

ΑΣΚΗΣΗ ΒΙΟΠΛΗΡΟΦΟΡΙΚΗΣ

ΑΘΑΝΑΣΟΥΛΗΣ ΑΛΕΞΑΝΔΡΟΣ ΑΕΜ:8407

2HB protein

Subunit one:

>sp|P69905|HBA_HUMAN Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2

MVLSPADKTNVKAAWGKVGAAHAGEYGAELERMFLSFPTTKTYFPHFDLSHGSAQVKGHG
KKVADALTNVAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTP
AVHASLSDKFLASVSTVLTSKYR

Number of amino acids: 142

Molecular weight: 15257.5

Theoretical pI: 8.72

Amino acid composition:

Ala (A)	21	14.8%
Arg (R)	3	2.1%
Asn (N)	4	2.8%
Asp (D)	8	5.6%
Cys (C)	1	0.7%
Gln (Q)	1	0.7%
Glu (E)	4	2.8%
Gly (G)	7	4.9%
His (H)	10	7.0%
Ile (I)	0	0.0%
Leu (L)	18	12.7%
Lys (K)	11	7.7%
Met (M)	3	2.1%
Phe (F)	7	4.9%
Pro (P)	7	4.9%
Ser (S)	11	7.7%
Thr (T)	9	6.3%
Trp (W)	1	0.7%
Tyr (Y)	3	2.1%
Val (V)	13	9.2%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Total number of negatively charged residues (Asp + Glu): 12
Total number of positively charged residues (Arg + Lys): 14

Atomic composition:

Carbon	C	690
Hydrogen	H	1080
Nitrogen	N	188
Oxygen	O	195
Sulfur	S	4

Formula: C₆₉₀H₁₀₈₀N₁₈₈O₁₉₅S₄

Total number of atoms: 2157

Extinction coefficients:

Extinction coefficients are in units of M⁻¹ cm⁻¹, at 280 nm measured in water.

Ext. coefficient 9970
Abs 0.1% (=1 g/l) 0.653, assuming all pairs of Cys residues form cystines

Ext. coefficient 9970
Abs 0.1% (=1 g/l) 0.653, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is M (Met).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).
 >20 hours (yeast, in vivo).
 >10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 6.97
This classifies the protein as stable.

Aliphatic index: 90.77

Grand average of hydropathicity (GRAVY): 0.048

HSP Results

Warning: Original output has been filtered to yield non-redundant similarities

blastp 2.2.26 [Sep-21-2011]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,

Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
_quot;Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs_quot;, Nucleic Acids Res. 25:3389-3402.

Query: unkown
(142 letters)

Database: prodom2010.1 multiple alignments
45,292,438 sequences; 2,147,483,647 total letters

ProDom domains producing High-scoring Segment Pairs:

Position	ProDom domain	Score	E value
1-40	#PD820594	212	3e-20
3-38	#PD859957	191	4e-17
6-71	#PDA8N7E0	97	0.001
6-76	#PD559047	97	0.001
34-90	#PDA1I509	189	1e-16
41-67	#PDA9Z7D9	140	7e-10
43-68	#PDA9Z7D5	136	3e-09
68-88	#PDB0N2Z0	99	0.0004
70-100	#PD748724	155	5e-12
89-111	#PD000377	115	2e-06
92-141	#PD688662	194	2e-17
102-141	#PD000054	193	2e-17
113-141	#PDA1F6T7	141	5e-10
114-141	#PDC64954	135	4e-09

>[PD820594](#) (Closest domain: HBA_HUMAN 1-40)

Number of domains in family: 643

Commentary (automatic):

FULL=HEMOGLOBIN HEME IRON METAL-BINDING OXYGEN ALTNAME: SUBUNIT SUBNAME:
ALPHA CHAIN

Length = 40

Score = 212 (86.3 bits), Expect = 3e-20

Identities = 40/40 (100%), Positives = 40/40 (100%)

```
Query:      1 MVLSPADKTNVKAAWGKVGHAHAGEYGAELERMFLSFPTT 40
             MVLSPADKTNVKAAWGKVGHAHAGEYGAELERMFLSFPTT
Sbjct:      1 MVLSPADKTNVKAAWGKVGHAHAGEYGAELERMFLSFPTT 40
```

>[PD688662](#) (Closest domain: HBPI_CHICK 91-141)

Number of domains in family: 19

Commentary (automatic):

HEME OXYGEN FULL=HEMOGLOBIN ALTNAME: METAL-BINDING IRON RECNAME: SUBNAME:
SEQUENCING DIRECT

Length = 51

Score = 194 (79.3 bits), Expect = 2e-17

Identities = 35/50 (70%), Positives = 44/50 (88%)

Query: 92 LRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKY 141
LRVDPVNFKLLSHC+L ++AA P++FTP VHA+ DKFL+S+S+VLT KY
Sbjct: 92 LRVDPVNFKLLSHCILCSVAARYPSDFTPEVHAAWDKFLSSISSVLTEKY 141

>[PD000054](#) (Closest domain: G3V1N2_HUMAN 70-109)

Number of domains in family: 776

Commentary (automatic):

FULL=HEMOGLOBIN ALTNAME: HEME IRON METAL-BINDING OXYGEN BETA SUBUNIT CHAIN
SUBNAME:

Length = 40

Score = 193 (79.0 bits), Expect = 2e-17

Identities = 40/40 (100%), Positives = 40/40 (100%)

Query: 102 LSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKY 141
LSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKY
Sbjct: 70 LSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKY 109

>[PD859957](#) (Closest domain: HBA_PANTR 3-38)

Number of domains in family: 1137

Commentary (automatic):

FULL=HEMOGLOBIN HEME IRON METAL-BINDING OXYGEN ALTNAME: SUBUNIT SUBNAME: BETA
CHAIN

Length = 36

Score = 191 (78.2 bits), Expect = 4e-17

Identities = 36/36 (100%), Positives = 36/36 (100%)

Query: 3 LSPADKTNVKAAWGKVGAGHAGEYGAEALERMFLSFP 38
LSPADKTNVKAAWGKVGAGHAGEYGAEALERMFLSFP
Sbjct: 3 LSPADKTNVKAAWGKVGAGHAGEYGAEALERMFLSFP 38

>[PDA1I509](#) (Closest domain: HBPI_CHICK 34-90)

Number of domains in family: 66

Commentary (automatic):

HEME OXYGEN SUBNAME: METAL-BINDING IRON RECNAME: ALTNAME: FULL=CYTOGLOBIN
FULL=HEMOGLOBIN REFERENCE

Length = 57

Score = 189 (77.4 bits), Expect = 1e-16

Identities = 33/57 (57%), Positives = 45/57 (78%)

Query: 34 FLSFPTTKTYFPFDLSHGSAQVKGHGKQVADALTNVAHVDDMPNALSALSDLHAH 90
F S+P TKTYFPFD+S GS Q++GHG KV +A+ AV ++DD+ AL+ LS+LHA+
Sbjct: 34 FASYPQTKTYFPFDVDSQGSVQLRGHGSKVLNAIGEAVKNIDDIRGALAKLSELHAY 90

>[PD748724](#) (Closest domain: HBA_PANTR 70-100)
Number of domains in family: 1213
Commentary (automatic):
FULL=HEMOGLOBIN ALTNAME: HEME IRON METAL-BINDING OXYGEN SUBUNIT SUBNAME:
CHAIN BETA
Length = 31
Score = 155 (64.3 bits), Expect = 5e-12
Identities = 31/31 (100%), Positives = 31/31 (100%)

Query: 70 AVAHVDDMPNALSALSDDLHAKLRVDPVNFK 100
AVAHVDDMPNALSALSDDLHAKLRVDPVNFK
Sbjct: 70 AVAHVDDMPNALSALSDDLHAKLRVDPVNFK 100

>[PDA1F6T7](#) (Closest domain: HBA_PANPA 113-141)
Number of domains in family: 714
Commentary (automatic):
FULL=HEMOGLOBIN HEME IRON METAL-BINDING OXYGEN ALTNAME: SUBUNIT SUBNAME:
ALPHA CHAIN
Length = 29
Score = 141 (58.9 bits), Expect = 5e-10
Identities = 29/29 (100%), Positives = 29/29 (100%)

Query: 113 HLPAEFTPAVHASLKDFLASVSTVLTSKY 141
HLPAEFTPAVHASLKDFLASVSTVLTSKY
Sbjct: 113 HLPAEFTPAVHASLKDFLASVSTVLTSKY 141

>[PDA9Z7D9](#) (Closest domain: HBA_MACSP 40-66)
Number of domains in family: 713
Commentary (automatic):
FULL=HEMOGLOBIN HEME IRON METAL-BINDING OXYGEN SUBNAME: SUBUNIT ALTNAME:
ALPHA CHAIN
Length = 27
Score = 140 (58.5 bits), Expect = 7e-10
Identities = 27/27 (100%), Positives = 27/27 (100%)

Query: 41 KTYFPHFDLSHGSAQVKGHGKKVADAL 67
KTYFPHFDLSHGSAQVKGHGKKVADAL
Sbjct: 40 KTYFPHFDLSHGSAQVKGHGKKVADAL 66

>[PDA9Z7D5](#) (Closest domain: HBA_PANTR 43-68)
Number of domains in family: 931
Commentary (automatic):

FULL=HEMOGLOBIN ALTNAME: HEME IRON METAL-BINDING OXYGEN SUBUNIT BETA CHAIN
SUBNAME:

Length = 26

Score = 136 (57.0 bits), Expect = 3e-09

Identities = 26/26 (100%), Positives = 26/26 (100%)

Query: 43 YFPHFDSLHGSAQVKGHGKKVADALT 68
YFPHFDSLHGSAQVKGHGKKVADALT
Sbjct: 43 YFPHFDSLHGSAQVKGHGKKVADALT 68

>[PDC64954](#) (Closest domain: G7Q017_MACFA 114-141)

Number of domains in family: 191

Commentary (automatic):

FULL=HEMOGLOBIN METAL-BINDING IRON HEME OXYGEN SUBNAME: ALTNAME: SUBUNIT
ALPHA CHAIN

Length = 28

Score = 135 (56.6 bits), Expect = 4e-09

Identities = 28/28 (100%), Positives = 28/28 (100%)

Query: 114 LPAEFTPAVHASLDKFLASVSTVLTSKY 141
LPAEFTPAVHASLDKFLASVSTVLTSKY
Sbjct: 114 LPAEFTPAVHASLDKFLASVSTVLTSKY 141

>[PDC00377](#) (Closest domain: HBA_ERIEU 88-110)

Number of domains in family: 544

Commentary (automatic):

FULL=HEMOGLOBIN IRON HEME METAL-BINDING OXYGEN SUBNAME: SUBUNIT ALPHA
ALTNAME: CHAIN

Length = 23

Score = 115 (48.9 bits), Expect = 2e-06

Identities = 23/23 (100%), Positives = 23/23 (100%), Gaps = 1/23 (4%)

Query: 89 AHKLRVDPVNFKLLSHCLLVTLA 111
AHKLRVDPVNFKLLSHCLLVTLA
Sbjct: 88 AHKLRVDPVNFKLLSHCLLVTLA 110

>[PDB0N2Z0](#) (Closest domain: HBA_CEBCA 67-87)

Number of domains in family: 90

Commentary (automatic):

FULL=HEMOGLOBIN ALTNAME: METAL-BINDING IRON HEME OXYGEN SUBUNIT ALPHA CHAIN
RECNAME:

Length = 21

Score = 99 (42.7 bits), Expect = 0.0004

Identities = 20/21 (95%), Positives = 21/21 (100%), Gaps = 1/21 (4%)

Query: 68 TNAVAHVDDMPNALSALSDLH 88
+NAVAHVDDMPNALSALSDLH
Sbjct: 67 SNAVAHVDDMPNALSALSDLH 87

>[PDA8N7E0](#) (Closest domain: E3TEM7 ICTPU 2-78)

Number of domains in family: 172

Commentary (automatic):

HEME OXYGEN METAL-BINDING IRON MUSCLE FULL=MYOGLOBIN RECNAME: SEQUENCING
DIRECT SUBNAME:

Length = 77

Score = 97 (42.0 bits), Expect = 0.001

Identities = 25/71 (35%), Positives = 36/71 (50%), Gaps = 5/71 (7%)

Query: 6 ADKTNVKAAWGKVGAGHAGEYGAERALERMFLSFPTTKTYFPHFDL-----SHGSAQVKGHG
60
+D V +WG V A+ G E L R+F+ P T+ +FP FD + G+ VK HG
Sbjct: 2 SDFDTVLTSWGSVEANYAAIGGEVLGRLEFVEHPETQKHFPKFDGISAADAAGNPAVKAHG
61

Query: 61 KKVADALTNV 71
+ V L + V
Sbjct: 62 ETVLKKLGLDV 72

>[PD559047](#) (Closest domain: GLB2A_SCAIN 14-91)

Number of domains in family: 65

Commentary (automatic):

HEME OXYGEN ALTNAME: SUBNAME: IRON METAL-BINDING RECNAME: SEQUENCING DIRECT
FULL=GLOBIN

Length = 78

Score = 97 (42.0 bits), Expect = 0.001

Identities = 25/74 (33%), Positives = 37/74 (50%), Gaps = 3/74 (4%)

Query: 6 ADKTNVKAAWGKVGAGHAGEYGAERALERMFLSFPTTKTYFPHF-DLSHGSA--QVKGHGKK
62
A K N++ +WG + A G + +F P TKTYF D+ G A +++GH
Sbjct: 14 AIKANLRRSWGVLSDIEATGLMLMSNLFTLRPDTKTYFTRLGDVQKKGKANSKLRGHAIT
73

Query: 63 VADALTNVAHVDD 76
+ AL N V +DD
Sbjct: 74 LTYALNNFVDSLDD 87

Subunit two:

>sp|P68873|HBB_PANTR Hemoglobin subunit beta OS=Pan troglodytes GN=HBB PE=1 SV=2

MVHLTPEEKSAVTALWGKVNVDVEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK
VKAHGKKVLGAFSDGLAHLDDLKGTFTATLSSELHCDKLHVDPENFRLLGNVLCVLAHFFG
KEFTPPVQAAYQKVVAGVANALAHKYH

Number of amino acids: 147

Molecular weight: 15998.4

Theoretical pI: 6.74

Amino acid composition:

Ala (A)	15	10.2%
Arg (R)	3	2.0%
Asn (N)	6	4.1%
Asp (D)	7	4.8%
Cys (C)	2	1.4%
Gln (Q)	3	2.0%
Glu (E)	8	5.4%
Gly (G)	13	8.8%
His (H)	9	6.1%
Ile (I)	0	0.0%
Leu (L)	18	12.2%
Lys (K)	11	7.5%
Met (M)	2	1.4%
Phe (F)	8	5.4%
Pro (P)	7	4.8%
Ser (S)	5	3.4%
Thr (T)	7	4.8%
Trp (W)	2	1.4%
Tyr (Y)	3	2.0%
Val (V)	18	12.2%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Total number of negatively charged residues (Asp + Glu): 15

Total number of positively charged residues (Arg + Lys): 14

Atomic composition:

Carbon	C	729
Hydrogen	H	1128
Nitrogen	N	196
Oxygen	O	202
Sulfur	S	4

Formula: C₇₂₉H₁₁₂₈N₁₉₆O₂₀₂S₄

Total number of atoms: 2259

Extinction coefficients:

Extinction coefficients are in units of $M^{-1} \text{ cm}^{-1}$, at 280 nm measured in water.

Ext. coefficient 15595
Abs 0.1% (=1 g/l) 0.975, assuming all pairs of Cys residues form cystines

Ext. coefficient 15470
Abs 0.1% (=1 g/l) 0.967, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is M (Met).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).
 >20 hours (yeast, in vivo).
 >10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 6.16
This classifies the protein as stable.

Aliphatic index: 93.47

Grand average of hydropathicity (GRAVY): 0.014

HSP Results

Warning: Original output has been filtered to yield non-redundant similarities

blastp 2.2.26 [Sep-21-2011]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
_quot;Gapped BLAST and PSI-BLAST: a new generation of protein database search programs_quot;; Nucleic Acids Res. 25:3389-3402.

Query: unkwown
 (147 letters)

Database: prodom2010.1 multiple alignments
 45,292,438 sequences; 2,147,483,647 total letters

ProDom domains producing High-scoring Segment Pairs:

Position	ProDom domain	Score	E value
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1-18	#PDD359J6	90	0.008
1-38	#PD859957	196	7e-18
4-39	#PD820594	101	0.0002
12-74	#PDA8N7E0	133	1e-08
36-94	#PDA1I509	107	4e-05
40-72	#PDA9Z7D5	172	2e-14
54-78	#PD792899	100	0.002
76-105	#PD748724	158	2e-12
97-146	#PD688662	119	9e-07
107-146	#PD000054	203	7e-19
119-146	#PDC64954	110	1e-05

>[PD000054](#) (Closest domain: HBB_PROLO 106-145)

Number of domains in family: 776

Commentary (automatic):

FULL=HEMOGLOBIN ALTNAME: HEME IRON METAL-BINDING OXYGEN BETA SUBUNIT CHAIN
SUBNAME:

Length = 40

Score = 203 (82.8 bits), Expect = 7e-19

Identities = 40/40 (100%), Positives = 40/40 (100%)

```

Query:      107 LGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKY 146
             LGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKY
Sbjct:      106 LGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKY 145

```

>[PD859957](#) (Closest domain: HBB_PANTR 1-38)

Number of domains in family: 1137

Commentary (automatic):

FULL=HEMOGLOBIN HEME IRON METAL-BINDING OXYGEN ALTNAME: SUBUNIT SUBNAME: BETA
CHAIN

Length = 38

Score = 196 (80.1 bits), Expect = 7e-18

Identities = 38/38 (100%), Positives = 38/38 (100%)

```

Query:      1 MVHLTPEEKSAVTALWGKVVNDEVGGEALGRLLVVYPW 38
             MVHLTPEEKSAVTALWGKVVNDEVGGEALGRLLVVYPW
Sbjct:      1 MVHLTPEEKSAVTALWGKVVNDEVGGEALGRLLVVYPW 38

```

>[PDA9Z7D5](#) (Closest domain: HBB_PANTR 40-72)

Number of domains in family: 931

Commentary (automatic):

FULL=HEMOGLOBIN ALTNAME: HEME IRON METAL-BINDING OXYGEN SUBUNIT BETA CHAIN
SUBNAME:

Length = 33

Score = 172 (70.9 bits), Expect = 2e-14

Identities = 33/33 (100%), Positives = 33/33 (100%), Gaps = 4/33 (12%)

Query: 40 QRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAF 72
QRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAF
Sbjct: 40 QRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAF 72

>[PD748724](#) (Closest domain: D9YZU5_HUMAN 76-105)
Number of domains in family: 1213
Commentary (automatic):
FULL=HEMOGLOBIN ALTNAME: HEME IRON METAL-BINDING OXYGEN SUBUNIT SUBNAME:
CHAIN BETA
Length = 30
Score = 158 (65.5 bits), Expect = 2e-12
Identities = 30/30 (100%), Positives = 30/30 (100%), Gaps = 4/30 (13%)

Query: 76 LAHLDNLKGTFFATLSELHCDKHLHVDPENFR 105
LAHLDNLKGTFFATLSELHCDKHLHVDPENFR
Sbjct: 76 LAHLDNLKGTFFATLSELHCDKHLHVDPENFR 105

>[PDA8N7E0](#) (Closest domain: E3TEM7 ICTPU 2-78)
Number of domains in family: 172
Commentary (automatic):
HEME OXYGEN METAL-BINDING IRON MUSCLE FULL=MYOGLOBIN RECNAME: SEQUENCING
DIRECT SUBNAME:
Length = 77
Score = 133 (55.8 bits), Expect = 1e-08
Identities = 32/65 (49%), Positives = 37/65 (56%), Gaps = 3/65 (4%)

Query: 12 VTALWGKV--NVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVL
69
V WG V N +GGE LGRL V +P TQ+ F F +S DA GNP VKAHG+ VL
Sbjct: 7 VLTSWGSVEANYAAIGGEVLGRLFVEHPETQKHF PKFDGISAADAA-GNPAVKAHGETVL
65

Query: 70 GAFSD 74
D
Sbjct: 66 KKLGD 70

>[PD688662](#) (Closest domain: HBPI_CHICK 91-141)
Number of domains in family: 19
Commentary (automatic):
HEME OXYGEN FULL=HEMOGLOBIN ALTNAME: METAL-BINDING IRON RECNAME: SUBNAME:
SEQUENCING DIRECT
Length = 51
Score = 119 (50.4 bits), Expect = 9e-07
Identities = 20/50 (40%), Positives = 33/50 (66%), Gaps = 3/50 (6%)

Query: 97 LHVDPENFRLLGNVLCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKY 146
L VDP NF+LL + ++C +A + +FTP V AA+ K ++ +++ L KY
Sbjct: 92 LRVDPVNFKLLSHCILCSVAARYPSDFTPEVHAAWDKFLSSISSVLTEKY 141

>[PDC64954](#) (Closest domain: Q03903_MACMU 119-146)

Number of domains in family: 191

Commentary (automatic):

FULL=HEMOGLOBIN METAL-BINDING IRON HEME OXYGEN SUBNAME: ALTNAME: SUBUNIT
ALPHA CHAIN

Length = 28

Score = 110 (47.0 bits), Expect = 1e-05

Identities = 20/28 (71%), Positives = 26/28 (92%), Gaps = 2/28 (7%)

Query: 119 FGKEFTPPVQAAYQKVVAGVANALAHKY 146
FGKEFTP VQA++QK+VAGVA+AL+ +Y
Sbjct: 119 FGKEFTPEVQASWQKMOVAGVASALSSRY 146

>[PDA1I509](#) (Closest domain: HBPI_CHICK 34-90)

Number of domains in family: 66

Commentary (automatic):

HEME OXYGEN SUBNAME: METAL-BINDING IRON RECNAME: ALTNAME: FULL=CYTOGLOBIN
FULL=HEMOGLOBIN REFERENCE

Length = 57

Score = 107 (45.8 bits), Expect = 4e-05

Identities = 21/59 (35%), Positives = 34/59 (57%), Gaps = 6/59 (10%)

Query: 36 YPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLAHLNKGTFATLSELHC 94
YP T+ +F F D G+ +++ HG KVL A + + ++D+++G A LSELH
Sbjct: 37 YPQTKTYFPHF-----DVSQGSVQLRGHGSKVLNAIGEAVKNIDDIRGALAKLSELHA 89

>[PD820594](#) (Closest domain: C0H805_SALSA 93-132)

Number of domains in family: 643

Commentary (automatic):

FULL=HEMOGLOBIN HEME IRON METAL-BINDING OXYGEN ALTNAME: SUBUNIT SUBNAME:
ALPHA CHAIN

Length = 40

Score = 101 (43.5 bits), Expect = 0.0002

Identities = 21/38 (55%), Positives = 24/38 (63%), Gaps = 2/38 (5%)

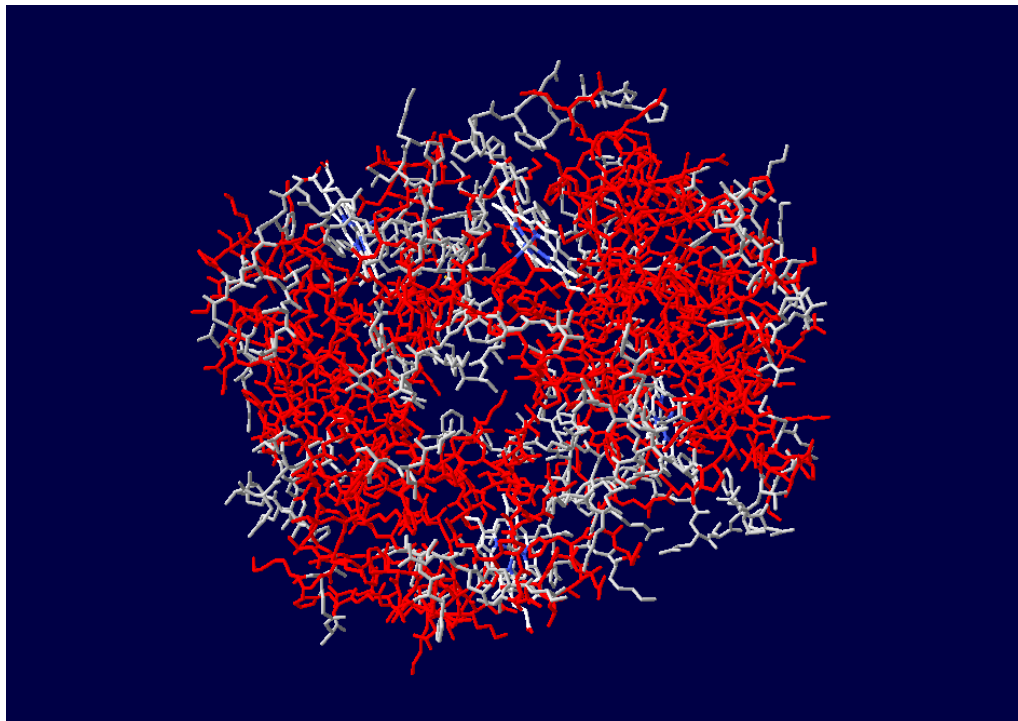
Query: 4 LTPEEKSAVTALWGKVN--VDEVGGEALGRLLVVYPWT 39
LT +KS V A WGK+ D VG EALGR+L YP T
Sbjct: 95 LTARDKSVVNAFWGKIKGKADVVGAEALGRMLTAYPQT 132

>[PD792899](#) (Closest domain: Q86QI8_PLABE 1-159)
Number of domains in family: 1
Commentary (automatic):
HEME OXYGEN SUBNAME: ANTIGEN FULL=31
Length = 159
Score = 100 (43.1 bits), Expect = 0.002
Identities = 19/25 (76%), Positives = 22/25 (88%), Gaps = 2/25 (8%)

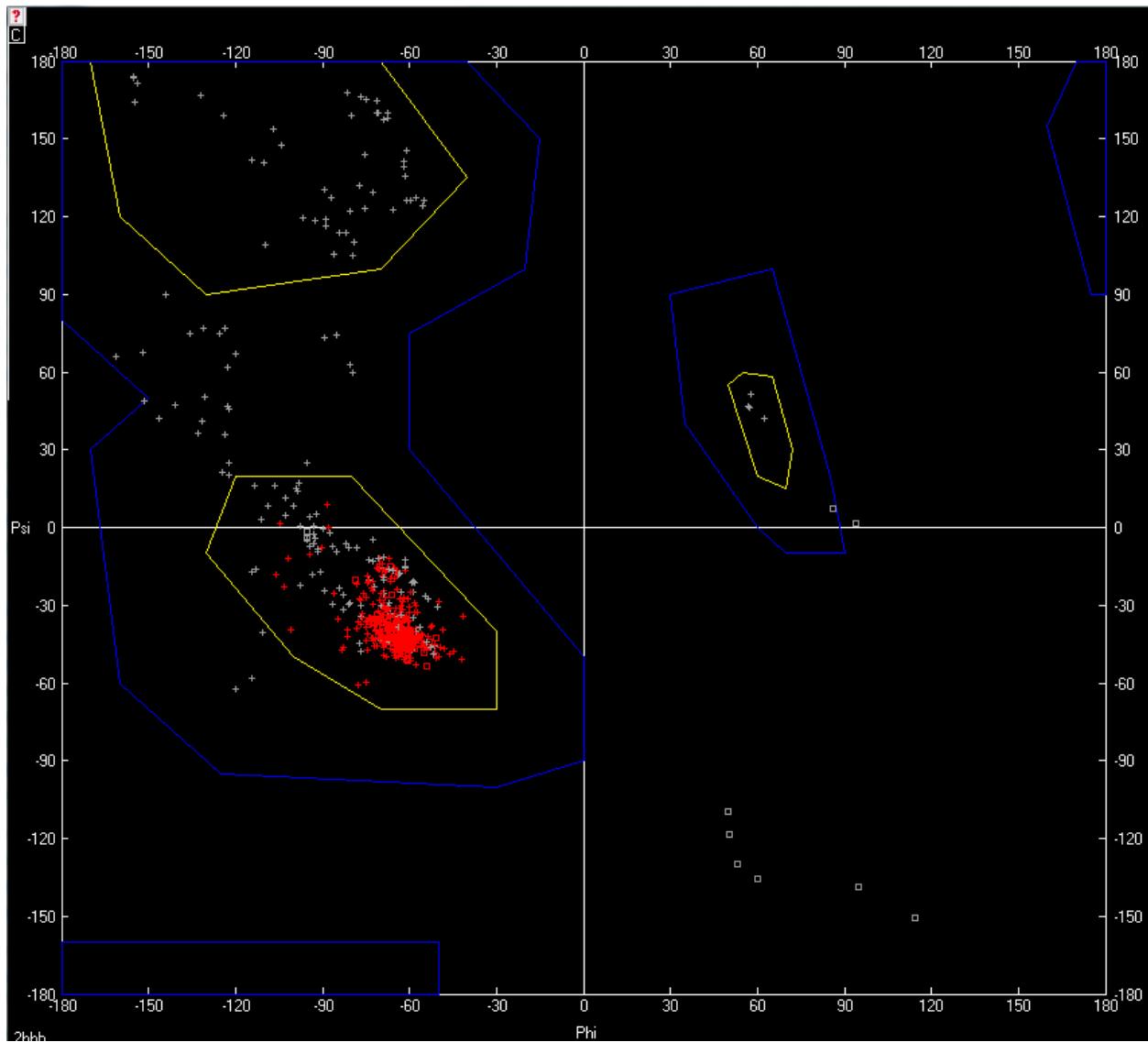
Query: 54 AVMGNPVKVKAHGKKVLGAFSDGLAH 78
A+MGN KVKAHGKKV+ AF+DGL H
Sbjct: 135 AIMGNAKVKAHGKKVITAFNDGLNH 159

>[PDD359J6](#) (Closest domain: Q2XP30_HUMAN 1-22)
Number of domains in family: 1
Commentary (automatic):
BETA-GLOBIN SUBNAME: FULL=MUTANT
Length = 22
Score = 90 (39.3 bits), Expect = 0.008
Identities = 17/18 (94%), Positives = 18/18 (100%), Gaps = 3/18 (16%)

Query: 1 MVHLTPEEKSAVTALWGK 18
MVHLTPEEKSAVTALWG+
Sbjct: 1 MVHLTPEEKSAVTALWQ 18



RAMACHANDRAN PLOT OF 2HHB:



Τα αμινοξέα που δεν επιτρέπεται να κινηθούν λόγω παρεμποδίσεων είναι: CGLY51, AGLY18, CGLY18, BGLY119, DGLY119, BGLY46 και τέλος το DGLY46.