using JalView. Secondary structure elements as seen in the final model of ChYtm1 are represented above the alignment. β-strands are marked with arrows, α-helices are depicted with coils. Secondary structure elements corresponding to UBL are shown in purple. Coloring and numbering of the following β-strands correspond to the WD repeats. Conserved residues are marked with shadows. The conserved glutamic acid proposed to bind the MIDAS domain of Rea1 is marked with a green box. The sequence corresponding to the knob-like structure is shown with orange line



Supplementary Figure S2. (a) UBL of ChYtm1 presents certain degree of flexibility because it appears in two different orientations depending on the symmetry of the crystals. UBL in purple: P 21 21 2 and in green: P 65 2 2 space groups. **(b)** Upon successful crystallization of ChYtm1/ChErb1[R486E]$_{432\text{-}801}$ we proved that the β-propeller structure was intact and the only difference between both dimers was the lack of D112-R486 salt bridge (left) that is not formed in the mutant (right).



Supplementary Figure S3. Electrostatic surface potential of the β-propeller of Erb1 represented as mesh shows that highly electropositive area possibly involved in binding to RNA (red arrow) is located on the opposite side to Ytm1 binding site (in green)