Class-I

Parameter	Possible values	Default value	Required	Description
sequence_text			*	Input protein sequence.
method	recommended, consensus, netmhcpan, ann, smmpmbec, smm, comblib_sidney2008	recommended		This allows selection from 8 different MHC class I binding prediction methods. 'recommended' method considers, for each allele-length combination, 'consensus' method (which includes ann, smm and comblib) first, and if not available, it uses 'netmhcpan'. To print the usage and list all available methods: `$ curl --data "" http://tools-api.iedb.org/tools_api/mhci/`
allele	Allele name		*	A comma-separated list of the alleles for which to make predictions. This list gets paired with the length list, so there must be a corresponding length for each allele. To list all available alleles for a specific method and species: `$ curl --data "method=ann&species=human" http://tools-api.iedb.org/tools_api/mhci/`
length	8, 9, 10, 11, 12, 13, 14		*	A comma-separated list of the lengths for which to make predictions. This list gets paired with the allele list, so there must be a corresponding allele for each length.

Class-II

Parameter	Possible values	Default value	Required	Description
sequence_text			*	Input protein sequence.
method	recommended, consensus3, NetMHCIIpan, nn_align, smm_align, comblib, tepitope	recommended		This allows selection from 8 different MHC class II binding prediction methods. 'recommended' method considers, for each allele-length combination, 'consensus3' method (which includes comblib, smm and nn) first, and if not available, it uses 'NetMHCIIpan'. To print the usage and list all available methods: `$ curl --data "" http://tools-api.iedb.org/tools_api/mhcii/`
allele	Allele name		*	A comma-separated list of the alleles for which to make predictions. To list all available alleles for a specific method: `$ curl --data "method=nn_align" http://tools-api.iedb.org/tools_api/mhcii/`

Class-I Processing

Parameter	Possible values	Default value	Required	Description
sequence_text			*	Input protein sequence.

method	recommended, consensus, netmhcpan, ann, smmpmbec, smm, comblib_sidney2008	recommended		This allows selection from 8 different MHC class I binding prediction methods. 'recommended' method considers, for each allele-length combination, 'consensus' method (which includes ann, smm and comblib) first, and if not available, it uses 'netmhcpan'. To print the usage and list all available methods: `$ curl --data "" http://tools-api.iedb.org/tools_api/processing/`
allele	Allele name		*	A comma-separated list of the alleles for which to make predictions. This list gets paired with the length list, so there must be a corresponding length for each allele. To list all available alleles for a specific method and species: `$ curl --data "method=ann&species=human" http://tools-api.iedb.org/tools_api/processing/`
length	8, 9, 10, 11, 12, 13, 14		*	A comma-separated list of the lengths for which to make predictions. This list gets paired with the allele list, so there must be a corresponding allele for each length.

MHC-NP

Parameter	Possible values	Default value	Required	Description
sequence_text			*	Input protein sequence.
method	mhcnp	mhcnp		This allows just one prediction method - 'mhcnp' method. To print the usage: `$ curl --data "" http://tools-api.iedb.org/tools_api/mhcnp/`
allele	Allele name		*	A comma-separated list of the alleles for which to make predictions. This list gets paired with the length list, so there must be a corresponding length for each allele. Currently, the tool supports only HLA-A*02:01, HLA-B*07:02, HLA-B*35:01, HLA-B*44:03, HLA-B*53:01, HLA-B*57:01, H-2-Db, and H-2-Kb alleles To list all available alleles for a specific method: `$ curl --data "method=mhcnp" http://tools-api.iedb.org/tools_api/mhcnp/`
length	8, 9, 10, 11		*	A comma-separated list of the lengths for which to make predictions. This list gets paired with the allele list, so there must be a corresponding allele for each length.