Dataset S5. Sequence comparison of Cph1 with PaBphP in the chromophore-binding GAF domains. The residue codes, ranging from 157–280, for PaBphP sequence are given in parentheses following the equivalent codes for Cph1 sequence (residue range of 170–293). Gray shading indicates residues conserved in both phytochromes. Entries in red boldface indicate the long-range intermolecular ^{1}H contacts of the chromophore detected in the Pr state, as shown in Fig. 1, *B* and *C*.

	PDB ID codes	
Residue	2VEA [6]	3C2W [14]
170 (157)	PHE	TYR
171 (158)	ASP	ASP
172 (159)	ARG	ARG
173 (160)	VAL	VAL
174 (161)	**MET**	MET
175 (162)	LEU	ALA
176 (163)	**TYR**	TYR
177 (164)	ARG	ARG
178 (165)	PHE	PHE
179 (166)	ASP	ARG
180 (167)	GLU	HIS
181 (168)	ASN	ASP
182 (169)	ASN	ASP
183 (170)	HIS	SER
184 (171)	GLY	GLY
185 (172)	ASP	GLU
186 (173)	**VAL**	VAL
187 (174)	ILE	VAL
188 (175)	ALA	ALA
189 (176)	GLU	GLU
190 (177)	ASP	SER
191 (178)	LYS	ARG
192 (179)	ARG	ARG
193 (180)	ASP	GLU
194 (181)	ASP	ASP
195 (182)	MET	LEU
196 (183)	GLU	GLU
197 (184)	PRO	SER
198 (185)	**TYR**	TYR
199 (186)	LEU	LEU
200 (187)	GLY	GLY
201 (188)	LEU	GLN
202 (189)	HIS	ARG
203 (190)	**TYR**	TYR
204 (191)	PRO	PRO
205 (192)	GLU	ALA
206 (193)	**SER**	SER
207 (194)	**ASP**	ASP
208 (195)	**ILE**	ILE
209 (196)	**PRO**	PRO
210 (197)	GLN	ALA
211 (198)	PRO	GLN
212 (199)	**ALA**	ALA
213 (200)	ARG	ARG
214 (201)	ARG	ARG
215 (202)	LEU	LEU
216 (203)	**PHE**	TYR
217 (204)	ILE	ILE
218 (205)	HIS	GLN
219 (206)	ASN	ASN
220 (207)	PRO	PRO
221 (208)	ILE	ILE
222 (209)	**ARG**	ARG
223 (210)	VAL	LEU
224 (211)	ILE	ILE
225 (212)	PRO	ALA
226 (213)	ASP	ASP
227 (214)	VAL	VAL
228 (215)	TYR	ALA
229 (216)	GLY	TYR
230 (217)	VAL	THR
231 (218)	ALA	PRO
232 (219)	VAL	MET
233 (220)	PRO	ARG
234 (221)	LEU	VAL
235 (222)	THR	PHE
236 (223)	PRO	PRO
237 (224)	ALA	ALA
238 (225)	VAL	LEU
239 (226)	ASN	ASN
240 (227)	PRO	PRO
241 (228)	SER	GLU
242 (229)	THR	THR
243 (230)	ASN	ASN
244 (231)	ARG	GLU
245 (232)	ALA	SER
246 (233)	VAL	PHE
247 (234)	ASP	ASP
248 (235)	LEU	LEU
249 (236)	THR	SER
250 (237)	GLU	TYR
251 (238)	SER	SER
252 (239)	ILE	VAL
253 (240)	LEU	LEU
254 (241)	**ARG**	ARG
255 (242)	SER	SER
256 (243)	**ALA**	VAL
257 (244)	**TYR**	SER
258 (245)	HIS	PRO
259 (246)	**CYS**	ILE
260 (247)	**HIS**	HIS
261 (248)	LEU	CYS
262 (249)	THR	GLU
263 (250)	**TYR**	TYR
264 (251)	LEU	LEU
265 (252)	LYS	THR
266 (253)	ASN	ASN
267 (254)	**MET**	MET
268 (255)	GLY	GLY
269 (256)	VAL	VAL
270 (257)	GLY	ARG
271 (258)	ALA	ALA
272 (259)	**SER**	SER
273 (260)	LEU	MET
274 (261)	**THR**	SER
275 (262)	ILE	ILE
276 (263)	SER	SER
277 (264)	LEU	ILE
278 (265)	ILE	VAL
279 (266)	LYS	VAL
280 (267)	ASP	GLY
281 (268)	GLY	GLY
282 (269)	HIS	LYS
283 (270)	LEU	LEU
284 (271)	TRP	TRP
285 (272)	GLY	GLY
286 (273)	LEU	LEU
287 (274)	ILE	PHE
288 (275)	**ALA**	SER
289 (276)	CYS	CYS
290 (277)	**HIS**	HIS
291 (278)	HIS	HIS
292 (279)	GLN	MET
293 (280)	THR	SER
-	-	-

170 (157)–194 (181)

195 (182)–219 (206)

220 (207)–244 (231)

245 (232)–269 (256)

270 (257)–293 (280)