Supporting Information

Insights into substrate and inhibitor selectivity among human GLUT transporters through comparative modeling and molecular docking

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Figure S1. Sequence alignment of GLUT1-14. Alignment performed with T-COFFEE and adjusted with Vito. N-terminal and C-terminal regions from several sequences are not shown, as indicated by slashes. TM1-12 indicate transmembrane helices, while ICH1-4 indicate helices from the intracelular helical domain. Stars indicate positions that hydrogen bond to glucose in PDB 4ZW9. Figure prepared with ESPript 3.0.¹

		TM1	TM1e	
GLUT1		20	1000000000000 00	فففقفقف
GLUT1	1	MEPSSKKLTGR I M I A V GG A V IG SL QFGY NTG VIN AP(PQKVI PQKVI	TLTT L W SL S
GLUT2	1	MTEDKVTGTLVFTVITAVLGSFQFGYDIGVINAP	PQQV I ISHYRHVLGVPLDDRKAINNYVINSTDELPTISYSMNPKPTPWAEEETVAAAQ	LITMLWSLS
GLUT3	1	MGTQKVTPALIFAITVATIGSFQFGYNTGVINAPE	PEKI \mathbf{I} KEFINKTLTDKGNAPPSEV	LLTSLWSLS
GLUT14	23	/ KPHTLAVTPALIFAITVATIGSFQFGYNTGVINAPE	PETI I KEFINKTLTDKANAPPSEV	LLTNLWSLS
GLUT4	13	/ E P P Q Q R V T G T L V L A V F S A V L G S L Q F G Y N I G V I N A P Ç	PQKV I EQSYNETWLGRQGPEGPSSIPPG	TLTT L WALS
GLUT5	7	/ M K E G R L T L V L A L A T L I A A F G S S F Q Y G Y N V A A V N S P F	PALL M QQFYNETYYGRTGEFMEDF	PLTL L W SV T
GLUT7	13	/ SREGRLQPTLLLATLSAAFGSAFQYGYNLSVVNTPF	PHKVFKSFYNETYFERHATFMDGK	LMLLWSCT
GLUT9	46	/ R R R K D W S C S L L V A S L A G A F G S S F L Y G Y N L S V V N A P 1	PTPY I KAFYNESWERRHGRPIDPD	TLTL L W SV T
GLUT11	3	/LRRLIQGRIL L LTICAAGIG G TF QFGY NLS IIN AP7	PTLH I QEFTNETWQARTGEPLPDH	LVLLMWSLI
GLUT6	27	/ A R V G T L Q N K R V F L A T F A A V L G N F S F G Y A L V Y T S P V I	VIPA L ERSLD	LTKSQASWF
GLUT8	15	/	AIPS <mark>L</mark> QRAAPPAPR	LDDAAASWF
GLUT12	29	/ P P W A R G C G M F T F L S S V T A A V S G L L V G Y E L G I I S G A I	ALLQ I KTLLA	LSCHEQEMV
GLUT10	1	MGHSPPVLPLCASVSLLGGLTFGYELAVISGAI	ALLP L QLDFG	LSCLEQEFL
GLUT13	70	/QFQQDETPAF V Y V V A VFSA LG GFL FGY DTG VVS GAN	AMLL <mark>I</mark> KRQLS	LDALWQELL

		TM2	TM3	TM4	TM5
GLUT1		22222222222222222222222	22222 22222222222 22222		222222222222
GLUT1	69	V AIFSVGGMIGSFSVGLFVNRFG	RNS MLM MNLLAFVSAVLMGFSKLG	GKSFEMLILGRFIIGVYCGLTTGFVPMYVGEVSPTA	LRGALGTLHQLGIVVGILI
GLUT2	101	VSSFAVGGMTASFFGGWLGDTLG	RIKAMLVANILSLVGALLMGFSKLG	GPSHILIIAGRSISGLYCGLISGLVPMYIGBIAPTA	LRGALGTFHQLAIVTGILI
GLUT3	67	VAIFSVGGMIGSFSVGLFVNRFG	RR NS MLIVNL LA V T G GCF M GLCKVA	AKSVEMLILGRLVIGLFCGLCTGFVPMYIGEISPTA	LRGAFGTLNQLGIVVGILV
GLUT14	91	VAIFSVGGMIGSFSVGLFVNRFG	R RNS MLI V NL LA A T G GC LM GLCKIA	AESVEMLILGRLVIGLFCGLCTGFVPMYIGEISPTA	LRGAFGTLNQLGIVIGILV
GLUT4	85	VAIFSVGGMISSFLIGIISQWLG	RK R A M L V N N V L A V L G G S L M G L A N A A	A A SYEMLILGRFLIGAYSGLTSGLVPMYVGEIAPTH	LRGALGTLNQLAIVIGILI
GLUT5	75	VSMFPFGGFIGSLLVGPLVNKFG	K GA LL FN NI FS IVP A ILM GCSRVA	A TISFELIIISRLLVGICAGVSSNVVPMVLGELAPKN	LRGALGVVPQLFITVGILV
GLUT7	81	VSMFPLGGLLGSLLVGLLVDSCG	K GT LLI N NI FA IIP A ILM GVSKVA	A KAFELIVFSRVVLGVCAGISYSALPMYLGELAPKN	LRGMVGTMTEVFVIVGVFL
GLUT9	114	VSIFAIGGLVGTLIVKMIGKVLG	r k ht lla n n gfa i saa llm acslqa	A GAFEMLIVGRFIMGIDGGVALSVLPMVLSEISPKE	IRG S LGQV TA I F I C IGV FT
GLUT11	71	VSLYPLGGLFGALLAGPLAITLG	R K K S L L V N N I F V V S A A I L F G F S R K A	A G S FE MIMLGR L LVGV NA GV SMNIQ PMVL G B SAPKE	LRGAV AMSSA I FT ALGIVM
GLUT6	85	GSVFTLGAAAGGLSAMILNDLLG	RKLSIMFSAVPSAAGYALMAGA	.HGLWMLLLGRTLTGFAGGLTAACIPVYVSEIAPPG	VRGALG ATPQ L M AV F G S L S
GLUT8	73	GAVVTLGAAAGGVLGGWLVDRAG	K LS LLL C SV PF VAG F AVI TAA	. QDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPA	VRGLLGSCVQLMVVVGILL
GLUT12	83	VSSLVIGALLASLTGGVLIDRYG	RTAIILSSCLLGLGSLVLILS	. LSYTVLIVGRIAIGVSISLSSIATCVYIAEIAPQH	RRGLLVSLNELMIVIGILS
GLUT10	51	VGSLLL LG ALLASLVG G FLIDCYG	r kqa il gs nl vl lag s l t l gla	. GSLAWLVLGRAVVGFAISLSSMACCIYVSELVGPR	Q RGVLVSL YE A GIT VGILL
GLUT13	124	V SSTVGAA AV SALAG G ALNGVF G	R AA ill A SA lf tag S Avl aaa	. NMKETLLAGRLVVGLGIGIASMTVPVYIAEVSPPN	L rg rlv ti ntlfitg g qff
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				TM6	ICH1	ICH2	ICH3	ICH4
GLUT1		eeee	عفعفف	د ففقفقفف	eee eeee	000000000	222222222222222	00000
GLUT1	171	AQVFGLDSIMGNKD	LWPLLLSI	IF IPALLO C I V I	LPFC PESPRFLLI	N R N E E N R A K S V L K K L R G 1	A D V TH D L O EM KEESROMMRE	KKVTILELFRS.PAY
GLUT2	203	SQIIGLEFILGNYD	LWHILLGL	SGVRAILQSLLI	LFFCPESPRYLYI	K L D E E V K A K Q S L K R L R G Y	(D V TK DI N EM RKEREEASSE	QKV S I I Q L FTN.SSY
GLUT3	169	AQIFGLEFILGSEE	LWPLLLGF	TILPAILQSAAI	LPFCPESPRFLLI	N R K E E E N A K Q I L Q R L W G 1	[Q DV SQ DIQEM KDESARMSQE	KQV T V L E L FRV.SSY
GLUT14	193	AQIFGLELILGSEE	LWPVLLGF	TILPAILQSAAI	LPCCPESPRFLLI	N R K K E E N A T R I L Q R L W G 1	ſQ DV SQ DI Q EM KDESARMSQE	KQV T V L E L FRV.SSY
GLUT4	187	AQVLGLESLLGTAS	SL W PL LL G L	TVLPALLQLVLI	LPFCPESPRYLYI	IQNLEGPARKSLKRLTG	∛ A D V S G V L A E L K D E K R K L E R E	RPLSLQLLGS.RTH
GLUT5	177	AQIFGL RNLLANVD	GWPILLGL	TGVPAALQLLLI	LPFFPESPRYLLI	Q K K D E A A A K K A L Q T L R G 🛙	∛ D S V D R E V A E I R Q E D E A E K A A	GFI S V L K L FRM.RSL
GLUT7	183	AQIFSLQAILGNPA	GMPVLLAL	TGVPALLQLLTI	LPFFPESPRYSLI	Q K G D E A T A R Q A L R R L R G F	HT DM EA EL E DM RAEARAERAE	GHLSVLHLCAL.RSL
GLUT9	216	GQLLGLPELLGKES	STMPYLFG V	IVVPAVVQLLSI	LPFLPDSPRYLLL	EKHN E AR A VK A FQTFL G H	<pre>KADVSQEVEVLAESRVQRSI</pre>	RLVSVLELLRA.PYV
GLUT11	173	GQVVGLRELLGGPQ	AWPLLLAS	CLVPGALQLASI	LPLLPESPRYLLI	d c g d t e a c l a a l r r l r g s	SG DL AG EL E EL EERAACQGC	RARRPWELFQH.RAL
GLUT6	184	LYALGLLL	PWRWLAVA	GEAPVLIMILLI	LSFMPNSPRFLLS	RG.R D EE A LR AL AW L R G 1	「. DV DVHWEFEQIQDNVRRQS	SRVSWAEARA PHV
GLUT8	172	AYLAGWVL	EWRWLAVL	GCVPPSLMLLL	MCFMPETPRFLLT	QH.RRQE A MA AL RF L W G S	SEQGWEDPPIG	AEQSFHLALLRQPGI
GLUT12	182	AYISNYA.FANVFH	IGWKYMFGL	VIPLGVLQAIA	MYFLPPSPRFLVM	KG.QEGAASK VL GRLRAI	LS D TTE EL TV I KSSLKDE	YQY S FWD L FRSKDNM
GLUT10	150	SYALNYA. LAGTPW	IG W RH M FGW	ATAPAVLQSLSI	LLFLPAGTDETA.		G. EA	PRYSFLDLFRARDNM
GLUT13	223	ASVVDGAFSYLQKD	GMRYMLGL	AAVPAVIQFFGF	FLFLPESPRWLIQ	. KGQTQKARRILSQMRG	≀Q[T I]DE E Y]D[S I KNNIEEEKE	VGSAGPVICRMLSY.PPT

		TM7		TM8	тм9	
GLUT1		2222222222222222	000000000000000	222222222222222222222222222222	000000000000000000000000000000000000000	
GLUT1	269	RQPILIAVVLQLSQQLS	GINAVFYYSTSIFEK AGV Q	. QPV YATI GS GIV NT A F TV VS L F VVERA	GRRTLHLIGLAGMAGCAILMTIALALLE	
GLUT2	301	R Q P I L V A L M L H V A Q Q F S	SGINGIFYYSTSIFQTAGIS	. KPVYATIGVGAVNMVFTAVSVFLVEKA	GRRSLFLIGMSGMFVCAIFMSVGLVLLN	
GLUT3	267	RQPIIISIVLQLSQQLS	GINAVFYYSTGIFKDAGVQ	. EPIYATIGAGVVNTIFTVVSLFLVERA	GRRTLHMIGLGGMAFCSTLMTVSLLLKD	
GLUT14	291	ROPITISIVLOLSQOLS	GINAVFYYSTGIFKDAGVQ	. OP IYATISAGVVNTIFTLLSLFLVERA	GRRTLHMIGLGGMAFCSTLMTVSLLLKN	•
GLUT4	285	RUPLIAVVLULSUULS	GINAVIIISTSIFEIAGVG.	PUVOYUMACTCAVNYVMMECAVEVUEL	GRRILHLLGLAGMCGCAILMIVALLLLE	• •
GLUT7	275	RWOLLSTIVLMACOOLS	SGINATITIADQITLSAGVPE.	A H S O Y V TY C S C V V N TY MT T T S A VI. VE B I	GRRHTLLAGYGICGSACLVITWVILFON	• •
GLUT9	314	RWOVVTVIVTMACYOLC	GLNAIWFYTNSIFGKAGIPP	AKIPYVTLSTGGIETLAAVFSGLVIEHI	GRRPLLIGGEGIMGLEEGTLTITLTLOD	
GLUT11	271	RROVTSLVVLGSAMELC	GNDSVYAYASSVFRKAGVPE.	AKIQYAIIGTGSCELLTAVVSCVVIERV	GRRVLLIGGYSLMTCWGSIFTVALCLQS	
GLUT6	273	CRPITVALLMRLLQQLT	GITPILVYLQSIFDSTAVLL.	. PPKDDAAIVGAVRLLSVLIAALTMDLA	GRK V L LF V SAAI M FAANLT L G L Y I HFGPRPLSPNS	ЗT
GLUT8	254	YKPFIIGVSLMAFQQLS	SGVNAVMFYAETIFEEAKFK	. DSSLASVVVGVIQVLFTAVAALIMDRA	GRR L L L VL SGVV M VFSTSAFG A YFK L TQGGPGNSS	βH
GLUT12	276	R TR IMI G L T L VFFV QIT	EG QPN I L FY A STV LKS VG FQSN	IEAASLASTGV GVV KVISTIPATL LVDHV	'G S K T F L C I G S S V M A A S L V T M G I V N L N I H M N F T H I C	CR
GLUT10	229	R GRTT V G L G L V L F QQLT	EG QPN V LC Y A STIF SS VG FHGC	SSAVLASVGL GAV KV A A TL TA M G LVDRA	GRR A L L LAG CAL M ALSVSG I G L VSF A VPMDSGPSC	ĽΓ
GLUT13	323	r ra liv gcg l q m f qqls	SGINTIMYYSATILQMSGVEDI	RLAI WL ASVTAFTNF I F TL VG V W LVEK V	GRR K L T <u>FGS</u> LAGTTVALII L A L GFV L SAQVSPRI1	I F
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GLUT1																																																l	200	22	يف	u	200	220	20	0
GLUT1	360																																													. QI	PV	MM	S Y I	Ls:	IVA	A I F	GF	VAE	FE	VG
GLUT2	392																									-																				.KF	SI	v M s	s Y 1	vs	MIA	A I F	LF	v s F	FE	ΙG
GLUT3	358	-	-				-			-			-													-															-					.NY	(N)	G M S	5 F 1	V C :	I G A	/I	VF	VAF	FE	ΙG
GLUT14	382	-	• •	• •	• •	• •	-	• •	• •			• •	•	• •	• •	•		• •	•	• •	• •	• •	• •	• •	•	-	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	-	• • •	• •	• •	• •	. H Y	(N)	GMS	SF1		I G A	1 I	VF	VA	FE	IG
GLUT4	376	-	• •	• •	• •	• •	-	• •	• •	•	• •	• •	•	• •	• •	•	• •	• •	•	• •	• •	• •	• •	• •	• •	-	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	•	•••	• •	• •	• •	. R\	/P/	AM:	Y	VS.		IF	GF	VAE	FE	IG
GLUT5	308	•	• •	• •	• •	• •	-	• •	• •	•	• •	• •	•	• •	• •	•	• •	• •	•	• •	• •	• •	• •	• •	• •	-	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	•	•••	• •	• •	• •	. 1 \ D (/ 5 V / D I	NUMUE PIT S					5 I			LG
GLUT9	407			• •	• •	• •		• •	• •		•••	• •	•	• •	• •		• •	• •	•	• •	• •	• •	• •	• •	•		• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	• •	•••	• •	• •	•		• •	• •	• •	. HZ		v	y i		TV	T	AT.	TA		SG
GLUT11	364				::				::	:		: :		: :	: :			::			::			: :			: :	::					::					::	::	::						. SI	PV	TI	YI	LA	AN	IF	AF	ILS	FG	IG
GLUT6	373	Α.																								-				G	LΕ	s.					. E	SW	GD	LΑ	Q.			. P :	LAA	A P A	A G Y	Y L I	r l I	VP	LLA	A T M	LF	IM	; Y A	VG
GLUT8	353																									-					.v	Α.					. I	SΑ	.P	VS	A			. Q1	9 V I	DAS	SVO	3 L 2	YM 1	LA	7 GS	S M C	LF	IA	FA	VG
GLUT12	378	SI	IN:	5 I	NQ	SL	DI	ΞS	VI	Y (GΡ	GN	IL.	SΤ	NN	N :	ΓL	RD	ΗE	ΥK	GΙ	SS	SΗ	SF	SS	5 L I	ΜP	LR	NI	DVI	DΚ	RG	ΕT	ΤS	AS	SLI	LΝ	AG	LS	ΗT	E	(Q]	[V]	ΓDΙ	P G I	DVE	AI	E L	(W)	LSI	LAS	S L I	νY,	VAZ	FS	IG
GLUT10	331	A	7 P I	A	TG	QT	GI	LP	GD	S	ΞL	LÇ	2D	SS	LP	P .	I P	RT	NE	ED	QR	EF	? I	LS	TA	K	КT	KP	HE	PR:	SG	DP	SA	PP	RI		LS	SA	LP	GP	Ρ.	•••		. Ll	PAI	RGH	IAI		RWD	IA			VF	VS	FS	FG
GLUT13	425	K i	11	ΑP	SG	QN	IA.	I C	IR	1:	51	CN	1 E	CM	Ъυ	PI	00	Gr	C	(K	MN	K S	5 1	VI	Da	55	CV	ΡV	Nľ	(A)	51	NE	AA	wG	RC	E	NE	ΙK	r K	ΙĿ	D .	•••	Lr	NA	INI	C F	11		5 W .	I A L		, Fi	LI	LV	E A	PG
																																																							- *	(

				TM11	TM12	
GLUT1		222222222	000000000000000000000000000000000000000	00000000000000000	222222222222222222222222222222222222222	
GLUT1	384	GPIPWFIVAELFS	QGP RPAA I AV AGFS NW T	SNFIVGMCEQYVEQLCG.	P Y V F I IF TVLL V LFF IF T Y FK V	PETKGRTFDEIASGFRQGGASQSDKTP/
GLUT2	416	GPIPWFMVABFFS	QGP RPAA L AI AAFS NW T	CNFIVALCEQYIADFCG.	PYVFFLFAGVLLAFTLFTFKV	PETKGKSFEEIAAEFQKKSGSAHRPKA/
GLUT3	382	GPIPWFIVAELFS	Q G P R P A A M A V A G C S N W T	SNFLVGLLFPSAAHYLG.	AYVFIIFTGFLITFLAFTFFKV	PETRGRT FE DI TRA F EGQAHGADRSGK/
GLUT14	406	GPIPWFIVABLES	QGP RPAAMAVAGCSNWT	SNFLVGLLEPSAAYYLG.	AYVFIIFTGFLITFLAFTFFKV	PETRGRTFEDITRAFEGQAHGADRSGK/
GLUT4	400	GPIPWFIVABLFS	Q G P R P A A MAV A G F S N T	SNFIIGMGEQYVAEAMG.	PYVFLLFAVLLLGFFIFTFLRV	PETRGRTFDOISAAFHRTPSLLE/
GLUT5	392	SPIPALLITEIFI	QSSRPSAFMVGGSVHWL	SNFTVGLIEPFIQEGLG.	PYSFIVFAVICLLTTIYIFLIV	PETKAKTFIEINQIFTKMNKVSEVY/
GLUT7	398	SPVPSVVRTEIFI	QSSRRAAFMVDGAVHWL	TNFIIGFLEPSIQEAIG.	AYSFIIFAGICLLTAIYIYVVI	PETKGKTFVEINRIFAKRNRVKLPE/
GLUT9	431	GGIPFILTGEFF	QSQRPAAFIIAGTVNWL	SNFAVGLLEPFIQKSLD.	TYCFLVFATICITGAIYLYFVL	PETKNRTYAEISQAFSKRNK/
GLUT11	388	AGVTGILATELFI	OMARPAACMVCGALMWI	MLILVGLGEPFIMEALS.	HFLYVPFLGVCVCGAIYTGLFL	PETKGKTFOEISKELHRLNFPRRAOGP/
GLUT6	414	GPITWLLMS DVLE	LRARGVASGLCVLASWL	TAFVLTKSFLPVVSTFGL	, OVPFFFFFAAICLVSLVFTGCCV	PETKGRSLEQIESFFRTGRRSFLR
GLUT8	390	GPIPWLLMSBIFE	LHVKGVATGICVLTNWL	MA FLV TKE F SS L MEV L RP	YGAFWLASAFCIFSVLFTLFCV	PETKGKTLEQITAHFEGR
GLUT12	480	GPMPWLVLSBIF	GGIRGRAMALTSSMNWG	INLLISLIELTVIDLIGL	PWVCFIYTIMSLASLLFVVMFI	PETKGCSLEQISMELAKVNYVKNNICF/
GLUT10	428	GPVTWLVLSBIYE	VEI RGRA F A FCNSF NW A.	ANLFISLSELDLIGTIGL	SWTFLLYGLTAVLGLGFIYLFV	PETKGQSLAEIDQQFQKRRFTLSFGHR/
GLUT13	525	GPMPWTVNSEIYE	LWARSTGNACSSGINWI	FNVLVSLTELHTAEYLTY	YGAFFLYAGFAAVGLLFIYGCL	PETKGKKLEEIESLFDNRLCTCGTSDS/
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	GLUT1	GLUT2	GLUT14	GLUT3	GLUT4	GLUT11	GLUT9	GLUT7	GLUT5	GLUT6	GLUT8	GLUT13	GLUT10	GLUT12
GLUT1	100.0	55.8	61.6	63.5	65.5	35.1	36.9	38.0	41.1	28.6	29.7	26.0	26.0	26.1
GLUT2	55.8	100.0	50.2	52.0	54.3	31.6	30.3	35.7	40.2	28.3	29.2	31.1	27.1	28.6
GLUT14	61.6	50.2	100.0	94.6	55.6	32.4	33.9	36.6	37.4	26.4	31.4	28.4	24.9	26.4
GLUT3	63.5	52.0	94.6	100.0	57.6	33.4	34.7	38.0	39.1	27.0	32.7	29.4	24.6	26.8
GLUT4	65.5	54.3	55.6	57.6	100.0	35.6	35.8	38.9	42.4	28.5	31.6	28.2	27.5	27.3
GLUT11	35.1	31.6	32.4	33.4	35.6	100.0	40.2	40.5	40.5	23.3	25.9	21.6	23.4	21.1
GLUT9	36.9	30.3	33.9	34.7	35.8	40.2	100.0	42.6	43.7	24.4	26.4	23.1	21.3	20.2
GLUT7	38.0	35.7	36.6	38.0	38.9	40.5	42.6	100.0	59.3	25.1	27.1	25.6	27.1	25.3
GLUT5	41.1	40.2	37.4	39.1	42.4	40.5	43.7	59.3	100.0	27.0	29.1	26.8	26.3	23.9
GLUT6	28.6	28.3	26.4	27.0	28.5	23.3	24.4	25.1	27.0	100.0	42.8	27.5	29.9	25.4
GLUT8	29.7	29.2	31.4	32.7	31.6	25.9	26.4	27.1	29.1	42.8	100.0	31.2	30.0	29.2
GLUT13	26.0	31.1	28.4	29.4	28.2	21.6	23.1	25.6	26.8	27.5	31.2	100.0	31.0	29.0
GLUT10	26.0	27.1	24.9	24.6	27.5	23.4	21.3	27.1	26.3	29.9	30.0	31.0	100.0	40.1
GLUT12	26.1	28.6	26.4	26.8	27.3	21.1	20.2	25.3	23.9	25.4	29.2	29.0	40.1	100.0

					R	EPORTED	SUBS	TRATES*2				
Receptor	glucose	galactose	2-desoxyglucose	mannose	glucosamine	fructose	xylose	urate	trehalose	dehydroascorbic acid	alfa-MG (alfa-methyl-glucose)	myo-inositol
GLUT1	3 mM ³	YES		YES	YES					YES		
GLUT2	17 mM³	YES		YES	YES	YES						
GLUT3	1.4 mM ³	YES		YES			YES			YES ⁴		
GLUT4	5 mM ³				YES					YES ³		
GLUT14	YES	YES		YES			YES			YES		
GLUT5	NO					YES⁵				NO^4		
GLUT7	YES	NO				YES⁵	NO			NO^4		
GLUT9	0.6 mM ³					0.4 mM ³		0.9 mM ³		NO^4		
GLUT11	YES	NO				YES				NO^4		
GLUT6	YES									NO^4		
GLUT8	2 mM ³	YES				YES			YES ⁶	YES ⁴		
GLUT10	YES	YES								NO^4		
GLUT12	YES ⁷	YES ⁷	YES ⁷			YES ⁷				YES ⁸	YES ⁷	
GLUT13	NO											$100 \ \mu M^3$

Table S2. Reported substrates for GLUT1-14.

*Unless another reference is especified. data was extracted from Yan. $2017.^2$ For cases where a K_d value was reported. the affinity is indicated. Otherwise. YES indicated the substrated is transported. NO indicates it is not transported. and blank cells indicates that no data was found.

	o binan	-5 Siec II		monogo	us seque	nees.	
Statistics after Clustal Omega alignment				Residue	e		
	E140	Q242	Q243	P248	K280	S424	W432
% conservation	100	100	100	100	100	100	97.2
Occupancy*	250	250	250	250	250	250	247

Table S3. Conservation of exofacial GLUT10 binding site in 250 homologous sequences.

*number of aligned sequences among a total of 250 sequences considered.

		0			0	-		
	Statistics after Clustal Omega alignment				Residue	e		
		E172	V289	Q290	P295	K327	S476	W484
	% conservation	99.6	100	99.6	100	100	100	88
	Occupancy*	249	250	250	250	250	250	236
-	% conservation Occupancy*	99.6 249	V 289 100 250	99.6 250	P295 100 250	K327 100 250	S476 100 250	w4 88 23

Table S4. Conservation of exofacial GLUT12 binding site in 250 homologous sequences.

*number of aligned sequences among a total of 250 sequences considered.

				Selecte	ed resid	ues in t	he bind	ing site		
Reference protein	GLUT13	T213	Q220	Q336	Q337	N342	N374	A521	W529	N552
	GLUT1	Q161	I168	Q282	Q283	N288	N317	E380	W388	N411
	GLUT2	Q193	I200	Q314	Q315	N320	N349	E412	W420	N443
	GLUT3	Q159	I166	Q280	Q281	N286	N315	E378	W386	N409
	GLUT4	Q177	I184	Q298	Q299	N304	N333	E396	W404	N427
	GLUT5	Q167	I174	Q288	Q289	N294	N325	A380	A396	H419
	GLUT6	Q174	S181	Q286	Q287	T292	R322	A410	W418	S441
Other GLUTs	GLUT7	E173	V180	Q294	Q295	N300	N331	S394	S402	H425
	GLUT8	Q162	I169	Q267	Q268	N273	Q302	A386	W394	N417
	GLUT9	A206	V213	Y327	Q328	N333	E364	C427	F435	N458
	GLUT10	E140	I147	Q242	Q243	P248	K280	S424	W432	N455
	GLUT11	A163	I170	M284	E285	D290	E321	G384	G392	M415
	GLUT12	E172	I179	V289	Q290	P295	K327	S476	W484	N507
	GLUT14	Q183	I190	Q304	Q305	N310	N339	E402	W410	N433
Top 250 Blastp hits	% conservation	96.4	99.6	100	100	99.6	99.6	96.8	96.8	96.4
	occupancy	249	249	250	250	250	250	243	243	242

Table S5. Myo-inositol binding site residues and their conservation within GLUTs.

*GLUT13 residues which are predicted to hydrogen bond to myo-inositol are shown in bold. For all other receptors. Cells are colored red if the residue differs from the one found in GLUT13 and green otherwise.

		Selec	ted resi	idues in	predic	ted ura	te bindi	ing site
Reference protein	GLUT9	Y71	Y327	Q328	N333	W336	C427	F435
	GLUT1	F26	Q282	Q283	N288	F291	E380	W388
	GLUT2	F24	Q314	Q315	N320	F323	E412	W420
	GLUT3	F24	Q280	Q281	N286	F289	E378	W386
	GLUT4	F38	Q298	Q299	N304	F307	E396	W404
	GLUT5	Y32	Q288	Q289	N294	Y297	A380	A396
	GLUT6	F52	Q286	Q287	T292	L295	A410	W418
Other GLUTs	GLUT7	Y38	Q294	Q295	N300	N303	S394	S402
	GLUT8	F40	Q267	Q268	N273	M276	A386	W394
	GLUT10	F22	Q242	Q243	P248	L251	S424	W432
	GLUT11	F28	M284	E285	D290	Y293	G384	G392
	GLUT12	V54	V289	Q290	P295	L298	S476	W484
	GLUT13	F95	Q336	Q337	N342	M354	A521	W529
	GLUT14	F48	Q304	Q305	N310	F313	E402	W410
top 250 GLUT9 Blastp hits	% conservation	95.6	100	100	100	99.6	99.6	99.7
	occupancy	243	250	250	250	249	250	249

Table S6. Urate binding site residues and their conservation within GLUTs.

*GLUT9 residues which are predicted to hydrogen bond to urate are shown in bold. For all other receptors. Cells are colored red if the residue differs from the one found in GLUT9 and green otherwise.

Statistics after Clustal Omega alignment				Resi	due			
	A163	M284	E285	N289	D290	E321	G384	G392
% conservation	90.8	88.0	92.0	92.5	96.0	92.0	98.8	97.2
Occupancy*	250	246	246	246	246	231	248	247

Table S7. Conservation of exofacial GLUT11 binding site in 250 homologous sequences.

*number of aligned sequences among a total of 250 sequences considered.

Protein	Ligand	Study type/ Study name	Template/	
			Anchor	
GLUT5	Cytochalasin B	Comparative docking/ Raw transfer	5EQI/ 5RH	
GLUT7	Cytochalasin B	Comparative docking/ Raw transfer	5EQI/ 5RH	
GLUT9	Cytochalasin B	Comparative docking/ Raw transfer	5EQI/ 5RH	
GLUT11	α-D-Glucose	Docking with PLANTS/ GLUT11ligsAnchor3	4ZW9/GLC_A_5 (best LPE)	
GLUT11	D-	Docking with PLANTS/ GLUT11ligsAnchor3	4ZW9/GLC A 5	
	Glucosamine		(best pKd)	
GLUT11	N-Acetyl-	Docking with PLANTS/ GLUT11ligsAnchor3	4ZWC/MAL_A_5	
	glucosamine		(best pKd)	
	thiazoline			
GLUT9	Urate	Docking with PLANTS/ GTR9uratePLANTS0constraint	4GC0/6BG_A	
GLUT3	Myo-inositol	Docking with PLANTS/ GTR3allPLANTS	4ZW9/GLC_A_5	
			(best LPE)	
GLUT13	Myo-inositol	Docking with PLANTS/ GTR13allPLANTSupload	4ZW9/GLC_A_5	
			(best LPE)	

Table S8. Reported complexes analyzed by comparative docking or docking with PLANTS.

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