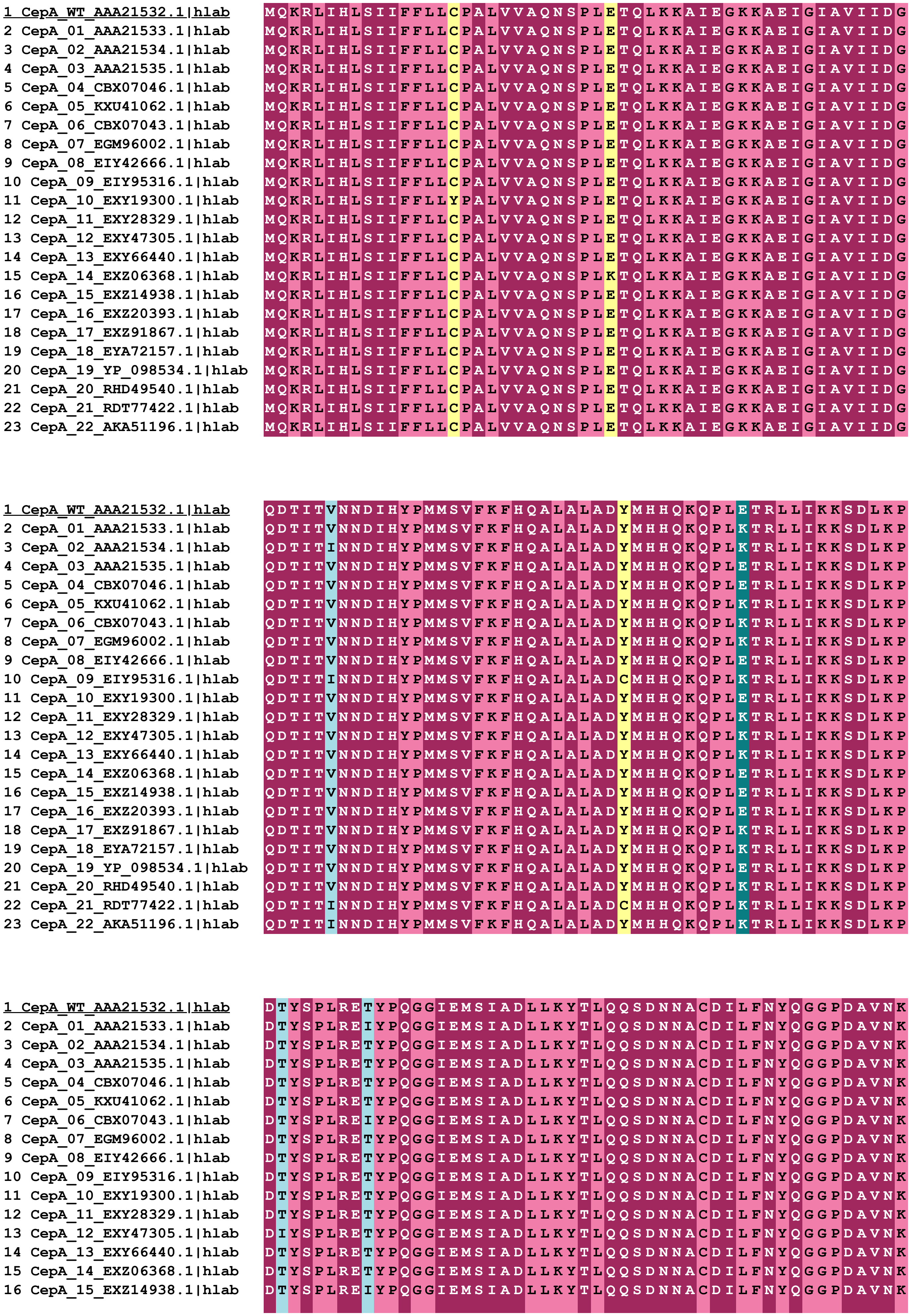
ConSurf Color-Coded MSA for Job:anuleka_cepa Date:24/10/2022



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2 CepA_01_AAA21533.1|hlab      MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
3 CepA_02_AAA21534.1|hlab      MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
4 CepA_03_AAA21535.1|hlab      MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
5 CepA_04_CBX07046.1|hlab      MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
6 CepA_05_KXU41062.1|hlab      MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
7 CepA_06_CBX07043.1|hlab      MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
8 CepA_07_EGM96002.1|hlab      MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
9 CepA_08_EIY42666.1|hlab      MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
10 CepA_09_EIY95316.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
11 CepA_10_EXY19300.1|hlab     MQKRLIHLSIIFFLLYPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
12 CepA_11_EXY28329.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
13 CepA_12_EXY47305.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
14 CepA_13_EXY66440.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
15 CepA_14_EXZ06368.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLKTQLKKAIEGKKAEIGIAVIIDG
16 CepA_15_EXZ14938.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
17 CepA_16_EXZ20393.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
18 CepA_17_EXZ91867.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
19 CepA_18_EYA72157.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
20 CepA_19_YP_098534.1|hlab    MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
21 CepA_20_RHD49540.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
22 CepA_21_RDT77422.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
23 CepA_22_AKA51196.1|hlab     MQKRLIHLSIIFFLLCPALVVAQNSPLETQLKKAIEGKKAEIGIAVIIDG
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1 CepA_WT_AAA21532.1|hlab      QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLETRLLIKKSDLKP
2 CepA_01_AAA21533.1|hlab      QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
3 CepA_02_AAA21534.1|hlab      QDTITINNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
4 CepA_03_AAA21535.1|hlab      QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLETRLLIKKSDLKP
5 CepA_04_CBX07046.1|hlab      QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLETRLLIKKSDLKP
6 CepA_05_KXU41062.1|hlab      QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
7 CepA_06_CBX07043.1|hlab      QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
8 CepA_07_EGM96002.1|hlab      QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
9 CepA_08_EIY42666.1|hlab      QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLETRLLIKKSDLKP
10 CepA_09_EIY95316.1|hlab     QDTITINNDIHYPMMSVFKFHQALALADCMHHQKQPLKTRLLIKKSDLKP
11 CepA_10_EXY19300.1|hlab     QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLETRLLIKKSDLKP
12 CepA_11_EXY28329.1|hlab     QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
13 CepA_12_EXY47305.1|hlab     QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
14 CepA_13_EXY66440.1|hlab     QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
15 CepA_14_EXZ06368.1|hlab     QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLETRLLIKKSDLKP
16 CepA_15_EXZ14938.1|hlab     QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLETRLLIKKSDLKP
17 CepA_16_EXZ20393.1|hlab     QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLETRLLIKKSDLKP
18 CepA_17_EXZ91867.1|hlab     QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
19 CepA_18_EYA72157.1|hlab     QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
20 CepA_19_YP_098534.1|hlab    QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLETRLLIKKSDLKP
21 CepA_20_RHD49540.1|hlab     QDTITVNNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
22 CepA_21_RDT77422.1|hlab     QDTITINNDIHYPMMSVFKFHQALALADCMHHQKQPLKTRLLIKKSDLKP
23 CepA_22_AKA51196.1|hlab     QDTITINNDIHYPMMSVFKFHQALALADYMHHQKQPLKTRLLIKKSDLKP
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1 CepA_WT_AAA21532.1|hlab      DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
2 CepA_01_AAA21533.1|hlab      DTYSPLREIYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
3 CepA_02_AAA21534.1|hlab      DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
4 CepA_03_AAA21535.1|hlab      DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
5 CepA_04_CBX07046.1|hlab      DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
6 CepA_05_KXU41062.1|hlab      DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
7 CepA_06_CBX07043.1|hlab      DTYSPLREIYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
8 CepA_07_EGM96002.1|hlab      DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
9 CepA_08_EIY42666.1|hlab      DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
10 CepA_09_EIY95316.1|hlab     DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
11 CepA_10_EXY19300.1|hlab     DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
12 CepA_11_EXY28329.1|hlab     DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
13 CepA_12_EXY47305.1|hlab     DIYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
14 CepA_13_EXY66440.1|hlab     DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
15 CepA_14_EXZ06368.1|hlab     DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
16 CepA_15_EXZ14938.1|hlab     DTYSPLREIYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
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18 CepA_17_EXZ91867.1|hlab   DTYSPLREIYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
19 CepA_18_EYA72157.1|hlab   DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
20 CepA_19_YP_098534.1|hlab  DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
21 CepA_20_RHD49540.1|hlab   DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
22 CepA_21_RDT77422.1|hlab   DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
23 CepA_22_AKA51196.1|hlab   DTYSPLRETYPQGGIEMSIADLLKYTLQQSDNNACDILFNYQGGPDAVNK
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2 CepA_01_AAA21533.1|hlab    YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNENLFD
3 CepA_02_AAA21534.1|hlab    YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNENLFD
4 CepA_03_AAA21535.1|hlab    YLHSLGIRECAVIHTENDMHKNLEFCYQNWTTPLAAAKLLEIFRNENLFD
5 CepA_04_CBX07046.1|hlab    YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNENLFD
6 CepA_05_KXU41062.1|hlab    YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNENLFD
7 CepA_06_CBX07043.1|hlab    YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNENLFD
8 CepA_07_EGM96002.1|hlab    YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNENLFD
9 CepA_08_EIY42666.1|hlab    YLHSLGIRECAVIHTENDMHKNLEFCYQNWTTPLAAAKLLEIFRNENLFD
10 CepA_09_EIY95316.1|hlab   YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNENLFD
11 CepA_10_EXY19300.1|hlab   YLHSLGIRECAVIHTENDMHKNLEFCYQNWTTPLAAAKLLEIFRNENLFD
12 CepA_11_EXY28329.1|hlab   YLHSLGIRECAVIHTENDMHKNLEFCYQNWTTPLAAAKLLEIFRNENLFD
13 CepA_12_EXY47305.1|hlab   YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNENLFD
14 CepA_13_EXY66440.1|hlab   YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNKNLFD
15 CepA_14_EXZ06368.1|hlab   YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNKNLFD
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18 CepA_17_EXZ91867.1|hlab   YLHSLGIRECAVIHTENDMHKNLEFCYQNWTTPLAAAKLLEIFRNENLFD
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20 CepA_19_YP_098534.1|hlab  YLHSLGIRECAVIHTENDMHKNLEFCYQNWTTPLAAAKLLEIFRNENLFD
21 CepA_20_RHD49540.1|hlab   YLNSLGIRECAVIHTENDMHKNLEFCYQNWTTPLAAAKLLEIFRNENLFD
22 CepA_21_RDT77422.1|hlab   YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNENLFD
23 CepA_22_AKA51196.1|hlab   YLHSLGIRECAVIHTENDMHENLEFCYQNWTTPLAAAKLLEIFRNENLFD
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3 CepA_02_AAA21534.1|hlab    KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
4 CepA_03_AAA21535.1|hlab    KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
5 CepA_04_CBX07046.1|hlab    KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
6 CepA_05_KXU41062.1|hlab    KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
7 CepA_06_CBX07043.1|hlab    KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
8 CepA_07_EGM96002.1|hlab    KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
9 CepA_08_EIY42666.1|hlab    KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
10 CepA_09_EIY95316.1|hlab   KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTIGHKTGTGDRNAKGQQIGC
11 CepA_10_EXY19300.1|hlab   KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
12 CepA_11_EXY28329.1|hlab   KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
13 CepA_12_EXY47305.1|hlab   KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
14 CepA_13_EXY66440.1|hlab   KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
15 CepA_14_EXZ06368.1|hlab   KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIAC
16 CepA_15_EXZ14938.1|hlab   KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
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18 CepA_17_EXZ91867.1|hlab   KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
19 CepA_18_EYA72157.1|hlab   KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
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22 CepA_21_RDT77422.1|hlab   KEYKNFIYQTMVECQTGQDRLIAPLLDKKVTMGHKTGTGDRNAKGQQIGC
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3 CepA_02_AAA21534.1|hlab    NDIGFILLPDGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVKQQID
4 CepA_03_AAA21535.1|hlab    NDIGFILLPDGHVYSIAVFVKDSEADNRENSEIIAEISHIVYEYVTQQID
5 CepA_04_CBX07046.1|hlab    NDIGFILLPDGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
6 CepA_05_KXU41062.1|hlab    NDIGFILLPDGHVYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
7 CepA_06_CBX07043.1|hlab    NDIGFILLPDGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
8 CepA_07_EGM96002.1|hlab    NEIGFILLPDGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
9 CepA_08_EIY42666.1|hlab    NDIGFILLPDGHVYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
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11 CepA_10_EXY19300.1|hlab	NDIGFILLPDGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
12 CepA_11_EXY28329.1|hlab	NDIGFILLPDGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
13 CepA_12_EXY47305.1|hlab	NDIGFILLPDGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
14 CepA_13_EXY66440.1|hlab	NDIGFILLPGGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
15 CepA_14_EXZ06368.1|hlab	NDIGFILLPSGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
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17 CepA_16_EXZ20393.1|hlab	NDIGFILLPDGHVYSIAVFVKDSEADNRENSKIIAEISRIVYEYVTQQID
18 CepA_17_EXZ91867.1|hlab	NDIGFILLPDGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID
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23 CepA_22_AKA51196.1|hlab	NDIGFILLPDGHAYSIAVFVKDSEADNRENSEIIAEISRIVYEYVTQQID

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3 CepA_02_AAA21534.1|hlab
4 CepA_03_AAA21535.1|hlab
5 CepA_04_CBX07046.1|hlab
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20 CepA_19_YP_098534.1|hlab
21 CepA_20_RHD49540.1|hlab
22 CepA_21_RDT77422.1|hlab
23 CepA_22_AKA51196.1|hlab

1	2	3	4	5	6	7	8	9

Variable Average Conserved

X - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.