

# Søren Skou Thirup

## List of Publications by Year in descending order

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36  
papers

2,474  
citations

361045

20  
h-index

344852

36  
g-index

37  
all docs

37  
docs citations

37  
times ranked

2681  
citing authors

#	ARTICLE	IF	CITATIONS
1	The crystal structure of elongation factor EF-Tu from <i>Thermus aquaticus</i> in the GTP conformation. <i>Structure</i> , 1993, 1, 35-50.	1.6	405
2	LysM domains mediate lipochitin oligosaccharide recognition and Nfr genes extend the symbiotic host range. <i>EMBO Journal</i> , 2007, 26, 3923-3935.	3.5	346
3	Legume receptors perceive the rhizobial lipochitin oligosaccharide signal molecules by direct binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13859-13864.	3.3	301
4	The crystal structure of Cys-tRNA <sup>Cys</sup> -EF-Tu-GDPNP reveals general and specific features in the ternary complex and in tRNA. <i>Structure</i> , 1999, 7, 143-156.	1.6	244
5	Helix unwinding in the effector region of elongation factor EF-Tu-GDP. <i>Structure</i> , 1996, 4, 1141-1151.	1.6	226
6	Evolution and Regulation of the <i>Lotus japonicus</i> LysM Receptor Gene Family. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 510-521.	1.4	117
7	Heparan sulfate proteoglycans present PCSK9 to the LDL receptor. <i>Nature Communications</i> , 2017, 8, 503.	5.8	89
8	A Unique Loop Extension in the Serine Protease Domain of Haptoglobin Is Essential for CD163 Recognition of the Haptoglobin-Hemoglobin Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 1072-1079.	1.6	69
9	High resolution crystal structure of bovine mitochondrial EF-tu in complex with GDP. <i>Journal of Molecular Biology</i> , 2000, 297, 421-436.	2.0	65
10	Improved Characterization of Nod Factors and Genetically Based Variation in LysM Receptor Domains Identify Amino Acids Expendable for Nod Factor Recognition in <i>Lotus</i> spp.. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 58-66.	1.4	62
11	Structural determination of the functional sites of <i>E. coli</i> elongation factor Tu. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1990, 1050, 203-208.	2.4	58
12	Crystal structure of the receptor-binding domain of Î±2-macroglobulin. <i>Structure</i> , 1998, 6, 595-604.	1.6	46
13	Cooperative binding of LysM domains determines the carbohydrate affinity of a bacterial endopeptidase protein. <i>FEBS Journal</i> , 2014, 281, 1196-1208.	2.2	45
14	Structure of the ternary complex of EF-Tu: macromolecular mimicry in translation. <i>Trends in Biochemical Sciences</i> , 1996, 21, 81-82.	3.7	44
15	Crystal structure of a transfer-ribonucleoprotein particle that promotes asparagine formation. <i>EMBO Journal</i> , 2010, 29, 3118-3129.	3.5	43
16	An intermolecular binding mechanism involving multiple LysM domains mediates carbohydrate recognition by an endopeptidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 592-605.	2.5	34
17	The identification of AF38469: An orally bioavailable inhibitor of the VPS10P family sorting receptor Sortilin. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2014, 24, 177-180.	1.0	33
18	Identification of the first small-molecule ligand of the neuronal receptor sortilin and structure determination of the receptor-ligand complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 451-460.	2.5	32

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19	Crystal structure of the TLDC domain of oxidation resistance protein 2 from zebrafish. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1694-1698.	1.5	31
20	A <i>Lotus japonicus</i> cytoplasmic kinase connects Nod factor perception by the NFR5 LysM receptor to nodulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14339-14348.	3.3	28
21	Structural information for explaining the molecular mechanism of protein biosynthesis. <i>FEBS Letters</i> , 1999, 452, 41-46.	1.3	19
22	Acidic Environment Induces Dimerization and Ligand Binding Site Collapse in the Vps10p Domain of Sortilin. <i>Structure</i> , 2017, 25, 1809-1819.e3.	1.6	19
23	Hidden Twins: SorCS Neuroreceptors Form Stable Dimers. <i>Journal of Molecular Biology</i> , 2017, 429, 2907-2917.	2.0	15
24	Purification and crystallization of the ternary complex of elongation factor Tu:GTP and Phe-tRNA <sup>Phe</sup> . <i>FEBS Letters</i> , 1994, 356, 165-168.	1.3	12
25	The identification of novel acid isostere based inhibitors of the VPS10P family sorting receptor Sortilin. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017, 27, 2629-2633.	1.0	12
26	PAK Kinases Target Sortilin and Modulate Its Sorting. <i>Molecular and Cellular Biology</i> , 2020, 40, .	1.1	12
27	Isolation, crystallization and X-ray analysis of the quaternary complex of Phe-tRNA <sup>Phe</sup> , EF-Tu, a GTP analog and kirromycin. <i>FEBS Letters</i> , 1996, 399, 59-62.	1.3	11
28	Functional effects of deleting the coiled-coil motif in <i>Escherichia coli</i> elongation factor Ts. <i>FEBS Journal</i> , 2003, 270, 4294-4305.	0.2	11
29	Analysis and crystallization of a 25 kDa C-terminal fragment of cloned elongation factor Ts from <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1995, 368, 49-54.	1.3	10
30	Crystal and solution structures of fragments of the human leucocyte common antigen-related protein. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 406-417.	1.1	9
31	Purification, crystallization and preliminary crystallographic studies of the TLDC domain of oxidation resistance protein 2 from zebrafish. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1253-1256.	0.7	6
32	Crystallisation and preliminary X-ray analysis of the receptor-binding domain of human and bovine $\alpha$ 2-macroglobulin. <i>FEBS Letters</i> , 1995, 372, 93-95.	1.3	5
33	Macromolecular mimicry in protein biosynthesis. <i>Folding &amp; Design</i> , 1997, 2, S7-S11.	4.5	5
34	Crystallization of human complement component C5. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 643-646.	2.5	4
35	Crystallization of <i>Escherichia coli</i> maltoporin in the trigonal space group $R\bar{3}$ . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 114-116.	0.7	2
36	Up, Down, and Around: Identifying Recurrent Interactions Within and Between Super-secondary Structures in $\beta$ -Propellers. <i>Methods in Molecular Biology</i> , 2012, 932, 35-50.	0.4	2