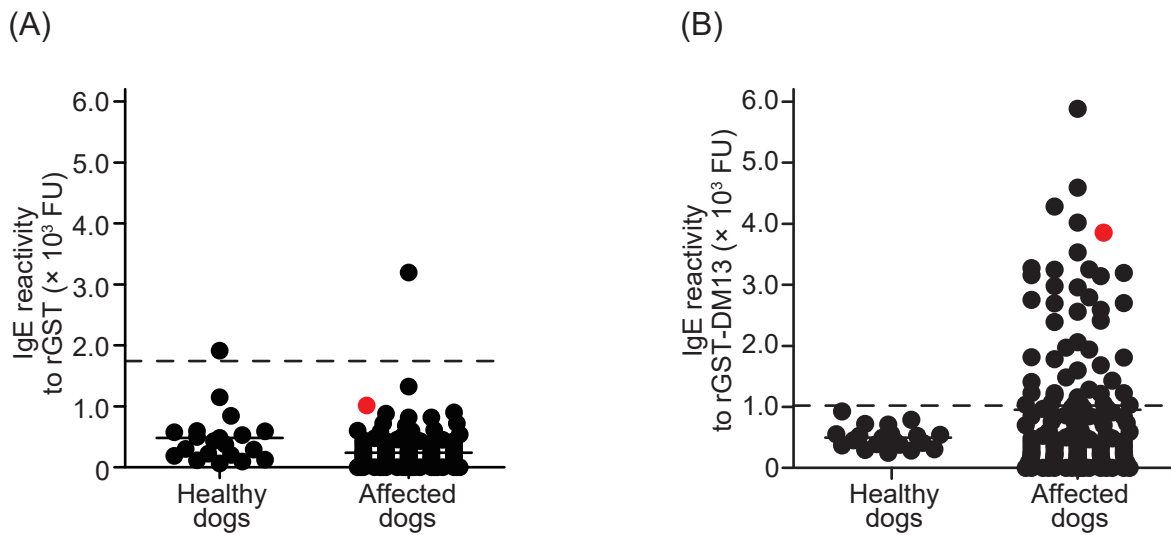
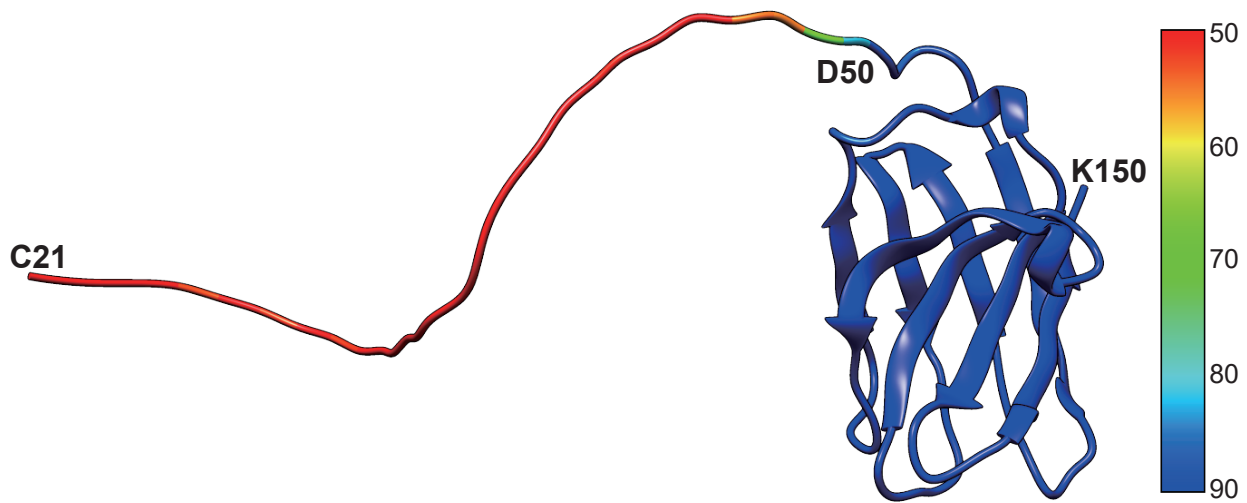


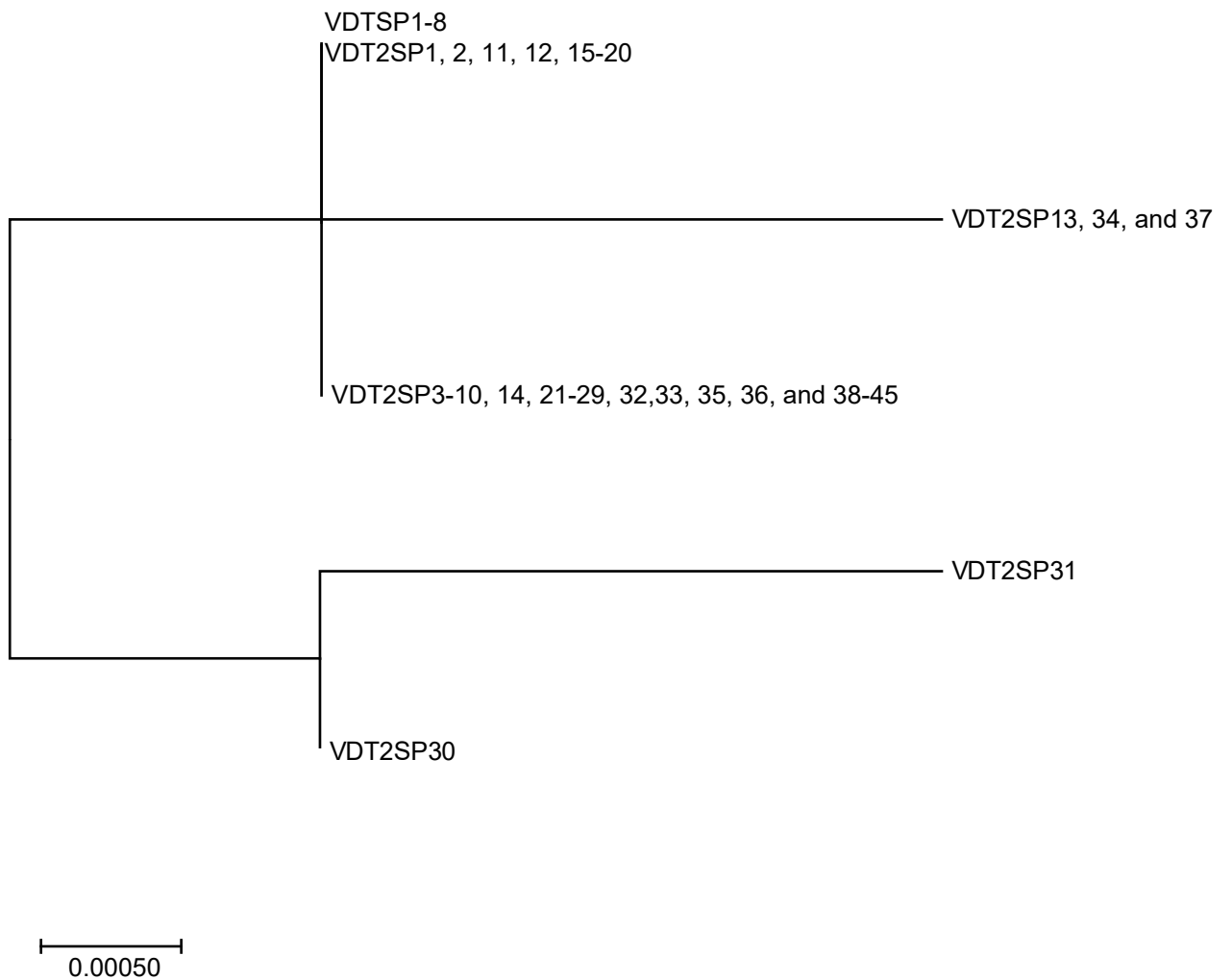
Supplementary Figure S1. ELISA to detect the specific IgE to *S. pseudintermedius* strain (A) VDTSP1, (B) VDTSP2, (C) VDTSP3, (D) VDTSP4, (E) VDTSP5, (F) VDTSP6, (G) VDTSP7 and (H) VDTSP8. The dotted horizontal lines indicate the cutoff value in fluorescent unit (FU). Black dots indicate the dog sera. The red dot indicates the serum of the immunized dog. A value more than the cutoff value was positivity. The positivity rates are shown in Table 3. The figures were generated using EZR statistical software (Saitama Medical Center, Jichi Medical University, Saitama, Japan; <https://www.jichi.ac.jp/saitama-sct/SaitamaHP.files/statmed.html>), which is a graphical user interface for R (The R Foundation for Statistical Computing, Vienna, Austria).



Supplementary Figure S2. ELISA to detect the specific IgE to DM13-domain-containing protein using canine sera. (A) IgE reactivity to rGST. (B) IgE reactivity to rGST-DM13. Black dots indicate the dog sera. The red dot indicates the serum of the immunized dog. The dotted horizontal lines indicate the cutoff value. A value more than the cutoff value was positivity. The figures were generated using EZR statistical software (Saitama Medical Center, Jichi Medical University, Saitama, Japan; <https://www.jichi.ac.jp/saitama-sct/SaitamaHP.files/statmed.html>), which is a graphical user interface for R (The R Foundation for Statistical Computing, Vienna, Austria).



Supplementary Figure S3. The ribbon model of the best-predicted structure of the DM13-domain-containing protein using AlphaFold2. The model is colored by the pLDDT confidence value as indicated by the bar in the figure. The locations of the residues Cys21, Asp50 and Lys150 are indicated. The figure was created using the UCSF Chimera software.



Supplementary Figure S4. Phylogenetic analysis of the gene sequence for DM13-domain-containing protein. The phylogeny was analyzed using the maximum likelihood method.

Supplementary Table S1. *S. pseudintermedius* genome sequences used for the in-house database of peptide mass fingerprints.

<i>S. pseudintermedius</i> strain	GenBank accession No. ^a
63228	CP015626
81661	CP016073
ED99	CP002478
HKU10-03	CP002439
NA45	CP016072

^a, The data were downloaded on 4th April 2018.

Supplementary Table S2. Candidate *S. pseudintermedius* proteins, reactive to IgE.

Protein name	No. of amino acids	Molecular weight (kDa)	pI	Result of MS data analysis by:						Signal peptide prediction by SignalP-5.0	
				MASCOT			SEQUEST			Probability	Description
				Coverage (%)	No. of peptide matches	Score	Coverage (%)	No. of peptide matches	Score		
DM13-domain containing protein	150	16.3	6.79	28.00	28	943.11	50.00	21	46.74	0.9994	Cleavage site between pos. 20 and 21: LGA-CG.
Immuno-dominant antigen B protein	171	19.0	8.88	23.39	5	80.04	26.90	7	5.44	0.5317	Cleavage site between pos. 34 and 35: AHA-AT.

Supplementary Table S3. Structurally similar proteins localized at outside bacterial cells, obtained from the DALI search.

PDB ID-Chain	Z-score^a	RMSD^b	No. of residues	Sequence identity (%)	Description
1o75-B	5.2	3.6	402	14	47 kDa membrane antigen
4ncd-A	5	3.2	211	13	Gram-negative pili assembly chaperone, N-terminal
6w8u-A	4.5	2.9	140	17	Pilin
4f8p-B	4	2.9	142	10	Ph 6 antigen
5tug-A	4	3.1	115	12	Flagellar biosynthesis protein FlaG
5fce-B	4	3	116	11	LPXTG family cell surface protein Fms2
4p94-B	4	3.4	130	15	Conserved flagellar protein F
7c7u-A	3.9	2.8	579	4	Biofilm-associated surface protein
3qzp-B	3.7	3.4	125	10	Iron-regulated surface determinant protein A
4mkm-A	3.7	2.9	292	12	Putative surface anchored protein
5tfy-A	3.5	3.3	164	9	Flagellin
5m11-A	3.4	3.6	748	3	Immunoreactive 84KD antigen PG93
6psn-A	3.3	2.8	562	8	Protective antigen
2q7a-A	3.2	3.8	152	6	Cell surface heme-binding protein
3lso-A	3.2	3.7	445	4	Putative membrane anchored protein
6m3a-A	3.2	3	105	13	Biofilm-associated surface protein
5o4u-A	3.2	2.8	207	18	Flagellin
5ftx-A	3.1	3.3	651	7	Surface layer protein
4ut1-A	2.9	3.3	551	11	Flagellar hook-associated protein
6qay-A	2.9	3.3	118	14	TasA anchoring/assembly protein
4b0m-M	2.9	3.1	212	3	F1 capsule-anchoring protein
5flu-B	2.7	2.7	163	11	PAP fimbrial major pilin protein
3f83-A	2.7	3.3	508	7	Fusion of the minor pilin CfaE and major pilin CF
2jty-A	2.7	3.1	184	9	Type-1 fimbrial protein, A chain
3zgh-A	2.6	3.1	177	4	Cell wall surface anchor family protein
6e57-A	2.5	3	399	9	Surface glycan binding protein B
4igb-B	2.4	3.3	435	9	LPXTG cell wall surface protein
6e3f-A	2.3	3.8	497	13	Probable cell-surface antigen I/II
5hbb-C	2	3.3	267	10	Cell surface protein SpaA
5u6f-A	2	3.8	288	9	LPXTG-motif cell wall anchor domain protein

^a, Similarity index obtained from the Dali search: family level similarity (> 4.5), superfamily level similarity (4.0–4.5), a twilight zone where some similarities of biological significance can be seen (3.7–4.0) and similarities of low significance (< 3.7).

^b, RMSD, root mean square deviation.