

CLUSTALW Result

[\[clustalw.fasta\]](#)[\[clustalw.dnd\]](#)[\[readme\]](#)

FastTree full



Exec

CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to Protein

Sequence format is Pearson

Sequence 1:	AAA98797.1	609 aa
Sequence 2:	XP_004038851.2	609 aa
Sequence 3:	XP_003832390.1	609 aa
Sequence 4:	NP_001127106.2	609 aa
Sequence 5:	XP_031520350.1	608 aa
Sequence 6:	XP_010357300.1	608 aa
Sequence 7:	XP_023054286.1	608 aa
Sequence 8:	XP_039086927.1	608 aa
Sequence 9:	BAA14130.1	511 aa
Sequence 10:	XP_030863335.1	511 aa
Sequence 11:	XP_003818736.2	511 aa
Sequence 12:	XP_024108681.1	511 aa
Sequence 13:	XP_010370880.1	511 aa
Sequence 14:	XP_009212204.3	511 aa
Sequence 15:	XP_023046681.1	511 aa
Sequence 16:	XP_039072587.1	511 aa
Sequence 17:	AAA16331.1	147 aa
Sequence 18:	XP_034787914.1	147 aa
Sequence 19:	NP_001162321.1	147 aa
Sequence 20:	XP_030773087.1	147 aa
Sequence 21:	XP_018891711.2	147 aa
Sequence 22:	XP_002822176.1	147 aa
Sequence 23:	XP_026303267.1	147 aa
Sequence 24:	XP_039080597.1	147 aa
Sequence 25:	AAH05278.1	180 aa
Sequence 26:	XP_003820986.1	263 aa
Sequence 27:	XP_002812569.1	263 aa
Sequence 28:	XP_004032757.2	180 aa
Sequence 29:	XP_023073103.1	261 aa
Sequence 30:	XP_010360153.1	263 aa
Sequence 31:	XP_003907591.1	263 aa
Sequence 32:	XP_039109363.1	179 aa
Sequence 33:	NP_000726.1	116 aa
Sequence 34:	XP_003822896.1	116 aa
Sequence 35:	XP_004044424.1	147 aa
Sequence 36:	XP_003776920.1	147 aa
Sequence 37:	XP_003897923.2	120 aa
Sequence 38:	XP_023061011.1	120 aa
Sequence 39:	XP_010386255.1	120 aa
Sequence 40:	XP_039075373.1	120 aa
Sequence 41:	CAA25109.1	154 aa
Sequence 42:	XP_008973239.1	166 aa
Sequence 43:	XP_018874109.1	166 aa
Sequence 44:	NP_001125556.1	154 aa
Sequence 45:	XP_023077864.1	192 aa
Sequence 46:	XP_003905518.1	154 aa
Sequence 47:	XP_010387444.1	154 aa
Sequence 48:	XP_039086409.1	154 aa
Sequence 49:	NP_036370.2	747 aa

Sequence 50: XP_018890589.2 749 aa
Sequence 51: XP_034786558.1 753 aa
Sequence 52: XP_002820941.2 747 aa
Sequence 53: XP_023060880.1 744 aa
Sequence 54: XP_030797002.1 743 aa
Sequence 55: XP_003903926.2 743 aa
Sequence 56: XP_039089208.1 743 aa
Sequence 57: AAH96305.1 736 aa
Sequence 58: XP_004057364.3 784 aa
Sequence 59: XP_034795441.1 827 aa
Sequence 60: XP_024097180.1 745 aa
Sequence 61: XP_023080805.1 745 aa
Sequence 62: XP_010386890.1 745 aa
Sequence 63: XP_009194393.2 784 aa
Sequence 64: XP_039090349.1 757 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 98
Sequences (1:3) Aligned. Score: 98
Sequences (1:4) Aligned. Score: 98
Sequences (1:5) Aligned. Score: 93
Sequences (1:6) Aligned. Score: 92
Sequences (1:7) Aligned. Score: 92
Sequences (1:8) Aligned. Score: 83
Sequences (1:9) Aligned. Score: 1
Sequences (1:10) Aligned. Score: 1
Sequences (1:11) Aligned. Score: 1
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Sequences (1:13) Aligned. Score: 1
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 Sequences (63:64) Aligned. Score: 66
 Guide tree file created: [\[clustalw.dnd\]](#)

There are 63 groups
 Start of Multiple Alignment

Aligning...

Group 1: Sequences:	2	Score:2532
Group 2: Sequences:	3	Score:2635
Group 3: Sequences:	4	Score:2507
Group 4: Sequences:	2	Score:2520
Group 5: Sequences:	3	Score:2514
Group 6: Sequences:	7	Score:2511
Group 7: Sequences:	8	Score:2422
Group 8: Sequences:	2	Score:2404
Group 9: Sequences:	3	Score:2397
Group 10: Sequences:	2	Score:2412
Group 11: Sequences:	3	Score:2404
Group 12: Sequences:	6	Score:2379
Group 13: Sequences:	2	Score:2274
Group 14: Sequences:	8	Score:2220
Group 15: Sequences:	16	Score:878
Group 16: Sequences:	2	Score:12321
Group 17: Sequences:	3	Score:12241
Group 18: Sequences:	4	Score:12078
Group 19: Sequences:	2	Score:12247
Group 20: Sequences:	3	Score:12204
Group 21: Sequences:	7	Score:11916
Group 22: Sequences:	8	Score:11372
Group 23: Sequences:	24	Score:1092
Group 24: Sequences:	2	Score:8661
Group 25: Sequences:	3	Score:8607
Group 26: Sequences:	4	Score:8527
Group 27: Sequences:	2	Score:8557
Group 28: Sequences:	3	Score:8494
Group 29: Sequences:	7	Score:8414
Group 30: Sequences:	8	Score:8251
Group 31: Sequences:	32	Score:1710
Group 32: Sequences:	2	Score:2984
Group 33: Sequences:	3	Score:2976
Group 34: Sequences:	4	Score:3431
Group 35: Sequences:	2	Score:4316
Group 36: Sequences:	3	Score:4303
Group 37: Sequences:	7	Score:3617
Group 38: Sequences:	8	Score:2872
Group 39: Sequences:	40	Score:1171
Group 40: Sequences:	2	Score:10056

Group 41: Sequences: 3 Score:10031
Group 42: Sequences: 4 Score:10031
Group 43: Sequences: 2 Score:9989
Group 44: Sequences: 3 Score:9928
Group 45: Sequences: 7 Score:9735
Group 46: Sequences: 8 Score:9284
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Group 48: Sequences: 3 Score:1872
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Group 52: Sequences: 4 Score:1842
Group 53: Sequences: 8 Score:1885
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Group 56: Sequences: 3 Score:12480
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Group 59: Sequences: 3 Score:12209
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Group 61: Sequences: 8 Score:11180
Group 62: Sequences: 24 Score:1727
Group 63: Sequences: 64 Score:1229

Alignment Score 225684

firstres = 1 lastres = 956

FASTA file created!

Fasta-Alignment file created [clustalw.fasta]

clustalw.fasta

>CAA25109.1

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LIRLFKGHPETLEKFDKFKHLK-----
-----SEDEMKASEDLK-----
-----KHGATVLTALGGILK-----KKGHHEAEIKP
LAQSHATKHKIPVKYLEFISECIIQVLQSKHPGDFGADAQGAMNKALELFRKDMASNYKE
LGFQG-----

>XP_008973239.1

-----MELGCQVCKHCAMGLSDGEWQLVLNVWGKVEAD
IPGHG-----QEV
LIRLFKGHPETLEKFDKFKHLK-----
-----SEDEMKASEDLK-----
-----KHGATVLTALGGILK-----KKGHHEAEIKP
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>AAH05278.1

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>XP_003820986.1

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>XP_002812569.1

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>XP_023073103.1

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>XP_003907591.1

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>XP_003832390.1

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VEEPQNLVKQN-----CELFEQ
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HQDSVSSKLKECCEKPLLE-----KSHCLAEVENDEMPADLP SLAADFVESKEVCKNYA
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VEEPQNLVKQN-----CELFEQ
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VEEPQNLVKQN-----CELFEQ
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>XP_003822896.1

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>XP_004044424.1

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>NP_000726.1

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>XP_003776920.1

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-----NFKVEN-----HTACHCST-----
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>XP 023061011.1

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>XP 010386255.1

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>XP 003897923.2

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>XP 039075373.1

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>AAH96305.1

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