DIONYSUS (inserm.fr)

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

PDB ID	Title	Keywords	Date added
<u>9BGE</u>	Cryo-EM structure of mAb8-24 bound to 426c.WITO.TM.SOSIP	IMMUNE SYSTEM	$ \begin{array}{c} & \alpha \\ & \alpha $
<u>8ULE</u>	The structure of NanH in complex with Neu5,9Ac	HYDROLASE	Neu5,9Ac
<u>8UM0</u>	The structure of NanH in complex with Neu5,7,9Ac(2,6)-LAcNAc	HYDROLASE	
<u>8ZUH</u>	Crystal structure of bovine Fbs2/Skp1/Man3GlcNAc2 complex	LIGASE	$\begin{array}{c} \alpha \\ \alpha \\ \alpha \\ \alpha \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta \end{array} \xrightarrow{6} \beta 4 \begin{array}{c} \beta \\ \beta \\ \beta \end{array} \xrightarrow{6} \beta \end{array} \xrightarrow{6} \beta \end{array} \xrightarrow{6} \beta \end{array} \xrightarrow{6} \beta $
<u>8RK0</u>	HCV E1/E2 homodimer complex, ectodomain	VIRAL PROTEIN	
<u>8U2A</u>	Crystal structure of NanI in complex with Neu5,9Ac	HYDROLASE	Neu5,9Ac
<u>9C20</u>	The Sialidase NanJ in complex with Neu5,9Ac	HYDROLASE	Neu5,9Ac
<u>8UL7</u>	The structure of NanH in complex with Neu5Ac	HYDROLASE	Neu5,9Ac
<u>9J4K</u>	Crystal structure of GH9I Inulinfructotransferases (IFTase) in complex with GF2	CARBOHYDRATE	$ \begin{array}{c} \alpha \\ \alpha \\ \beta \\ \end{array} $
<u>8RJJ</u>	HCV E1/E2 homodimer complex	VIRAL PROTEIN	
<u>9IK1</u>	Cryo-EM structure of the human P2X3 receptor-compound 26a complex	MEMBRANE PROTEIN	bDGlcpNAc
<u>9J4J</u>	Crystal structure of GH9I Inulin fructotransferases(IFTase)incomplex with nystose(F3)	CARBOHYDRATE	$ \begin{array}{c} & & \\ & & $
<u>9J4I</u>	Crystal structure of GH9I Inulin fructotransferases (IFTase) in compex with fruetosyl nystose (GF4)	CARBOHYDRATE	Nystose α^2
<u>8UVV</u>	The NanJ sialidase catalytic domain in complex with Neu5Ac	HYDROLASE	Neu5,9Ac
<u>8RU4</u>	Crystal structure of Human Catenin Beta-1 in complex with stitched peptide inhibitor	SIGNALING PROTEIN	Glc
<u>8W96</u>	SmChiA with diacetyl chitobiose	HYDROLASE	
<u>8U50</u>	The structure of the catalytic domain of Nanl sialdase in complex with Neu5Gc	HYDROLASE	Neu5GC
<u>8TXU</u>	Fab 3864-10 in complex with influenza HA H3-SING16	ANTIVIRAL PROTEIN	$ \begin{array}{c} \alpha & \alpha \\ \alpha & \beta \\ \alpha & \beta \\ \alpha & \alpha \end{array} $
8WBY	Cryo-EM structure of ACE2-B0AT1 complex with JX98		$\beta_{\beta} 4 \beta_{\beta}$
8W2J	Human liver phosphofructokinase-1 filament in the T-state conformation	TRANSPORT/HYDROLASE TRANSFERASE	1,6-di-O-phosphono-beta-D-fructofuranose
8TX9	Nan Regulatory Protein (core isomerase domain) from Streptococcus pneumoniae	TRANSCRIPTION	2-acetamido-2-deoxy-6-O-phosphono-alpha-D-mannopyranose
<u>8QLI</u>	Crystal structure of Paradendryphiella salina PL7C alginate lyase mutant H124 soaked with with tetra-mannuronic acid	LYASE	
<u>9EQG</u>	CryoEM structure of human full-length alpha1beta3gamma2L GABA(A)R in complex with GABA and puerarin	MEMBRANE PROTEIN	$\begin{array}{c} \alpha & 2 \\ \alpha & \alpha \\ \alpha & \alpha \\ \alpha & \alpha \\ \alpha & 2 \\ \alpha & 2 \\ \alpha & \alpha \\$
<u>8X8K</u>	Crystal structure of STBD1 CBM20 domain in complex with maltotetraose	PROTEIN BINDING	
<u>8XPY</u>	Structure of Nipah virus Malaysia string G protein ectodomain monomer bound to single-domain antibody n425 at 3.63 Angstroms overall resolution	VIRAL PROTEIN	$ \bigcirc \alpha \ \overline{6} \bigcirc \alpha \ \overline{6} \bigcirc \beta \ \overline{4} \bigcirc \overline{6} \bigcirc \beta \ \overline{4} \bigcirc \overline{6} $
<u>8QX6</u>	Novel laminarin-binding CBM X584	SUGAR BINDING PROTEIN	
<u>80LC</u>	SA11 Rotavirus Trypsinized Triple Layered Particle	VIRUS	bDGlcpNAc
<u>80lb</u>	SA11 Rotavirus Non-tripsinized Triple Layered Particle	VIRUS	bDGlcpNAc
<u>8ZDW</u>	The cryoEM structure of H5N1 HA split from symmetric filament in conformation A	VIRAL PROTEIN/IMMUNE SYSTEM	$ \begin{array}{c c} & & & \\ $
<u>9AT9</u>	Crystal structure of Klebsiella pneumoniae FimH lectin domain bound to D-mannose	CELL ADHESION	aDManp
	The 1.26 angstrom resolution structure of Bacillus cereus beta-amylase in complex with maltose	HYDROLASE	
<u>8ZRZ</u>			
8ZRZ 8QSR	Cryo-EM structure of the glucose-specific PTS transporter IICB from E. coli in the inward-facing conformation	TRANSPORT PROTEIN	bDGlcp