

[illegible][illegible]

The protein structure is shown with alpha helices labeled $\alpha 4$, $\alpha 5$, $\alpha 6$, $\alpha 7$, and $\beta 6$. The sequence is divided into segments of 130, 140, 150, 160, 170, and 180 residues.

The sequence alignment shows the following residues (H indicates a histidine residue):

Residue	130	140	150	160	170	180
1	DL	SL	SL	SL	SL	SL
2	LL	LG	LG	LG	LG	LG
3	KY	IR	IR	IR	IR	IR
4	TL	EC	EC	EC	EC	EC
5	QSD	AV	AV	AV	AV	AV
6	NN	IH	IH	IH	IH	IH
7	AC	TN	TN	TN	TN	TN
8	DI	DM	DM	DM	DM	DM
9	LF	HL	HL	HL	HL	HL
10	NY	FC	FC	FC	FC	FC
11	QGG	YQ	YQ	YQ	YQ	YQ
12	PD	NV	NV	NV	NV	NV
13	AV	KN	KN	KN	KN	KN
14	NK	LE	LE	LE	LE	LE
15	YLV	FC	FC	FC	FC	FC
16	QSD	YQ	YQ	YQ	YQ	YQ
17	NN	NV	NV	NV	NV	NV
18	AC	IH	IH	IH	IH	IH
19	DI	DM	DM	DM	DM	DM
20	LF	HL	HL	HL	HL	HL
21	NY	FC	FC	FC	FC	FC
22	QGG	YQ	YQ	YQ	YQ	YQ
23	PD	NV	NV	NV	NV	NV
24	AV	KN	KN	KN	KN	KN
25	NK	LE	LE	LE	LE	LE
26	YLV	FC	FC	FC	FC	FC
27	QSD	YQ	YQ	YQ	YQ	YQ
28	NN	NV	NV	NV	NV	NV
29	AC	IH	IH	IH	IH	IH
30	DI	DM	DM	DM	DM	DM
31	LF	HL	HL	HL	HL	HL
32	NY	FC	FC	FC	FC	FC
33	QGG	YQ	YQ	YQ	YQ	YQ
34	PD	NV	NV	NV	NV	NV
35	AV	KN	KN	KN	KN	KN
36	NK	LE	LE	LE	LE	LE
37	YLV	FC	FC	FC	FC	FC
38	QSD	YQ	YQ	YQ	YQ	YQ
39	NN	NV	NV	NV	NV	NV
40	AC	IH	IH	IH	IH	IH
41	DI	DM	DM	DM	DM	DM
42	LF	HL	HL	HL	HL	HL
43	NY	FC	FC	FC	FC	FC
44	QGG	YQ	YQ	YQ	YQ	YQ
45	PD	NV	NV	NV	NV	NV
46	AV	KN	KN	KN	KN	KN
47	NK	LE	LE	LE	LE	LE
48	YLV	FC	FC	FC	FC	FC
49	QSD	YQ	YQ	YQ	YQ	YQ
50	NN	NV	NV	NV	NV	NV
51	AC	IH	IH	IH	IH	IH
52	DI	DM	DM	DM	DM	DM
53	LF	HL	HL	HL	HL	HL
54	NY	FC	FC	FC	FC	FC
55	QGG	YQ	YQ	YQ	YQ	YQ
56	PD	NV	NV	NV	NV	NV
57	AV	KN	KN	KN	KN	KN
58	NK	LE	LE	LE	LE	LE
59	YLV	FC	FC	FC	FC	FC
60	QSD	YQ	YQ	YQ	YQ	YQ
61	NN	NV	NV	NV	NV	NV
62	AC	IH	IH	IH	IH	IH
63	DI	DM	DM	DM	DM	DM
64	LF	HL	HL	HL	HL	HL
65	NY	FC	FC	FC	FC	FC
66	QGG	YQ	YQ	YQ	YQ	

CepA_WT_AAA21532.1/hlab											
		190	200	210	220	230	240				
CepA_WT_AAA21532.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_01_AAA21533.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_02_AAA21534.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_03_AAA21535.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_04_CBX07046.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_05_KXU41062.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_06_CBX07043.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_07_EGM96002.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_08_EIY42666.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_09_EIY95316.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_10_EXY19300.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_11_EXY28329.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_12_EXY47305.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_13_EXY66440.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_14_EXZ06368.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_15_EXZ14938.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_16_EXZ20393.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_17_EXZ91867.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_18_EYA72157.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_19_YP_098534.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_20_RHD49540.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_21_RDT77422.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD
CepA_22_AKA51196.1 hlab		TTPLAAAKLLEIFRN	E	NLFDKEYKNFIYQ	TMVE	CQTG	D	RLIAPLLDKKVT	M	GHKTGT	GD

CepA_WT_AAA21532.1/hlab											
		250	260	270	280	290	300				
CepA_WT_AAA21532.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_01_AAA21533.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_02_AAA21534.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_03_AAA21535.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_04_CBX07046.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_05_KXU41062.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_06_CBX07043.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_07_EGM96002.1 hlab		RNAKGQOI	SCNE	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_08_EIY42666.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_09_EIY95316.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_10_EXY19300.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_11_EXY28329.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_12_EXY47305.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_13_EXY66440.1 hlab		RNAKGQOI	ACND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_14_EXZ06368.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_15_EXZ14938.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_16_EXZ20393.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_17_EXZ91867.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_18_EYA72157.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_19_YP_098534.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_20_RHD49540.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_21_RDT77422.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID
CepA_22_AKA51196.1 hlab		RNAKGQOI	SCND	IGFILLP	DGHAYSIAV	FVKDSEADN	RENS	E	IIAEIS	RIVVEYV	TQQID