

TABLE 4: Number of patients with and without anti-BCOADC-E1 $\alpha$  and anti-PDC-E1 $\alpha$  antibodies.

		Anti-PDC-E1 $\alpha$		Total
		Positive	Negative	
Anti-BCOADC-E1 $\alpha$	Positive	7/16 (43.8%)	9/16 (56.3%)	16
	Negative	4/14 (28.6%)	10/14 (71.4%)	14
Total		11/30 (36.7%)	19/30 (63.3%)	30

Note: the incidences of the anti-BCOADC-E1 $\alpha$  and anti-PDC-E1 $\alpha$  antibodies are independent of each other by Fischer's exact test ( $P = 0.466$ ).

BCDC-E1 $\alpha$	1	SSLDKPKQFPGSAEFIDKLEFIQPNVISGIP	YRVMDRGGQ	INPSEDPH	51
PDC-E1 $\alpha$	1	FANDATFEIKKCDLHRLEEGPPVTTV			26
BCDC-E1 $\alpha$	52	LPKEKVLKLYKSMTLLNTMDRILYESQRQGR	ISFYMTNYGEEGTHVGSAAALDNTDLVF		110
PDC-E1 $\alpha$	27	LTREDGLKYYRMQTVRRMELKADLYKQK	IRGFCHLCDGQEAACVGLGAGINPTDHLI		86
BCDC-E1 $\alpha$	111	GQYREAGVLMYRDYPLELFMAQCYGNISDLGKGROMPVHYGKERHFT	ISSPLATQIPQ		170
PDC-E1 $\alpha$	87	TAYRAHGFTFTRGLSVREILAELTGRKGGCAKGGSMHMYAK	NFYGGNGIVGAQVPL		144
BCDC-E1 $\alpha$	171	AVGAAYAANKRANRNVICYFGEAASEGDAHAGFNFAATLECP	IFFCRNNGYAISTPT		230
PDC-E1 $\alpha$	145	GAGIALACKYNGKDEVCLTYGDGAANQGOIFEAYNMAALWKLPC	IFICENRYGMGTSV		204
BCDC-E1 $\alpha$	231	SEQYRGDGI AARGPGYGI	MSIRVDGNDVFAVYNATKEARRRAVAENQPFL	IEAMTYRIGH	290
PDC-E1 $\alpha$	205	ERAAASTDYKRGDF	IPGLRVDGNDILCVREATRFAAAYCRSGKGP	ILMELQTYRYHG	262
BCDC-E1 $\alpha$	291	HSTSDSSAYSRSVDEVNYWDKQDHPISRLRHY	LLSQGWDEEQEAKWRKQSPRKVMEAFE		350
PDC-E1 $\alpha$	263	HSMSDPGVSRYTREEIQEVRKSDPIMLLKDRMVNSNLASVEELKE	IDVEVRKEIEDAAQ		322
BCDC-E1 $\alpha$	351	QAERKPKPNPNNLLFSDVYQEMPAQLRKQQESLARHLQTYGEHYPLDHF	DK		400
PDC-E1 $\alpha$	323	FATADPEPPELEELGYHIYSSDPPFEVRGANQWI	KFKSVS		361

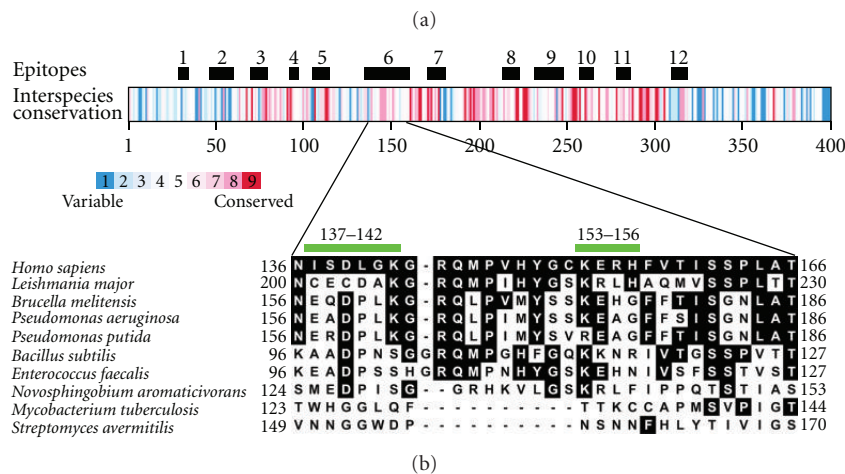


FIGURE 4: Comparative analyses between the epitopes and the conserved structures of BCOADC-E1 $\alpha$ . (a) Comparison of the epitopes between BCOADC-E1 $\alpha$  (BCDC-E1 $\alpha$ ) and PDC-E1 $\alpha$ . The amino acid sequences of BCOADC-E1 $\alpha$  and PDC-E1 $\alpha$  were aligned using the BLAST2 Program [27]. Vertical lines represent identical residues, while dots denote similar residues. The epitopes of BCOADC-E1 $\alpha$  and PDC-E1 $\alpha$  determined by the multipin ELISA are indicated in pink and blue, respectively. The major determinant region is underlined for each antigen. (b) Comparison of the epitopes and the interspecies conservation of BCOADC-E1 $\alpha$ . (a) Upper: interspecies conservation was calculated by the ConSurf program [29] with the aid of the ClustalW2 program [28]. The epitope regions are also indicated. The conservation indices for the individual amino acid residues are drawn in graded colors (blue to red) as indicated. (b) Lower: sequence alignments of the major determinant region of human BCOADC-E1 $\alpha$  and homologous proteins from various infectious microorganisms. Inverted letters represent residues that are identical to the human protein. The two regions (aa 137–142 and 153–156) that exhibited high solvent accessibilities (Supplementary Figure S2) are also indicated.