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https://www.dsimb.inserm.fr/DIONYSUS/news/structures.html

Month 2024 : 04/09/2024-30/10/2024

<u>8YRL</u>	Crystal structure of Aspergillus fumigatus Galactofuranosylransferase (AfGfsA) in complex with UDP and galactofuranose	TRANSFERASE	bDGalf
<u>9JUB</u>	Cryo-EM structure of human hyaluronidase PH-20	HYDROLASE/IMMUNE SYSTEM	
<u>9DQC</u>	Hare calicivirus protruding domain and A-trisaccharide complex	VIRAL PROTEIN	
<u>8ZE2</u>	Drosophila melanogaster gustatory receptor 64a(Gr64a) in Sucrose-bound state	PROTEIN TRANSPORT	$\alpha 2^{\alpha}$
<u>8R53</u>	The complex of Glycogen Phosphorylase with (-)-Epigallocatechin-3-gallate (EGCG) and glucose.	TRANSFERASE	aDGlcp
8ZE3	Drosophila mojavensis gustatory receptor 43a(Gr43a) in Fructose-bound state	PROTEIN TRANSPORT	bDFruf
<u>8R5L</u>	E-selectin complexed with glycomimetic ligand BW850	CELL ADHESION	bDGlcpNAc
8R5M	E-selectin complexed with glycomimetic ligand DS0567	CELL ADHESION	bDGlcpNAc
8ROV	Human dectin-2 with dimerization domain	SUGAR BINDING PROTEIN	aDManp
<u>8X3Q</u>	tll1591 with alpha-glucan 4sugar	TRANSFERASE	
<u>8X3U</u>	tll1591 with alpha_glucan 3sugar	TRANSFERASE	$\alpha_2 \alpha_2 \beta_{\beta}$
<u>8VLT</u>	Crystal structure of glycan-targeting antibody 2526 Fab bound to Mannose	IMMUNE SYSTEM	aDManp
9GCJ	The crystal structure of beta-glucosidase from the thermophilic bacterium Caldicellulosiruptor saccharolyticus in complex with beta-D-glucose determined at 1.95 A resolution	HYDROLASE	bDGlcp
<u>9FYO</u>	Lacto-N-biosidase from Trueperella pyogenes	HYDROLASE	$\beta_{\beta} = \beta_{\beta} = \beta_{\beta}$
9BAL	Surface glycan-binding protein A (SGBP-A, SusD-like) from a mixed-linkage beta- glucan utilization locus in Segatella copri in complex with cellopentaose	SUGAR BINDING PROTEIN	
<u>9BMK</u>	$GH5_4$ endo-beta(1,3/1,4)-glucanase E331A from Segatella copri in complex with cellotriose	HYDROLASE	
<u>8R49</u>	Plastidial phosphorylase Pho1 from Solanum tuberosum in complex with beta cyclodextrin	TRANSFERASE	
8R4G	Plastidial phosphorylase Pho1 from Solanum tuberosum in complex with a-D- glucose	TRANSFERASE	aDGlcp
9DT7	Crystal structure of ADP-ribose diphosphatase from Klebsiella pneumoniae (5-O- phosphono-alpha-D-ribofuranose bound)	HYDROLASE	5-O-phosphono-alpha-D-ribofuranose
<u>8XUZ</u>	Structure of SARS-CoV-2 BA.2.86 spike glycoprotein in complex with ACE2 (2-up and 1-down state)	VIRAL PROTEIN/PROTEIN BINDING	$ \begin{array}{c} \bullet \\ & & \bullet \\ & & \bullet \\ & $