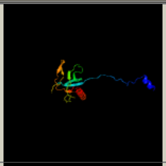
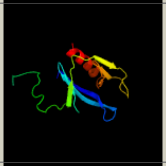
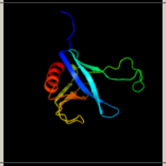
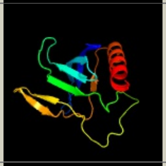
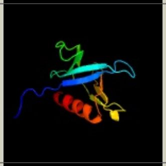
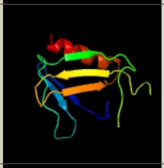
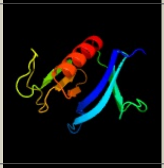
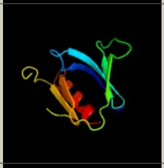
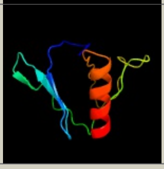
Email	fatima.cvrckova@natur.cuni.cz
Description	PH______
Date	Sun Dec 3 14:59:00 GMT 2023
Unique Job ID	e8c093519bd97f3a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6bbqA_	Alignment		99.8	23	**PDB header:** lipid binding protein **Chain:** A: **PDB Molecule:** cytohesin-3,adp-ribosylation factor 6; **PDBTitle:** model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein **PDB Entry:** PDBe RCSB PDBj
2	c2fjlA_	Alignment		98.5	27	**PDB header:** hydrolase **Chain:** A: **PDB Molecule:** 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase **PDBTitle:** solution structure of the split ph domain in phospholipase c-gamma1 **PDB Entry:** PDBe RCSB PDBj
3	c2r09A_	Alignment		99.8	21	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** cytohesin-3; **PDBTitle:** crystal structure of autoinhibited form of grp1 arf gtpase exchange2 factor **PDB Entry:** PDBe RCSB PDBj
4	d1wjma_	Alignment		99.6	23	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
5	c2d9wA_	Alignment		99.6	20	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** docking protein 2; **PDBTitle:** solution structure of the ph domain of docking protein 2 from human **PDB Entry:** PDBe RCSB PDBj
6	c2dn6A_	Alignment		99.6	21	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** kiaa0640 protein; **PDBTitle:** solution structure of the ph domain of kiaa0640 protein from human **PDB Entry:** PDBe RCSB PDBj
7	d1u29a1	Alignment		99.7	19	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
8	d1u5ea1	Alignment		99.7	17	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
9	c2dhkA_	Alignment		99.7	20	**PDB header:** immune system **Chain:** A: **PDB Molecule:** tbc1 domain family member 2; **PDBTitle:** solution structure of the ph domain of tbc1 domain family member 22 protein from human **PDB Entry:** PDBe RCSB PDBj
10	d1fgya_	Alignment		99.7	18	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
11	c2dkpA_	Alignment		99.7	18	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** pleckstrin homology domain-containing family a member 5; **PDBTitle:** solution structure of the ph domain of pleckstrin homology domain-2 containing protein family a member 5 from human **PDB Entry:** PDBe RCSB PDBj

12	c3a8qB_	Alignment		99.7	22	**PDB header:** signaling protein **Chain:** B: **PDB Molecule:** t-lymphoma invasion and metastasis-inducing **PDBTitle:** low-resolution crystal structure of the tiam2 phccex domain **PDB Entry:** PDBe RCSB PDBj
13	c2z0qA_	Alignment		97.3	20	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** rho guanine nucleotide exchange factor 3; **PDBTitle:** crystal structure of dh-ph domain of rhogef3(xpln) **PDB Entry:** PDBe RCSB PDBj
14	c7kk7B_	Alignment		99.6	19	**PDB header:** cell adhesion **Chain:** B: **PDB Molecule:** pleckstrin homology domain-containing family a member 7; **PDBTitle:** crystal structure of ligand-free plekha7 ph domain **PDB Entry:** PDBe RCSB PDBj
15	d1dbha2	Alignment		98.1	16	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
16	c1u5fA_	Alignment		99.7	17	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** src-associated adaptor protein; **PDBTitle:** crystal structure of the ph domain of skap-hom with 8 vector-derived2 n-terminal residues **PDB Entry:** PDBe RCSB PDBj
17	c3mpxA_	Alignment		97.9	17	**PDB header:** lipid binding protein **Chain:** A: **PDB Molecule:** fyve, rhogef and ph domain-containing protein 5; **PDBTitle:** crystal structure of the dh and ph-1 domains of human fgd5 **PDB Entry:** PDBe RCSB PDBj
18	c4gzuB_	Alignment		99.7	20	**PDB header:** signaling protein **Chain:** B: **PDB Molecule:** ferm, rhogef and pleckstrin domain-containing protein 2; **PDBTitle:** crystal structure of the dh-ph-ph domain of farp2 **PDB Entry:** PDBe RCSB PDBj
19	c7syfA_	Alignment		97.9	20	**PDB header:** oncoprotein **Chain:** A: **PDB Molecule:** phosphatidylinositol 3,4,5-trisphosphate-dependent rac **PDBTitle:** reconstruction of full-length prex-1 (ptdins(3,4,5)p3-dependent rac2 exchanger 1) **PDB Entry:** PDBe RCSB PDBj
20	c1ki1B_	Alignment		97.2	23	**PDB header:** signaling protein **Chain:** B: **PDB Molecule:** intersectin long form; **PDBTitle:** guanine nucleotide exchange region of intersectin in complex with2 cdc42 **PDB Entry:** PDBe RCSB PDBj
21	c5hzkB_	Alignment	not modelled	97.0	23	**PDB header:** signaling protein **Chain:** B: **PDB Molecule:** intersectin-1,nph1-1,intersectin-1; **PDBTitle:** crystal structure of photoinhibitable intersectin1 containing wildtype2 lov2 domain in complex with cdc42 **PDB Entry:** PDBe RCSB PDBj
22	d2coca1	Alignment	not modelled	99.8	19	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
23	d2dyna_	Alignment	not modelled	99.8	18	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
24	d1droa_	Alignment	not modelled	99.6	16	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
25	c4h8sA_	Alignment	not modelled	99.6	17	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** dcc-interacting protein 13-beta; **PDBTitle:** crystal structure of human appl2barph domain **PDB Entry:** PDBe RCSB PDBj
26	c3ksyA_	Alignment	not modelled	97.4	14	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** son of sevenless homolog 1; **PDBTitle:** crystal structure of the histone domain, dh-ph unit, and catalytic2 unit of the ras activator son of sevenless (sos) **PDB Entry:** PDBe RCSB PDBj
27	c2yryA_	Alignment	not modelled	99.7	17	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** pleckstrin homology domain-containing family a member 6; **PDBTitle:** solution structure of the ph domain of pleckstrin homology domain-2 containing family a member 6 from human **PDB Entry:** PDBe RCSB PDBj

28	c3odoA_	Alignment	not modelled	98.0	17	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** rho guanine nucleotide exchange factor 1; **PDBTitle:** crystal structure of the dh/ph domains of p115-rhogef **PDB Entry:** PDBe RCSB PDBj
29	d1v88a_	Alignment	not modelled	99.7	15	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
30	d1zc3b1	Alignment	not modelled	98.6	18	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
31	d1u5fa1	Alignment	not modelled	99.6	16	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
32	d1v89a_	Alignment	not modelled	99.6	15	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
33	c4c0aA_	Alignment	not modelled	98.3	15	**PDB header:** protein transport **Chain:** A: **PDB Molecule:** iq motif and sec7 domain-containing protein 1; **PDBTitle:** arf1(delta1-17)in complex with brag2 sec7-ph domain **PDB Entry:** PDBe RCSB PDBj
34	c5mr1A_	Alignment	not modelled	99.6	19	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** interactor protein for cytohesin exchange factors 1; **PDBTitle:** crystal structure of the pleckstrin homology domain of interactor2 protein for cytohesin exchange factors 1 (ipcef1) **PDB Entry:** PDBe RCSB PDBj
35	c3ky9B_	Alignment	not modelled	98.1	14	**PDB header:** apoptosis **Chain:** B: **PDB Molecule:** proto-oncogene vav; **PDBTitle:** autoinhibited vav1 **PDB Entry:** PDBe RCSB PDBj
36	d2adza1	Alignment	not modelled	91.8	20	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
37	c4nswB_	Alignment	not modelled	99.7	16	**PDB header:** protein transport **Chain:** B: **PDB Molecule:** arf-gap with coiled-coil, ank repeat and ph domain- **PDBTitle:** crystal structure of the bar-ph domain of acap1 **PDB Entry:** PDBe RCSB PDBj
38	d1v5pa_	Alignment	not modelled	99.7	15	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
39	d1btna_	Alignment	not modelled	99.6	17	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
40	c2y7bA_	Alignment	not modelled	99.6	15	**PDB header:** cell cycle **Chain:** A: **PDB Molecule:** actin-binding protein anillin; **PDBTitle:** crystal structure of the ph domain of human actin-binding protein2 anillin anln **PDB Entry:** PDBe RCSB PDBj
41	d1upqa_	Alignment	not modelled	99.7	16	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
42	c2q13A_	Alignment	not modelled	99.6	19	**PDB header:** protein transport **Chain:** A: **PDB Molecule:** dcc-interacting protein 13 alpha; **PDBTitle:** crystal structure of bar-ph domain of appl1 **PDB Entry:** PDBe RCSB PDBj
43	d1foea2	Alignment	not modelled	74.7	22	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
44	c3tcaA_	Alignment	not modelled	99.5	15	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** amyloid beta a4 precursor protein-binding family b member **PDBTitle:** crystal structure of the ras-associating and pleckstrin-homology2 domains of riam **PDB Entry:** PDBe RCSB PDBj
45	d1ki1b2	Alignment	not modelled	99.1	15	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
46	c6bcbA_	Alignment	not modelled	98.5	18	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** rho guanine nucleotide exchange factor 18; **PDBTitle:** a complex between ph domain of p114rhogef and activated rhoa bound to2 a gtp analog **PDB Entry:** PDBe RCSB PDBj
47	c4h6yA_	Alignment	not modelled	99.6	20	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** ferm, rhogef and pleckstrin domain-containing protein 1; **PDBTitle:** crystal structure of the dh-ph-ph domain of farp1 **PDB Entry:** PDBe RCSB PDBj
48	c2d9vA_	Alignment	not modelled	99.7	14	**PDB header:** membrane protein **Chain:** A: **PDB Molecule:** pleckstrin homology domain-containing protein family b **PDBTitle:** solution structure of the ph domain of pleckstrin homology domain-2 containing protein family b member 1 from mouse **PDB Entry:** PDBe RCSB PDBj
49	c2dhiA_	Alignment	not modelled	99.7	14	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** pleckstrin homology domain-containing family b member 2; **PDBTitle:** solution structure of the ph domain of evectin-2 from mouse

						PDB Entry: PDBe RCSB PDBj
50	c4yonA_	Alignment	not modelled	97.6	17	**PDB header:** protein binding **Chain:** A: **PDB Molecule:** phosphatidylinositol 3,4,5-trisphosphate-dependent rac **PDBTitle:** p-rex1:rac1 complex **PDB Entry:** PDBe RCSB PDBj
51	c3hk0B_	Alignment	not modelled	99.5	14	**PDB header:** signaling protein **Chain:** B: **PDB Molecule:** growth factor receptor-bound protein 10; **PDBTitle:** crystal structure of the ra and ph domains of grb10 **PDB Entry:** PDBe RCSB PDBj
52	d1w1ha_	Alignment	not modelled	99.5	16	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
53	c7ctpA_	Alignment	not modelled	98.9	13	**PDB header:** protein binding **Chain:** A: **PDB Molecule:** protein niban 2; **PDBTitle:** crystal structure of human fam129b/minerva/niban2 **PDB Entry:** PDBe RCSB PDBj
54	c2rovA_	Alignment	not modelled	99.7	15	**PDB header:** transferase **Chain:** A: **PDB Molecule:** rho-associated protein kinase 2; **PDBTitle:** the split ph domain of rock ii **PDB Entry:** PDBe RCSB PDBj
55	c3fehA_	Alignment	not modelled	99.8	16	**PDB header:** hydrolase activator **Chain:** A: **PDB Molecule:** centaurin-alpha-1; **PDBTitle:** crystal structure of full length centaurin alpha-1 **PDB Entry:** PDBe RCSB PDBj
56	c6bc1D_	Alignment	not modelled	98.2	17	**PDB header:** signaling protein **Chain:** D: **PDB Molecule:** rho guanine nucleotide exchange factor 28; **PDBTitle:** a complex between ph domain of p190rhogef and activated rac1 bound to2 a gtp analog **PDB Entry:** PDBe RCSB PDBj
57	c2dfkA_	Alignment	not modelled	97.9	14	**PDB header:** cell cycle **Chain:** A: **PDB Molecule:** collybistin ii; **PDBTitle:** crystal structure of the cdc42-collybistin ii complex **PDB Entry:** PDBe RCSB PDBj
58	d1txda2	Alignment	not modelled	98.0	17	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
59	c6e31A_	Alignment	not modelled	99.6	14	**PDB header:** cell adhesion **Chain:** A: **PDB Molecule:** rap1-interacting adapter molecule; **PDBTitle:** crystal structure of riam in an autoinhibited configuration. **PDB Entry:** PDBe RCSB PDBj
60	c2rsgA_	Alignment	not modelled	99.6	16	**PDB header:** lipid transport **Chain:** A: **PDB Molecule:** collagen type iv alpha-3-binding protein; **PDBTitle:** solution structure of the cert ph domain **PDB Entry:** PDBe RCSB PDBj
61	c2da0A_	Alignment	not modelled	99.6	16	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** 130-kda phosphatidylinositol 4,5-biphosphate-dependent arf1 **PDBTitle:** solution structure of the ph domain of pip2-dependent arf1 gtpase-2 activating protein from human **PDB Entry:** PDBe RCSB PDBj
62	c3ml4D_	Alignment	not modelled	99.2	16	**PDB header:** signaling protein **Chain:** D: **PDB Molecule:** protein dok-7; **PDBTitle:** crystal structure of a complex between dok7 ph-ptb and the musk2 juxtamembrane region **PDB Entry:** PDBe RCSB PDBj
63	d1v5ma_	Alignment	not modelled	96.6	19	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
64	c2ys3A_	Alignment	not modelled	99.7	14	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** unc-112-related protein 2; **PDBTitle:** solution structure of the ph domain of kindlin-3 from human **PDB Entry:** PDBe RCSB PDBj
65	c4k81C_	Alignment	not modelled	99.6	14	**PDB header:** signaling protein **Chain:** C: **PDB Molecule:** growth factor receptor-bound protein 14; **PDBTitle:** crystal structure of the grb14 ra and ph domains in complex with gtp-2 loaded h-ras **PDB Entry:** PDBe RCSB PDBj
66	c3tfmA_	Alignment	not modelled	99.7	15	**PDB header:** motor protein **Chain:** A: **PDB Molecule:** myosin x; **PDBTitle:** myosin x ph1n-ph2-ph1c tandem **PDB Entry:** PDBe RCSB PDBj
67	d1u5da1	Alignment	not modelled	99.7	15	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
68	c1x86A_	Alignment	not modelled	97.4	15	**PDB header:** signaling protein/membrane protein **Chain:** A: **PDB Molecule:** rho guanine nucleotide exchange factor 12; **PDBTitle:** crystal structure of the dh/ph domains of leukemia-associated rhogef2 in complex with rhoa **PDB Entry:** PDBe RCSB PDBj
69	c2rloA_	Alignment	not modelled	99.6	14	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** centaurin-gamma 1; **PDBTitle:** split ph domain of pi3-kinase enhancer **PDB Entry:** PDBe RCSB PDBj
70	d1x1ga1	Alignment	not modelled	99.6	14	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
71	c4iapB_	Alignment	not modelled	99.7	19	**PDB header:** lipid binding protein/ hydrorase **Chain:** B: **PDB Molecule:** oxysterol-binding protein homolog 3,endolysin,oxysterol- **PDBTitle:** crystal structure of ph domain of osh3 from

						saccharomyces cerevisiae **PDB Entry:** PDBe RCSB PDBj
72	c4xh9D_	Alignment	not modelled	97.3	16	**PDB header:** signaling protein **Chain:** D: **PDB Molecule:** neuroepithelial cell-transforming gene 1 protein; **PDBTitle:** crystal structure of human rhoa in complex with dh/ph fragment of the2 guanine nucleotide exchange factor net1 **PDB Entry:** PDBe RCSB PDBj
73	d1wgqa_	Alignment	not modelled	99.7	14	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
74	d1qqga1	Alignment	not modelled	99.6	15	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Phosphotyrosine-binding domain (PTB) **PDB entry:** PDBe RCSB PDBj
75	d2coda1	Alignment	not modelled	99.6	16	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
76	d1omwa2	Alignment	not modelled	97.9	16	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
77	d1v5ua_	Alignment	not modelled	99.6	13	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
78	c3odxA_	Alignment	not modelled	98.1	16	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** rho guanine nucleotide exchange factor 1; **PDBTitle:** crystal structure of an n-terminally truncated linker-dh/ph domains of2 p115-rhogef **PDB Entry:** PDBe RCSB PDBj
79	c1xdvB_	Alignment	not modelled	97.8	16	**PDB header:** signaling protein **Chain:** B: **PDB Molecule:** son of sevenless protein homolog 1; **PDBTitle:** experimentally phased structure of human the son of sevenless protein2 at 4.1 ang. **PDB Entry:** PDBe RCSB PDBj
80	c2lulA_	Alignment	not modelled	99.7	13	**PDB header:** transferase **Chain:** A: **PDB Molecule:** tyrosine-protein kinase tec; **PDBTitle:** solution nmr structure of ph domain of tyrosine-protein kinase tec2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr3504c **PDB Entry:** PDBe RCSB PDBj
81	c3pp2A_	Alignment	not modelled	99.7	14	**PDB header:** hydrolase activator **Chain:** A: **PDB Molecule:** rho gtpase-activating protein 27; **PDBTitle:** crystal structure of the pleckstrin homology domain of arhgap27 **PDB Entry:** PDBe RCSB PDBj
82	c3o96A_	Alignment	not modelled	98.7	14	**PDB header:** transferase **Chain:** A: **PDB Molecule:** rac-alpha serine/threonine-protein kinase; **PDBTitle:** crystal structure of human akt1 with an allosteric inhibitor **PDB Entry:** PDBe RCSB PDBj
83	d2elba2	Alignment	not modelled	99.6	15	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
84	c3bjiA_	Alignment	not modelled	98.5	12	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** proto-oncogene vav; **PDBTitle:** structural basis of promiscuous guanine nucleotide exchange by the t-2 cell essential vav1 **PDB Entry:** PDBe RCSB PDBj
85	d2fjla1	Alignment	not modelled	99.7	14	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
86	d1plsa_	Alignment	not modelled	99.6	14	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
87	c4d0nB_	Alignment	not modelled	97.9	15	**PDB header:** cell cycle **Chain:** B: **PDB Molecule:** a-kinase anchor protein 13; **PDBTitle:** akap13 (akap-lbc) rhogef domain in complex with rhoa **PDB Entry:** PDBe RCSB PDBj
88	c1ntyA_	Alignment	not modelled	97.4	15	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** triple functional domain protein; **PDBTitle:** crystal structure of the first dh/ph domain of trio to 1.7 a **PDB Entry:** PDBe RCSB PDBj
89	c6fsfA_	Alignment	not modelled	99.7	16	**PDB header:** endocytosis **Chain:** A: **PDB Molecule:** gtpase-activating protein bem3; **PDBTitle:** crystal structure of the tandem px-ph-domains of bem3 from2 saccharomyces cerevisiae **PDB Entry:** PDBe RCSB PDBj
90	c7c3mA_	Alignment	not modelled	98.1	16	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** fermitin family homolog 3,fermitin family homolog 3, **PDBTitle:** structure of ferm protein **PDB Entry:** PDBe RCSB PDBj
91	c4xohB_	Alignment	not modelled	99.6	14	**PDB header:** cell cycle **Chain:** B: **PDB Molecule:** division mal foutue 1 protein; **PDBTitle:** mechanistic insights into anchorage of the contractile ring from yeast2 to humans **PDB Entry:** PDBe RCSB PDBj
92	c4gmvB_	Alignment	not modelled	99.5	14	**PDB header:** cell adhesion **Chain:** B: **PDB Molecule:** ras-associated and pleckstrin homology domains-containing **PDBTitle:** crystal structure of the coiled-coil, ra and ph domains of2 lamellipodin **PDB Entry:** PDBe RCSB PDBj

93	d1wi1a_	Alignment	not modelled	99.6	13	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
94	c2j59O_	Alignment	not modelled	99.7	16	**PDB header:** hydrolase **Chain:** O: **PDB Molecule:** rho-gtpase activating protein 10; **PDBTitle:** crystal structure of the arf1:arhgap21-arfbd complex **PDB Entry:** PDBe RCSB PDBj
95	d2j59m1	Alignment	not modelled	99.7	16	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
96	c3a8nA_	Alignment	not modelled	99.7	16	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** t-lymphoma invasion and metastasis-inducing protein 1; **PDBTitle:** crystal structure of the tiam1 phccex domain **PDB Entry:** PDBe RCSB PDBj
97	c7z6eD_	Alignment	not modelled	98.7	14	**PDB header:** lipid binding protein **Chain:** D: **PDB Molecule:** serine/threonine-protein kinase mrck-1; **PDBTitle:** structure of the c1-ph-cnh regulatory module of mrck1 **PDB Entry:** PDBe RCSB PDBj
98	c2lg1A_	Alignment	not modelled	98.1	14	**PDB header:** metal binding protein **Chain:** A: **PDB Molecule:** a-kinase anchor protein 13; **PDBTitle:** solution structure of the human akap13 ph domain and stabilizing dh2 helix **PDB Entry:** PDBe RCSB PDBj
99	d1xx0a1	Alignment	not modelled	99.5	13	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
100	c4mt6A_	Alignment	not modelled	97.8	12	**PDB header:** protein binding **Chain:** A: **PDB Molecule:** rho guanine nucleotide exchange factor 9; **PDBTitle:** crystal structure of closed inactive collybistin **PDB Entry:** PDBe RCSB PDBj
101	c3odwB_	Alignment	not modelled	98.1	15	**PDB header:** signaling protein **Chain:** B: **PDB Molecule:** rho guanine nucleotide exchange factor 1; **PDBTitle:** crystal structure of the linker-dh/ph domains of p115-rhogef **PDB Entry:** PDBe RCSB PDBj
102	c2p0fA_	Alignment	not modelled	99.7	12	**PDB header:** ligand binding protein **Chain:** A: **PDB Molecule:** rho gtpase-activating protein 9; **PDBTitle:** arhgap9 ph domain in complex with ins(1,3,5)p3 **PDB Entry:** PDBe RCSB PDBj
103	c7vs3A_	Alignment	not modelled	99.7	13	**PDB header:** exocytosis **Chain:** A: **PDB Molecule:** calcium-dependent secretion activator 1; **PDBTitle:** the crystal structure of rat calcium-dependent activator protein for2 secretion (caps) c2ph **PDB Entry:** PDBe RCSB PDBj
104	d1wg7a_	Alignment	not modelled	99.6	13	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
105	d1ntya2	Alignment	not modelled	98.0	15	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
106	c2kcjA_	Alignment	not modelled	99.6	13	**PDB header:** membrane protein **Chain:** A: **PDB Molecule:** pleckstrin homology domain-containing family a member 3; **PDBTitle:** solution structure of fapp1 ph domain **PDB Entry:** PDBe RCSB PDBj
107	c3t06E_	Alignment	not modelled	97.6	14	**PDB header:** signaling protein **Chain:** E: **PDB Molecule:** rho guanine nucleotide exchange factor 11; **PDBTitle:** crystal structure of the dh/ph fragment of pdzrhogef with n-terminal2 regulatory elements in complex with human rhoa **PDB Entry:** PDBe RCSB PDBj
108	c2d9xA_	Alignment	not modelled	99.6	13	**PDB header:** lipid transport **Chain:** A: **PDB Molecule:** oxysterol binding protein-related protein 11; **PDBTitle:** solution structure of the ph domain of oxysterol binding protein-2 related protein 11 from human **PDB Entry:** PDBe RCSB PDBj
109	c4y93A_	Alignment	not modelled	99.2	13	**PDB header:** transferase **Chain:** A: **PDB Molecule:** non-specific protein-tyrosine kinase,non-specific protein- **PDBTitle:** crystal structure of the ph-th-kinase construct of bruton's tyrosine2 kinase (btk) **PDB Entry:** PDBe RCSB PDBj
110	d1unqa_	Alignment	not modelled	99.6	12	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
111	c2dx1A_	Alignment	not modelled	96.5	16	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** rho guanine nucleotide exchange factor 4; **PDBTitle:** crystal structure of rhogef protein asef **PDB Entry:** PDBe RCSB PDBj
112	c7yirA_	Alignment	not modelled	99.6	14	**PDB header:** cytosolic protein **Chain:** A: **PDB Molecule:** arf-gap with rho-gap domain, ank repeat and ph domain- **PDBTitle:** crystal structure of n-terminal ph domain of arap3 protein from human **PDB Entry:** PDBe RCSB PDBj
113	d1faoa_	Alignment	not modelled	99.6	13	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
						PDB header: signaling protein **Chain:** A: **PDB Molecule:** dual adaptor of phosphotyrosine and 3-

114	c1faoA_	Alignment	not modelled	99.6	13	phosphoinositides; **PDBTitle:** structure of the pleckstrin homology domain from dapp1/phish in2 complex with inositol 1,3,4,5-tetrakisphosphate **PDB Entry:** PDBe RCSB PDBj
115	d2cofa1	Alignment	not modelled	99.6	14	**Fold:** PH domain-like barrel **Superfamily:** PH domain-like **Family:** Pleckstrin-homology domain (PH domain) **PDB entry:** PDBe RCSB PDBj
116	c2vszA_	Alignment	not modelled	96.3	14	**PDB header:** apoptosis **Chain:** A: **PDB Molecule:** engulfment and cell motility protein 1; **PDBTitle:** crystal structure of the elmo1 ph domain **PDB Entry:** PDBe RCSB PDBj
117	c2d9zA_	Alignment	not modelled	99.8	12	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** protein kinase c, nu type; **PDBTitle:** solution structure of the ph domain of protein kinase c, nu type from2 human **PDB Entry:** PDBe RCSB PDBj
118	c3nsuA_	Alignment	not modelled	99.6	12	**PDB header:** signaling protein **Chain:** A: **PDB Molecule:** phosphatidylinositol 4,5-bisphosphate-binding protein slm1; **PDBTitle:** a systematic screen for protein-lipid interactions in saccharomyces2 cerevisiae **PDB Entry:** PDBe RCSB PDBj
119	c3cxbB_	Alignment	not modelled	99.7	13	**PDB header:** signaling protein **Chain:** B: **PDB Molecule:** pleckstrin homology domain-containing family m **PDBTitle:** crystal structure of sifa and skip **PDB Entry:** PDBe RCSB PDBj
120	c1qqgA_	Alignment	not modelled	99.6	13	**PDB header:** signal transduction **Chain:** A: **PDB Molecule:** insulin receptor substrate 1; **PDBTitle:** crystal structure of the ph-ptb targeting region of irs-1 **PDB Entry:** PDBe RCSB PDBj