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## Structure of the Roc-COR domain tandem of C-tepidum, a prokaryotic homologue of the human LRRK2 Parkinson kinase

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## Supplemental data

### Structure of the RocCOR domain tandem of *C. tepidum*, a prokaryotic homologue of the human LRRK2 parkinson kinase

Katja Gotthardt, Michael Weyand, Arjan Kortholt, Peter J.M Van Haastert and Alfred Wittinghofer

**Table S1:** Crystallographic data, phasing and refinement statistic

Data collection	COR SeMet	COR native	RocCOR E917R native
X-ray source	SLS X10SA	SLS X10SA	SLS X10SA
Space group	P3(2)21	P3(2)21	P2(1)2(1)2(1)
Cell parameters	a = 130.74 Å	a = 130.11 Å	a = 83.20 Å
	b = 130.74 Å	b = 130.11 Å	b = 106.10 Å
	c = 129.42 Å	c = 129.20 Å	c = 139.00 Å
Resolution (Å)	50.0–3.2 (3.3 – 3.2)	50.0–2.9 (3.0–2.9)	50.0–2.9 (3.0–2.9)
Wavelength (Å)	0.980	0.980	0.979
Completeness (%)	99.6 (99.9)	99.9 (100.0)	99.0 (99.7)
Unique reflections	40676 (3605)	28455 (2715)	27475 (2628)
Redundancy	7.2 (7.3)	8.8 (9.2)	3.7 (3.7)
$R_{\text{sym}}$ (%) <sup>a</sup>	8.3 (38.4)	12.7 (69.9)	7.1 (46.6)
$I/\sigma I$	17.19 (5.40)	12.7 (5.23)	20.52 (4.20)
<i>Phasing</i>			
Resolution (Å)	20–3.2		
No. of sites	16 of 18		
FOM after SOLVE	0.35		
FOM after RESOLVE (centric/acentric)	0.63/0.71		
<i>Refinement</i>			
PDB code			
$R_{\text{work}}^b/R_{\text{free}}^c$ (%)		21.0/24.3	23.0/27.0
Reflections (work/free)		27016/1422	26101/1374
No. of atoms		4643	6235
R.m.s.d.			
Bond length (Å)/ weight		0.009 / 0.022	0.009/ 0.022
Bond angle (°)		1.200	1.300
Wilson-B factor (Å <sup>2</sup> )		61.13	48.10
Ramachandran plot <sup>d</sup>			
Core (%)		87.9	88.8
Additionally (%)		11.5	10.6
Generously (%)		0.6	0.6
Disallowed (%)		0.0	0.0

Values in parentheses correspond to those in the outer resolution shell

a  $R_{\text{sym}} = (\sum (I - \langle I \rangle)) / (\sum I)$  where  $\langle I \rangle$  is the average intensity of multiple measurements

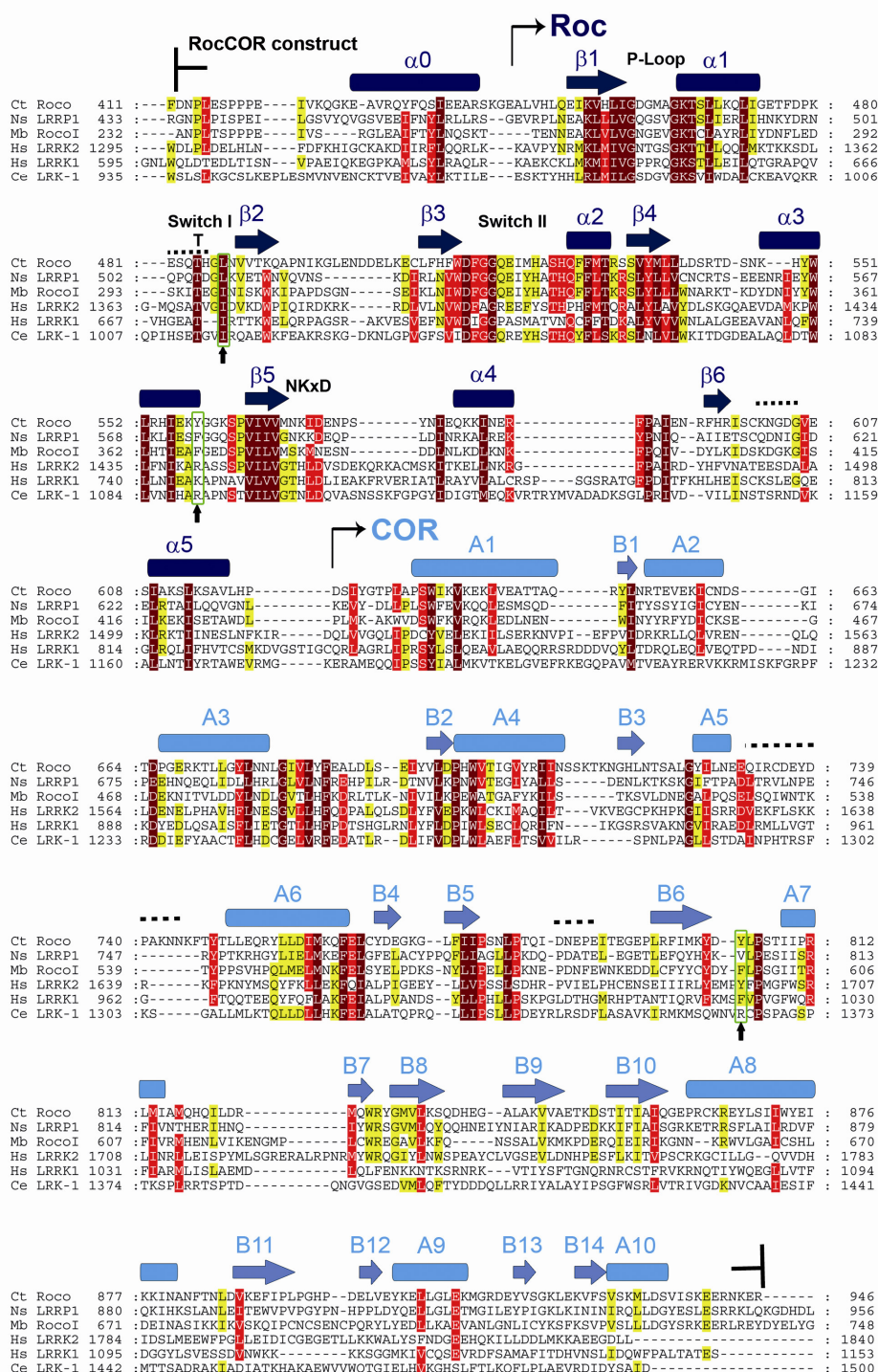
FOM, figure of merit

b  $R_{\text{work}} = (\sum |F_{\text{obs}} - F_{\text{calc}}|) / (\sum |F_{\text{obs}}|)$

c  $R_{\text{free}}$  is the R-factor based on 5% of the data excluded from refinement

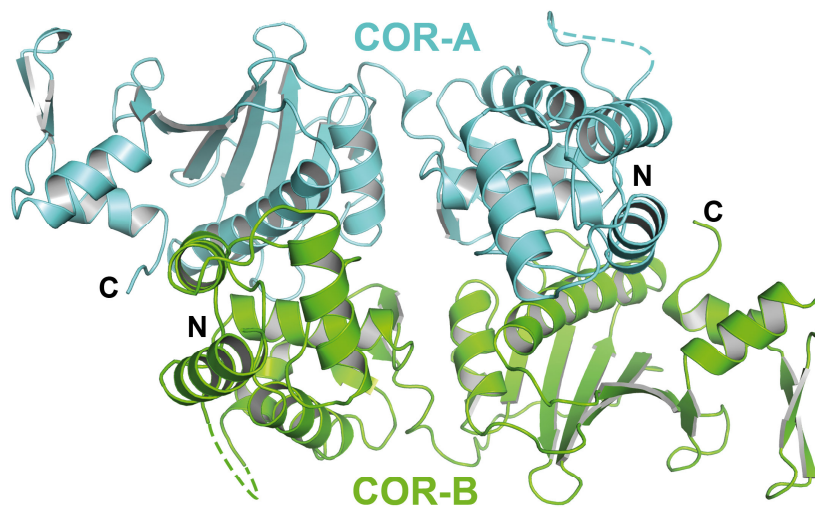
d Geometrical quality of the final models was confirmed with PROCHECK (CCP4-suite)

**Fig. S1**



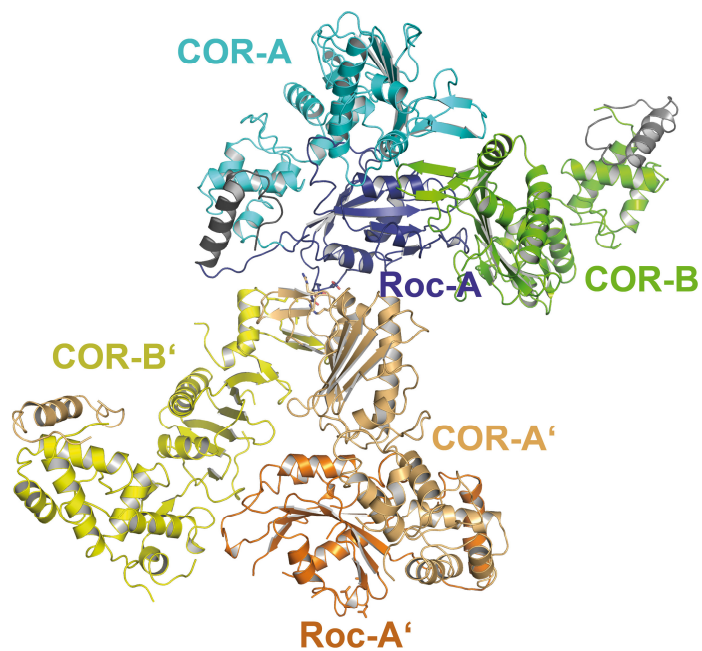
**Fig. S1** Sequence alignment and secondary structure assignment of the RocCOR tandem, with sequences from *Chlorobium tepidum* Roco, *Nostoc sp.* LRRP1, *Methanosarcina barkeri* Roco1, human LRRK2 and LRRK1 and *Caenorhaditis elegans* LRK-1 (Swiss-Prot accession numbers: Q8KC98, Q8Z0H2, Q466H0, Q5S007, Q38SD2, Q9TZM3). Positions of the Parkinson mutations are indicated with black arrows. Disordered regions of the structure are indicated with dashed lines. The RocCOR construct used for the structure is indicated.

**Fig. S2**



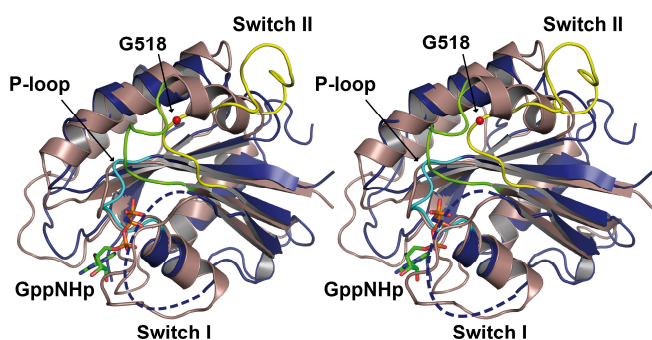
**Fig. S2** Ribbon diagram of the non-physiological COR dimer found in the asymmetric unit. Different protomers are coloured in green and cyan. Disordered loops are indicated with dashed lines.

**Fig. S3**



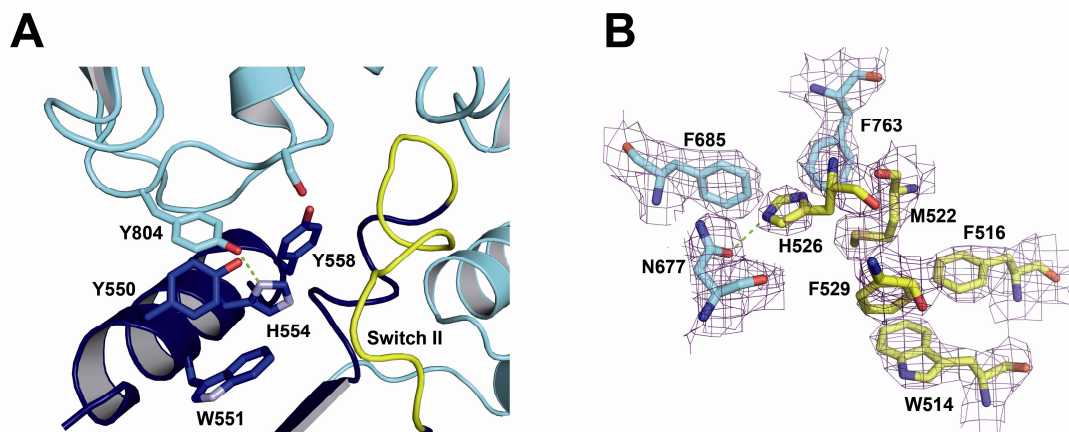
**Fig. S3** Crystal packing contact of the Roc domain A to a neighbouring molecule. RocCOR is coloured as in the main text. The adjacent molecule is shown in various shades of orange.

**Fig. S4**



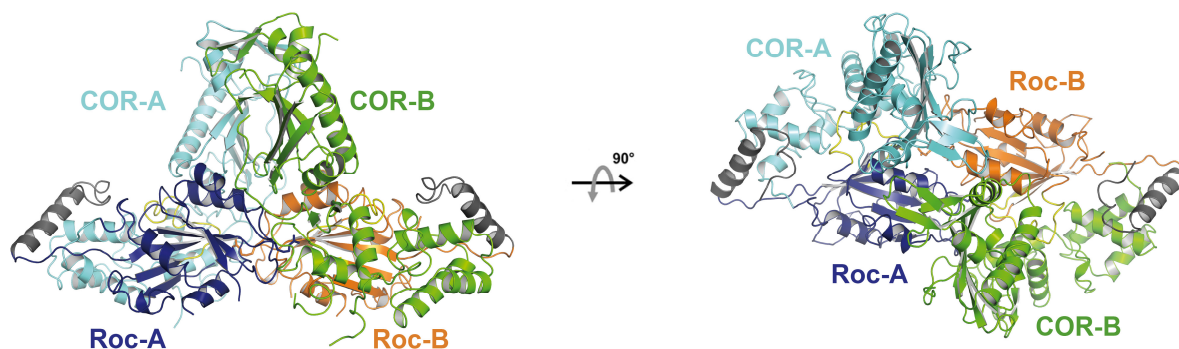
**Fig. S4** Stereo ribbon representation of the superimposition of the Roc domain A in blue (as in Figs 4,5,6) with Ras•GppNHp in light pink (Pai *et al.*, 1990).

**Fig. S5**



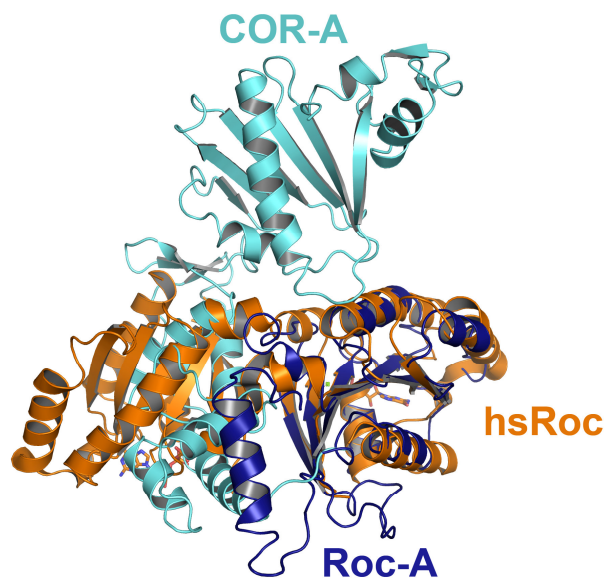
**Fig. S5 Roc-COR interface and Switch II.** A. Interface between Roc (blue) and COR (cyan) involving Switch II (yellow) Hydrogen bond between Tyr804 and His554 is indicated with green dashed line. B. 2Fo-Fc electron density (contoured at  $1\sigma$ ) and corresponding atomic model of the COR-Switch II interface. Colours as in A.

**Fig. S6**



**Fig. S6** Model of the complete RocCOR dimer, in two different orientations, with colours as in the main text. The modelled second G domain (Roc-B) is coloured in orange. The alpha0 helices of both G domains are shown in grey.

**Fig. S7**



**Fig. S7** Model of the RocCOR tandem, using the domain-swapped dimer of human LRRK2 Roc as found in the crystal by Deng *et al.*, (Deng *et al.*, 2008) superimposed onto the *Ct*Roc domain of the structure described here. The superimposition leads to serious clashes between the hsRoc dimer (orange) and the N-terminal domain of COR (cyan) of *Ct* RocCOR.