

Table S1. DesKABD-homologous structures. The list was obtained using DALI, the scoring figures included follow the reported definitions of the algorithm. Key residues described in the text, are detailed on the last five columns, giving the equivalent residues for each homologous protein (for uncertain equivalence, a question mark is used; no equivalent residues are left as blank boxes).

PDB	Z score	RMSD (Å)	lali	nres	%id	Resolution (Å)	PDB description	Glu289	Asn293	Lys296	His297	His335
1i59	13.8	2.3	119	180	24	1.80	CHEMOTAXIS PROTEIN CheA	His405	Asn409	Asp412? Arg408?	His413	Arg503?
2c2a	13.7	2.5	121	240	21	1.90	SENSOR HISTIDINE KINASE	Asn376	Asn380	Lys383	Tyr384	?
1ysr	13.7	2.6	119	137	18	1.78	SENSOR-TYPE HISTIDINE KINASE PrrB	Asn349	Asn353	Lys356	His357	Arg396?
1gkz	13.1	2.5	119	316	16	2.20	3-METHYL-2-OXOBUTANOATE DEHYDROGENASE	Glu285	Asn249	Arg252		?
1id0	12.9	2.6	118	146	18	1.60	PhoQ HISTIDINE KINASE	Asn385	Asn389	Lys392	Tyr393	Arg434
3d2r	12.8	2.6	119	362	16	2.03	PYRUVATE DEHYDROGENASE [LIPOAMIDE] KINASE	Glu254	Asn258	Arg261		?
2bu8	12.7	2.6	119	359	18	2.50	PYRUVATE DEHYDROGENASE KINASE ISOENZYME 2	Glu243	Asn247	Arg250		?
3d36	12.4	2.4	119	221	16	2.03	SPORULATION KINASE B	Asn320	Asn324	Glu327	Ala328	?
1r62	12.3	2.5	111	136	14	1.60	NITROGEN REGULATION PROTEIN NR(II)	Asn244	Asn248	Gln251	Ala252	?
3cgz	11.5	2.9	112	143	17	1.90	VIRULENCE SENSOR HISTIDINE KINASE PhoQ	Asn386	Asn390	Lys393		His423?
1til	10.6	2.2	98	141	18	2.70	ANTI-SIGMA F FACTOR	Glu46	Asn50	Arg105?		Arg105?
2ftk	9.4	2.8	106	182	8	3.05	SPORULATION INITIATION PHOSPHOTRANSFERASE B	Lys716	Leu720	Gln723		?
1mx0	6.3	2.3	88	461	17	2.30	TYPE II DNA TOPOISOMERASE VI SUBUNIT B	Glu38	Asn42	Asp45		?