

Mview

Multiple Sequence Alignment (MSA)

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Results for Job ID

mview-I20250609-145946-0041-85960689-p1m

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Tool Output

Result Files

Submission Details

Tool output

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MVview

Reference sequence (1): 6WX6_A
Identities normalised by aligned length.
Colored by: identity

	cov	pid	1 [.	.	:	.	.	.
80									
1	6wX6_A	100.0%	100.0%						
2	NP_000137.2	77.1%	99.4%						
3	AAP36762.1	77.5%	89.2%						
4	2FG4_A	76.7%	99.4%						

Index	Sequence	Score	Identity
5	CAE11873.1	91.2%	74.7%
6	CAG32996.1	77.1%	98.9%
7	AAA35831.1	77.1%	98.9%
8	AKI70338.1	77.1%	98.9%
9	AKI70336.1	77.1%	98.9%
10	ATC54405.1	77.1%	98.9%
	consensus/100%		
	consensus/90%		
	consensus/80%		
	consensus/70%		

	cov	pid	81	1	:																																																															
160																																																																								
1	6MX6_A	100.0%	100.0%	AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
2	NP_000137.2	77.1%	99.4%	AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
3	AP36762.1	77.5%	99.2%	AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
4	2FG4_A	76.7%	99.4%	AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
5	CAE11873.1	91.2%	74.7%	AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
6	CAG32996.1	77.1%	98.9%	AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
7	AAA35831.1	77.1%	98.9%	AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
8	AKT70338.1	77.1%	98.9%	AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
9	AKT70336.1	77.1%	98.9%	AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
10	AIC544405.1	77.1%	98.9%	AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
	consensus/100%			AA	s	N	S	V	N	Y	Q	A	S	V	T	Y	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P
	consensus/90%			AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
	consensus/80%			AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								
	consensus/70%			AAVNS	VN	LY	QAS	VTY	S	L	G	F	Y	E	D	R	D	V	A	L	E	G	V	S	H	F	F	R	E	A	E	K	R	E	G	E	R	L	L	K	N	O	N	R	G	G	R	A	L	F	O	I	K	K	P	A	E	D	E	V	E	K	T	P								

	240	cov	pid	161
1	6MX6_A	100.0%	100.0%	DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
2	NP_000137.2	77.1%	99.4%	DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
3	AAP36762.1	77.5%	99.2%	DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
4	2FG4_A	76.7%	99.4%	DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
5	CAG11873.1	91.2%	74.7%	DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
6	CAE32996.1	77.1%	98.9%	DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
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8	AK170338.1	77.1%	98.9%	DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
9	AK170336.1	77.1%	98.9%	DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
10	AIC54405.1	77.1%	98.9%	DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
	consensus/100%			DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
	consensus/90%			DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
	consensus/80%			DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH
	consensus/70%			DANKAAMALEKKI NQALLDHALCSARIDPH CDFL EHTFDEEV KKKMDH TNHR GGPEAGLC EYFER TIRH

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cov      pid 241      : ] 261

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DGGSGGSGGSGGASGG

2	NP_000137.2	77.1%	99.4%	D -----
3	AAP36762.1	77.5%	89.2%	D -----L
4	2FG4_A	76.7%	99.4%	D -----
5	CAE11873.1	91.2%	74.7%	D -----
6	CAG32996.1	77.1%	98.9%	D -----
7	AAA35831.1	77.1%	98.9%	D -----
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9	AKI70336.1	77.1%	98.9%	D -----
10	AIC54405.1	77.1%	98.9%	D -----
	consensus/100%			D
	consensus/90%			D
	consensus/80%			D
	consensus/70%			D

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