

H. armiger
R. siamensis
R. episcopus
R. marshalli
R. osgoodi
R. pusillus
R. rex
R. sinicus

267
(0.979*)

ALLSGA E I FAEEVVKGVKPAHCE	KTTVFKSLGM	AVAAKLV Y DSWSS
ALLSGA E I FAEEVVKGVKPAHCE	KTTVFKSLGM	AVAAKLV Y DSWLL
ALLSGA E I FAEEVVKGVKPAHCE	KTTVFKSLGM	AVAAKLV Y DSWLS
GFVSGGQVAATSSLGWARGCPC	RAVVLVQNARVA	EGRRGTWEPWKT
ALLSGA E I FAEEVVKGVKPAHCE	KTTVFKSLGM	AVAAKLV Y DSWLS
ALLSGA E I FAEEVVKGVKPAHCE	KTTVFKSLGM	AVAAKLV Y DSWLS
ALLSGA E I FAEEVVKGVKPAHCE	KTTVFKSLGM	AVAAKLV Y DSWLS
ALLSGA E I FAEEVVKGVKPAHCE	KTTVFKSLGM	AVAAKLV Y DSWLS

H. armiger
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2 **4**
(0.993*) **(0.991*)**

KPLDPGGLK
KPLDPGGLK
RMLCPAGLK
QPLDPGGLK
KPLDPGGLK
KPLDPGGLK
QPLDPGGLK
KPLDPGGLK

H. armiger
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96
(0.999*)

[illegible]

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378
(0.997*)

390
(0.985*)

V	V	L	S	W	G	V	V	A	I	Q	V	G	S	L	L	G
V	V	S	T	L	G	I	L	R	Q	R	G	R	Q	R	G	R
V	V	L	S	W	G	V	V	A	I	Q	V	G	S	L	L	G
V	V	L	S	W	G	V	V	A	I	Q	V	G	S	L	L	G
V	V	L	S	W	G	V	V	A	I	Q	M	G	S	L	L	G
V	V	L	S	W	G	V	V	A	I	Q	V	G	S	L	L	G
V	V	L	S	W	G	V	V	A	I	Q	V	G	S	L	L	G
V	V	L	S	W	G	V	V	A	I	Q	V	G	S	L	L	G
V	V	L	S	W	G	V	V	A	I	Q	V	G	S	L	L	G

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152
(1.000*)

163
(1.000*)

AGGVGI TCWI LVCN
AGGVGI TCWI LVCN
AGKSLL ENMVEECG
AGGVGI TCWI LVCN
AGGVGI TCWI LVCN
AGGVGI TCWI LVCN
AGGVGI TCWI LVCN
AGGVGI TCWI LVCN

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388 **390**
(0.957*) (0.958*)

PKKKLAEA
PKKKLAEA
PKKDLSEP
PKKKLAEA
PKKKLAEA
PKKKLAEA
PKKKLAEA
PKKKLAEA

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266 267 272 275
(0.985*) (0.977*) (0.982*) (0.982*)

The diagram illustrates sequence alignment with vertical red bars highlighting mismatches. The sequences are as follows:

LFLCLWCYLP	AKGCLK
LFLCLWCYLP	AKGCLK
LFLCLWCYLP	AKGCLK
LFLCLWCYLP	AKGCLK
LFFALF	MVLPSSQGLP
LFFALF	MVLPSSQGLP
LFLCLWCYLP	AKGCLK
LFLCLWCYLP	AKGCLK

Vertical red bars highlight mismatches at positions 4, 5, 6, and 7. Horizontal blue lines are present under the 4th and 5th rows.