

```

/AF-P02239-F1-model_v4 46 51 56 61 66 71 76 81 86 # No: Chain Z rmsd lali nres %id PDB Description
ANIPKNTHRFFTLVLEIAPGAKDLFSFLKGSSEVPQNNPDLQAHAGKVFKLTYEAAIQLQVNGAVASDNLKLG 21: t001-A 32.0 0.0 154 154 100 MOLECULE: LEGHEMOGLOBIN-1;
DEVGGEALGRLLVYPWTQRFFESFGDLSTPDVGMGNPKVKAHGKKVLGAFSDGLAHLNLTGTFATLSELGDK 2: 1ird-B 14.1 2.5 138 146 12 MOLECULE: HEMOGLOBIN ALPHA CHAIN;

```

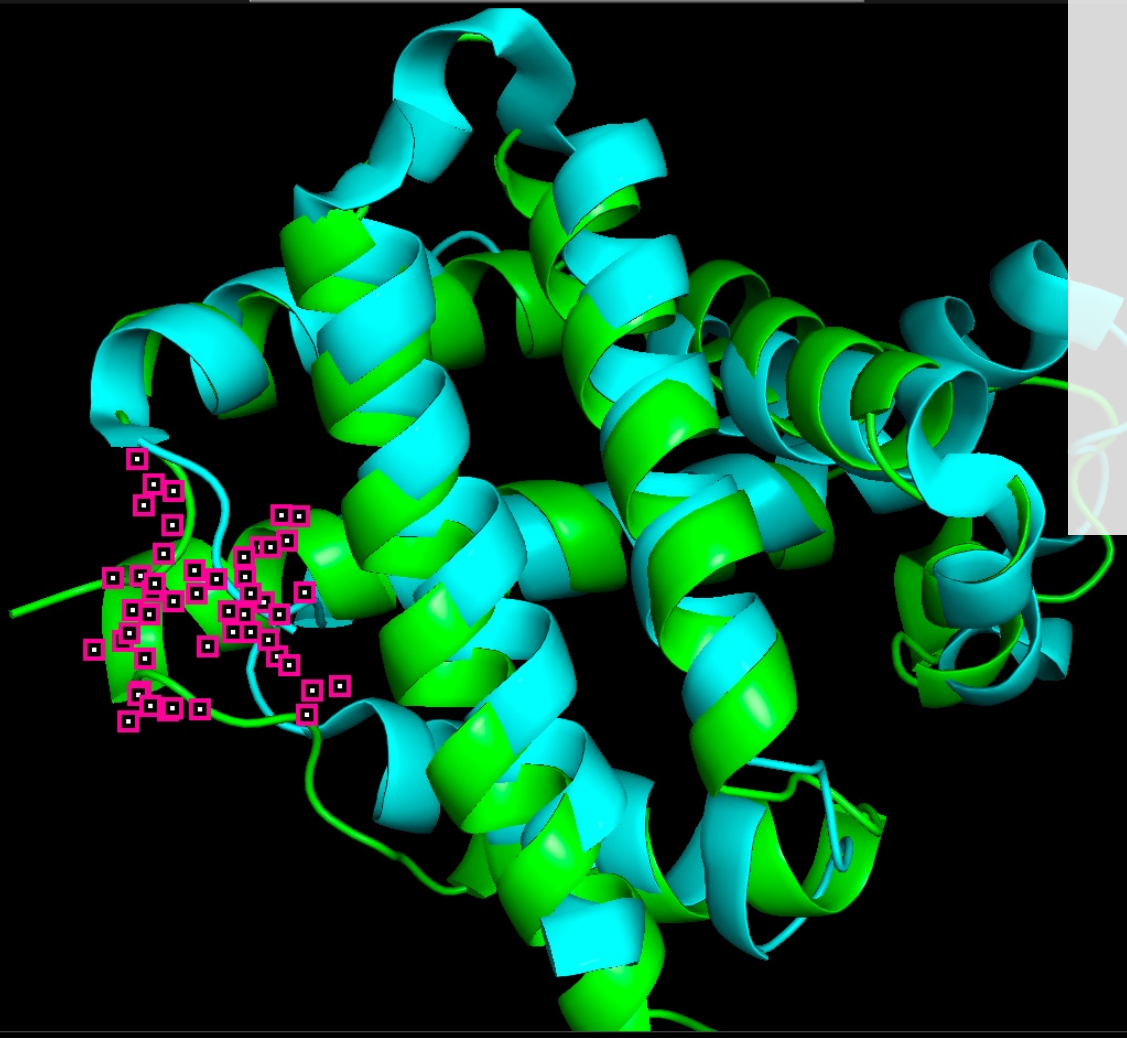
```

No 2: Query=s001A Sbjct=1irdB Z-score=14.1
Query mgVLTDVQVALVKSSFEEFnaNIPKNTHRFFTLVLEIAPGAKDLFSFLKGSS----EVPQ 56
ident || | | | | | | | |
Sbjct -vHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVVYPWTQRFFESFGDLStpdaVMGN 57

Query NN-PDLQAHAGKVFKLTYEAAIqlqvnGAVASdatLKSLGSVHV-SKGVVDAHFPVVKEA 114
ident | | | | |
Sbjct PKvKAHGKKVLGAFSDGLAHL-----DNLKG--tFATLSELHCdKLHVDPENFRLLGNV 109

Query ILKTIKEVVGDKWSEELNTAWTIAYDELAIIKKEMKdaa 154
ident | | |
Sbjct LVCVLAHHFGKEFTPPVQAAYQKVVGAGVANALAHKYH--- 146

```



```
# Identity:      22/83 (26.5%)
# Similarity:   31/83 (37.3%)
# Gaps:         20/83 (24.1%)
# Score: 54.5
```

```
#
#
#=====
```

CAA68462.1	58	NPDQLQAHAGKV-----FKLTYEAAIQLQVNGAVASDATLKSL	94
		.: .. . :..... :.....:	
AAA35597.1	58	NPKVKAHGKKVLGAFSDGLAHLDNLKGTATLSELHCDKLHVDPENFRLL	107

CAA68462.1	95	GSVHVS	KGVD	AHF----	PV	KEA	ILK	TIK	GV	122
		: .	:..		:.		
AAA35597.1	108	GNVXVC--	VLAH	HFGKE	FTPP	VXAA	YOK	VVAG	V	138

NW Score		Identities	Positives	Gaps	
-8		27/158(17%)	55/158(34%)	15/158(9%)	
Query	1	MGVLTDVQVALVKSSFEEFNANIPKNTHRFFTLVLEIAPGAKDLFSFLKGSSEVP---QN			57
		M T V+ + V + + + N+ + +L + P + F G P			
Sbjct	1	MVHXTPEKSAVTALWGK--VNVDEXGGEALGXLLVYPWTQR-FXXSFGDLXTPXAVMG			57
Query	58	NPDLQAHAGKVFKLTYEAAIQLQVNGAVASDATLKSLSVHVSKEGVDA-HFPVVKEAIL			116
		NP ++AH KV + L T +L +H K VD +F ++ +			
Sbjct	58	NPKVKAHGKKVLGAFSDGLAHLN-----NLKGTATLSELHCDKLHVDPENFRLLGNVXV			112
Query	117	KTIKGVVGDKWSEELNTAWTIAYDELAIIKKEMKDAA			154
		+ G +++ + A+ +A + +			
Sbjct	113	CVLAHHFGKEFTPPVXAAYQKVVAGVANALAHKYH---			147

#	No:	Chain	Z	rmsd	lali	nres	%id	PDB	Description
1:	t001-A	32.0	0.0	154	154	100		MOLECULE: LEGHEMOGLOBIN-1;	
2:	1ird-B	14.1	2.5	138	146	12		MOLECULE: HEMOGLOBIN ALPHA CHAIN;	

No 2: Query=s001A Sbjct=1irdB Z-score=14.1

```

Query  mgVLTDVQVALVKSSFEEFNaNIPKNTHRFFTLVLEIAPGAKDLFSFLKGSS----EVPQ    56
ident  ||      |      |      |      |      |      |      |
Sbjct  -vHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVYPWTQRRFFESFGDLStpdaVMGN    57

```

Query NN-PDLQAHAGKVFKLTYEAA**iqqlqvn**GAVASdatLKSLSGVSHV-SKGVVDAHFPPVKEA 114
ident | | | | |
Sbjct PKvKAHGKKVLGAFSDGLAHL-----DNLKG--tFATLSELHCdKLHVDPENFRLLGNV 109

Query	ILKTIKEVVGDKWSEELNTAWTIAAYDELAIIIKKEMKdaa	154
ident		
Sbjct	LVCVLAHHFGKEFTPPVOAAYOKVVAGVANALAHKYH---	146

```

/AF-P02239-F1-model_v4 46 51 56 61 66 71 76 81 86 91 96
ANIPKNTRHFFTLVLEIAPGAKDLFSFLKGSSEVPQNNPDLQAHAGKVFKLTYEAAFDLVNIGAVASDATLKSLSGVHV
/vbird-mov 246 251 256 261 266 271 276 281 286 291 296
DEVGGEALGRLLVYVPYPTQRFESFGDLPSTPDAMVGNPKVKAHGKKVLGAFSDGLAHLNLDKGTFTLSELHCDKILHVD

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