

Conservation Threshold: 2 (Maximum: 3)
 Number of gaps ignored: 2
 Percentage of unusual residues ignored: 12%

Sub-group A, sequences: 1 to 10
 Sub-group B, sequences: 23 to 33
 Sub-group C, sequences: 45 to 55
 Sub-group D, sequences: 67 to 77

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Identity between all sub-groups

(36) ALL [R]

Identity between sub-group pairs

(10) A,B [D]
 (25) A,D [D]
 (26) A,B [E]
 (70) A,D [E]

Identity within one sub-group

(31) B [E] C [R]
 (38) C [E]
 (40) C [D]
 (41) A [R]
 (57) B [E]
 (64) D [E]
 (68) C [D]

2

Conservation between all sub-groups

NONE

Conservation between sub-group pairs

(10) A,D (2) A-[D] D-[D]	Cons: Negative Charged	Diff:
B,D (2) B-[D] D-[D]	Cons: Negative Charged	Diff:
(64) B,C (2) B-[D] C-[ED]	Cons: Negative Charged	Diff:
B,D (2) B-[D] D-[E]	Cons: Negative Charged	Diff:
C,D (2) C-[ED] D-[E]	Cons: Negative Charged	Diff:
(71) B,C (2) B-[KR] C-[K]	Cons: Positive Charged	Diff:

Difference between sub-group pairs

(13) B,C (1) B-[E] C-[KR]	Cons: Charged	Diff: Positive	% B-[0] C-[90]
		Negative	% B-[90] C-[0]
(31) B,C (1) B-[E] C-[R]	Cons: Charged	Diff: Positive	% B-[0] C-[100]
		Negative	% B-[100] C-[0]
(40) C,D (1) C-[D] D-[H]	Cons: Charged	Diff: Positive	% C-[0] D-[90]
		Negative	% C-[100] D-[0]
(68) A,C (1) A-[H] C-[D]	Cons: Charged	Diff: Positive	% A-[90] C-[0]
		Negative	% A-[0] C-[100]

Conserved within one sub-group

(8) D (2) D-[ED]	Cons: Negative Charged
(12) C (2) C-[ED]	Cons: Negative Charged
(15) B (2) B-[KR]	Cons: Positive Charged
(19) C (2) C-[K]	Cons: Positive Charged
(21) D (2) D-[KR]	Cons: Positive Charged
(43) D (2) D-[HKR]	Cons: Positive Charged
(45) C (2) C-[KR]	Cons: Positive Charged
(54) A (2) A-[KR]	Cons: Positive Charged
(59) B (2) B-[D]	Cons: Negative Charged
(61) A (2) A-[K]	Cons: Positive Charged

Figure 5b