### Zadanie 1

### Gen1.txt

Gn.Ex Type S .Begin ...End .Len Fr Ph I/Ac Do/T CodRg P.... Tscr..

1.01 Sngl + 53 3781 3729 1 0 110 36 3485 0.849 336.62

3.02 Term - 51355 51246 110 2 2 82 36 136 0.870 5.49

3.01 Init - 56840 56606 235 2 1 67 19 205 0.368 9.85

Descriptions Graphic Summary Alignments	Taxonomy							
Sequences producing significant alignments		Download	d V Nev	Selec	t colur	nns Y	Show	100 🗸 🔞
select all 0 sequences selected			k <u>Graph</u>	ics [	istance	e tree of I	esults N	ew MSA Viewe
Description	Scientific Name	Max Score	Total Score	Query	E value	Per.	Acc. Len	Accession
	Transcripts							_
Homo sapiens insulin receptor substrate 1 (IRS1), mRNA	Homo sapiens	9118	16140	12%	0.0	100.00%	9771	NM_005544.3
	Genomic sequences							-
Homo sapiens chromosome 2, GRCh38,p13 Primary Assembly	Homo sapiens	1.246e+05	1.246e+05	100%	0.0	100.00%	242193529	NC_000002.12

### Gen2.txt

2.09 Intr + 83127 83209 83 2 2 95 109 29 0.938 4.14

3.05 Term - 93759 93695 65 1 2 58 46 76 0.820 -1.55

4.01 Init + 101351 101737 387 1 0 60 72 196 0.747 12.01

	Transcripts							- E
V	PREDICTED: Homo sapiens uncharacterized LOC105370834 (LOC105370834), transcript vari Homo sapiens	1930	1930	0%	0.0	94.46%	2308	XR_001751554.2
~	PREDICTED: Homo sapiens OCA2 melanosomal transmembrane protein (OCA2), transcript v Homo sapiens	1544	6852	1%	0.0	100.00%	3681	XM_017022261.1
~	$\underline{PREDICTED}; \underline{Homo \ sapiens \ OCA2 \ melanosomal \ transmembrane \ protein \ (\underline{\mathsf{OCA2}), \underline{transcript \ v} \ \underline{Homo \ sapiens \ }}$	1533	5441	0%	0.0	100.00%	2893	XM_017022265.1
~	Homo sapiens ribosomal protein L5 (RPL5), transcript variant 1, mRNA Homo sapiens	1225	1225	0%	0.0	89.16%	1028	NM_000969.5
$\checkmark$	Homo sapiens OCA2 melanosomal transmembrane protein (OCA2), transcript variant 2, mRNA Homo sapiens	1116	5800	0%	0.0	100.00%	3071	NM_001300984.2
$\checkmark$	Homo sapiens OCA2 melanosomal transmembrane protein (OCA2), transcript variant 1, mRNA Homo sapiens	1116	5938	0%	0.0	100.00%	3143	NM_000275.3
$\checkmark$	$\underline{PREDICTED}; \underline{Homo \ sapiens \ OCA2 \ melanosomal \ transmembrane \ protein \  \underline{(OCA2)}, \underline{transcript \ v} \ \underline{Homo \ sapiens \ }$	1116	5627	0%	0.0	100.00%	2980	XM_017022263.1
V	$\underline{PREDICTED}. \ Homo \ \underline{sapiens} \ OCA2 \ \underline{melanosomal} \ \underline{transmembrane} \ \underline{protein} \ \underline{(OCA2)}. \ \underline{transcript} \ \underline{v} \ \underline{Homo} \ \underline{sapiens}$	1116	5680	0%	0.0	100.00%	3049	XM_017022260.1
~	$\underline{PREDICTED}; \underline{Homo \ sapiens \ OCA2 \ melanosomal \ transmembrane \ protein \ (\underline{\mathsf{OCA2}). \ transcript \ y \ \mathsf{Homo \ sapiens \ ocapiens \$	1116	5803	0%	0.0	100.00%	3073	XM_017022259.1
V	$\underline{PREDICTED}. \ Homo \ \underline{sapiens} \ OCA2 \ \underline{melanosomal} \ \underline{transmembrane} \ \underline{protein} \ \underline{(OCA2)}. \ \underline{transcript} \ \underline{v} \ \underline{Homo} \ \underline{sapiens}$	1116	5805	0%	0.0	100.00%	3115	XM_017022257.1
$\checkmark$	$\label{eq:predicted:predicted:protein} \begin{picture}{ll} PREDICTED: Homo sapiens OCA2 melanosomal transmembrane protein (OCA2), transcript v Homo sapiens ocas description of the protein of the protein ocas description of the protein ocas description ocas$	1116	6818	1%	0.0	100.00%	3620	XM_017022256.1
~	$\underline{PREDICTED}; \underline{Homo} \ \underline{sapiens} \ \underline{OCA2} \ \underline{melanosomal} \ \underline{transmembrane} \ \underline{protein} \ \underline{(OCA2)}, \underline{transcript} \ \underline{v} \ \underline{Homo} \ \underline{sapiens}$	1116	5939	0%	0.0	100.00%	3214	XM_011521640.2
~	$\underline{PREDICTED}; \underline{Homo \ sapiens \ OCA2 \ melanosomal \ transmembrane \ protein \ (\underline{\mathsf{OCA2}), \underline{transcript \ v} \ \underline{Homo \ sapiens \ }}$	1116	5902	0%	0.0	100.00%	3165	XM_017022255.1
~	$\underline{PREDICTED}; \underline{Homo \ sapiens \ OCA2 \ melanosomal \ transmembrane \ protein \ (\underline{\mathsf{OCA2}), \underline{transcript \ v} \ \mathsf{Homo \ sapiens \ ocapiens \ ocapie$	1107	5568	0%	0.0	100.00%	2957	XM_017022262.1
V	Homo sapiens ribosomal protein L5 (RPL5), transcript variant 2, non-coding RNA Homo sapiens	815	1204	0%	0.0	91.09%	1024	NR_146333.1
~	$\underline{PREDICTED}; \underline{Homo \ sapiens \ OCA2 \ melanosomal \ transmembrane \ protein \  \underline{(OCA2)}, \underline{transcript \ v} \ \underline{Homo \ sapiens \ }$	464	3730	0%	2e-125	100.00%	1974	XR_001751294.1
$\checkmark$	${\tt PREDICTED: Homo\ sapiens\ OCA2\ melanosomal\ transmembrane\ protein\ (OCA2),\ transcript\ v\ \ Homo\ sapiens}$	464	4510	0%	2e-125	100.00%	2701	XM_017022264.1
~	PREDICTED: Homo sapiens OCA2 melanosomal transmembrane protein (OCA2), transcript v Homo sapiens	464	4825	0%	2e-125	100.00%	2866	XM_017022258.1

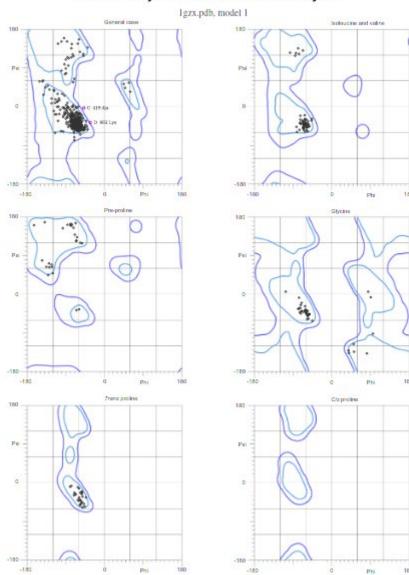
	Genomic s	equences							_
	Homo sapiens chromosome 15, GRCh38,p13 Primary Assembly	Homo sapiens	6.361e+05	6.529e+05	100%	0.0	100.00%	101991189	NC_000015.10
$\checkmark$	Homo sapiens chromosome 15 genomic patch of type FIX, GRCh38.p13 PATCHES HG2139_P.	Homo sapiens	4.304e+05	4.356e+05	67%	0.0	99.92%	4998962	NW_011332701.1
$\checkmark$	Homo sapiens chromosome 15 genomic scaffold, GRCh38,p13 alternate locus group ALT_RE	Homo sapiens	4.304e+05	4.356e+05	67%	0.0	99.92%	5161414	NT_187660.1
~	Homo sapiens chromosome 22, GRCh38.p13 Primary Assembly	Homo sapiens	1155	1910	0%	0.0	87.54%	50818468	NC_000022.11
$\checkmark$	Homo sapiens chromosome 1, GRCh38,p13 Primary Assembly	Homo sapiens	1149	4480	0%	0.0	88.22%	248956422	NC_000001.11
$\checkmark$	Homo sapiens chromosome 2, GRCh38.p13 Primary Assembly	Homo sapiens	1149	1979	0%	0.0	87.43%	242193529	NC_000002.12
~	Homo sapiens chromosome 11, GRCh38.p13 Primary Assembly	Homo sapiens	1112	2560	0%	0.0	86.97%	135086622	NC_000011.10
~	Homo sapiens chromosome 5, GRCh38,p13 Primary Assembly	Homo sapiens	1053	2276	0%	0.0	85.90%	181538259	NC_000005.10
$\checkmark$	Homo sapiens chromosome 8, GRCh38.p13 Primary Assembly	Homo sapiens	1051	3078	0%	0.0	86.00%	145138636	NC_000008.11
$\checkmark$	Homo sapiens chromosome 11 genomic scaffold, GRCh38.p13 alternate locus group ALT_REF.	<u>Homo sapiens</u>	1051	1051	0%	0.0	85.77%	200998	NW_003871073.1
V	Homo sapiens chromosome 19, GRCh38.p13 Primary Assembly	Homo sapiens	1027	2104	0%	0.0	86.14%	58617616	NC_000019.10
$\checkmark$	Homo sapiens chromosome 4, GRCh38,p13 Primary Assembly	Homo sapiens	1005	2198	0%	0.0	86.18%	190214555	NC_000004.12
$\checkmark$	Homo sapiens chromosome 6, GRCh38.p13 Primary Assembly	Homo sapiens	985	985	0%	0.0	85.38%	170805979	NC_000006.12
V	Homo sapiens chromosome 10, GRCh38,p13 Primary Assembly	Homo sapiens	942	3212	0%	0.0	84.45%	133797422	NC_000010.11
V	Homo sapiens chromosome 3, GRCh38,p13 Primary Assembly	Homo sapiens	813	813	0%	0.0	82.22%	198295559	NC_000003.12
¥	Homo sapiens chromosome 17, GRCh38.p13 Primary Assembly	Homo sapiens	651	651	0%	0.0	82.38%	83257441	NC_000017.11

Zadanie 2

W bialku dominuja aphla-heliksy.

Wygląd mapy miałby wskazywać na przewagę aphla-heliks.

## MolProbity Ramachandran analysis





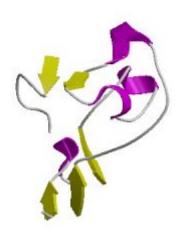
# Top of CATH Hierarchy (4 classes)

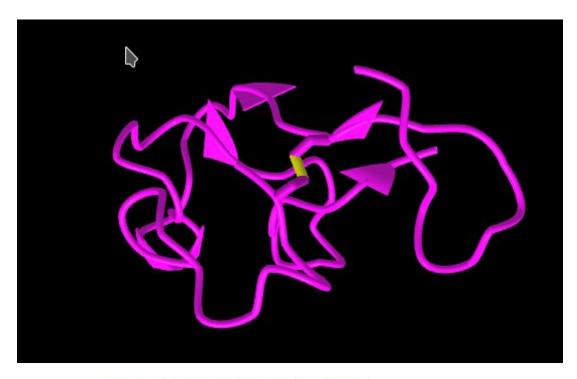
Þ	[C]	1	Mainly Alpha	5 Architectures, 4
$\triangleright$	[C]	2	Mainly Beta	21 Architectures, 2-
Þ	[C]	3	Alpha Beta	14 Architectures, 6:
Þ	C	4	Few Secondary Structures	1 Architecture
$\triangleright$	C	6	Special	2 Architecture

## H Leishmanolysin domain 3

### Go to Superfamily >

CATH ID	2.10.55.10
Domains	1
Example Domain	1lmlA03 [PDB]





## MolProbity Ramachandran analysis

