GCK PM1 Residues

Applicable for glucose and ATP-binding sites[1-9]

Residue	Domain	Comment
Glucose binding site (<u>22 residues</u>)[1]		
Ser151 - Pro153	S	Ser151 makes H-bond interaction with Glc in closed conf.
Thr168 - Lys169	S	Thr168 and Lys169 make H-bond interaction with Glc in closed conf. Lys169 is a general acid catalyst in the catalytic ternary complex.
Asn204 - Thr206	L / CRII	Asn204 and Asp205 make H-bond interaction with Glc in closed conf. Asp205 is part of the catalytic ternary complex (general base catalyst).
Ile225 - Asn231	L	Asn231 makes H-bond interaction with Glc in closed conf[2,3].
Asn254 - Gly258	L	Glu256 makes H-bond interaction with Glc in closed conf[2,3].
Gln287	L	Gln287 makes H-bond interaction with Glc in closed conf.
Glu290	L	Glu290 makes H-bond interaction with Glc in closed conf[2,3].
Mg^{2+}- ATP binding site (<u>29 residues</u>)		
Asp78 - Arg85	S	Phosphate 1 motif. Asp78 is important for coordinating the Mg2+ ion in ternary complex. Thr82 H-binding to ATP-y-S in crystal structure 3VEY[6].
Ser151	S	Ser151 is important for coordinating the Mg2+ ion in ternary complex[1].
Lys169	S	Lys169 makes H-bond interaction with ATP in closed conf. Lys169 is a general acid catalyst in the catalytic ternary complex[7].
Asp205	L / CRII	Part of the Connect 1 motif. Asp205 makes H-bond interactions with Mg^{2+} and ATP. Part of the catalytic ternary complex (general base catalyst)[1].
Ile225 - Gly229	L	Phosphate 2 motif. Thr228 makes H-bond interaction with ATP and is part of the catalytic scaffold of GK[1,8].
		Gly229: H-binding to AMP-PNP according to crystal structure GK•Glc•AMP-PNP[1].
Gly295 - Lys296	L	
Glu331 - Arg333	L	
Ser336	L	H-binding to AMP-PNP according to crystal structures[1,4,5].
Gly410 - His416	L	Adenosine motif. Ser411: H-binding to AMP-PNP according to crystal structures[1].

References

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