

File Edit View Find Analysis Help

Name 1: Name 2: Name 3:
Sort Sequences By: Sort Order: Font Size:

User assigned number: num 100
Residue index: res 221
Alignment column index: aln 386
seq 9 of 14



Name panels

NT3_MOUSE	2	
NT3_RAT	2	
NT3_HUMAN	2	TRKC
NT3_FELCA	2	
NT3_CHICK	2	
NT3_XENLA	2	
Q9N2F0_9PRIM	1	
NGF_PANTR	1	
<input checked="" type="checkbox"/> NGF_HUMAN	1	TRKA NGFR
sec.struct.graphics		
Q9N2E9_PONPY	1	
NGF_BOVIN	1	
NGF_MOUSE	1	
NGF_XENLA	1	
Q9XY95_LAMFL	-1	

V	K	N	G	C	R	G	I	D	D	K	-	H	W	N	S	Q	C	K	T	S	Q	T	Y	V	R	A	L	T	S	E	N	N	K	L	V	G	W	R	W	I	R	I	D	T	S	C	V	C	A	L	S	R	K	I	G	R	T	-
V	K	N	G	C	R	G	I	D	D	K	-	H	W	N	S	Q	C	K	T	S	Q	T	Y	V	R	A	L	T	S	E	N	N	K	L	V	G	W	R	W	I	R	I	D	T	S	C	V	C	A	L	S	R	K	I	G	R	T	-
V	K	N	G	C	R	G	I	D	D	K	-	H	W	N	S	Q	C	K	T	S	Q	T	Y	V	R	A	L	T	S	E	N	N	K	L	V	G	W	R	W	I	R	I	D	T	S	C	V	C	A	L	S	R	K	I	G	R	T	-
V	K	N	G	C	R	G	I	D	D	K	-	H	W	N	S	Q	C	K	T	S	Q	T	Y	V	R	A	L	T	S	E	N	N	K	L	V	G	W	R	W	I	R	I	D	T	S	C	V	C	A	L	S	R	K	I	G	R	T	-
V	K	N	G	C	R	G	I	D	D	K	-	H	W	N	S	Q	C	K	T	S	Q	T	Y	V	R	A	L	T	S	E	N	N	K	M	V	G	W	R	W	I	R	I	D	T	S	C	V	C	A	L	S	R	K	I	G	R	S	-
V	D	S	G	C	R	G	I	D	S	K	-	H	W	N	S	Y	C	T	T	H	T	F	V	K	A	L	T	M	D	G	K	Q	-	A	A	W	R	F	I	R	I	D	T	A	C	V	C	V	L	S	R	K	A	V	R	R	A	-
V	D	S	G	C	R	G	I	D	S	K	-	H	W	N	S	Y	C	T	T	H	T	F	V	K	A	L	T	M	D	G	K	Q	-	A	A	W	R	F	I	R	I	D	T	A	C	V	C	V	L	S	R	K	A	V	R	R	A	-
V	D	S	G	C	R	G	I	D	S	K	-	H	W	N	S	Y	C	T	T	H	T	F	V	K	A	L	T	M	D	G	K	Q	-	A	A	W	R	F	I	R	I	D	T	A	C	V	C	V	L	S	R	K	A	V	R	R	A	-
V	D	S	G	C	R	G	I	D	S	K	-	H	W	N	S	Y	C	T	T	H	T	F	V	K	A	L	T	M	D	G	K	Q	-	A	A	W	R	F	I	R	I	D	T	A	C	V	C	V	L	S	R	K	A	V	R	R	A	-
V	S	S	G	C	R	G	I	D	A	K	-	H	W	N	S	Y	C	T	T	H	T	F	V	K	A	L	T	M	E	G	K	Q	-	A	A	W	R	F	I	R	I	D	T	A	C	V	C	V	L	S	R	K	-	G	R	T	-	
T	G	S	A	C	R	G	A	D	E	L	-	R	W	R	S	Q	C	K	T	T	Q	S	F	V	R	A	L	T	E	D	A	R	G	R	L	A	W	R	W	I	R	L	D	T	A	C	V	C	T	L	T	R	R	Y	G	G	A	-

Column selection panel

Column filter and column sort box

Double click residue annotation

Double click sequence annotations

VNE blosum62



Conservation score

Consensus sequence