

A20	-MNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	59
A20-10	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A20-12	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGLCASGYRPLTRDEAMSIKG	60
A20-14	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A20-17	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A20-5	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A20-8	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A21	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A21-10	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A21-11	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGLCASGYRPLTRDEAMSIKG	60
A21-13	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A21-14	-MNKVISVNIILLSTIFMLMKVQAAEPIYPAQVKWYGLGQGVCAANGYRPLTRDEAMSIKN	59
A21-15	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A21-16	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A21-19	MMNKLITANLAFASSLMLLIQAQAAEPVYPDQVKWYGLGEGVCASGYRPLTRDEAMSIKG	60
A21-4	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCSSGYRPLTRDEAMSIKG	60
A21-5	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKLAGLGTGVCASGYRPLTRDEAMSIKG	60
A21-6	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A21-8	MMNRIITASLAFASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A26	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A27	MMNRIITANLAFWASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A29V	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A7	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
A8	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKS	60
A9	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCSSGYRPLTRDEAMSIKG	60
BC88	-MNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	59
FC951	-----	0
126-14	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWASLGTGVCASGYRPLTRDEAMSIKG	60
312M	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
VBF557	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWAGLGTGVCASGYRPLTRDEAMSIKG	60
ERR1305902-bin.15	MMNRIITANLAFLASSLMLAQVQAAEPVYPDQVKWASLGTGVCASGYRPLTRDEAMSIKG	60
A20	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	117
A20-10	NLVSRMGQWQITGLADRWWIMGSGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A20-12	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A20-14	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A20-17	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A20-5	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A20-8	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A21	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A21-10	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A21-11	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A21-13	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A21-14	SLVSRMGFWQITGLADGWVIMGPGYNGEIKKSLVSAGESWCYPNSPVSGEIPTLSDWNIP	119
A21-15	NLVSRMGQWQITGLAERWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A21-16	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A21-19	NLVSRMGQWQITGLANRWVIMGSGYNGEIKQG--TAGETWCYPTSPISGEIPLSAWNIP	118
A21-4	NLVSRMGQWQITGLADRWWIMGSGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A21-5	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A21-6	NLVSRMGQWQITGLANRWVIMGPGYNGEIKQG--SAGETWCYPNSPVSGEIPTLSVWNIP	118
A21-8	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A26	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A27	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A29V	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A7	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A8	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
A9	NLVSRMGQWQITGLADRWWIMGSGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
BC88	NLVSRMGQWQITGLADRWWIMGSGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	117
FC951	-----	0
126-14	NLVSRMGQWQITGLADRWWIMGSGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
312M	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
VBF557	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118
ERR1305902-bin.15	NLVSRMGQWQITGLADRWWIMGPGYNGEIKQG--TAGETWCYPNSPVSGEIPTLSDWNIP	118

[illegible]

A20	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQHHGGSTTE	297
A20-10	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A20-12	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A20-14	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A20-17	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQHHGGSTTE	298
A20-5	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A20-8	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A21	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A21-10	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A21-11	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A21-13	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A21-14	VVTLKYDKSTKWSKTDYSLGELVEIKTSFQIPQVSKTEYSVEISSTQSWASQQGEETRE	299
A21-15	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A21-16	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A21-19	VVTLKYDKATNWSKTDYSLSEKVGKKTFQIPQVSSSTEYSVEISSTQSWASQKGGSTTE	298
A21-4	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A21-5	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A21-6	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQHHGGSTTE	298
A21-8	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A26	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQHHGGSTTE	298
A27	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A29V	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A7	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A8	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
A9	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
BC88	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	297
FC951	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	174
126-14	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
312M	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
VB557	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
ERR1305902-bin.15	VVTLKYDKATNWSKTDYSLSEKVTTKNKFQWPLVGETELAIEIAASQSWASQKGGSTTE	298
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A20	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPDN	357
A20-10	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A20-12	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPDN	358
A20-14	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A20-17	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A20-5	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A20-8	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A21	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A21-10	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A21-11	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A21-13	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A21-14	TVLVEARPTVPPYSSLPVRIALYKSNISYPYEFKAEVNYDLTMKGFLRRNGNAWYTHPEN	359
A21-15	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A21-16	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A21-19	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPAN	358
A21-4	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPDN	358
A21-5	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A21-6	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPTN	358
A21-8	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A26	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPDN	358
A27	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A29V	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A7	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A8	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
A9	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPDN	358
BC88	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	357
FC951	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	234
126-14	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
312M	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
VB557	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
ERR1305902-bin.15	TVSVEARPTVPPHSSLPVRVALYKSNISYPYEFKAEVNYDLTMKGFLRWGGNAWYTHPEN	358
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A20	RPTREHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	417
A20-10	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A20-12	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A20-14	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A20-17	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A20-5	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A20-8	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21-10	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21-11	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21-13	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21-14	GPTLEHTFAVGPFPRDKASSIRYQWDKRYIPGEMKWWDNWNTISEYGLSTMQNNLGLVLRP	419
A21-15	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21-16	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21-19	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21-4	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21-5	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21-6	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A21-8	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A26	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A27	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A29V	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A7	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A8	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
A9	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
BC88	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	417
FC951	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	294
126-14	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
312M	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
VB557	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
ERR1305902-bin.15	RPTWEHTFAVGPFPRDKASSIRYQWDKRYIPGEVKWWDNWTISEYGLSTMQNNLGRVLRP	418
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A20	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRNASAEGVALTGVDLDQEALANEGFG	477
A20-10	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A20-12	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRHASAEGVALTGVDLDQEALANEGFG	478
A20-14	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A20-17	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRNSSAEGVALTGVDLDSEALASEGFG	478
A20-5	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A20-8	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A21	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRNASAEGVALTGVDLDSEALANEGFG	478
A21-10	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A21-11	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRNASAEGVALTGVDLDSEALANEGFG	478
A21-13	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRNASAEGVALTGVDLDQEALANEGFG	478
A21-14	VHASVTGDFYAESQFAGDIEIGLPPTTSTKA-LLRSASVNMVELTDLKLDKKNLASEGFG	478
A21-15	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A21-16	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A21-19	IRSAVTGDFYAESQFAGDIEIGQPQSGSTKAAQLRSASADEVALTGVDLDSEALANEGFG	478
A21-4	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A21-5	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A21-6	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRNSSAEGVALTGVDLDSETLASEGFG	478
A21-8	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRNASAEGVALTGVDLDQEALANEGFG	478
A26	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A27	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRNASAEGVALTGVDLDQEALANEGFG	478
A29V	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRNASAEGVALTGVDLDQEALANEGFG	478
A7	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A8	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
A9	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
BC88	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	477
FC951	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	354
126-14	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
312M	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGFG	478
VB557	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRNASAEGVALTGVDLDQEALANEGFG	478
ERR1305902-bin.15	IRSAVTGDFYAESQFAGDIEIGQPQTRSAASAQLRSASADEVALTGVDLDSEALANEGVG	478
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A20	NVSLTIVTPAY	487
A20-10	NVSLTIVPVQ	488
A20-12	NVSLTIVTPAY	488
A20-14	NVSLTIVPVQ	488
A20-17	NVSLTIAPVQ	488
A20-5	NVSLTIVPVQ	488
A20-8	NVSLTIVPVQ	488
A21	NVSLTIVPVQ	488
A21-10	NVSLTIVPVQ	488
A21-11	NVSLTIVPVQ	488
A21-13	NVSLTIVPVQ	488
A21-14	NVSLTLAPAH	488
A21-15	NVSLTIVPVQ	488
A21-16	NVSLTIVPVQ	488
A21-19	NVSLTIVPVQ	488
A21-4	NVSLTIVPVQ	488
A21-5	NVSLTIVPVQ	488
A21-6	NVSLTMAPVQ	488
A21-8	NVSLTIVPVQ	488
A26	NVSLTIVPVQ	488
A27	NVSLTIVPVQ	488
A29V	NVSLTIVTPAY	488
A7	NVSLTIVPVQ	488
A8	NVSLTIVPVQ	488
A9	NVSLTIVPVQ	488
BC88	NVSLTIVPVQ	487
FC951	NVSLTIVPVQ	364
126-14	NVSLTIVPVQ	488
312M	NVSLTIVPVQ	488
VBF557	NVSLTIVPVQ	488
ERR1305902-bin.15	NVSLTIVPVQ	488
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Additional file 2 Protein sequence alignment of aerolysin from *Aeromonas veronii* strains isolated from patients with gastrointestinal disease. Protein alignment was performed with Clustal Omega.