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**Supporting information for article:**

**Crystal structures of the naturally fused CS and cytochrome *b5* reductase domains of Ncb5or reveal an expanded CS fold, extensive CS–*b5*R interactions and productive binding of the NAD(P)<sup>+</sup> nicotinamide ring**

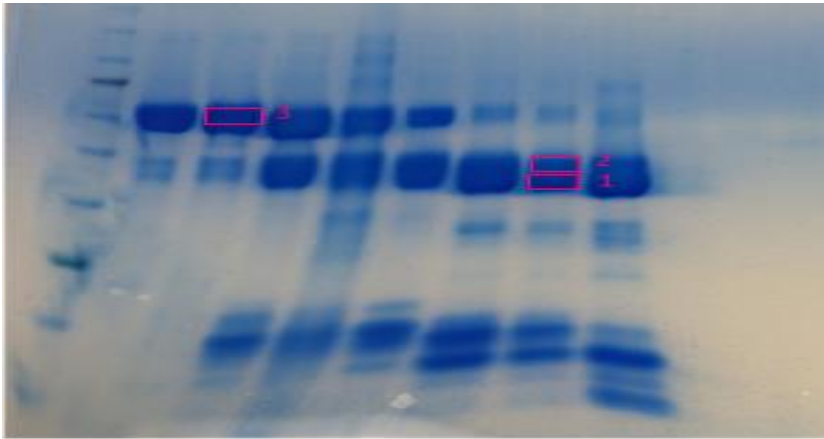
**David R. Benson, Scott Lovell, Nurjahan Mehzabeen, Nadezhda Galeva, Anne Cooper, Philip Gao, Kevin P. Battaile and Hao Zhu**

**Table S1.** A partial list of known structures of the CS domain and its partner. N/A: not available.

Protein	PDB #	Partner	Function	Reference
Ncb5or-CS (human)	6MV1, 6MV2	Ncb5or-b5R (human)	inter-domain (and inter-protein) electron transfer	This study
PIH1D1 (human)	6GXZ	RPAP3 (human)	HSP90 co-chaperone R2TP complex	(Henri <i>et al.</i> , 2018)
SHQ1 (human)	4PBD	Dyskerin (human)	H/ACA ribonucleoprotein particle assembly	(Singh <i>et al.</i> , 2015)
SHQ1 (yeast)	3EUD	Cbf5 (yeast)	H/ACA ribonucleoprotein particle assembly	(Singh <i>et al.</i> , 2009), (Singh <i>et al.</i> , 2015)
SGT1 (cress)	2JKI	Hsp90 (barley)	kinetochore complex	(Zhang <i>et al.</i> , 2008)
SGT1 (cress)	2XCM	RAR1 (cress)	regulation of innate immunity	(Zhang <i>et al.</i> , 2010)
p23/Hsp20 (human)	1EJF	N/A	heat shock (stress) response	(Weaver <i>et al.</i> , 2000)
NudC (human)	3QOR	N/A	maintenance of nuclear migration	(Zheng <i>et al.</i> , 2011)
NudC (mouse)	1WFI	N/A	maintenance of nuclear migration	N/A
NudCD2 (mouse)	2RH0	homo-dimer	maintenance of nuclear migration (?)	N/A
$\alpha$ B crystallin (human)	2WJ7	Hsp20 (rat)	heat shock (stress) response	(Bagneris <i>et al.</i> , 2009)
$\alpha$ A crystallin (bovine)	3L1E, 3L1F	$\alpha$ B crystallin (human)	heat shock (stress) response	(Laganowsky <i>et al.</i> , 2010)
USP19 (human)	1WH0	N/A	Ubiquitin Carboxyl- terminal Hydrolase	N/A
HspB2 (human)	6F2R	HspB3 (human)	heat shock (stress) response	N/A
Nuclear movement protein ( <i>E. cuniculi</i> )	2O30	homo-dimer	nuclear movement	N/A
AgsA ( <i>S. typhimurium</i> )	4ZJ9	homo-dimer	heat shock (stress) response	(Mani <i>et al.</i> , 2016)
KIAA1068 (human)	1WGV	N/A	unknown	N/A
Sgt1 (human)	1RL1	N/A	protein degradation	(Lee <i>et al.</i> , 2004)

**Figure S1.** A) SDS-PAGE of limited proteolysis of full-length Ncb5or with trypsin. Lanes (left-right): molecular marker, uncut, 0, 1, 2, 5, 24, 30, 48 hrs (digestion). Bands 1, 2 and 3 were excised from the gel and subjected to peptide mapping with chymotrypsin. The LC-MS/MS results of their products are listed in **B**).

**A**

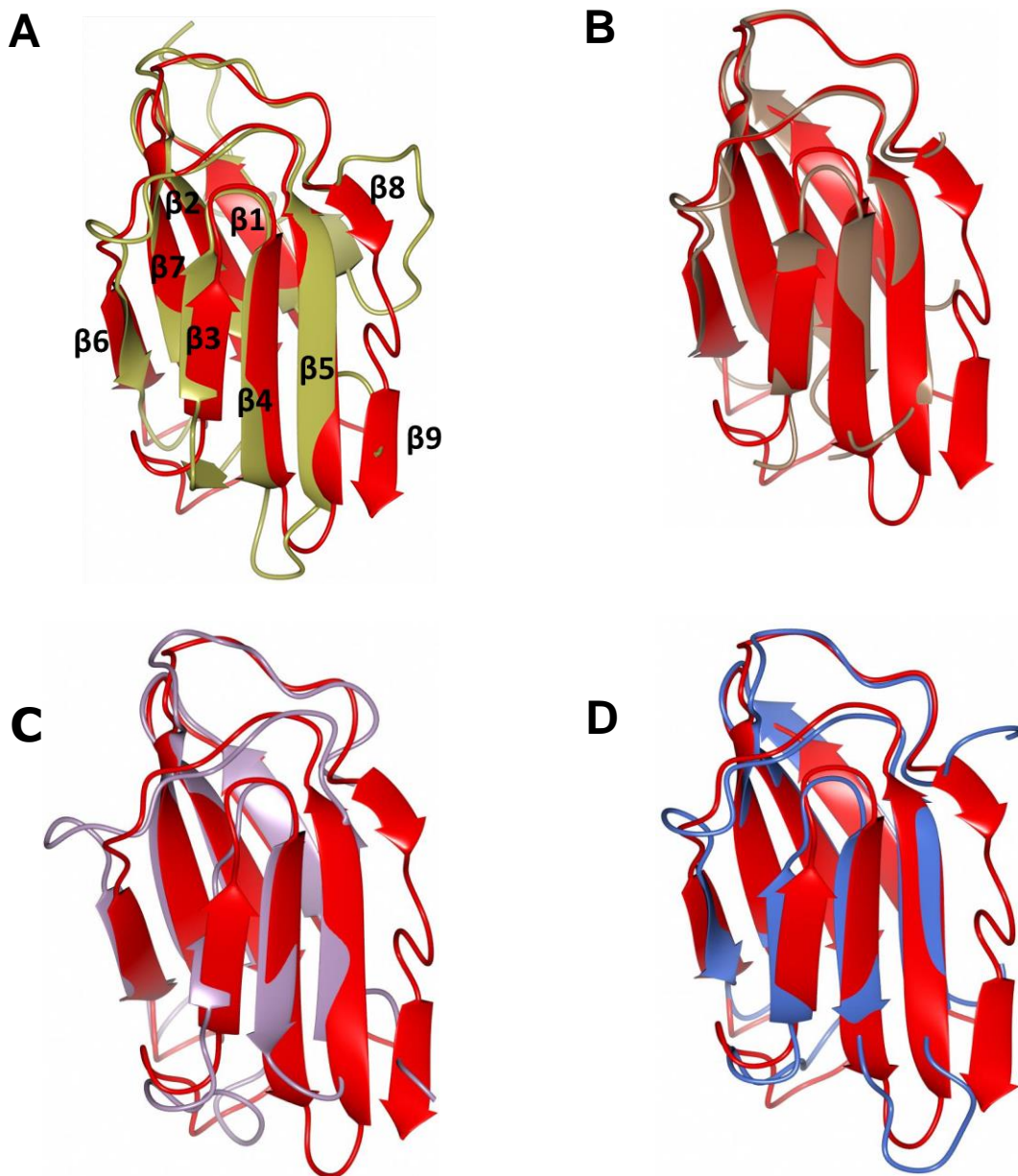


**B**

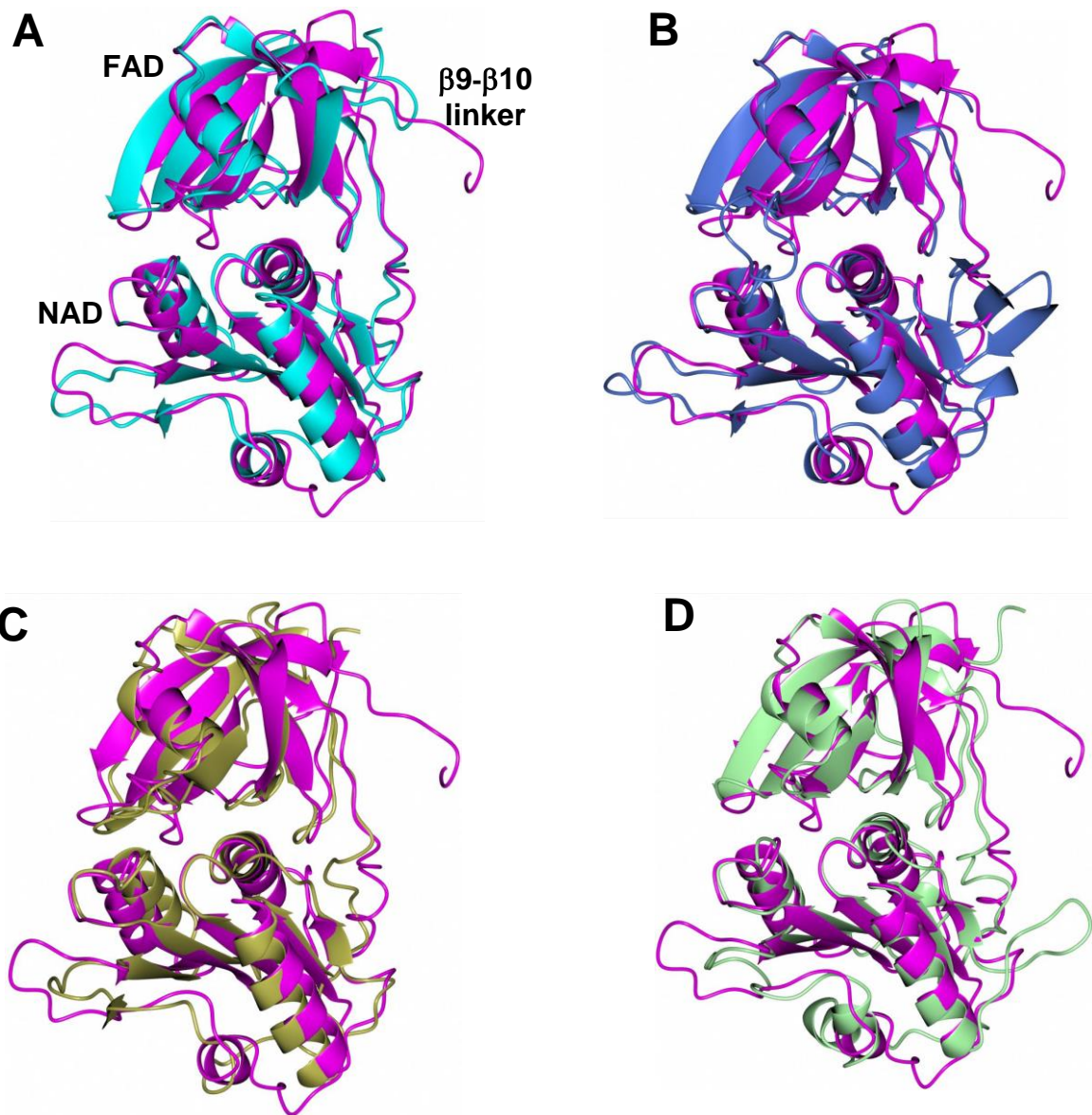
Peptide Sequence	Begin Position	End Position	Precursor Mz	Precursor Charge	Peptide retention time	Sample 1 Ion peak area	Sample 2 Ion peak area	Sample 3 Ion peak area
NVPSQSFPAPR	10	21	600.312	2	14.61	0	27675	2236017
VASGGRSKVPL	25	36	535.8195	2	10.4	0	0	9834564
SGKDLTGL	50	58	395.7189	2	13.5	3981	0	2240638
ICIRGFVY	80	88	514.2733	2	25.77	38293	37061	2327473
ICIRGF	80	86	383.2074	2	21.12	0	0	40993764
VYVNSPY	86	93	421.2082	2	16.54	0	0	703489
DQVHRW	116	122	420.7092	2	9.69	0	0	461359
DQVHRWVNY	116	125	608.7965	2	17.99	0	0	3066170
ESMLKECL	125	133	505.2383	2	18.72	0	0	2762120
<u>EGPSYPSYDWF</u>	<u>170</u>	<u>181</u>	<u>674.28</u>	<u>2</u>	<u>31.95</u>	<u>4761810</u>	<u>1579519</u>	<u>0</u>
<u>DINLDSIIVDHQNSFR</u>	<u>196</u>	<u>213</u>	<u>1000.987</u>	<u>2</u>	<u>28.3</u>	<u>424810</u>	<u>0</u>	<u>0</u>
<u>DINLDSIIVDHQNSFR</u>	<u>196</u>	<u>213</u>	<u>667.6606</u>	<u>3</u>	<u>28.3</u>	<u>1795294</u>	<u>201435</u>	<u>0</u>
LIHIGLSHEVQEDF	223	237	818.9201	2	25.89	5930836	4460630	3302128
LIHIGL	223	229	333.2209	2	24.21	4296662	2649834	1914309
DFLGHPL	260	267	399.7109	2	23.22	25892176	14434548	17119236
CLMLPPSTHLQVPIGQHVY	301	320	1095.564	2	31.1	14668356	10471283	19999802
CLMLPPSTHLQVPIGQHVY	301	320	730.7115	3	31.1	20912006	17936324	31948456
CLMLPPSTHL	301	311	584.7963	2	24.08	2863936	500939	1053886
MLPPSTHLQVPIGQHVY	303	320	639.6732	3	23.98	1934978	611568	1671057

QVPIGQHVY	311	320	520.7798	2	15.31	15002936	8494890	7484312
QVPIGQHYYL	311	321	577.3218	2	21.68	7734609	4201766	3757868
LKLPITGTEIVKPY	320	334	786.474	2	26.59	1.58E+08	1.09E+08	160966512
LKLPITGTEIVKPY	320	334	524.6518	3	26.59	1.97E+08	1.48E+08	202504352
KLPITGTEIVKPY	321	334	729.932	2	21.88	64155364	46617284	73147008
KLPITGTEIVKPY	321	334	486.9571	3	21.88	53522968	40591712	58519704
TPVSGSLLSEF	334	345	568.7953	2	30.48	67067796	41762596	36763948
KEPVLNNKY	345	355	601.3324	2	13.04	6903187	4025524	2494419
KEPVLNNKY	345	355	401.224	3	13.04	2089857	1047379	620918
IKIYPTGLF	359	368	526.313	2	29.02	889565	454892	150452
TPELDRL	368	375	422.2322	2	17.86	1000109	412504	110493
QIGDFVSVSSPEGNF	375	390	791.8728	2	27.6	3125253	1734724	718776
VSVSSPEGNF	380	390	511.7431	2	18.21	1607199	949887	426350
ALTDIPSLR	419	428	493.2875	2	21.1	63188620	34123092	29151366
FNKTEDDIW	434	444	640.8115	2	25.67	11851054	6974407	7392802
NKTEDDIW	435	444	567.2773	2	23.42	46864804	26914894	28664094
VLSAPISEW	462	471	501.2688	2	27.07	13970847	5699884	10266745
NGKQGHISPALL	471	483	617.8488	2	17.3	2049715	709153	1163179
VCICGPVPF	497	506	524.7514	2	27.16	44645556	28843044	47993448
TEQGVRL	506	513	401.7245	2	12.2	8292545	6069676	8043911
TEQGVRL	506	514	458.2665	2	18.24	78778544	56141264	68987392
NFSKNEIHSF	517	527	611.7962	2	16.87	119918	46362	59720
SKNEIHSF	519	527	481.2405	2	10.88	3565085	2245790	1371276
SKNEIHSF	519	527	321.1628	3	10.88	643460	314515	171685
SKNEIHSFTA	519	529	567.2829	2	12.66	1436111	965453	2004352

**Figure S2.** Superposition of the CS domain of CS-b5R-NAD (red) with **A**) human chaperone protein p23 (gold; PDB entry 1EJF, (Weaver *et al.*, 2000)), **B**) nuclear movement protein from *E. cuniculi* GB-M1 (brown; PDB entry 2O30, <http://www.rcsb.org/structure/2O30>), **C**) CS domain of the essential baker's yeast H/ACA ribonucleoparticle assembly protein (lilac; PDB entry 3EUD (Singh *et al.*, 2009)), **D**) cress *Arabidopsis thaliana* SGT1-like protein (blue, 2XCM, (Zhang *et al.*, 2010)).

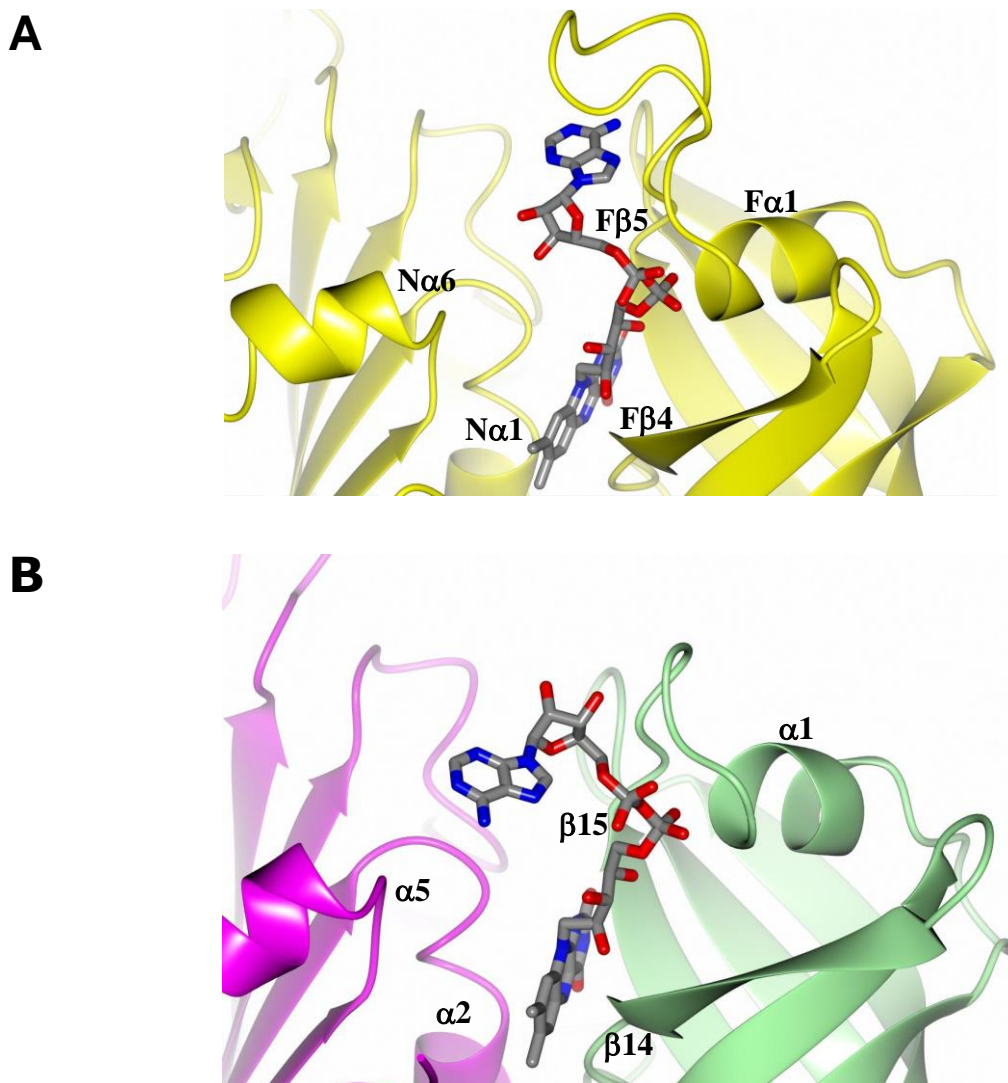


**Figure S3.** Superposition of the b5R domain of CS-b5R-NAD (magenta) with **A)** *P. polycephalum* b5R (2EIX, cyan); **B)** corn NADH dependent nitrate reductase (2CND, blue) (Lu *et al.*, 1995), **C)** nitric oxide dioxygenase from *Vibrio cholerae* O1 biovar El Tor (4EH1, gold) and **D)** ferredoxin NADP reductase from *Neisseria gonorrhoeae* (5TR9, gold). The NAD and FAD sub-domains and the linker between strands  $\beta 9$  and  $\beta 10$  in CS-b5R-NAD are indicated in panel A.



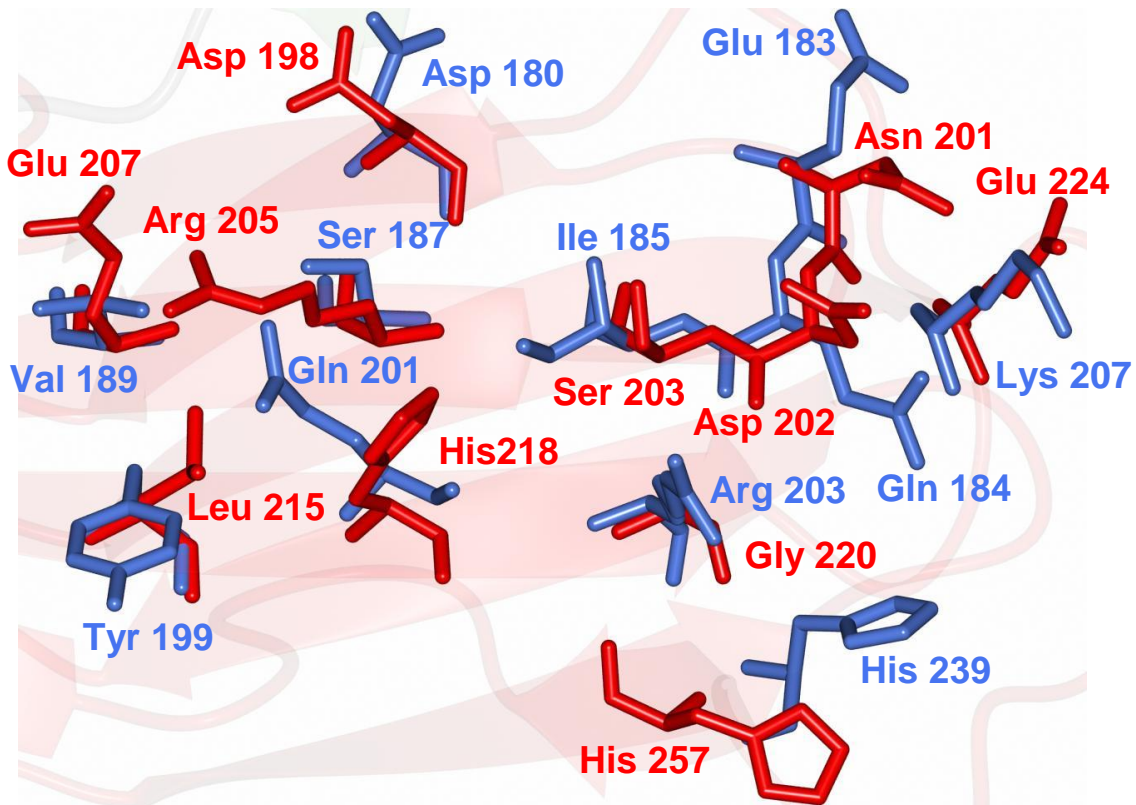


**Figure S4.** Comparison of the environment for the FAD adenine ring in human Cyb5R3 (1UMK, **A**) and CS-b5R (**B**).

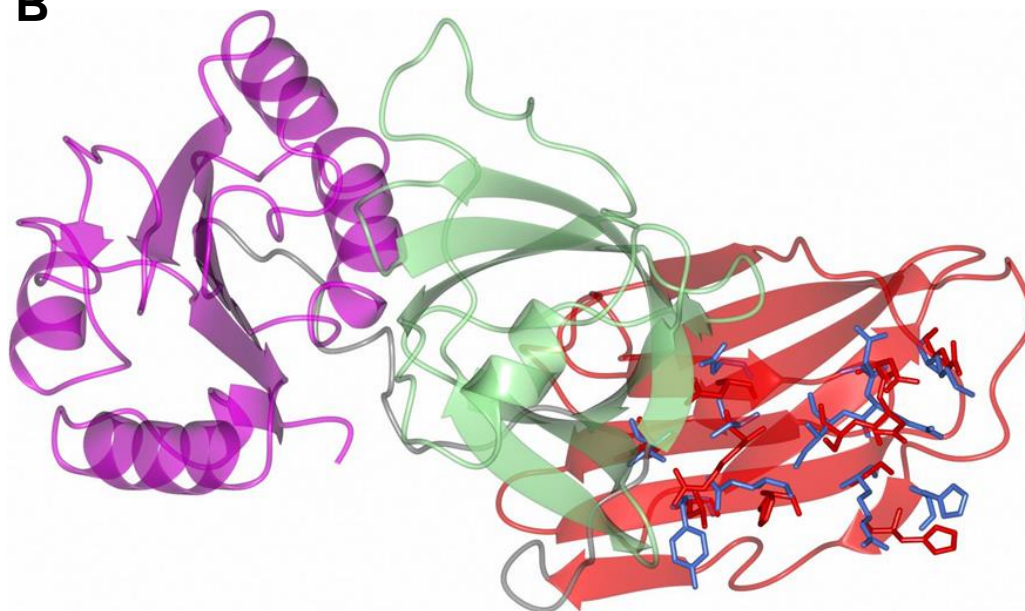


**Figure S5.** **A)** Comparison of the CS-domain surface residues of 2XCM (blue) and CS-b5R-NAD (red). **B)** Same as **A)** with the b5R domain shown.

**A**



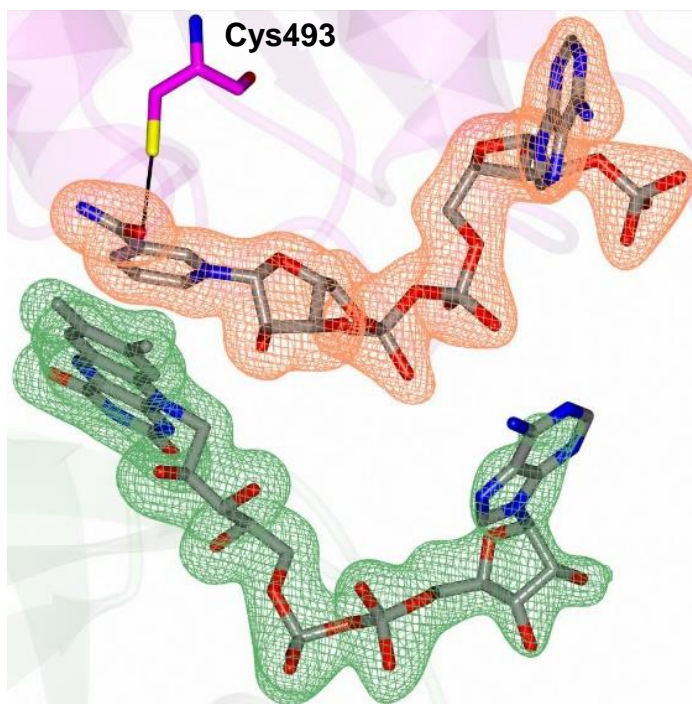
**B**



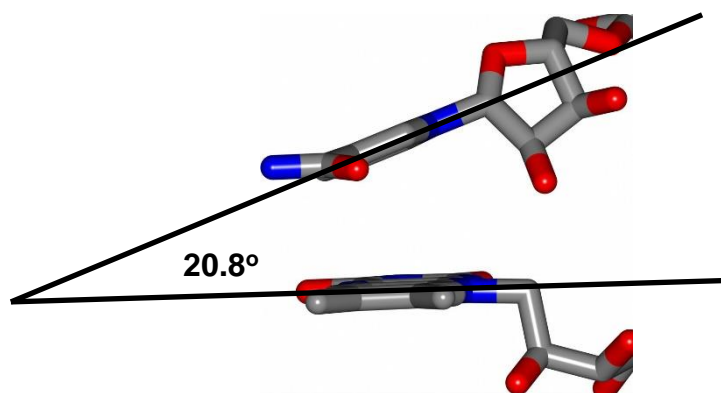


**Figure S6.** Interaction between FAD and NADP<sup>+</sup> in CS-b5R-NADP. **A)** Electron density maps (Fo-Fc polder omit, Adams *et al.*, 2010) for FAD (green) and NADP<sup>+</sup> (coral). **B)** Angle between the mean planes of the FAD (flavin) and NADP<sup>+</sup> (nicotinamide) rings.

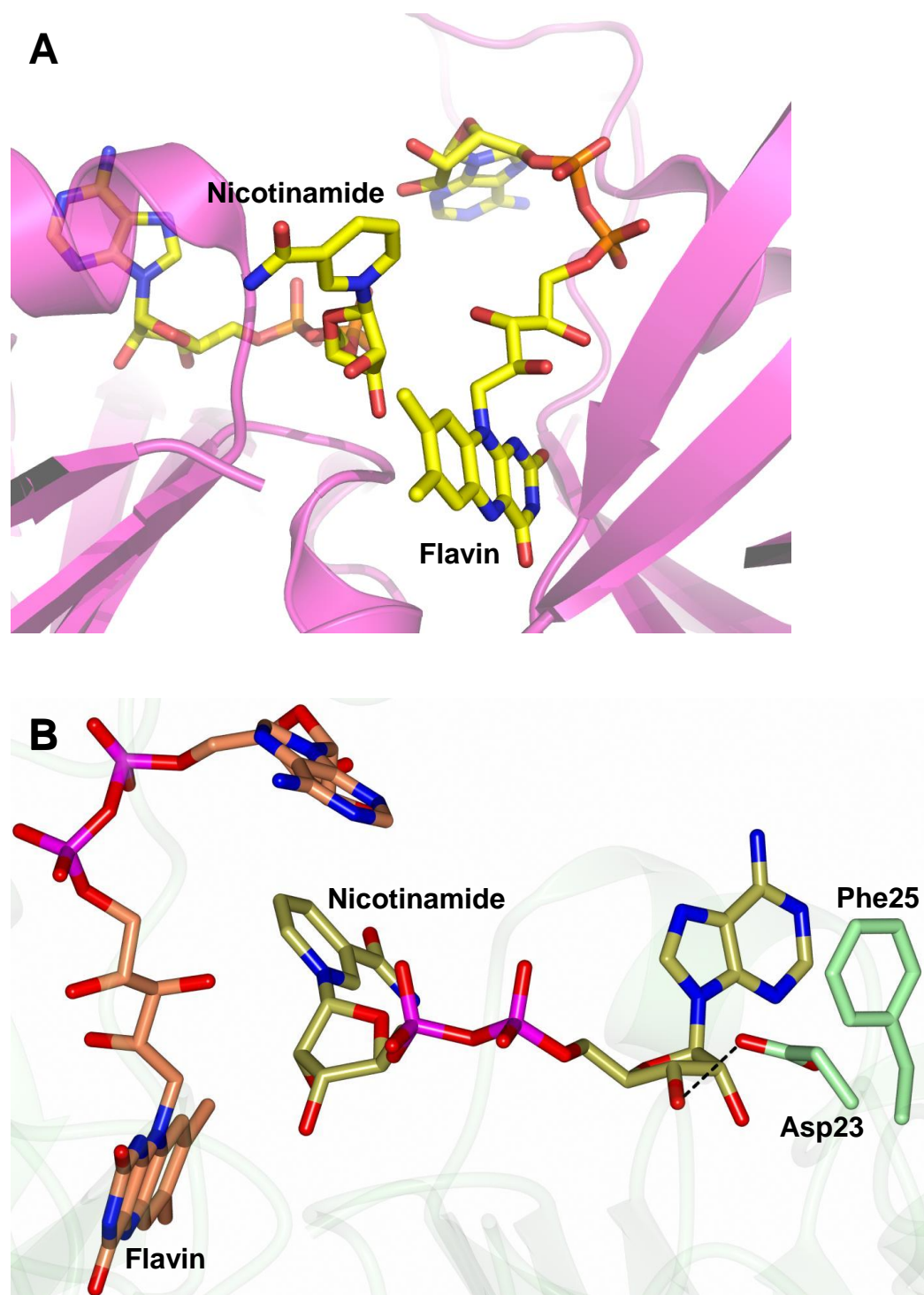
**A**



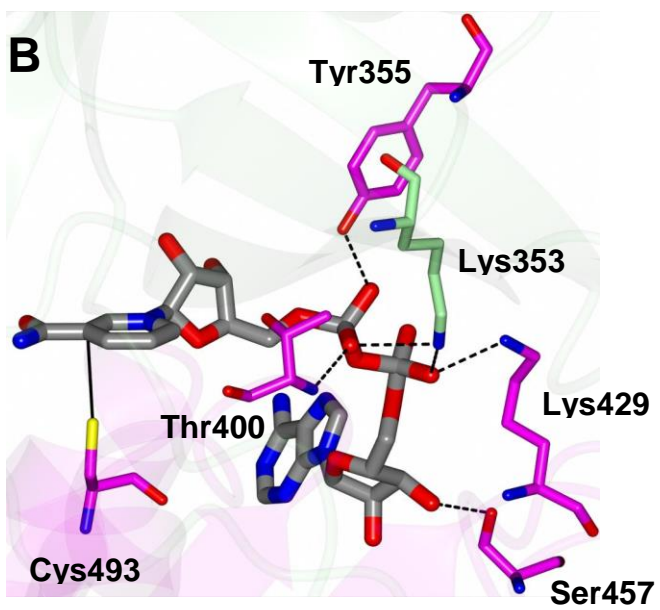
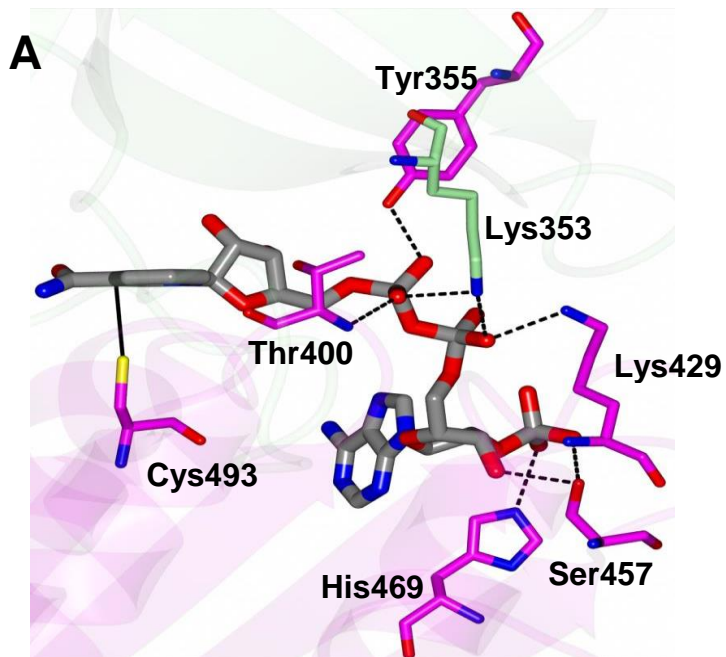
**B**



**Figure S7.** Two views of the structure of oxidized rat Cyb5R3 (PDB entry 1IB0) showing that the nicotinamide ring of bound NAD<sup>+</sup> is outside of the active site. Panel B further highlights interactions between the NAD<sup>+</sup> adenine ring and the protein (Bewley *et al.*, 2001)



**Figure S8.** Side chain interactions with (A) NADP<sup>+</sup> in CS-b5R-NADP; and (B) NAD<sup>+</sup> in CS-b5R-NAD.



**Figure S9.** BlastP-guided sequence alignment of mammalian Cyb5R1-4 and homologous reductases from slime mold, plants and fungi. Gene Bank accession numbers are listed for all entries. Open-ended N-terminal sequences are indicated by ..., and C-terminal stop codon by \*.

MNSRRREPITLQDPEAKYPLPLIEKEKISHNTRRRFRFGLPSPDHVLGLPVGNYVQ  
MSVKKKDLITLQDPEAKYPLPLIEKEQISHNTRRRFRFGLPSPDHVLGLPVGNYVH  
MSVKKKDLITLQDPEAKYPLPLIEKEQINHNTRRRFRFGLPSPDHVLGLPVGNYVH  
MGAQLSTLGHMVLPVWFLY SLLMKLFQRSTPAITLESPIKYLRLIDREIISHDTRRRFRFALPPPQHILGLPVGQHIY  
MGAQLSTLSHVLPVWFIY SLFMKLFQRSTPAITLENPDIKYPLRLIDKEVISPDTRRRFRFALPSPQHILGLPVGQHIY  
MGAQLSTLSRVVLPVWVY SLFMKLFQRSSPAITLENPDIKYPLRLIDKEIISHDTRRRFRFALPSPQHILGLPVGQHIY  
MDILTAPVLIQVSIIVITVLYLFLKPAQSNSTPPKPQNKIPKALQDPSVKYPLPLIEKEEINHDTKRFRFGLPSSSHVLGLPVGQHIY  
MVENNTLIITGVVVVSSIAIYIYLKATNTCPF SLCKKSKKRTLVDDSVKYPLPLIEKEEINHDTKRFRFGLPSPKHILGLPVGQHIY  
MGIQTSVLLASLGVGLVTLGLAVGSYLVRSSRRPQVTLDPNEKYLLRLLDKTTVSHNTRRRFRFALPTAHHTLGLPVGKHIY  
MGIQSPVLLASLGVGLTLLGLALGTYLVRSSRRPQVTLQDPDEKYLLRLLDKTTVSHNTRRRFRFALPTAHHILGLPVGKHVY  
MGIQSPVLLASLGVGLFTLFLGALGTYLVRSSRRPQVTLQDPDEKYLLRLLDKTTVSHNTRRRFRFALPTAHHILGLPVGKHVY  
MSYAMSTTVAVTVGVVLPVSTAGLLGYYFNRKRKILITLIDPSEKYKLRLLVDKEIISHDTRRRFRFALPSPHVLGLPVGKHVY  
MVENNTLAITGGVLISSVSLFLYLRQLRAEKSKRTLEDDSVKYLLPLIEKEEINHDTKRFRFGLPSPKHILGLPVGHHVY  
.HEVQEDFSVRVSVGKIEIVLQKKENTSWDFLGHPLKNHNSLIPKDTGLY YRKCQLISKEDVTHDTRLFLCLMLPPSTHL QVPIGNHVY  
.HEVQENFSVRVIENVGKIEIVLQKKESVSWQCLGDHLEKHDSFIPKDTGLY YRRCQLISKEDVTHDTRLLCLMLPPSTHL QVPVQGHVY  
.HEVQENFSVRVIENVGKIEIVLQKKETVSWKCLGDPLEKHDSFIPKDTGLY YRQCQLISKEDVTHDTRLFLCLMLPPSTHL QVPVQGHVY  
. .KREPALNPNEYKFKMLREKQIINHNTLRFNHLHHPEDVVLPIGQHMS  
. .KKGQVEKALDPQEYRKFQKKEFIVNHNTRIIFRFPALPNEDDILGLPIGQHIS  
MDTEFLRTLDRQILLGVFAVAVGAGAAYFLTSSKRRVCLDPENFKEFKLVKRHQLSHNVAKVFELPTSTSVLGLPIGQHIS  
MEFSQSHRDEMISMAVALVAIVGGTAYYYYVTKPKGCLDPENFKEFKLVKRTQLSHNVATFRFDLPTPKSVLGLPIGQHIS  
MDFLQAQENQILVGVAVA VVAIGLGAVALYSSKTKGCLDPENFKAFLKVKRAQLSHNVAKFTFALPTPTSVLGLPIGQHIS  
.FPLLDKSFPTTENLNPELLGHVVALVAVGFTAAYIYRKHAKPKGSLDPKNFKEFKLIKKTQLSHNVARFKFALPTPSSVLGLPVGKNIL  
. .HGVIIPVFLIIFGTIVKREWVGYAIVVAFSLGFHFKWRQRVRKVLSDKIQQFELSDKAVLNHNTAIYRFRPRANDVLGLPIGQHLK  
MAIDAQKLVVIVIVVPLLFKFIIGPKTKPVLDPKRNDFQSFPLVEKTIILHNTSMYKGLPHADDVLGLPIGQHIY  
. .CTGLLLNCVVTPLYFWKTQNGRIVVSLQFVVLVYATAFISIGTDKSLYRNKVALPLSKKTRISRNNTSLYCFKLYPFRERLHIPMGYHLA  
. .YIPAALFVVGVAITTYMSGELKILQSLPILFMIIFVRAISAYKRRRSYLPDRWTSLELEDQTIISKNTALYRFLKTRLESLELDIPAGHHVA  
. .PIKEITTPRQRKVALNSREKISCKLVSKTYISHNTRLFRFALPSEDQLLGLPIGKHIF  
. .RAPALSNPRGRIHCRVLVAKKELSRDVRLEFRFSLPSPDQVGLPIGKHIF  
. .RTFVVREKQVESAYVTSF VLVPADGGAVLDYQPGQYIG  
. .HHTPKLITFAISRPEY RFKAGQFSR

Cyb5R2 / Human (NP\_057313)  
Cyb5R2 / Mouse (NP\_796190)  
Cyb5R2 / Rat (NP\_001014266)  
Cyb5R3 / Human (NP\_000389)  
Cyb5R3 / Mouse (NP\_084063)  
Cyb5R3 / Rat (NP\_620232)  
Cyb5R3 / Zebrafish (NP\_001038825)  
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Cyb5R1 / Human (NP\_057327)  
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b5R/slime mold (Dictyostelium, XP\_638259)  
b5R/Arabidopsis (NP\_197279)  
b5R/Glycine (XP\_003556838)  
b5R/Glycine (XP\_003520929, 003554059)  
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nitrate reductase/Glycine (XP\_003544771)  
nitrate reductase/corn (2CND)  
nitric oxide dioxygenase (4EH1)  
ferredoxin reductase/Neisseria (5TR9)

FAD/1

FAD/2

LLAKIDNELVVRAYTPVSSD  
LLAQINNELVIRAYTPVSSD  
LLAQINNELVIRAYTPVSSD  
LSARIDGNLVVRPYTPVSSD  
LSTRIDGNLVIRPYTPVSSD  
LSTRIDGNLVIRPYTPVSSD  
LSAKVNGSLVVRAYTPVSSD  
LTANIDGKIIVRPYTPVSSD  
LSTRIDGNLVIRPYTPVTS  
LSARIDGSLVIRPYTPVTS  
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LKLSTGAEIVKPYTPVSESLSDSDFKEPVLSPNKYIYFLIKIY  
VKATVDGKEIYRYPYTPVSSD  
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PAGLFTPELDRLQIGDFISVS  
PAGLFTPELDRLQIGDFVSVS  
EKGQMSQYIDHLNPGDFLQVR  
EKGAMSGYVDNMFIDGSDIEVK  
PQGRMSSHFFREMRVGDHLAVK  
PQGRMSSHFFREIREGDYMAVK  
PQGRMSSHFFREMRVGDYLSVK  
PNGKMSHHFRQMKEGDFLAVR  
PNGKVSKKFSELKIGDTIGVR  
PTGNVSKMIGELKIGDSIQIK  
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Cbr1p/S.cerevisiae (NP\_012221)  
b5R/S.cerevisiae (NP\_013623)  
b5R/S.cerevisiae (NP\_013581)  
nitrate reductase/Glycine  
nitrate reductase/corn (2CND)  
nitric oxide dioxygenase (4EH1)  
ferredoxin reductase/Neisseria (5TR9)



NADPH/1

PDQTSEPKKTLADHLGMIAGGTGITPMLQLIRHITKD
ANKTSEPEKKLVHHLGMIAGGTGITPMLQLIRHITKD
TDKTSEPEKKLVHHLGMIAGGTGITPMLQLIRHITKD
PDKKSNPIIRTVKSVMGIAGGTGITPMLQVIRAIMKD
ADKKSNPVVRTVKSVMGIAGGTGITPMLQVIRAVLKD
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PDKKSEAEVRKFKHVAMIAGGTGITPMLQLVRSITAD
ADKKAEPKNRVFKHLSMIAGGTGITPMLQVIAAILRD
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PNKKSPPPELRVAKKLGMIAGGTGITPMLQLIRAILKV
PNKKSPPPELRVAKKLGMIAGGTGITPMLQLIRAILKV
ADKKAPAETKTVKSLGLIAGGTGITPMLQLIRDITKN
MDKKAEPKNRFFKHLSMIAGGTGITPMLQVIAAILRD

LFLLAAGTGFTPMVKILNYALTD
LFLLAAGTGFTPMVTVLNYALSH
LFLLAAGTGFTPMVTVLNHALTH
MGMIAGGTGITPMLQVARAIKKN
IGMLAGGTGITPMLQVIKAILKN
FGMLAGGSGITPMFQVARAIKEN
LGMIAGGTGITPMFQVTRAIKEN
FGMLAGGSGITPMFQVARAIKEN
FGMIAGGSGITPMFQLIRAIKEN
FGMIAGGTGITPMLQIIRAVLSN
LGMIAGGTGIAPMYQIMKAIAMD
LGI IAGGSGITPVLQVLQEIIPS
LGI VAGGSGITPVLQILNEIITV
HGKQKFAKRLAMLAGGTGITPIYQVAQAILKD
NGKQRNARRLAMICGGSGITPMYQIIQAVLRDQ
LISAGVGATPMQAILHTLAKQN
VMLCTGSGIAPFLSILEQPEIRQRFDTVNLIHSVSFPEELIFNDRLAALSEHPLVGEYGHSEFRFVPTT

PSDRTRMSLIFANQTEEDILVRKELEEIARTHPDQFDLWYTL
TSDETRMSLLFANQTEEDILLRKELEEVATTHHKQFNWYTL
TSDGTRMSLLFANQTEEDILLRKELEEVATTHQNQFSLWYTL
PDDHTVCHLLFANQTEKDILLRPELEELRNKHSARFKLWYTL
PNDHTVCYLLFANQSEKDILLRPELEELRNEHSARFKLWYTV
PNDHTVCYLLFANQSEKDILLRPELEELRNEHSARFKLWYTV
SSDETVCSLIFANQTEKDILLRNELEDEVHRNHPKSLKLWYTL
PTDQTQIRLLFANQTEDDILCRQELDDLAKEHPTRFRVWYTV
PEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFLWFTL
PEDPTQCFLLFANQTERDIILREDLEELQAQYPNRFLWFTL
PEDPTQCFLLFANQTEKDIILREDLEELQAQYPIRFLWFTL
PNDTTCSLLFANQTEKDILLKDELEEIQARHSRFLWFTV
PIDATQIRLLFANQTEDDILCRKELDELAEKHPTRFRVWYTV
IPSLRKVKLMFFNKTEDDIIWRSQLEKLAFKD KRLDVEFVL
MSSLRKVKLMFFNKTEDDIIWRCQLEKLALRE KRFDVEFVL
MSSLRKVKLMFFNKTEDDIIWRCQLEKLALKD KRFHVEYVL
PKEKTIINLIFANVNEDDILLRTELDDMAKKY SNFKVYVVL
PSDKTEISLVFGNITEEDILLKKELEDELAEKHP QFKVYVVL
PTDKTKVHLIYANVTYDDILLKEELEGLTNYPEQFKIFYVL
QQDKTNINLIYANVTYFDDILLKEELDAFAIKFPNQFKVYVVL
PNDRTKVHLIYANVTYEDILLKEELDGLASNYPDRFKIYVVL
PKDKTKVHLVYANVTYVDDILLKEELDNFANKFAQRFEVYHVL
FEDPTEITLLYANVSEGDIVLRDEIDALAKKP RFTVHYVVL
PHDTTKVSLVFGNVHEEDILLKKELEALVAMKPSQFKIVYVVL
PEDLTHISLIYANETEDDILMKSQLDHMAKEYPHFKVHYVVIH
PEDLTKVSLLYANETENDILLKDELEDEMAEKYPHFQVHYVVIH
PEDHTEMHLVYANHAEDDILLREELDAWAKTHCDRFKVVYVVI
PEDHTEMHLVYANRTEDDILLRDELDRWAAEYPRDLKVVYVVI

KSGVTYLYACNSAKEHTFAGETAGLIA
KSGVTYLYACNSAKEHTFAGETAGLIA

Cyb5R2 / Human (NP\_057313)
Cyb5R2 / Mouse (NP\_796190)
Cyb5R2 / Rat (NP\_001014266)
Cyb5R3 / Human (NP\_000389)
Cyb5R3 / Mouse (NP\_084063)
Cyb5R3 / Rat (NP\_620232)
Cyb5R3 / Zebrafish (NP\_001038825)
Cyb5R3 / C.elegans (NP\_504638)
Cyb5R1 / Human (NP\_057327)
Cyb5R1 / Mouse (NP\_082333)
Cyb5R1 / Rat (NP\_001013144)
Cyb5R1 / Zebrafish (NP\_956483)
Cyb5R1 / C.elegans (NP\_504639)
Cyb5R4 / Human (NP\_057314)
Cyb5R4 / Mouse (NP\_077157)
Cyb5R4 / Rat (NP\_596918)
b5R/slime mold (Physarum, 2EIX)
b5R/slime mold (Dictyostelium, XP\_638259)
b5R/Arabidopsis (NP\_197279)
b5R/Glycine (XP\_003556838)
b5R/Glycine (XP\_003520929, 003554059)
b5R/Glycine (XP\_003531792)
b5R/S.pombe (NP\_587852)
Cbr1p/S.cerevisiae (NP\_012221)
b5R/S.cerevisiae (NP\_013623)
b5R/S.cerevisiae (NP\_013581)
nitrate reductase/Glycine (XP\_003544771)
nitrate reductase/corn (2CND)
nitric oxide dioxygenase (4EH1)
ferredoxin reductase/Neisseria (5TR9)

NADPH/2

DRPPIGWKYSSGFVTADMKEHLPP
DRPPSDWKYSSGFVSADMKEHLPP
DRPPSGWEYSSGFITADMKEHLPP
DRAPEAWDYQGQGFVNEEMIRDHLPP
DKAPDAWDYSQGFVNEEMIRDHLRT
DKAPDAWDYSQGFVNEEMIRDHLPP
DRPSEGWKYSEGFVNAAMMKDHLPP
DRPPVMWSYSSGFINDSMIKENLFP
DHPPKDWAYSKGFVTADMIREHLPA
DSPPEDWTYSKGFVTADMIEHLPA
DYPPEDWTYSKGFVTADMIEHLPA
DRAPADWEYSQGFISAEMIKDHLPP
SKASKDWRYSTGHINEEMIKHLFP
SAPISEWNGKQGHISRALISEFLKRNLS
SAPSPWNGKQGHISRALISEFLQRSS
SAPSPWNGKQGHISRALISEFLQRSL
NNPPAGWTGGVGFVSADMKEHLPP
NNPPKGTQGVGFVSKEIIESRLPS
NQPPPEVWDGGVGFVSKEMIQTHCPA
NQPPEIWDGGVGFVTKEMIQDFPA
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NKPPEQWNGGIGFISKEIKSHCPE
NNPPENWKGSVGFVTQELIKAHFPA
DSPDREDWTGGVGYITKDVIEHLPA
KPNKQWNGDVGVTLEEMKRYLPK
YPSDRWTGDVGYITKDMNRYLPE
GIAKEGWQYSVGRITESIMREHLPP
DQVKRPEEGWKYSVGFVTEAVLREHVPE
QQGWMQVWYRDESADDVLQEMQLAELILPIEDGDFYLCGPIGFMQYVVKQLLA
RAANPSGLSGKRIPELLKNNSIEQALHTKLTPESTRFMICGNPEMVKDTFQTLTD
MGYAMHRNRIPGGIMMENGFF\*

NADPH/3

PAKSTLILVCGPPPLIQTAHPNLEKLGYTQDMIFTY\*
PGEDTLILVCGPPPLIQAAAHPNLEKLGYTQDMIFTY\*
PGEATLILVCGPPPLIQEAAHPNLEKLGYTQDMIFTY\*
PEEEPLVLMCGPPPMIQYACLPLNDHVGHPTECFVF\*
PGEEPLILMCGPPPMIQFACLPLNLERVGHKERCFTF\*
PGEETLILMCGPPPMIQFACLPLNLERVGHKERCFTF\*
ADSDVLVVMCGPPPMIEKACLPLNLLKLGKYNIFAY\*
PGDSDAVLLCGPPPMINFACIPNLEKLEYDPANRLLF\*
PGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY\*
PAEDVLLLLCGPPPMVQLACHPNLDKLGYSQKMRFTY\*
PAEDVLLLLCGPPPMVQLACHPNLDKLGYSQKMRFTY\*
PSDSDMILMCGPPPMIQFACNPNLDKLGYSQKMRFTY\*
SNEESAVLLCGPPPMINACIPNLDKLGHSNENYLIFF\*
DKSKVLVLCGPPVPEFTEQGV RLLHDLNFSKNEIHSFTA\*
ENSRAFLCICGPTPFTDEGI RLLHDLNFSDEIHHGFTA\*
ENSKVFLCICGPTPFTDEGI RLLHDLNFSDEIHHGFTA\*
PSSDIKVMCGPPPMNKMAMQ GHLETGTYTPEQWFIF\*
PSDQTMVIMCGPPPMNKMAMT GHLETIGFNESNIFTF\*
PASDIQILRCGPPPMNKMAMA ANLEALGYSPQMQFQF\*
PASDIKILRCGPPPMNKMAMA ANLEALGYSPQMQFQF\*
PAQDIKILRCGPPPMNKMAMA AHLEALGYASEMQFQF\*
PAQDIQILRCGPPPMNKMAMA THLDALGYTSNMQFQF\*
PSPETKVLICGPTPMVNSLR EATVALGYEKSRAISKLEDOQVVF\*
ATMDNVQILICGPPPMNVSVR RSTVDLGFRRSKPLSKMEDQVVF\*
QAEDHRLILICGPPPMNEMVL NYAKELGWSNGFHKNGNTDKVVF\*
YSEDNRLLICGPDGMNLLAL QYAKELGWKNSTRSSGDDQVVF\*
SSSDALALTCGPPPMIEFAVQPNLEKMGYDIKNDLLVF\*
GGDDTLALACGPPPMIQFAISPNEKMKYDMANSFV\*

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