Supplemental Table S1. NGO0690 predicted linear (LE) and conformational (CE) epitopes

NGO0690

`>WP_003691259.1 hypothetical protein [Neisseria gonorrhoeae]`
`MNKTLSILPAAILLGGCAAGGNTFGSLDGGTGMGGSIVKMTVESQCRAELDRRSEWRLTALAMSAEKQAEWENKICGCATEEAPNQLTGND`
`VMQMLNQSTRNQALAALTVKTVSACFKRLYR`

			Linear Epitopes (LE)			
n.	**Start**	**End**	**Sequence**	**Residues**	**ElliPro Score**	**Color ***
1	20	33	GGNTFGSLDGGTGM	14	0.8	Trsp Wheat
2	52	70	RRSEWRLTALAMSAEKQAE	19	0.7	Lt Pink
3	93	100	MQMLNQST	8	0.64	Green
			Conformational epitopes (CE)			
1			G20-T23	4	0.94	Trsp Dk Gray
2			F24-M33	10	0.75	Trsp Dk Gray
3			R53-E55, R57-E70	17	0.74	Dk Gray
4			L87-N90, M93-Q94, L96-T100, Q103	12	0.67	Dk Gray

Gray-highlighted residues in the sequence above: predicted signal peptide, not shown in the cartoon models in **Figure 11A, 11A$_I$** and **11A$_{II}$**

Dashed underlined: Low confidence regions predicted by AlphaFold (yellow / orange in **Figure 11A**)

* Epitope color in **Figure 11A$_I$ and A$_{II}$**

Supplemental Table S2. NGO0948 predicted linear (LE) and conformational (CE) epitopes

NGO0948

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>WP_003693315.1 outer membrane protein assembly factor BamC [Neisseria gonorrhoeae]
MPSEPFGRHNMTNTLISITQDDTMTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPAGSGAVRASDLE
KRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVVDGKSPAEIWPLLKAFWQENGFDIESEEPAIGQMETEWAENRAKIPQDSLRRLFDTVGLG
GIYSTGERDKFIVRIEQGKNGVSDIFFAHKAMKEVYGDKNKDTTMWQPSASDPNLEAAFLTRFMQYLGVDGRQAENALAKKPTLPAANEMARIE
GKSLIVFGDYGRNWRRTGLALDRIGLTVVGQNTERHAFLVQKAPNESNAVTEQKPGLFKRLLGKGKAEKPAEQPELIVYAEPVADGSRIVLLNK
DGSAYAGKDASALLGKLHSELR
```

n.	Start	End	Sequence	Residues	ElliPro Score	Color *
Linear epitopes (LE)						
1	1	44	MPSEPFGRHNMTNTLISITQDDTMTHIKPVIAALALIGLAACSG	44	0.87	Trsp White
2	61	115	LIKLEVPPDLNNPDQGNLYRLPAGSGAVRASDLEKRRTPAVQQPADAEVLKSVKG	55	0.74	Trsp Wheat
3	173	192	IPQDSLRRLFDTVGLGGIYS	20	0.68	$ Trsp Lt Pink
4	224	233	YGDKNKDTTM	10	0.71	Trsp Green
5	280	292	RIEGKSLIVFGDY	13	0.58	Dk Pink
6	314	319	NTERHA	6	0.63	Ruby
7	331	387	AVTEQKPGLFKRLLGKGKAEKPAEQPELIVYAEPVADGSRIVLLNKDGSAYAGKDAS	57	0.66	Taupe
Conformational epitopes (CE)						
1			M1-T19	19	0.97	-
2			Q20-H26	7	0.94	-
3			P29-A40, C42-G44	15	0.72	Trsp White
4			L61-I62, L64	3	0.58	Trsp Dk Gray
5			E65-Y79	15	0.82	Trsp Dk Gray
6			L81-K95, T98-L110	28	0.74	Trsp $$ Dk Gray
7			K111-K114, G256	5	0.56	Dk Gray$$
8			G115, D130-S133, E136, G206-V210	11	0.53	Dk Gray
9			I173-P174, D176-L178, L181-F182	7	0.64	Dk Gray $
10			D183-Y191	9	0.74	Dk Gray
11			Y224-M233, S329, N330-Q335	17	0.62	Dk Gray
12			R280-S285, I287, F289-Y292, N314-A319, K351-I359, Y361-R370, V372-S387	52	0.63	Dk Gray
13			K336-K341	6	0.79	Dk Gray $
14			L343-E350	8	0.80	Dk Gray $

Gray-highlighted residues in the sequence: predicted putative signal peptide, only shown in the cartoon model in **Figure 11b and 11B.**

Dashed underlined: Low confidence regions predicted by AlphaFold (yellow / orange in **Figure 11B**)

* Epitope color in **Figure 11B$_I$ and 11B$_{II}$**

$ Partial view in the cartoon model in **Figure 11B$_{II}$**

$$ Not visible in the cartoon model in **Figure 11B$_{II}$**

Italic: Residues not predicted in LE

Supplemental Table S3. NGO1701 predicted linear (LE) and conformational (CE) epitopes

```
NGO1701
>WP_003689877.1 four-helix bundle copper-binding protein [Neisseria gonorrhoeae]
MNRRQFLGSAAAVSLASAASFARAHGHADYHHHHDMQPAAASAYTAVRQTAAHCLDAGQVCLTHCLSLLTQGDTSMSDCAVAVRQMLALCGAV
HDLAAQNSPLTRDAAKVCLEACKQCAKACKEHSAHHAECKACYESCLDCIKECEKLAA
```

			Linear epitopes (LE)			
n.	Start	End	Sequence	Residues	ElliPro Score	Color *
1	25	44	HGHADYHHHHDMQPAAASAY	20	0.82	Wheat
2	63	78	THCLSLLTQGDTSMSD	16	0.74	Lt Pink
3	99	106	QNSPLTRD	8	0.63	Green
4	123	133	KEHSAHHAECK	11	0.62	Dk Pink
5	147	151	EKLAA	5	0.75	Ruby
			Conformational epitopes (CE)			
1			H25-H31	7	0.96	Trsp Dk Gray
2			Q37-Y44, Q99-L103, R105-D106, *K109*, K149-A151	20	0.68	Dk Gray
3			T63-D78, K123-E131, K133, *E137*	27	0.70	Dk Gray

Gray-highlighted residues in the sequence: predicted signal peptide, not shown in the cartoon models in **Figure 11C, 12C$_I$ and 11C$_{II}$**

Dashed underlined: Low confidence regions predicted by AlphaFold (yellow / orange in **Figure 11C**)

* Epitope color in **Figure 11C$_I$ and 11C$_{II}$**

Italic: Residues not predicted in LE