

# Integrins

Cuddapah Sunku Chennakesava

Dianne Cooper

Albena Kantardzhieva

Sebastian Komorowski

Mikhail Paveliev

## Integrins-Function

Receptor proteins that mediate cell-  
extracellular matrix and cell-cell interactions

wound healing

cell differentiation

tumour cell homing

leukocyte recruitment

# Integrins-structure

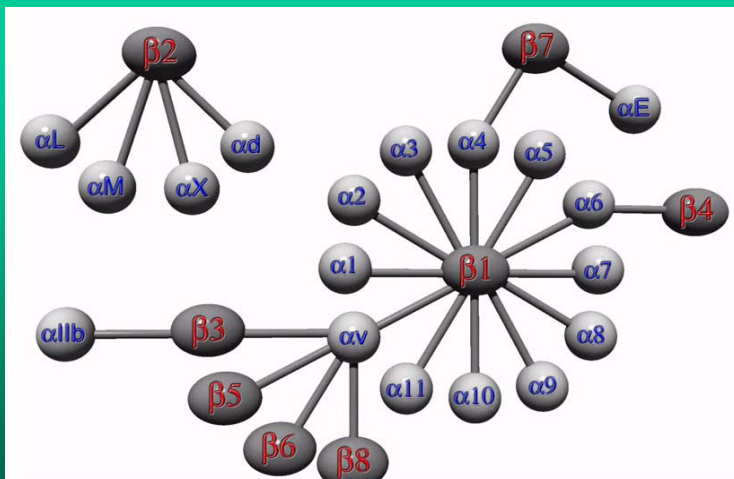
Integrins consist of two non-covalently linked transmembrane glycoprotein subunits

All are heterodimeric and consist of one alpha and one beta subunit

18 alpha subunits identified

8 beta subunits identified

# Integrins-isoforms



# AIMS

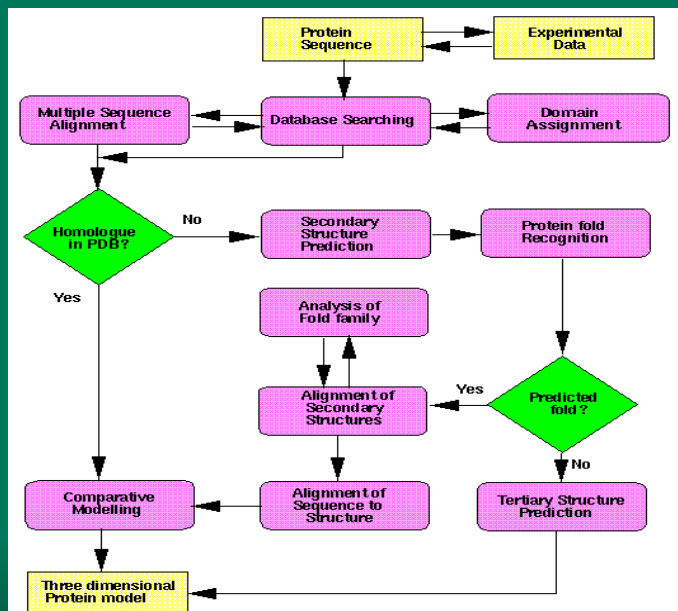
Compare amino acid sequences of alpha and beta integrins

Identify conserved regions

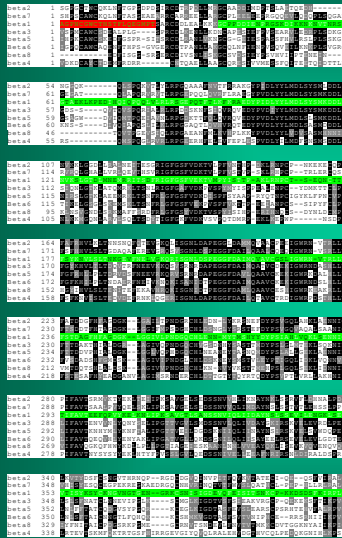
Predict molecular weights, isoelectric points and potential phosphorylation sites

Determine 3D structure

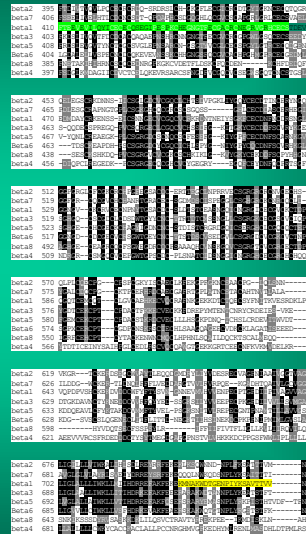
## Flowchart of protein 3D structure analysis



# BOXSHADE 3.21



1-20 signal sequence  
34-464 integrin beta chain



729-751 transmembrane domain

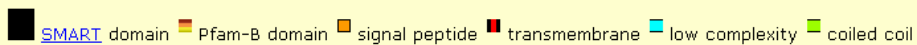
# Pfam 14.0 (Saint Louis)

## Domain structure of proteins in the integrin-beta alignment

Pfam-A domains



Other annotation

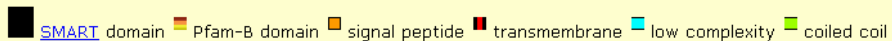


## Domain structure of proteins in the integrin-alpha alignment

Pfam-A domains



Other annotation



## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6

Family members	Score	Expect	Identities	Positives	Gaps
Beta1 vs beta 2	686 bits (1769),	0.0	344/791 (43%)	468/791 (58%)	40/791 (5%)
Beta1 vs beta 3	655 bits (1690),	0.0	332/780 (42%)	462/780 (58%)	28/780 (3%)
Beta1 vs beta4	440 bits (1132),	e-121	265/723 (36%),	383/723 (52%)	62/723 (8%)
Beta1 vs beta5	611 bits (1576),	e-173	323/787 (41%),	452/787 (57%),	33/787 (4%)
Beta1 vs beta6	626 bits (1615),	e-178	315/774 (40%),	440/774 (56%),	26/774 (3%)
Beta1 vs beta7	668 bits (1724),	0.0	332/770 (43%),	470/770 (60%),	31/770 (4%)
Beta1 vs beta8	430 bits (1105),	e-118	230/598 (38%),	333/598 (55%),	35/598 (5%)
<b>AVERAGE</b>			<b>~40%</b>	<b>~55%</b>	<b>~5%</b>

Family members	Score	Expect	Identities	Positives	Gaps
alpha5 vs alpha1	43.9 bits (102)	0.036	35/124 (28%)	51/124 (40%)	17/124 (13%)
alpha5 vs alpha2	142 bits (359)	6e-32	186/785 (23%)	313/785 (39%)	97/785 (12%)
alpha5 vs alpha3	188 bits (478)	9e-46	256/981 (26%),	381/981 (38%)	142/981 (14%)
alpha5 vs alpha4	225 bits (574)	7e-57	225/856 (26%)	364/856 (42%)	95/856 (11%)
alpha5 vs alpha6	217 bits (553)	2e-54	255/993 (25%),	408/993 (40%),	140/993 (14%)
alpha5 vs alpha7	233 bits (595),	2e-59	254/898 (28%),	386/898 (42%),	125/898 (13%)
alpha5 vs alpha8	825 bits (2130),	0.0	427/979 (43%),	601/979 (60%),	28/979 (2%)
alpha5 vs alpha9	229 bits (585),	4e-58	243/931 (26%),	389/931 (41%),	104/931 (11%)
alpha5 vs alpha10	120 bits (300),	4e-25	126/473 (26%),	192/473 (39%),	62/473 (13%)
alpha5 vs alpha11	124 bits (312),	2e-26	144/583 (24%),	226/583 (38%),	104/583 (17%)
alpha5 vs alpha_d	120 bits (302),	2e-25	138/498 (27%),	208/498 (41%),	57/498 (11%)
alpha5 vs alpha_E	115 bits (289),	7e-24	144/557 (25%),	223/557 (39%),	71/557 (12%)
alpha5 vs alpha_L	109 bits (273),	5e-22	153/616 (24%),	248/616 (39%),	96/616 (15%)
alpha5 vs alpha_M	117 bits (293),	3e-24	138/523 (26%),	217/523 (41%),	70/523 (13%)
alpha5 vs alpha_v	808 bits (2086),	0.0	440/1021 (43%),	607/1021 (59%),	32/1021 (3%)
alpha5 vs alpha_x	118 bits (296),	1e-24	179/755 (23%),	179/755 (23%),	110/755 (14%)
alpha5 vs alpha_llb	564 bits (1453),	e-159	359/976 (36%),	507/976 (51%),	58/976 (5%)
<b>AVERAGE</b>			<b>~29%</b>	<b>~42%</b>	<b>~17%</b>

# ExPASy Compute pI/Mw

Integrin	Molecular weight	Isoelectric point
Alpha 1	128	5.82
Alpha 2	129	5.1
Alpha 3	119	6.51
Alpha 4	115	5.91
Alpha 5	115	5.5
Alpha 6	119	6.36
Alpha 7	124	5.59
Alpha 8	117	5.37
Alpha 9	115	5.72
Alpha 10	128	6.21
Alpha 11	134	6.29
Alpha d	127	5.47
Alpha E	130	5.43
Alpha L	119	5.42
Alpha M	127	6.74
Alpha v	116	5.51
Alpha X	129	6.28
Alpha IIb	113	5.21
Beta 1	89	5.27
Beta 2	85	6.57
Beta 3	88	5.04
Beta 4	202	5.79
Beta 5	88	5.62
Beta 6	86	5.27
Beta 7	87	5.63
Beta 8	86	6.96

# MotifScan

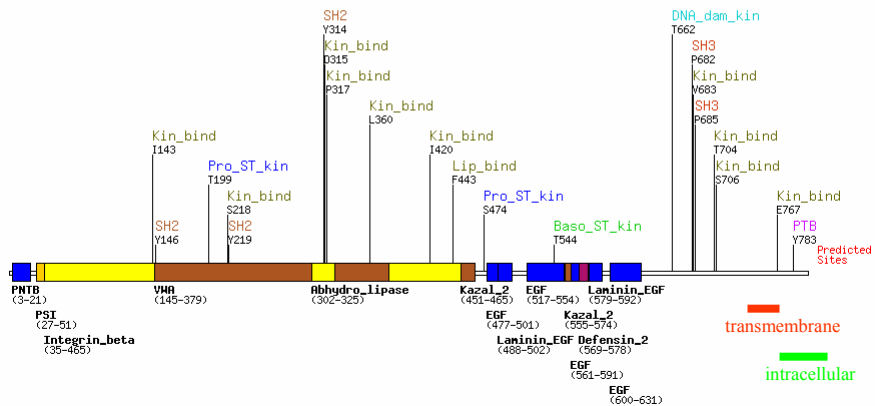
## Motif Scan Graphic Results: BETA\_INTEGRIN

Description: User-entered sequence

Motifs scanned: All

Stringency: Medium

Show domains: Yes



# MotifScan

Phosphotyrosine binding group (PTB)				
Shc PTB			Gene Card SHC1	
Site	Score	Percentile	Sequence	SA
Y783	0.5526	0.463 %	DTGENPIYKSAVTTV	1.054

Lipid binding group (Lip_bind)				
PIP3-binding PH			Gene Card PIP3_E	
Site	Score	Percentile	Sequence	SA
F443	0.6903	0.413 %	PKRDSDSFKIRPLGF	1.219

Src homology 2 group (SH2)				
Crk SH2			Gene Card CRK	
Site	Score	Percentile	Sequence	SA
Y314	0.4200	0.327 %	MYTMSHYDYDPSIAH	3.098

Nck SH2			Gene Card NCK1	
Site	Score	Percentile	Sequence	SA
Y314	0.4596	0.429 %	MYTMSHYDYDPSIAH	3.098

p85 SH2			Gene Card PIK3R1	
Site	Score	Percentile	Sequence	SA
Y146	0.5024	0.809 %	EDYPIDLYLMDLSY	0.632

Grb2 SH2			Gene Card GRB2	
Site	Score	Percentile	Sequence	SA
Y219	0.5132	0.718 %	NCTTPFSYKNVLSLT	1.033

Src homology 3 group (SH3)				
PLCg SH3			Gene Card PLCG1	
Site	Score	Percentile	Sequence	SA

Kinase binding site group (Kin_bind)				
PDK1 Binding			Gene Card PDPK1	
Site	Score	Percentile	Sequence	SA
T704	0.3070	0.050 %	DDCWFFYFTYSVNGN	0.699

Erk1 Binding			Gene Card EPHB2	
Site	Score	Percentile	Sequence	SA
P317	0.5468	0.545 %	MSHYDYDPSIAHLVQ	0.880

PDK1 Binding			Gene Card PDPK1	
Site	Score	Percentile	Sequence	SA
S218	0.5644	0.317 %	QNCTTPFSYKNVLSL	2.152

PDK1 Binding			Gene Card PDPK1	
Site	Score	Percentile	Sequence	SA
S706	0.5983	0.650 %	CWFYFTYSVNGNNEV	0.852

Erk D-domain			Gene Card MAPK1	
Site	Score	Percentile	Sequence	SA
I420	0.6051	0.280 %	RKCSNISIGDEVOFE	0.432

Erk D-domain			Gene Card MAPK1	
Site	Score	Percentile	Sequence	SA
I143	0.6054	0.282 %	KRAEDYPIDLYLMD	0.840

PDK1 Binding			Gene Card PDPK1	
Site	Score	Percentile	Sequence	SA
E767	0.6144	0.855 %	RREFAKFEKEKMNAK	4.760

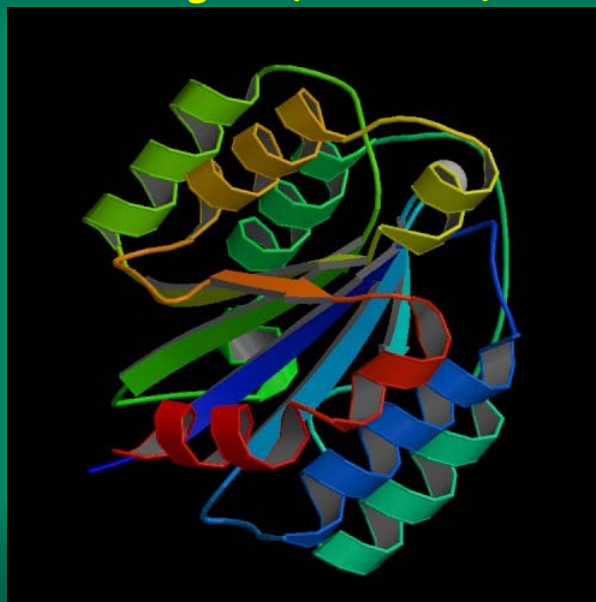
PDK1 Binding			Gene Card PDPK1	
Site	Score	Percentile	Sequence	SA
D315	0.6261	0.995 %	YTM SHYDYDPSIAHL	3.051

Erk D-domain			Gene Card MAPK1	
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## 3-dimensional structure of alpha1 integrin (I domain)

RasMol



## Credits

**Sequence alignment engineers: Sebastian Komorowski and Dianne Cooper**

**Animation and graphics: Albena Kantardzhieva**

**Sound engineer: Cuddapah Sunku Chennakesava**

**Screenplay by: Mikhail Paveliev**

**Scientific consultant: Geraint Thomas**

**Produced by: EMBO productions, France.**

**For any questions please refer to:**

**<http://integrins.hypermart.net/>**

