

CPF-member	Name	Motif	Comment	Reference(s)
DASH-CRY	dlr	YWVxFELLWRD	<ul style="list-style-type: none"> • CPD lesion repair • 2 mismatches allowed 	[25,26,165]
	dlr1	MSNRGRQ	<ul style="list-style-type: none"> • Part of D-R salt bridge • CPD lesion repair • 1 mismatch allowed 	[25,26,165]
	dlr2	DYDxxSNYGNWxY	<ul style="list-style-type: none"> • Part of D-R salt bridge • CPD lesion repair • Trp-triad • 2 mismatches allowed 	[25,26,53,165]
CPD class I/III	c1/3-1	DGDLxxxNxGWQW	<ul style="list-style-type: none"> • Generated from alignment of sequences from references • 2 mismatches allowed 	[9,175, 176]
	c3-2	PxFRxFNPxxQxEKFD	<ul style="list-style-type: none"> • From Alignment of 5 CPDIII sequences (see supplement in Nie et al., 2021) • 2 mismatches allowed 	[176]
	c3	WQWxAGxGxD	<ul style="list-style-type: none"> • From Alignment of 5 CPDIII sequences (see supplement in Nie et al., 2021) • 1 mismatch allowed 	[176]
CPD class II	mts	MHGFxRMYWAK	<ul style="list-style-type: none"> • Mitochondrial target sequence (MTS) • 2 mismatches allowed 	[9,173-175]
	cc1	EExxVRREL	<ul style="list-style-type: none"> • 1 mismatch allowed 	[175]
	cc2	YMNyGCKRKf	<ul style="list-style-type: none"> • 2 mismatches allowed • Only conserved in eukaryots 	[174,175]
	cc3	NGYxG (microorganisms & animals) SGYxG (plants)	<ul style="list-style-type: none"> • N in microorganisms and animals • S in many plants 	[9]

CPF-member	Name	Motif	Comment	Reference(s)
	cab	FxLxxxFxxAxxxxYxxM	<ul style="list-style-type: none"> antenna loop (antenna binding site) 1 mismatch allowed 	[36]
DCRY	dcl	WVSxS	<ul style="list-style-type: none"> C-terminal lid 	[172]
	dct	PPHCxPSxxxxxRQFxWL	<ul style="list-style-type: none"> C-terminal tail 3 mismatches allowed 	[172]
	d2pu	FIFDG	<ul style="list-style-type: none"> Secondary pocket upper helix 	[171]
	d2pl	EQDCEPxWxxR	<ul style="list-style-type: none"> Secondary pocket lower helix 2 mismatches allowed 	[171]
	dm1	HTLWxP	<ul style="list-style-type: none"> DCRY motif1 	New motif
MCRY	mpm	ERKA W V A x F x R PxMx xxSLLxS	<ul style="list-style-type: none"> Phosphate motif 2 mismatches allowed 	[172]
	mcl	WMWLSCSSFFQ Q FF H C Y	<ul style="list-style-type: none"> C-terminal lid 2 mismatches allowed 	[172]
	ml	YKxxK	<ul style="list-style-type: none"> Protrusion loop 	[172]
	m2pu	DPWFAGSSN	<ul style="list-style-type: none"> Secondary pocket upper helix 2 mismatches allowed 	[171]

CPF-member	Name	Motif	Comment	Reference(s)
	mct	YRGLCLLASVPS	<ul style="list-style-type: none"> Conserved C-terminal extension 2 mismatches allowed 	[170]
	m2pl	EYDSEPF G KER (non-insects) EEDPEP x GRVR (insects)	<ul style="list-style-type: none"> Secondary pocket lower helix 1 mismatch allowed (non-insects) 2 mismatches allows (insects) 	[171]
	mnc	VYxxL	<ul style="list-style-type: none"> MCRY non-chordate specific 	New motif
	I	VWPGG	<ul style="list-style-type: none"> MCRY1 specific 	New motif
	II	RLDKHL	<ul style="list-style-type: none"> MCRY2 specific 	New motif
(6-4) photolyase	α 15	HHLARHxVACFLTRG DL	<ul style="list-style-type: none"> Conserved α-Helix 15 2 mismatches allowed 	[169]
	α 10	SPYLxFGCLS	<ul style="list-style-type: none"> Conserved α-Helix 10 1 mismatch allowed 	[169]
	sl	MxGNxxCxQIPW	<ul style="list-style-type: none"> Conserved sulfur loop 1 mismatch allowed 	[169]

CPF-member	Name	Motif	Comment	Reference(s)
	α 12	PPxSLxGQLxWREFxYTxA	<ul style="list-style-type: none"> Conserved α-helix 12 2 mismatches allowed 	[169]
	α 11	SxRxFxxxL	<ul style="list-style-type: none"> Conserved α-helix 11 no mismatches allowed 	[169]
	α 8	GGExEALxR	<ul style="list-style-type: none"> Conserved α-helix 8 1 mismatch allowed 	[169]
	α 14	PxIDAIMxQLxxxG	<ul style="list-style-type: none"> Conserved α-helix 14 1 mismatch allowed 	[169]
	α 16	WExGxxVFxxLLxD	<ul style="list-style-type: none"> Conserved α-helix 16 1 mismatch allowed 	[169]
	α 17	DxxxNxGxWMWL	<ul style="list-style-type: none"> Conserved α-helix 17 1 mismatch allowed 	[169]
	α 18	YxPxxFGxxxDPxG	<ul style="list-style-type: none"> Conserved α-helix 18 1 mismatch allowed 	[169]
	6-4	YIYEPWKAP	<ul style="list-style-type: none"> 6-4 photolyase specific 	New motif
PCRY	pd1	DQxVP	<ul style="list-style-type: none"> Part of DAS-motif1 	[167,168]
	pd2	STxExxS	<ul style="list-style-type: none"> Part of DAS-motif2 	[167,168]

CPF-member	Name	Motif	Comment	Reference(s)
	pc1	QGRTGYPLVDAGMR ELWATGWxH	<ul style="list-style-type: none"> Conserved in all plant CRYs 3 mismatches allowed 	[166]
	pc	DLLYEPW	<ul style="list-style-type: none"> All plant CRY1s 1 mismatch allowed 	[166]
	pn	VWFRRDLRxEDNPAL	<ul style="list-style-type: none"> N-terminal 2 mismatches allowed 	[166]
PCRY-like	pl1	VGLR	<ul style="list-style-type: none"> PCRY-like specific 1 	New motif
	pl2	WRDLAY	<ul style="list-style-type: none"> PCRY-like specific 2 	New motif
	pl3	MWQNxG	<ul style="list-style-type: none"> PCRY-like specific 3 	New motif
CRY4	4a	GXPPLTYKxF	<ul style="list-style-type: none"> CRY4 motif a 	New motif
	4b	PNSLLPSTTGL	<ul style="list-style-type: none"> CRY4 motif b 	New motif
	4c	TxNFTxMX	<ul style="list-style-type: none"> CRY4 conserved 	[83]
	4Y	WYEDAERL	<ul style="list-style-type: none"> CRY4 conserved Y 2 mismatches allowed 	[83]

CPF-member	Name	Motif	Comment	Reference(s)
ppl	ppl1	ESxSxxPVYCFDPR	<ul style="list-style-type: none"> 2 mismatches allowed 	New motif
	ppl2	BSJYGANFCKI	<ul style="list-style-type: none"> 2 mismatches allowed 	New motif
	ppl3	FFRFxTxK		New motif

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