aligned.fasta

File Edit Structure Headers Numberings Tree Info Preferences

	1	11	21	31	41	51	61	71
Consensus	mvLSaaDKtn	vkaaWsKigg	HageyGAEAL	ERMFlgyPtT	KTYFPHF-Dl	sHGSaQiKaH	GKKVvdALtl	AVgHiDDlpg
Conservation	▁▃▅▅▃▂▅▅▃▁	▃▃▅▅▅▅▅▅▃▃	▅▃▃▃▂▅▅▅▅▅	▅▅▅▅▃▃▂▅▅▅	▅▅▅▅▅▅▅ ▃▅	▂▅▅▅▃▅▃▅▃▅	▅▅▅▅▃▃▅▅▃▅	▅▃▅▅▃▅▅▃▂▂
1pbx_A	SLSDKDKAA	VRALWSKIGK	SADAIGNGAL	SRMIVVYQWT	KTYFSHWTDV	THGSHIKAH	GKKVMGGIAL	AVSKIDDLKT
HBAD_ALDGI	-MLTEDDKQL	IQHVWETVLE	HQEDFGAEAL	ERMFTVYPST	KTYFPHF-DL	HHGSEQIRHH	GKKVVGALGD	AVRHIDDLSA
HBA_MELGA	MVLSAADKNN	VKGIFTKIAG	HAEEYGAETL	ERMFITYPST	KTYFPHF-DL	SHGSAQIKGH	GKKVVAALIE	AANHIDDIAG
HBA_RABIT	MVLSPADKTN	IKTAWEKIGS	HGGEYGAEAV	ERMFLGFPTT	KTYFPHF-DF	THGSEQIKAH	GKKVSEALTK	AVGHLDDLPG
P69905	MVLSPADKTN	VKAAWGKVGA	HAGEYGAEAL	ERMFLSFPTT	KTYFPHF-DL	SHGSAQVKGH	GKKVADALTN	AVAHVDDMPN
HBA_HORSE	MVLSAADKTN	VKAAWSKVGG	HAGEYGAEAL	ERMFLGFPTT	KTYFPHF-DL	SHGSAQVKAH	GKKVGDALTL	AVGHLDDLPG

	111	121	131	141
Consensus	laaHlPaefT	PaVHaSLDKF	LaaVstVLts	KYR
Conservation	▅▃▃▅▃▅▃▃▃▅	▅▃▅▅▃▅▅▅▅▅	▅▃▃▅▃▃▅▅▃▃	▅▅▅
1pbx_A	ISTMFGKGFT	QEANVLDKF	LSCVALALAE	RYR
HBAD_ALDGI	LGAHLGREYT	PQVQVAYDKF	LAAVSAVLAE	KYR
HBA_MELGA	VAIHHPAALT	PEVHASLDKF	LCAVGTVLTA	KYR
HBA_RABIT	LANHHPSEFT	PAVHASLDKF	LANVSTVLTS	KYR
P69905	LAAHLPAEFT	PAVHASLDKF	LASVSTVLTS	KYR
HBA_HORSE	LAVHLPNDFT	PAVHASLDKF	LSSVSTVLTS	KYR

UCSF Chimera

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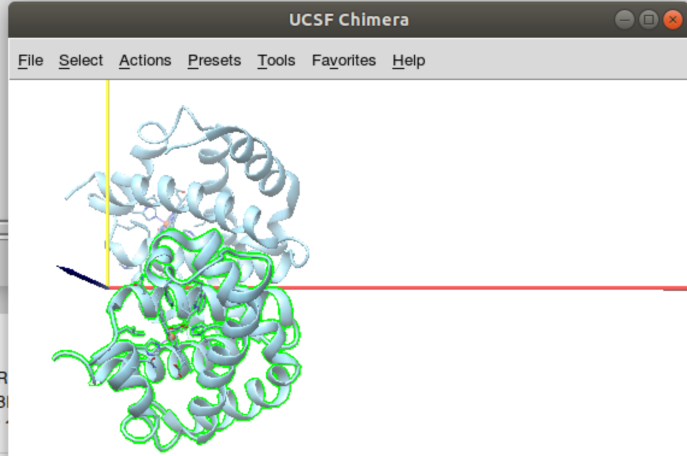
- ⓟ xmipp3 - extract unit cell
- ⓟ chimera - rigid fit
- ⓟ scipion - model from template
- ⓟ powerfit - powerfit
- ⓟ ccp4 - coot refinement
- ⓟ ccp4 - refmac
- ⓟ phenix - emringer

Summary | Methods | Output Log

▽ Input
  ▽ inputSequencesToAlign
    001 (from scipion - import sequence HOR...
    002 (from scipion - import sequence RABI...
    003 (from scipion - import sequence MEL...
SUMMARY