

Table S3. Summary of hits and structures found for MPXV (NC_003310) antigenic proteins

MPXV virion	MPXV protein	Structures found (n)	Available structures	Chain	Rank	E-value	% Match identity	% Coverage
MV	A29	1	3VOP	C	1	3.13752E-20	90.69767442	38.73873874
MV	E8	1309	4E9O	X	1	1.2234E-158	93.13304721	75.40983607
			4ETQ	X	2	2.5556E-156	91.4893617	74.75409836
			5USH	X	3	1.7373E-158	92.73504274	75.40983607
			4ETQ	C	4	2.8765E-153	90.98712446	73.7704918
			5USH	A	5	1.201E-152	90.94827586	73.1147541
			5USL	X	6	1.5539E-155	92.24137931	74.42622951
			6B9J	X	7	2.0503E-155	91.45299145	74.42622951
			5USL	A	8	9.871E-155	91.81034483	74.09836066
			6KLZ	A	9	2.22323E-36	37.33333333	69.83606557
			6KM2	A	10	2.22323E-36	37.33333333	69.83606557
MV	H3	1	5EJO	A	1	1.6013E-142	84.38818565	65.23076923
MV	M1	6	1YPY	A	1	1.093E-131	98.9010989	72.50996016
			1YPY	B	2	3.0146E-121	99.4047619	66.93227092
			2I9L	I	3	4.5356E-125	99.42196532	68.92430279
			4U6H	J	4	2.2423E-121	99.4047619	66.93227092
			4U6H	E	5	5.7892E-120	99.39759036	66.13545817
			6CJ6	B	6	1.67502E-08	26.31578947	57.37051793
EV	A35	7	4M1G	A	1	2.77992E-48	87.80487805	43.40659341
			3K7B	B	2	4.00405E-50	88.23529412	45.05494505
			3K7B	A	3	3.96318E-48	87.95180723	43.95604396
			4M1G	B	4	1.08783E-44	82.92682927	41.20879121
			4LU5	A	5	1.13535E-50	90.36144578	45.05494505
			4LU5	B	6	9.92339E-50	89.15662651	44.50549451
			4LQF	A	7	9.12281E-44	81.70731707	40.65934066
EV	B6	36	5FOB	C	1	1.00571E-11	29.58333333	67.9245283
			6V06	A	2	1.35695E-07	33.05785124	34.90566038
			6XSD	A	3	1.35695E-07	33.05785124	34.90566038
			6V08	A	4	1.46339E-07	33.05785124	34.90566038
			2UWN	A	5	5.34893E-08	28.05755396	39.93710692
			7JIK	A	6	1.39262E-07	33.05785124	34.90566038
			1QUB	A	7	1.36882E-07	33.05785124	34.90566038
			2V8E	A	8	1.47132E-07	28.05755396	39.93710692
			1C1Z	A	9	1.33245E-07	33.05785124	34.90566038
			4AYI	E	10	2.204E-07	31.95876289	28.30188679

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Description

STRUCTURE OF VACCINIA VIRUS A27

VACCINIA D8L ECTODOMAIN STRUCTURE

VACCINIA VIRUS D8L IMV ENVELOPE PROTEIN IN COMPLEX WITH FAB OF MURINE IGG2A LA5

STRUCTURE OF VACCINIA VIRUS D8 PROTEIN BOUND TO HUMAN FAB VV66

VACCINIA VIRUS D8L IMV ENVELOPE PROTEIN IN COMPLEX WITH FAB OF MURINE IGG2A LA5

STRUCTURE OF VACCINIA VIRUS D8 PROTEIN BOUND TO HUMAN FAB VV66

STRUCTURE OF VACCINIA VIRUS D8 PROTEIN BOUND TO HUMAN FAB VV304

STRUCTURE OF VACCINIA VIRUS D8 PROTEIN BOUND TO HUMAN FAB VV138

STRUCTURE OF VACCINIA VIRUS D8 PROTEIN BOUND TO HUMAN FAB VV304

HUMAN CARBONIC ANHYDRASE II V143I VARIANT 00 ATM CO2

HUMAN CARBONIC ANHYDRASE II V143I VARIANT 15 ATM CO2

VACCINIA VIRUS H3 ENV PROT; TARGET OF NEUT AB, EXHIBITS GLYCOSYLTRANSFERASE FOLD & BINDS UDP-GLUCOSE

CRYSTAL STRUCTURE OF VACCINIA VIRUS L1 PROTEIN

CRYSTAL STRUCTURE OF VACCINIA VIRUS L1 PROTEIN

STRUCTURE OF FAB 7D11 FROM A NEUTRALIZING ANTIBODY AGAINST THE POXVIRUS L1 PROTEIN

VACCINIA L1/M12B9-FAB COMPLEX

VACCINIA L1/M12B9-FAB COMPLEX

STRUCTURE OF THE POXVIRUS PROTEIN F9

STRUCTURE OF MURINE IGG2A A27D7-FAB IN COMPLEX WITH VACCINIA ANTIGEN A33R AT THE RESOLUTION OF 1.6 ANG.

THE STRUCTURE OF THE POXVIRUS A33 PROTEIN REVEALS A DIMER OF UNIQUE C- TYPE LECTIN-LIKE DOMAINS.

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STRUCTURE OF MURINE IGG2A A27D7-FAB IN COMPLEX WITH VACCINIA ANTIGEN A33R AT THE RESOLUTION OF 1.6 ANG.

STRUCTURE OF MURINE IGG2A A20G2-FAB IN COMPLEX WITH VACCINIA ANTIGEN A33R AT RESOLUTION OF 2.9 ANG.

STRUCTURE OF MURINE IGG2A A20G2-FAB IN COMPLEX WITH VACCINIA ANTIGEN A33R AT THE RESOLUTION OF 2.9 ANG.

STRUCTURE OF MURINE IGG2B A2C7-FAB IN COMPLEX WITH VACCINIA ANTIGEN A33R AT THE RESOLUTION OF 2.3 ANG.

CRYSTAL STRUCTURE OF HUMAN COMPLEMENT C3B IN COMPLEX WITH SMALLPOX INHIBITOR OF COMPLEMENT (SPICE)

CRYSTAL STRUCTURE OF BETA-2 GLYCOPROTEIN I PURIFIED FROM PLASMA (PB2GPI)

PATIENT-DERIVED B2GPI

CRYSTAL STRUCTURE OF HUMAN RECOMBINANT BETA-2 GLYCOPROTEIN I (HRB2GPI)

CRYSTAL STRUCTURE OF HUMAN COMPLEMENT FACTOR H, SCR DOMAINS 6-8 (H402 RISK VARIANT).

HUMAN RECOMBINANT BETA-2-GLYCOPROTEIN 1

CRYSTAL STRUCTURE OF THE GLYCOSYLATED FIVE-DOMAIN HUMAN BETA2- GLYCOPROTEIN I.

CRYSTAL STRUCTURE OF HUMAN COMPLEMENT FACTOR H, SCR DOMAINS 6-8 (H402 RISK VARIANT).

CRYSTAL STRUCTURE OF HUMAN BETA-2-GLYCOPROTEIN-I (APOLIPOPROTEIN-H)

STRUCTURE OF A COMPLEX BETWEEN CCPS 6 AND 7 OF HUMAN COMPLEMENT FACTOR H.
