Supporting Information

Engineering DszC mutants from transition state macrodipole considerations and evolutionary sequence analysis

Rui P. P. Neves, Maria J. Ramos, Pedro A. Fernandes*

LAQV, REQUIMTE, Departamento de Química e Bioquímica, Faculdade de Ciências, Universidade do Porto, Rua do Campo Alegre, s/n, 4169-007 Porto, Portugal

*E-mail for P.A.F.: pafernan@fc.up.pt.

INDEX

MODELING OF THE QM/MM MODEL OF THE DSZC:DBT COMPLEX	2
TRANSITION STATE MACRODIPOLE CALCULATIONS WITH DIFFERENT DENSITY FUNCTIONALS AND BASIS SETS	3
POSITIONAL CONSERVATION SCORES OBTAINED FROM THE CONSURF SERVER	3
REFERENCES	5

Modeling of the QM/MM model of the DszC:DBT complex

The DszC:DBT complex was modelled in the catalytically-competent homodimeric form (chain A and F, with 417 residues each, from PDB ID 3X0Y with 2.3 Å resolution), in complex with the FMN cofactor in the oxidized form and with all X-ray waters within 6 Å of each catalytic site.¹ The FMN cofactor was modelled as C^{4a}-hydroperoxyflavin intermediate (C^{4a}OOH), as there was a well-defined electronic density for FMN in the active site of DszC that suggested a tight-binding of FMN to the active site of DszC. The binding pose of DBT was modelled as in the TdsC homolog enzyme from *Paenibacillus sp.* (64% identity and identical active site residues) binding oxidized FMN and DBT (PDB ID: 5XDE),² after aligning the conserved FMN cofactor and the backbone of catalytic residues His92, Ser163, His391 of both DszC and TdsC. As predicted by the Propka3.1 program,³ physiological protonation states were attributed to all residues except His92, His388 and His391: His92 and His388 were protonated as δ -tautomers and His391 was doubly-protonated as in the imidazolium form.

The DszC homodimer was described with the ff10 force field⁴, whereas DBT and C^{4a}OOH were parameterized with the GAFF⁵ and with RESP charges derived after geometry optimization of each molecule at the HF/6-31G* level – using the Antechamber module available in AMBER12 and the Gaussian software for QM calculations⁶. The Xleap module of AMBER12 was used to add 33 Na⁺ ions to counteract the overall positive charge of the system, and to add TIP3P waters⁷ to fill a rectangular box with faces at a minimum distance of 12 Å from the solute. Afterwards, a four-step molecular mechanics (MM) energy minimization protocol was applied to remove bad contacts in the system: (1) positional harmonic restraints of 50 kcal·mol⁻¹ were applied to water molecules; (2) positional harmonic restraints of 50 kcal·mol⁻¹ were applied to all heavy atoms; (3) positional harmonic restraints of 10 kcal·mol⁻¹ were applied backbone atoms of the solute; and (4) no restraints were applied.

The QM/MM model proceeding for ONIOM calculations was taken from the final minimized structure of the MM protocol. It comprised one monomer binding C^{4a}OOH and DBT, all residues of the second monomer within a radius of 18 Å from the His92, Tyr96, Asn129, Ser163, His388 and His391, C^{4a}OOH and DBT in the first monomer, and the water molecules at least 6 Å away from the catalytic site – in a total of 7238 atoms and total charge of -15. The QM layer included all atoms of DBT, the isoalloxazine ring (except for the two methyl groups in the phenyl moiety), the N¹⁰-bound hydroxymethyl of the ribitol tail of C^{4a}OOH, and the side chains of residues His92, Tyr96, Asn129, Ser163, His388 and His391 – a total of 112 atoms, zero total charge and singlet multiplicity – whereas the MM layer comprised all the remaining atoms of the model. All atoms beyond a radius of 15 Å from the molecules composing the QM layer were kept rigid throughout the ONIOM calculations. All ONIOM calculations were ran with the Gaussian software.

All QM/MM calculations were carried out at the B3LYP/6-31G(d):ff10 level of theory,⁸⁻¹⁶ with the Coulomb QM/MM interactions calculated with the electrostatic embedding scheme, as implemented in Gaussian 09.⁶ The B3LYP/6-31G(d) level has been successfully employed in other QM/MM studies of the catalytic mechanism of enzymes.¹⁷⁻²⁰ In particular, to study the triplet-singlet spin inversion taking place upon formation of the C^{4a}OOH, we allowed break of the symmetry of the singlet configuration by accepting the inclusion of imaginary coefficients and/or mixed-spin orbitals in the wavefunction.²¹⁻²³ We used hydrogens as link atoms to complete the valence of the bonds in the boundary of the two layers.²⁴⁻²⁷



Transition state macrodipole calculations with different density functionals and basis sets

Figure S1. Activation energy differences upon alanine mutation for different density functionals (BLYP, B3LYP, mPW1N and M06-2X) as a function of the relative proximity of each residue to the O_p and the S_{DBT} atoms. Activation energy differences are calculated relatively to the activation energy of the wild-type form at the same level of theory; to determine the representative position of charged residues, only the heavy atoms of the charged group were considered to describe the position of the residue relatively to the active site, whereas the heavy atoms of the whole sidechain were considered for the remaining residues. Larger markers represent bulkier amino acids. Residues whose mutation provides a change larger than |1.0 kcal·mol-1| in the activation energy are labelled. Residues colored in blue and red correspond to positively and negatively charged residues, and those colored in green and gray correspond to polar and apolar residues. All calculations were performed at the ONIOM(DFT/6-31G(d):AMBER) level of theory.



Figure S2. Activation energy differences upon alanine mutation for different basis sets (6-31G(d) and 6-311+G(2d,2p)) as a function of the relative proximity of each residue to the O_p and the S_{DBT} atoms. Activation energy differences are calculated relatively to the activation energy of the wild-type form at the same level of theory; to determine the representative position of charged residues, only the heavy atoms of the charged group were considered to describe the position of the residue relatively to the active site, whereas the heavy atoms of the whole sidechain were considered for the remaining residues. Larger markers represent bulkier amino acids. Residues whose mutation provides a change larger than |1.0 kcal·mol-1| in the activation energy are labelled. Residues colored in blue and red correspond to positively and negatively charged residues, and those colored in green and gray correspond to polar and apolar residues. All calculations were performed at the ONIOM(B3LYP:AMBER) level of theory.



Figure S3. Activation energy differences for different density functionals (BLYP, B3LYP, mPW1N and M06-2X) upon insertion of a unitary probe charge in the geometric centre of the sidechain of the residues within 10 Å of the active site of DszC, as a function of the distance of the sidechain centre of mass to the O_p and S_{DBT} atoms. Larger markers represent bulkier amino acids. Since most residues are composed of C, N and O, we assumed for simplicity that the geometric center of each sidechain should closely resemble their centre of mass. Residues in which the probe insertion leads to a change larger than 50% of the maximum energy difference relative to the activation energy are labelled. Residues colored in blue and red correspond to positively and negatively charged residues, and those colored in green and gray correspond to polar and apolar residues.



Figure S4. Activation energy differences for different basis sets (6-31G(d) and 6-311+G(2d,2p)) upon insertion of a unitary probe charge in the geometric centre of the sidechain of the residues within 10 Å of the active site of DszC, as a function of the distance of the sidechain centre of mass to the O_p and S_{DBT} atoms. Larger markers represent bulkier amino acids. Since most residues are composed of C, N and O, we assumed for simplicity

that the geometric center of each sidechain should closely resemble their centre of mass. Residues in which the probe insertion leads to a change larger than 50% of the maximum energy difference relative to the activation energy are labelled. Residues colored in blue and red correspond to positively and negatively charged residues, and those colored in green and gray correspond to polar and apolar residues.

Positional conservation scores obtained from the ConSurf server

			01/0	A 0 D	0111			1110				MET	401				050	TUD	1/41				ConSurf	Table
	pos	ALA	CYS	ASP	GLU	PHE	GLY	HIS	ILE	LYS	LEU	MEI	ASN	PRO	GLN	ARG	SER	THK	VAL	IRP	IYR	MAX AA	Grade	S1.
MEI	1											100.0						100.0				M 100.000	0*	resid
	2										400.0							100.0				1 100.000	<u>8</u> ^	varie
LEU	3										100.0						40.0	00.0				L 100.000	7*	for e
SER	4													00.0			40.0	60.0	00.0			T 60.000		posit
PRO	5	00.0			40.0									80.0				00.0	20.0			P 80.000	0"	in
GLU	0	20.0		00.0	40.0			00.0		40.0				20.0		00.0		20.0				E 40.000	3"	
	/ 0			20.0		20.0		20.0		40.0					40.0	20.0		20.0		20.0		K 40.000	<u> </u>	
	0					20.0		50.0							40.0		16.7	20.0		20.0		Q 40.000	4*	
110 /A1	9			10.5			10 E	50.0			10 E				10.7		10.7	10.7	27 E			H 30.000	4	
	10	20.0		12.5			12.5			10.0	12.5					40.0	10.0	25.0	37.5			V 37.500	2 0*	
	11	16.7		0.2			10.0			10.0				66.7		40.0	10.0	0.0				R 40.000		
	12	05.0		0.5			6.2							6.2	6.2	0E 0		10.5			6.2	AD 25 000	1	
RG CD	13	20.0		12.5		4.5	0.3				0.1		4 5	0.0	0.3	25.0		12.5			0.3	AR 20.000	1	
	14	10.Z		9.1	2.2	4.5	4.5	2.2			9.1		4.5	10.0	4.5	4.5	16.7	4.5				P 30.304		
	10	00.5 20 F		3.3 20 0	3.3 7 7		3.3	J.J						10.0	0.6	0./	10.7	20 F	26			A 00.005	2	
LA CD	10	20.5		20.2	1.1	04	2.0	4.0			7.0		24	4.0	2.0	1.1	1.1	20.5	2.0			D 26.205	3 1	
SN	10	1Z.Z		04.1	4.9	∠.4 3.0	2.4	4.9		57	1.3		Z.4	4.9	4.9	1.3	4.9	1.3	10		10	D 34.140	1	
SN CD	10	JZ.1		9.4 40.6	0.1 20.2	J.Ö	47	24		J./			9.4	1.5	9.4 2.4	1.9	5./ 6.2	J./	1.9		1.9	H 32.0/5	4	
00 00	19	4./ 25 4		40.0	20.3	1 F	4./	ی. ا ۱ ج	20		20		4./	ა.I ეი ი	J.1	0.1	0.3	1.ŏ	1 5	<u> </u>	60	D 40.020	4	
AU AI	20 21	20.4 1 /		1 /		1.5 0 7		1.3	3.U 20 =		J.U		1 /	29.9	1 /	1 /	1.5		0.6	20.9	0.0	F 23.001	<u> </u>	
	21	1.4 50.4		1.4	6.4	Z.1	1 1	11	20.5	1 1	01.0		1.4	0.1	1.4	1.4	2.0	2.0	9.0	Z.1		L 37.334	2	
	22	52.1		0.4	0.4		1.1	1.1	17.0	1.1	2.1	1.0	1.1	2.1	9.0	0.5	3.2	3.2	2.1			A 52.128	4	
	23	8.9		1.0		0.0			17.8	5.0	4.0	1.0		1.0	3.0	15.8	4.0	9.9	28.7			V 28.713	<u> </u>	
	24	84.Z		40.0	42.0	0.9	2.2	2.2	0.9	2.2	4.4				44.5	00.0	0.5	1.8	1.9			A 84.211	8	
RG	25	16.4		12.3	13.9	10	3.3	3.3	1.6	3.3	2.4				11.5	26.2	2.5	4.1	1.6			R 26.230	1	
	20	19.4		11.0	27.9	1.0	2.3	0.8	2.0	3.1	3.1	0.7			8.5	9.3	10.9	1.0	22.2			E 27.907	7	
	21	3.7	0.7			0.7	0.7		3.0		50.3	0.7				0.5	0.5	2.2	33.3			L 50.290	7	
	28	74.6	0.7	40.0	47.0		0.7	0.7	3.6		2.2			0.0	10.4	6.5	6.5	1.4	3.6			A 74.638	1	
	29	30.7		18.0	17.3		0.7	0.7	77	1.4	0.7		1.4	Z.Z	10.1	4.3	2.2	2.9	1.4		0.7	A 30.091	1	
13	30	12.7		0.0	21.0	22.0	1.4	1.4	1.1	4.Z	2.0		0.7		7.0	12.7	Z.1	0.0	1.1	0.4	0.7	E 21.001	7	
	31	50.4		1 4	0.0	JJ.0	0.7	0.4	Z. I	0.7	01.3				0.7	00.4	4.0	25	0.7	Z.1	1.4	L 01.200	6	
KG I A	32 22	24.2		0.7	2.0		0.7	Z.1	1.4	6.0	6.2			4.1	1.0	22.4	4.Z	0.0	0.7		1.4	A 39.441	1	
	33	34.Z		0.7	10.5		75		1.4	0.0	0.2		0.7	4.1	4.0	9.0	0.0	0.9	9.0			A 34.247	7	
HR	34	02.0		32.1			1.5		0.7		0.7		Z.1		0.7	4.1	8.8	44.Z	0.7			1 44.218	1	
	30	93.9	0.7	0.7	0.7		1.4		0.7		0.7		1.2	4.0	0.7		47	0.7	2.1			A 93.070	9	
	30	35.0	0.7	0.7	0.7		1.3	4.0	2.0	0.0	7.4		1.3	4.0	F 4	4.0	4.7	0.7	40.9			V 40.940	4	
	ა/ 20	22.ŏ		4./	51.U		0.7	1.3		2.0	2.1 1 7				J.4	1.J	0.7	4.0	ა.4			E 01.00/	ა ი	
RU CD	ა ბ			00.6	74						4./					90.3						R 90.302	9	
57 DC	39	0.4		92.0	1.4			07	1 2	12.4	1 2				1/ 0	E1 0	07	07			07	D 52.01/	3	
1.4	40	9.4 11 G		27	4.0		07	2.1	1.3	13.4	1.J				14.0	01.U	1.2	0.7	1 2		0.7	K 01.00/	4	
	41 10	41.0		2.1	10.ŏ		0.7	0.7	0.7	4./	0.4		10 5		10.7	IU./ g 1	1.3	2.1	1.3			A 41.011	3 7	
	42	3.4		0.7	07		50.4		07	10.4	0.7		19.5		0./	0.1		0.7	07			G 00.443	6	
	43	14.8		07	0.7		52.3	16.0	0.7	12.1	4.0		4.0	0.4	J.4	10.7	0.4	0.7	0.7		07	G 52.349	0	
	44	0.0		2.1	2.1			10.0	0.7		ŏ./		4.0	9.4 70 5	1.3	5.4	9.4	30.9	1.3		0.7	I 30.8/2	0	
	45	27.5	0 -	4.0	4.0	0-		10		00.0	40.4			72.5	4.0	40.4	0-	0.0	0-	4.0	4 -	P /2.483	8	
HR	46	14.1	0.7	1.3	1.3	ŏ./	4.0	4.0	0.0	20.8	10.1		4.0	4.0	1.3	16.1	2.7	b.U	6.7	1.3	4./	K 20.805	1	
LA	4/	4/./		10.7	9.4	2.0	1.3	3.4	2.0	3.4	1.3		1.3	1.3	4.0	4./	2.0	2.0	2.0		1.3	A 47.651	1	
	48	2.0		0.7	89.9						0.7				6.7							E 89.933	9	
RG	49	2.7			0 6 <i>i</i>				20.8	6.0	9.4					38.3			22.8			R 38.255	7	
	50	14.8		26.8	22.1		2.0	4.0	1.3	0.7		4.0	1.3		14.8	8.1	4.0	1.3	2.7			D 26.846	3	
.SP	51	10.7		1.3	1.3	o -		1.3	0.7	4.0	54.4	1.3			1.3	15.4	0.7	0.7	0.7	6.0		L 54.362	4	
EU	52					2.7			23.5	or -	72.5	0.7				o · -	a –		0.7			L 72.483	7	
RG	53	4.7						• -		25.5						61.7	6.7	1.3			• -	R 61.745	8	
LA.	54	20.8		20.1	18.1		2.0	8.7		3.4			4.0		14.8	4.7	2.0	0.7			0.7	A 20.805	1	

sequence of DszC, after the multi-sequence analysis performed by the ConSurf server

SER	55	22.1			0.7		0.7	3.4			1.3		1.3		1.3		67.8		0.7		0.7	S 67.785	7
GLY	56			4.0			94.6			0.7						0.7						G 94.631	9
LEU	57										100.0											L 100.000	9
LEU	58	0.7					0.7				81.2		1.3	2.0	0.7			2.7	9.4	1.3		L 81.208	8
SER	59	18.9		2.7	1.4		7.4	0.7		10.1	1.4		7.4	3.4	3.4	4.1	12.2	26.4			0.7	T 26.351	2
LEU	60	8.1				1.4			5.4		68.9	0.7							15.5			L 68.919	7
LEU	61	17.8				0.7	2.7		4.8		33.6	1.4			2.7		21.9	11.0	2.7	0.7		L 33.562	6
VAL	62	2.7		1.4	4.1	0.7	14.4	4.8	38.4		2.7		0.7				0.7	2.7	26.7			1 38.356	6
PRO	63	6.8					0.7				0.7			89.7			1.4			0.7		P 89.726	8
ARG	64	22.6	0.7		3.4		3.4	0.7		17.1			0.7	6.2	2.7	21.2	0.7	10.3	10.3			A 22.603	2
GLU	65	21.9	0.7	3.4	47.9		0.7	0.7		6.2			0.7	0.7	10.3	3.4	2.1	0.7		0.7		E 47.945	3
TYR	66	2.1			0.7	21.9		21.2	4.8		9.6		0.7				0.7		2.1	1.4	34.9	Y 34.932	2
GLY	67			07			98.6								07							G 98 630	9
GLY	68			0.7			99.3								•							G 99 315	9
TRP	69	19.2		27	48	07	26.7	48	07		13.0	07	07	07	13.0	14	34	14	07	34	21	G 26 712	1
GLV	70	2.1		6.8	11.6	0.1	76.0	1.0	0.1	07	10.0	0.1	0.7	0.1	1 /		0.7		0.1	0.1	2.1	G 76 027	5
	71	40.5		0.0	7 /		8.1	1/	0.7	0.7	1/1 2		0.7		17.6		0.7	0.7	71	0.7		Δ 10.5/1	5
ASD	72	2.0		26.2	27		6.0	2.0	0.7	0.7	14.2		0.4	15 /	0.7	71	20.8	7.4	7.4	0.7		D 26 174	1
	72	2.0		20.2	2.1	27	0.0	1.0			4.0		5.4	0.7	1.2	1.4	20.0	0.7	0.7	70.2	5.4	W 70 105	7
	73	4.0		2.4	5 /	2.1	27	2.0	0.7	2.0	4.0			20.1	0.1	24	10 1	0.7 E 4	0.7	19.2	5.4	D 20 124	1
	74	13.4		3.4	0.4	0.7	Z.1	2.0	2.7	2.0	4.7		0.7	20.1	0.1	3.4	0.1	0.4 20.2	0.7			P 20.134	4
	75	3.4		12.1	11.4	0.7	0.4		2.1		1.4	0.7	0.7		10.7	1.3	2.1	30.3	0.7			1 30.200	4
	76	30.2	0.7			2.0	9.4	0.7	17.5		10.7	0.7	0.7		1.3		2.0	10.1	10.1		00.0	A 30.201	0
	70	7.4	0.7	4.0	47.5	11.4	0.4	2.7	1.3	44.0	35.6	2.0	0.7		4.0	00.0	1.3	1.3	1.3		30.2	L 35.570	4
GLU	78	10.1	0.7	4.0	17.5		3.4	4.0	05.5	14.8	2.7		1.3		13.4	20.8	1.3	0.7	40.0			R 20.840	2
VAL	/9	10.7	0.7			• •	1.3	1.3	25.5		8.7		<u> </u>				<u>.</u>	8.7	43.0			V 42.953	4
VAL	80	1.3				6.0	1.3		26.2		4.0		0.7				3.4	7.4	49.7			V 49.664	5
ARG	81	1.3					0.7			0.7					3.4	93.3		0.7				R 93.289	9
GLU	82	5.4			31.5		0.7	0.7	18.1	2.0	8.7				4.0	21.5		4.7	2.7			E 31.544	3
ILE	83					18.8			30.9		28.2	2.0							20.1			1 30.872	5
ALA	84	88.6					3.4								_		8.1					A 88.591	9
ALA	85	22.1			4.0					18.8					8.7	36.9	5.4	3.4	0.7			R 36.913	4
ALA	86	40.3					19.5				0.7						1.3	5.4	32.9			A 40.268	6
ASP	87			95.3	4.7																	D 95.302	9
GLY	88	8.1					36.2							3.4			47.0	5.4				S 46.980	8
SER	89	18.8											2.0				79.2					S 79.195	9
						0.7					100	· -					07					1 42 953	6
LEU	90	0.7				0.7			43.0		40.9	0.7					0.7		13.4			142.000	
LEU GLY	90 91	0.7 61.7				0.7	38.3		43.0		40.9	0.7					0.7		13.4			A 61.745	8
LEU GLY HIS	90 91 92	0.7 61.7				0.7	38.3	59.7	43.0		40.9	0.7 6.7			33.6		0.7		13.4			A 61.745 H 59.732	8 9
LEU GLY HIS LEU	90 91 92 93	0.7 61.7				0.7	38.3	59.7	43.0 9.4		65.1	0.7 6.7			33.6		0.7		13.4 25.5			A 61.745 H 59.732 L 65.101	8 9 7
LEU GLY HIS LEU PHE	90 91 92 93 94	0.7 61.7				29.5	38.3	59.7	43.0 9.4 3.4		65.1 44.3	0.7 6.7		8.1	33.6		0.7		13.4 25.5 2.7		12.1	A 61.745 H 59.732 L 65.101 L 44.295	8 9 7 6
LEU GLY HIS LEU PHE GLY	90 91 92 93 94 95	0.7 61.7 19.5				29.5	38.3 66.4	59.7	43.09.43.4		40.9 65.1 44.3 1.3	0.7 6.7		8.1	33.6 8.1		3.4	0.7	13.4 25.5 2.7 0.7		12.1	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443	8 9 7 6 6
LEU GLY HIS LEU PHE GLY TYR	90 91 92 93 94 95 96	0.7 61.7 19.5	2.0			29.5 36.9	38.3 66.4	59.7 0.7	43.09.43.4		40.9 65.1 44.3 1.3	0.7 6.7	6.0	8.1	33.6 8.1		3.4 5.4	0.7	13.4 25.5 2.7 0.7		12.1 49.0	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993	8 9 7 6 6 8
LEU GLY HIS LEU PHE GLY TYR HIS	90 91 92 93 94 95 96 97	0.7 61.7 19.5	2.0			29.5 36.9	38.3	59.7 0.7 82.6	43.09.43.4		40.9 65.1 44.3 1.3	0.7	6.0 0.7	8.1	33.6 8.1 15.4		3.4 5.4	0.7	13.4 25.5 2.7 0.7		12.1 49.0	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550	8 9 7 6 6 8 8 8
LEU GLY HIS LEU PHE GLY TYR HIS LEU	90 91 92 93 94 95 96 97 98 92	0.7 61.7 19.5	2.0			29.5 36.9 16.1	38.3	59.7 0.7 82.6 35.6	43.0 9.4 3.4		40.9 65.1 44.3 1.3	6.7	6.0 0.7	8.1	33.6 8.1 15.4 1.3		3.4 5.4	0.7	13.4 25.5 2.7 0.7 0.7		12.1 49.0 30.9	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570	8 9 7 6 6 8 8 8 8 6
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR	90 91 92 93 94 95 96 97 98 99	0.7 61.7 19.5 5.4	2.0			29.5 36.9 16.1 3.4	38.3 66.4 2.0	59.7 0.7 82.6 35.6 0.7	 43.0 9.4 3.4 1.3 0.7 		40.3 65.1 44.3 1.3 10.7 65.8	0.7	6.0 0.7 1.3	8.1	33.6 8.1 15.4 1.3		3.4 5.4	0.7 1.3 0.7 2.0	13.4 25.5 2.7 0.7 0.7 13.4		12.1 49.0 30.9 0.7	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772	8 9 7 6 6 8 8 8 8 6 6 6
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN	90 91 92 93 94 95 96 97 98 99 100	0.7 61.7 19.5 5.4	2.0 2.7 2.0			29.5 36.9 16.1 3.4	38.3 66.4 2.0 3.4	59.7 0.7 82.6 35.6 0.7 4.0	 43.0 9.4 3.4 1.3 0.7 40.4 		40.3 65.1 44.3 1.3 10.7 65.8 13.4	0.7	6.0 0.7 1.3 12.1	8.1	33.6 8.1 15.4 1.3 26.8		0.7 3.4 5.4 4.7 2.0	0.7 1.3 0.7 2.0	13.4 25.5 2.7 0.7 0.7 13.4	14.8	12.1 49.0 30.9 0.7 6.0	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846	8 9 7 6 6 8 8 8 6 6 6 6
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA	90 91 92 93 94 95 96 97 98 99 100 101	0.7 61.7 19.5 5.4 6.0	2.0 2.7 2.0		0.7	29.5 36.9 16.1 3.4 2.7	38.3 66.4 2.0 3.4 3.4	59.7 0.7 82.6 35.6 0.7 4.0	 43.0 9.4 3.4 1.3 0.7 10.1 		40.3 65.1 44.3 1.3 10.7 65.8 13.4 28.9	0.7 6.7 11.4 0.7	6.0 0.7 1.3 12.1 1.3	8.1	33.6 8.1 15.4 1.3 26.8 3.4		3.4 5.4 4.7 2.0 17.5	0.7 1.3 0.7 2.0 3.4	13.4 25.5 2.7 0.7 13.4 22.1	14.8	12.1 49.0 30.9 0.7 6.0	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859	8 9 7 6 8 8 8 8 6 6 6 6 6
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO	90 91 92 93 94 95 96 97 98 99 100 101 102	0.7 61.7 19.5 5.4 6.0 34.2	2.0 2.7 2.0	0.7	0.7	29.5 36.9 16.1 3.4 2.7 0.7	38.3 66.4 2.0 3.4 3.4 2.0	59.7 0.7 82.6 35.6 0.7 4.0	43.0 9.4 3.4 1.3 0.7 10.1 4.0	0.7	40.3 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3	0.7 6.7 11.4 0.7	6.0 0.7 1.3 12.1 1.3 8.1	8.1 4.0 1.3	33.6 8.1 15.4 1.3 26.8 3.4 7.4	4.0	3.4 5.4 4.7 2.0 17.5 0.7	0.7 1.3 0.7 2.0 3.4 8.1	13.4 25.5 2.7 0.7 13.4 22.1 9.4	14.8	12.1 49.0 30.9 0.7 6.0 0.7	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228	8 9 7 6 6 8 8 8 8 6 6 6 6 6 5
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET	90 91 92 93 94 95 96 97 98 99 100 101 102 103	0.7 61.7 19.5 5.4 6.0 34.2 9.4	2.0 2.7 2.0	0.7	0.7	29.5 36.9 16.1 3.4 2.7 0.7 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4	0.7	40.3 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4	0.7 6.7 11.4 0.7 2.0	6.0 0.7 1.3 12.1 1.3 8.1 6.0	8.1 4.0 1.3	 33.6 8.1 15.4 1.3 26.8 3.4 7.4 	4.0	3.4 5.4 4.7 2.0 17.5 0.7 15.4	0.7 1.3 0.7 2.0 3.4 8.1 30.2	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1	14.8 14.1 3.4	12.1 49.0 30.9 0.7 6.0 0.7 4.7	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201	8 9 7 6 8 8 8 6 6 6 6 6 5 6
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1	2.0 2.7 2.0	0.7	0.7	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7	 43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 	0.7	40.3 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4	0.7 6.7 11.4 0.7 2.0 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0	8.1 4.0 1.3 9.4	33.6 8.1 15.4 1.3 26.8 3.4 7.4	4.0	0.7 3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9	14.8 14.1 3.4	12.1 49.0 30.9 0.7 6.0 0.7 4.7	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872	8 9 7 6 8 8 8 6 6 6 6 6 5 6 4
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0	2.0 2.7 2.0	0.7	0.7 0.7 6.0	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7	 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 	0.7	40.3 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7	0.7 6.7 11.4 0.7 2.0 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0	8.1 4.0 1.3 9.4	33.6 8.1 15.4 1.3 26.8 3.4 7.4	4.0 4.0 30.2	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7	14.8 14.1 3.4	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201	8 9 7 6 6 8 8 8 6 6 6 6 6 6 5 6 4 2
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU LEU	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0 1.3	2.0 2.7 2.0	0.7	0.7 0.7 6.0	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7 2.0	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 10.7	0.7	40.3 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7 51.0	0.7 6.7 11.4 0.7 2.0 0.7 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0	8.1 4.0 1.3 9.4	33.6 8.1 15.4 1.3 26.8 3.4 7.4 7.4	4.0 4.0 30.2 6.7	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0 1.3	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7 10.7	14.8 14.1 3.4	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201 L 51.007	8 9 7 6 8 8 8 6 6 6 6 6 6 6 5 6 4 2 2 6
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU LEU LEU	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0 1.3 6.7	2.0 2.7 2.0	0.7	0.7 0.7 6.0 0.7	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7 0.7 9.4 36.9	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7 0.7 1.3	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7 0.7	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 10.7 0.7	0.7	40.9 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7 51.0 5.4	0.7 6.7 11.4 0.7 2.0 0.7 0.7 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0	8.1 4.0 1.3 9.4	33.6 8.1 15.4 1.3 26.8 3.4 7.4 7.4	4.0 4.0 30.2 6.7 4.7	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4 2.7	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0 1.3 1.3 1.3	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7 10.7 16.1	14.8 14.1 3.4 7.4 4.7	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0 11.4	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201 L 51.007 F 36.913	8 9 7 6 8 8 8 6 6 6 6 6 5 6 4 2 6 5
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU LEU LEU GLY	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0 1.3 6.7 15.3	2.0 2.7 2.0	0.7 5.4 2.0	0.7 0.7 6.0 0.7 1.3	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7 9.4 36.9 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7 0.7 1.3 70.7	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7 0.7	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 10.7 0.7 0.7	0.7	65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7 51.0 5.4 2.0	0.7 6.7 11.4 0.7 2.0 0.7 0.7 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0	8.1 4.0 1.3 9.4	33.6 8.1 15.4 1.3 26.8 3.4 7.4 7.4 6.0 0.7	4.0 4.0 30.2 6.7 4.7 0.7	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4 2.7 4.7	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0 1.3 1.3 0.7	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7 10.7 16.1 0.7	14.8 14.1 3.4 7.4 4.7	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0 11.4	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201 L 51.007 F 36.913 G 70.667	8 9 7 6 8 8 8 6 6 6 6 6 6 5 6 4 2 6 5 5 5
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU LEU LEU ILE GLY SER	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0 1.3 6.7 15.3 3.4	2.0 2.7 2.0	0.7 5.4 2.0 5.4	0.7 0.7 6.0 0.7 1.3 4.0	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7 0.7 9.4 36.9 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7 0.7 1.3 70.7 3.4	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7 0.7	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 10.7 0.7 0.7 0.7	0.7	65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7 51.0 5.4 2.0	0.7 6.7 11.4 0.7 2.0 0.7 0.7 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0	8.1 4.0 1.3 9.4	33.6 8.1 15.4 1.3 26.8 3.4 7.4 7.4 6.0 0.7 4.0	4.0 4.0 30.2 6.7 4.7 0.7 11.4	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4 2.7 4.7 22.8	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0 1.3 1.3 0.7 34.2	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7 10.7 16.1 0.7 1.3	14.8 14.1 3.4 7.4 4.7	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0 11.4	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201 L 51.007 F 36.913 G 70.667 T 34.228	8 9 7 6 8 8 8 6 6 6 6 6 6 6 6 6 4 2 6 5 5 5 3
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU LEU LEU LEU LEU SER GLN	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0 1.3 6.7 15.3 3.4 12.8	2.0 2.7 2.0	0.7 5.4 2.0 5.4 10.1	0.7 0.7 6.0 0.7 1.3 4.0 10.7	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7 0.7 9.4 36.9 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7 0.7 1.3 70.7 3.4 2.7	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7 0.7	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 10.7 0.7 0.7	0.7	40.9 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7 51.0 5.4 2.0 2.0	0.7 6.7 11.4 0.7 2.0 0.7 0.7 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0 7.4 0.7	8.1 4.0 1.3 9.4 0.7 47.7	33.6 8.1 15.4 1.3 26.8 3.4 7.4 7.4 6.0 0.7 4.0 2.7	4.0 4.0 30.2 6.7 4.7 0.7 11.4 5.4	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4 2.7 4.7 2.8 1.3	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0 1.3 1.3 0.7 34.2 2.7	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7 10.7 16.1 0.7 1.3	14.8 14.1 3.4 7.4 4.7	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0 11.4	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201 V 30.872 R 30.201 L 51.007 F 36.913 G 70.667 T 34.228 P 47.651	8 9 7 6 8 8 8 6 6 6 6 6 5 5 5 5 3 1
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU ILE GLU ILE GLU SER GLU GLU	90 91 92 93 94 95 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0 1.3 6.7 15.3 3.4 12.8 31.8	2.0 2.7 2.0	0.7 5.4 2.0 5.4 10.1 8.1	0.7 0.7 6.0 0.7 1.3 4.0 10.7 45.3	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7 0.7 9.4 36.9 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7 0.7 1.3 70.7 3.4 2.7 2.7	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7 0.7 0.7 1.4	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 10.7 0.7 0.7 0.7	0.7	40.9 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7 51.0 5.4 2.0 0.7	0.7 6.7 11.4 0.7 2.0 0.7 0.7 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0 7.4 0.7	8.1 4.0 1.3 9.4 0.7 47.7 0.7	33.6 8.1 15.4 1.3 26.8 3.4 7.4 7.4 6.0 0.7 4.0 2.7 3.4	4.0 4.0 30.2 6.7 4.7 0.7 11.4 5.4 1.4	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4 2.7 4.7 2.7 3.4 1.3 1.4	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0 1.3 1.3 0.7 34.2 2.7 1.4	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7 10.7 16.1 0.7 1.3 1.4	14.8 14.1 3.4 7.4 4.7	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0 11.4	A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201 U 51.007 F 36.913 G 70.667 T 34.228 P 47.651 E 45.270	8 9 7 6 8 8 8 6 6 6 6 6 5 5 6 4 2 2 6 5 5 3 3 1 3
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU LEU LEU LEU LEU LEU GLY SER GLN GLU GLN	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 111 111 112	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0 1.3 6.7 15.3 3.4 12.8 31.8 0.7	2.0 2.7 2.0	0.7 5.4 2.0 5.4 10.1 8.1	0.7 0.7 6.0 0.7 1.3 4.0 10.7 45.3 0.7	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7 9.4 36.9 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7 0.7 1.3 70.7 3.4 2.7 2.7 0.7	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7 0.7 1.4 1.4	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 10.7 0.7 0.7 0.7	0.7	40.9 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7 51.0 5.4 2.0 0.7 5.4	0.7 6.7 11.4 0.7 2.0 0.7 0.7 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0 7.4 0.7	8.1 4.0 1.3 9.4 0.7 47.7 0.7	33.6 8.1 15.4 1.3 26.8 3.4 7.4 7.4 7.4 6.0 0.7 4.0 2.7 3.4 82.4	4.0 4.0 30.2 6.7 4.7 0.7 11.4 5.4 1.4 4.7	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4 2.7 4.7 2.7 1.3 1.4	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0 1.3 1.3 0.7 34.2 2.7 1.4 2.0	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7 10.7 16.1 0.7 1.3 1.4 1.4	14.8 14.1 3.4 7.4 4.7	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0 11.4	A 61.745 A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201 U 30.872 R 30.201 L 51.007 F 36.913 G 70.667 T 34.228 P 47.651 E 45.270 Q 82.432	8 9 7 6 8 8 8 6 6 6 6 5 5 5 5 3 1 3 8
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU LEU LEU LEU LEU LEU SER GLN GLU GLU	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0 1.3 6.7 15.3 3.4 12.8 31.8 0.7 23.0	2.0 2.7 2.0	0.7 5.4 2.0 5.4 10.1 8.1	0.7 0.7 6.0 0.7 1.3 4.0 10.7 45.3 0.7 1.4	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7 9.4 36.9 0.7 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7 0.7 1.3 70.7 3.4 2.7 2.7 0.7 2.0	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7 0.7 1.4 1.4 3.4	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 10.7 0.7 0.7 0.7 0.7 6.8	0.7 1.3 0.7 0.7 8.8	40.9 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7 5.4 2.0 0.7 5.4 0.7	0.7 6.7 11.4 0.7 2.0 0.7 0.7 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0 7.4 0.7	8.1 4.0 1.3 9.4 0.7 47.7 0.7	33.6 8.1 15.4 1.3 26.8 3.4 7.4 7.4 6.0 0.7 4.0 2.7 3.4 82.4 12.8	4.0 4.0 30.2 6.7 4.7 0.7 11.4 5.4 1.4 4.7 14.2	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4 2.7 4.7 2.8 1.3 1.4	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0 1.3 1.3 0.7 34.2 2.7 1.4 2.0 0.7	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7 10.7 16.1 0.7 1.3 1.4 1.4 4.1	14.8 14.1 3.4 7.4 4.7	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0 11.4 4.1	A 61.745 A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201 V 30.872 R 30.201 L 51.007 F 36.913 G 70.667 T 34.228 P 47.651 E 45.270 Q 82.432 A 22.973	8 9 7 6 8 8 8 6 6 6 6 6 6 6 5 5 5 3 3 1 3 8 5 5
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU LEU ILE GLU LEU ILE GLY SER GLN GLU GLU GLU	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0 1.3 6.7 15.3 3.4 12.8 31.8 0.7 23.0 18.2	2.0 2.7 2.0	0.7 5.4 2.0 5.4 10.1 8.1 7.4	0.7 0.7 6.0 0.7 1.3 4.0 10.7 45.3 0.7 1.4 35.8	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7 9.4 36.9 0.7 0.7	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7 0.7 1.3 70.7 3.4 2.7 2.7 0.7 2.0 0.7	59.7 0.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7 0.7 1.4 1.4 3.4 2.7	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 10.7 0.7 0.7 0.7 6.8	0.7 1.3 0.7 8.8 3.4	40.9 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7 5.4 2.0 0.7 5.4 0.7	0.7 6.7 11.4 0.7 2.0 0.7 0.7 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0 7.4 0.7	8.1 4.0 1.3 9.4 0.7 47.7 0.7	33.6 8.1 15.4 1.3 26.8 3.4 7.4 7.4 6.0 0.7 4.0 2.7 3.4 82.4 12.8 15.5	4.0 4.0 30.2 6.7 4.7 0.7 11.4 5.4 1.4 4.7 14.2 9.5	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4 2.7 4.7 2.8 1.3 1.4 1.4	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0 1.3 1.3 0.7 34.2 2.7 1.4 2.0 0.7 1.4	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7 10.7 16.1 0.7 1.3 1.4 1.4 4.1 0.7	14.8 14.1 3.4 7.4 4.7 16.9 1.4	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0 11.4 4.1	A 61.745 A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201 V 30.872 R 30.201 L 51.007 F 36.913 G 70.667 T 34.228 P 47.651 E 45.270 Q 82.432 A 22.973 E 35.811	8 9 7 6 8 8 8 6 6 6 6 6 6 6 6 6 6 5 5 5 5 3 1 3 8 5 1
LEU GLY HIS LEU PHE GLY TYR HIS LEU THR ASN ALA PRO MET ILE GLU LEU LEU LEU LEU GLU SER GLU GLU GLU GLU HIS	90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115	0.7 61.7 19.5 5.4 6.0 34.2 9.4 22.1 4.0 1.3 6.7 15.3 3.4 12.8 31.8 0.7 23.0 18.2 15.5	2.0 2.7 2.0	0.7 5.4 2.0 5.4 10.1 8.1 7.4 4.1	0.7 0.7 6.0 0.7 1.3 4.0 10.7 45.3 0.7 1.4 35.8 4.1	29.5 36.9 16.1 3.4 2.7 0.7 0.7 0.7 9.4 36.9 0.7 0.7 8.8	38.3 66.4 2.0 3.4 3.4 2.0 4.7 2.0 4.7 0.7 1.3 70.7 3.4 2.7 2.7 0.7 2.0 0.7 2.0 0.7	59.7 82.6 35.6 0.7 4.0 2.0 0.7 8.7 0.7 1.4 1.4 3.4 2.7 6.1	43.0 9.4 3.4 1.3 0.7 10.1 4.0 7.4 18.1 2.0 10.7 0.7 0.7 0.7 6.8	0.7 1.3 0.7 8.8 3.4 2.7	40.9 65.1 44.3 1.3 10.7 65.8 13.4 28.9 1.3 3.4 7.4 10.7 5.10 5.4 2.0 0.7 5.4 0.7 5.4 0.7	0.7 6.7 11.4 0.7 2.0 0.7 0.7 0.7 0.7	6.0 0.7 1.3 12.1 1.3 8.1 6.0 6.0 7.4 0.7 0.7 2.7	8.1 4.0 1.3 9.4 0.7 47.7 0.7 1.4 10.1	33.6 8.1 15.4 1.3 26.8 3.4 7.4 7.4 6.0 0.7 4.0 2.7 3.4 82.4 12.8 15.5 4.1	4.0 4.0 30.2 6.7 4.7 0.7 11.4 5.4 1.4 4.7 14.2 9.5 33.1	3.4 5.4 4.7 2.0 17.5 0.7 15.4 2.7 3.4 2.7 4.7 2.8 1.3 1.4 1.4 2.0	0.7 1.3 0.7 2.0 3.4 8.1 30.2 6.0 2.0 1.3 1.3 0.7 34.2 2.7 1.4 2.0 0.7 1.4 2.7	13.4 25.5 2.7 0.7 13.4 22.1 9.4 8.1 30.9 2.7 10.7 16.1 0.7 1.3 1.4 1.4 4.1 0.7 0.7	14.8 14.1 3.4 7.4 4.7 16.9 1.4	12.1 49.0 30.9 0.7 6.0 0.7 4.7 6.0 11.4 4.1 4.1	A 61.745 A 61.745 H 59.732 L 65.101 L 44.295 G 66.443 Y 48.993 H 82.550 H 35.570 L 65.772 Q 26.846 L 28.859 A 34.228 T 30.201 V 30.872 R 30.201 V 30.872 R 30.201 L 51.007 F 36.913 G 70.667 T 34.228 P 47.651 E 45.270 Q 82.432 A 22.973 E 35.811 R 33.108	8 9 7 6 8 8 8 6 6 6 6 6 6 6 6 6 6 5 5 5 5 5 5

TYR	117	4.7		1.4	10.1	18.9	4.7	1.4	2.0		26.4				8.1	0.7	6.8	2.0		0.7	12.2	L 26.351	3
THR	118	10.8		1.4	15.5		6.8			8.8	0.7			1.4	2.7	35.1	5.4	9.5	2.0			R 35.135	2
GLN	119	10.0		4.0	22.0	1.3	11.3	2.7	1.3	2.7	11.3		0.7	2.7	11.3	16.0	0.7		0.7	1.3		E 22.000	1
ILE	120	8.0				0.7	0.7		9.3		2.7		4.0				12.7	51.3	8.0		2.7	T 51.333	7
ALA	121	36.7	0.7				2.7		8.7		9.3	0.7				0.7	0.7	9.3	30.7			A 36.667	5
GLN	122	22.0		2.7	23.3		1.3	1.3		4.0			2.0		8.7	20.0	10.0	4.7				E 23.333	1
ASN	123	2.0		1.3	18.0	0.7	18.7	10.7		8.7	2.0		22.7	0.7	9.3	4.0	1.3					N 22.667	2
ASN	124	2.0		5.3	1.3		93	2.0		73	0.7		32.7		93	25.3	4.0	07				N 32 667	3
TRP	125	0.7	07			07	0.7	13			22.0		0.7	07	13	8.0		0.7		54 7	8.0	W 54 667	4
TRP	126	0.1	33			71 3	•		07		93		•	•		0.0		0.1	20	87	47	F 71 333	7
THR	127		0.0			8.0		07	1.4		0.0				36			14	5.8	77.5	1.1	W 77 536	8
GLV	128	53	27			0.0	88.0	0.7	1.4						0.0		4.0	1.4	0.0	11.0	1.4	G 88 000	8
	120	4.7	2.1	33			20.3						60.0				2.0	0.7				N 60.000	0
	129	70.7		5.5			29.5		2.0				00.0				2.0	6.7	10.7			A 70 667	9
SED	130	27				47	1.0		2.0		22.2	0.7	0.7		10.0		4.7	0.7	20.7			A 70.007	6
SER	420	2.1		0.7		4./	4.0	6.7	2.0		33.3	0.7	0.7		0.7		0.7	2.1	30.7			L 33.333	0
SER	132	5.5		0.7	4.0		0.7	0.7					00.7	75.0	0.7	0.0	2.0	0.0	7.4			N 00.007	9
GLU	133	5.4			1.3		0.7						100.0	/5.8		2.0	5.4	2.0	7.4			P 75.839	1
ASN	134												100.0									N 100.000	0
ASN	135												100.0									N 100.000	6*
SER	136							400.0									100.0					S 100.000	6*
HIS	137							100.0														H 100.000	6*
VAL	138																		100.0			V 100.000	6*
LEU	139	3.3				2.7		0.7			40.0	2.0	1.3		8.0	38.7		0.7	2.7			L 40.000	7
ASP	140			84.7	3.3		4.7						1.3		0.7		4.7				0.7	D 84.667	9
TRP	141	9.3		2.7	1.3		5.3		6.7	12.0	2.7		3.3	18.7	2.7	12.0	5.3	16.0	0.7	1.3		P 18.667	2
LYS	142	4.7		18.0	1.3		10.0	2.0		2.7			0.7	2.0	1.3	46.7	6.7	3.3		0.7		R 46.667	6
VAL	143	5.3	0.7	0.7			1.3	0.7	1.3		43.3						6.7	30.0	10.0			L 43.333	6
ARG	144	2.7			7.3	2.0		0.7	6.7	10.7	4.0	0.7			6.0	17.3	2.7	20.7	18.7			T 20.667	1
ALA	145	30.7	1.3				4.7		14.0		33.3	1.3					2.0		12.7			L 33.333	6
THR	146	7.3		0.7	6.0		0.7	2.0	1.3	7.3	2.0		0.7		4.0	12.0	7.3	45.3	2.7		0.7	T 45.333	3
PRO	147	8.0		10.0	10.7		0.7	1.3		7.3	1.3		0.7	22.0	3.3	24.7	6.7	1.3	0.7	1.3		R 24.667	1
THR	148	3.3		26.7	10.0	5.3	1.3	2.7	1.3	0.7	3.3		1.3		4.0	12.7	3.3	14.7	8.7		0.7	D 26.667	1
GLU	149	12.5			6.3		25.0						3.1	37.5		6.3	9.4					P 37.500	1
ASP	150	8.0		28.7	8.7		42.7			2.0			2.0	4.7	0.7		2.0	0.7				G 42.667	1
GLY	151	1.3		28.0	10.0		41.3	1.3		2.0			7.3	0.7	1.3		1.3	4.7			0.7	G 41.333	1
GLY	152	1.3		6.0	5.3	0.7	48.7	7.3	0.7	1.3			4.7		2.0	1.3	7.3	3.3		8.7	1.3	G 48.667	1
TYR	153		0.7			20.7		4.0	6.7		12.7				0.7	5.3	0.7		2.0	11.3	35.3	Y 35.333	1
VAL	154	3.3			10.7	2.0			6.7		12.7				1.3	26.7	0.7	2.0	32.7		1.3	V 32.667	1
LEU	155					27.3			5.3		52.0								11.3		4.0	L 52.000	6
ASN	156	1.3		24.0	2.0			5.3		0.7			37.3		3.3	1.3	16.0	8.0	0.7			N 37.333	5
GLY	157						100.0															G 100.000	9
THR	158	4.0		4.0	2.7	6.7		2.7	4.7	13.3	4.0		0.7	1.3	4.7	26.7	4.7	5.3	13.3		1.3	R 26.667	1
LYS	159									83.3					3.3	13.3						K 83.333	9
HIS	160	0.7				5.3	10.0	10.7					2.7	6.0		2.7	46.0	15.3			0.7	S 46.000	6
PHE	161					86.7															13.3	F 86.667	9
CYS	162	20.7	40.7				2.0						6.0				28.0	1.3	1.3			C 40.667	7
SER	163	1.3															54.7	44.0				S 54.667	9
GLY	164	2.7					96.0						1.3									G 96.000	9
ALA	165	55.3					9.3										20.7	8.7	6.0			A 55.333	7
LYS	166	8.0			0.7		2.0	9.3	4.0	8.7	18.0	1.3	1.3	0.7	2.0	10.7	13.3	3.3	16.0		0.7	L 18.000	3
GLY	167	0.7	07	26.0		8.0	18.7		12.0		27						0.7	13	29.3			V 29 333	6
SER	168	31.3					53										63.3					S 63 333	8
ASP	169			78.0	8.0			4.0							8.7		1.3					D 78.000	8
LEU	170	2.7	0.7		5.5			0.7	6.0		13.3	17.3			4.7	20.0			15.3	10.0	9.3	R 20.000	4
I FU	171		0.1					•	19.3		53.3	73	07			13	0.7	14 7	27		0.0	1 53 333	7
PHF	172	20				07		07	12.0		13.3	0.7	7.3	10.0	20	1.0	47	20.0	25.3	07	07	V 25 333	6
VAI	173	16.0	27			20		0.1	10.7		18.7	0.1	1.0	10.0	2.0			20.0	48.0	0.1	0.1	V 48 000	6
PHF	174	3.3			14 7	1.3	33				87		53			47	49.3	8.7	.0.0	07		S 49 333	8
GLY	175	64.0			1-1.1	0.7	23.3		07		2.0		0.0			۱.ד	т Ј.Ј	0.1	40	53		A 64 000	7
VAI	176	67		20	40	20	20.0	60	6.0		6.0			20	60	87	47	73	24.7	87	53	V 24 667	1
VAI	177	0.1		2.0		10.0		0.0	20.0		30.0			2.0	0.0	0.1		10.0	30.0	0.1	0.0	I V 30 000	2*
GIN	178	20.0			20.0	10.0	20.0		20.0		00.0				40.0			10.0	00.0			0 40 000	<u>د</u> 4*
JLN		20.0			20.0		20.0								-0.0							Q TU.UUU	-1

ASP	179			66.7									33.3									D 66.667	6*
ASP	180			60.0			40.0															D 60.000	5*
SER	181	7.5		25.6	2.3	1.5	4.5	10.5	1.5	3.8	15.8	0.8	5.3	0.8	3.8	7.5	1.5	4.5	1.5		1.5	D 25.564	1
PRO	182	10.9		10.9	35.7		3.9		0.8	3.1			1.6	13.2	6.2	1.6	5.4	3.9	2.3		0.8	E 35.659	2
GLN	183	12.1		22.7	9.1	3.0	20.5	1.5	0.8	1.5	6.1		3.0	3.8	1.5	0.8	6.1	3.8	3.0		0.8	D 22.727	1
GLN	184	6.8	1.5	11.3	3.0		14.3	2.3	1.5		0.8		3.0	3.8	2.3	1.5	10.5	36.1	1.5			T 36.090	1
GLY	185	4.0		21.5	8.1		46.3			2.0			3.4		5.4	2.0	5.4	2.0				G 46.309	1
ALA	186	12.0		10.7	15.3		5.3			19.3			3.3		8.7	14.0	4.7	6.0	0.7			K 19.333	1
ILE	187	4.7		0.7		4.0	0.7	14.7	6.0	4.0	36.0	0.7		12.7		9.3	0.7	1.3	4.7			L 36.000	4
ILE	188	6.7						6.0	14.7		30.0					3.3	0.7	1.3	32.0	2.7	2.7	V 32.000	4
ALA	189	6.0				28.7	2.0	1.3	21.3		5.3	1.3	2.7		0.7		2.7	8.0	18.0		2.0	F 28.667	4
ALA	190	57.3				11.3	9.3				11.3						0.7	1.3	7.3		1.3	A 57.333	6
ALA	191	29.3	0.7			4.7		1.3	12.0		7.3				2.0		3.3	2.7	30.0		6.7	V 30.000	4
ILE	192	1.3		• •	• •				30.7		17.3					<u> </u>		0.7	50.0			V 50.000	6
PRO	193	1.3		9.3	3.3		0.0	0.7		2.7	0.7			82.0		0.7	40.0	0.7			0.7	P 82.000	/
	194	13.3		00.7	0.7	0.7	6.0	0.7	0.7	2.7	0.7		0.7	4.0	<u> </u>	8.7	13.3	49.3			0.7	T 49.333	5
SER	195	9.3		28.7	Z.1	0.7	14.7	2.0	0.7	3.3	0.7		8.7	0.7	0.0	10.0	8.0	4.0	10			D 28.007	7
AKG	190	12.7		10.7	10 7		0.7	2.1	0.7	0.7	0.7			20.2	13.3	0.7	4.0	5.5	1.5			R 00.000	1
	100	10.0		12.7	10.7		0.7	3.3		2.0				29.5	3.3	0.7	0.0	5.5				F 29.333	0
VAI	100	1.5				53	30.7		173		12.0								30.7		17	1 47 333	5
	200	53	0.7	0.7	2.0	0.0	33	2.0	33	13	2.0		13		10.0	8.0	87	35.3	14.7		0.7	T 35 333	1
PRO	200	6.0	0.7	0.1	2.0	22.0	0.0	2.0	16.7	0.7	7.3		1.0	40	10.0	1.3	1.3	0.7	32.7		4.0	V 32 667	5
ASN	202	7.3	0.1	20	53	0.7	10 7	17.3	4.0	0.7	18.7	07	14 0	0.7	6.0	27	1.3	1.3	5.3		1.3	1 18 667	1
ASP	203	2.7		50.7	1.3	•	17.3	10.7		0		0.1	7.3	2.7	4.0	1.3	1.3		0.0		0.7	D 50.667	3
ASP	204			95.3			1.3						3.3									D 95.333	9
TRP	205	2.0					1.3													96.7		W 96.667	9
ALA	206	2.0		80.7	0.7			2.7		0.7			12.0				1.3					D 80.667	7
ALA	207	15.3					14.0	0.7					55.3	7.3			4.7	2.0			0.7	N 55.333	8
ILE	208					18.0			39.3		16.7	20.7							5.3			1 39.333	6
GLY	209						100.0															G 100.000	9
	240										~ ~												
MEI	210										6.0	2.0			92.0							Q 92.000	9
ARG	210									2.0	6.0	2.0			92.0	96.7		1.3				Q 92.000 R 96.667	9 9
ARG GLN	210 211 212	0.7	0.7							2.0	6.0 37.3	2.0			92.0 50.7	96.7 2.7		1.3 7.3	0.7			Q 92.000 R 96.667 Q 50.667	9 9 9
ARG GLN THR	210 211 212 213	0.7	0.7	54.0	40.0		<u> </u>			2.0	6.0 37.3	2.0			92.0 50.7	96.7 2.7	12.0	1.3 7.3 84.7	0.7			Q 92.000 R 96.667 Q 50.667 T 84.667	9 9 9 9
ARG GLN THR ASP	210 211 212 213 214	0.7 3.3 22.0	0.7	54.0	16.0		6.0			2.0	6.0 37.3	2.0			92.0 50.7	96.7 2.7	12.0 0.7	1.3 7.3 84.7	0.7 1.3			Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000	9 9 9 9 9 8
MET ARG GLN THR ASP SER	210 211 212 213 214 215 216	0.7 3.3 22.0	0.7	54.0	16.0 0.7		6.0 2.7			2.0	6.0 37.3	2.0	1 2		92.0 50.7	96.7 2.7	12.0 0.7 96.7	1.3 7.3 84.7	0.7 1.3			Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667	9 9 9 9 8 9
MET ARG GLN THR ASP SER GLY SEP	210 211 212 213 214 215 216 217	0.7 3.3 22.0	0.7	54.0 1.3	16.0 0.7		6.0 2.7 97.3			2.0	37.3	2.0	1.3		92.0	96.7 2.7	12.0 0.7 96.7	1.3 7.3 84.7	0.7 1.3			Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667	9 9 9 9 8 9 9 9 9 7
MET ARG GLN THR ASP SER GLY SER THR	210 211 212 213 214 215 216 217 218	0.7 3.3 22.0	0.7	54.0 1.3	16.0 0.7	13	6.0 2.7 97.3 10.0		53	2.0	6.0 37.3	2.0	1.3 4.0		92.0 50.7 0.7	96.7 2.7 1.3	12.0 0.7 96.7 52.7 2.7	1.3 7.3 84.7 30.0 2.7	0.7		0.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000	9 9 9 9 9 9 9 9 9 7 8
MET ARG GLN THR ASP SER GLY SER THR ASP	210 211 212 213 214 215 216 217 218 219	0.7 3.3 22.0 1.3 4.7 2.0	0.7	54.0 1.3	16.0 0.7	1.3	6.0 2.7 97.3 10.0	6.0	5.3	2.0	6.0 37.3 0.7 2.0	2.0	1.3 4.0 2.7		92.0 50.7 0.7	96.7 2.7 1.3	12.0 0.7 96.7 52.7 2.7	1.3 7.3 84.7 30.0 2.7 18.0	0.7 1.3 82.0 6.7		0.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000	9 9 9 9 9 9 9 7 8 1
MET ARG GLN THR ASP SER GLY SER THR ASP PHE	210 211 212 213 214 215 216 217 218 219 220	0.7 3.3 22.0 1.3 4.7 2.0	0.7	54.0 1.3 4.0	16.0 0.7 17.3	1.3 1.3 74.0	6.0 2.7 97.3 10.0 0.7	6.0	5.3 4.7 12.0	2.0	6.0 37.3 0.7 2.0 10.7	2.0	1.3 4.0 2.7		92.0 50.7 0.7 3.3	96.7 2.7 1.3 15.3	12.0 0.7 96.7 52.7 2.7 10.7	1.3 7.3 84.7 30.0 2.7 18.0	0.7 1.3 82.0 6.7 1.3		0.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000	9 9 9 9 9 9 9 9 7 8 1 8
MET ARG GLN THR ASP SER GLY SER THR ASP PHE HIS	210 211 212 213 214 215 216 217 218 219 220 221	0.7 3.3 22.0 1.3 4.7 2.0 4.7	0.7	54.0 1.3 4.0 28.0	16.0 0.7 17.3 29.3	1.3 1.3 74.0	6.0 2.7 97.3 10.0 0.7	6.0	5.3 4.7 12.0	2.0 5.3 4.0	6.0 37.3 0.7 2.0 10.7	2.0	1.3 4.0 2.7 9.3		92.0 50.7 0.7 3.3 2.7	96.7 2.7 1.3 15.3 4.7	12.0 0.7 96.7 52.7 2.7 10.7	1.3 7.3 84.7 30.0 2.7 18.0 4.0	0.7 1.3 82.0 6.7 1.3 3.3		0.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333	9 9 9 9 8 9 9 7 8 1 8 1 8 2
MET ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN	210 211 212 213 214 215 216 217 218 219 220 221 222	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7	0.7	54.0 1.3 4.0 28.0 24.7	16.0 0.7 17.3 29.3 0.7	1.3 1.3 74.0	6.0 2.7 97.3 10.0 0.7	6.0 8.7 1.3	5.3 4.7 12.0	2.0 5.3 4.0 4.7	6.0 37.3 0.7 2.0 10.7	2.0	1.3 4.0 2.7 9.3 21.3		92.0 50.7 0.7 3.3 2.7 12.0	96.7 2.7 1.3 15.3 4.7 12.7	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0	1.3 7.3 84.7 30.0 2.7 18.0 4.0	0.7 1.3 82.0 6.7 1.3 3.3		0.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667	9 9 9 9 8 9 9 9 7 8 1 8 1 8 2 2
MET ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL	210 211 212 213 214 215 216 217 218 219 220 221 222 223	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7	0.7	54.0 1.3 4.0 28.0 24.7	16.0 0.7 17.3 29.3 0.7	1.3 1.3 74.0	6.0 2.7 97.3 10.0 0.7 14.0	6.0 8.7 1.3	5.3 4.7 12.0	2.0 5.3 4.0 4.7	6.0 37.3 0.7 2.0 10.7 2.7	2.0	1.3 4.0 2.7 9.3 21.3		92.0 50.7 0.7 3.3 2.7 12.0	96.7 2.7 1.3 15.3 4.7 12.7	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7	0.7 1.3 82.0 6.7 1.3 3.3 86.0		0.7 2.0	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000	9 9 9 9 8 9 9 7 8 1 8 1 8 2 2 9
MET ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7	0.7	54.0 1.3 4.0 28.0 24.7	16.0 0.7 17.3 29.3 0.7 8.7	1.3 1.3 74.0 4.0 2.7	6.0 2.7 97.3 10.0 0.7 14.0	6.0 8.7 1.3 2.0	5.3 4.7 12.0 1.3 0.7	2.0 5.3 4.0 4.7 6.7	6.0 37.3 0.7 2.0 10.7 2.7 8.0	2.0	1.3 4.0 2.7 9.3 21.3	12.7	92.0 50.7 0.7 3.3 2.7 12.0 2.0	96.7 2.7 1.3 15.3 4.7 12.7 37.3	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7		0.7 2.0 0.7 0.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333	9 9 9 9 8 9 9 7 8 1 8 1 8 2 2 9 1
MET ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3	0.7	54.0 1.3 4.0 28.0 24.7	16.0 0.7 17.3 29.3 0.7 8.7	1.3 1.3 74.0 4.0 2.7	6.0 2.7 97.3 10.0 0.7 14.0	6.0 8.7 1.3 2.0	5.3 4.7 12.0 1.3 0.7 15.3	2.0 5.3 4.0 4.7 6.7	6.0 37.3 0.7 2.0 10.7 2.7 8.0 13.3	2.0	1.3 4.0 2.7 9.3 21.3	12.7	92.0 50.7 0.7 3.3 2.7 12.0 2.0	96.7 2.7 1.3 15.3 4.7 12.7 37.3	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0		0.7 2.0 0.7 0.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000	9 9 9 9 8 9 9 7 8 1 8 2 2 9 1 6
MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3 12.0	0.7	54.0 1.3 4.0 28.0 24.7 6.0	16.0 0.7 17.3 29.3 0.7 8.7 24.0	1.3 1.3 74.0 2.7 2.0	6.0 2.7 97.3 10.0 0.7 14.0	6.0 8.7 1.3 2.0 2.7	5.3 4.7 12.0 1.3 0.7 15.3	2.0 5.3 4.0 4.7 6.7 3.3	6.0 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7	2.0	1.3 4.0 2.7 9.3 21.3	12.7 23.3	92.0 50.7 0.7 3.3 2.7 12.0 2.0 1.3	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0		0.7 2.0 0.7 0.7 6.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000	9 9 9 9 8 9 9 7 8 1 8 2 2 9 1 6
MEI ARG GLN THR ASP GLY SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU PRO	210 211 212 213 214 215 216 217 218 219 220 221 222 223 222 223 224 225 226 227	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3 12.0 18.9	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1	16.0 0.7 17.3 29.3 0.7 8.7 24.0 12.8	1.3 1.3 74.0 2.7 2.0 0.7	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4	6.0 8.7 1.3 2.0 2.7 6.1	5.3 4.7 12.0 1.3 0.7 15.3	2.0 5.3 4.0 4.7 6.7 3.3 5.4	6.0 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7 0.7	2.0	1.3 4.0 2.7 9.3 21.3	12.7 23.3 16.2	92.0 50.7 0.7 3.3 2.7 12.0 2.0 1.3 0.7	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7	14.9	0.7 2.0 0.7 0.7 6.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919	9 9 9 9 9 9 9 9 7 8 8 1 8 2 2 9 1 6 1 1
MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU PRO ASP	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 4.7 4.7 6.7 3.3 12.0 18.9 12.8	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1	16.0 0.7 17.3 29.3 0.7 8.7 24.0 12.8 12.2	1.3 1.3 74.0 2.7 2.0 0.7 0.7	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4	6.0 8.7 1.3 2.0 2.7 6.1 8.1	5.3 4.7 12.0 1.3 0.7 15.3	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7	6.0 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7 0.7 0.7		1.3 4.0 2.7 9.3 21.3 2.0 4.1	12.7 23.3 16.2	92.0 50.7 0.7 3.3 2.7 12.0 2.0 1.3 0.7 1.4	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7	14.9	0.7 2.0 0.7 0.7 6.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135	9 9 9 9 9 9 7 8 1 6 1 1 1
MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU PRO ASP GLU	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3 12.0 18.9 12.8 7.3	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1 22.7	16.0 0.7 17.3 29.3 0.7 8.7 24.0 12.8 12.2 50.0	1.3 1.3 74.0 2.7 2.0 0.7 0.7	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4	6.0 8.7 1.3 2.0 2.7 6.1 8.1 1.3	5.3 4.7 12.0 1.3 0.7 15.3	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7	6.0 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7 0.7 0.7 1.3		1.3 4.0 2.7 9.3 21.3 2.0 4.1 1.3	12.7 23.3 16.2	92.0 50.7 0.7 3.3 2.7 12.0 2.0 1.3 0.7 1.4 4.7	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4 6.0	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5 4.0	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7	14.9	0.7 2.0 0.7 0.7 6.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135 E 50.000	9 9 9 9 9 9 7 8 1 6 1 1 6
MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU VAL	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3 12.0 18.9 12.8 7.3 15.3	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1 22.7	16.0 0.7 17.3 29.3 0.7 8.7 24.0 12.8 12.2 50.0	1.3 1.3 74.0 2.7 2.0 0.7 0.7 4.7	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4	6.0 8.7 1.3 2.0 2.7 6.1 8.1 1.3	5.3 4.7 12.0 1.3 0.7 15.3	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7	6.0 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7 0.7 0.7 1.3 18.7	2.0	1.3 4.0 2.7 9.3 21.3 2.0 4.1 1.3	12.7 23.3 16.2	92.0 50.7 0.7 3.3 2.7 12.0 2.0 1.3 0.7 1.4 4.7	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4 6.0 1.3	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5 4.0	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7 0.7 40.0	14.9	0.7 2.0 0.7 0.7 6.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135 E 50.000 V 40.000	9 9 9 9 9 9 9 7 8 2 9 1 6 1 1 6 1 6 6 6 6 6 6
MEI MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU VAL LEU	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3 12.0 18.9 12.8 7.3 15.3 7.3	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1 22.7	16.0 0.7 17.3 29.3 0.7 8.7 24.0 12.8 12.2 50.0	1.3 1.3 74.0 2.7 2.0 0.7 0.7 0.7 4.7 4.0	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4	6.0 8.7 1.3 2.0 2.7 6.1 8.1 1.3	5.3 4.7 12.0 1.3 0.7 15.3	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7	6.0 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7 0.7 0.7 1.3 18.7 78.0	1.3	1.3 4.0 2.7 9.3 21.3 2.0 4.1 1.3	12.7 23.3 16.2	92.0 50.7 0.7 3.3 2.7 12.0 2.0 1.3 0.7 1.4 4.7	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4 6.0 1.3	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5 4.0	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7 40.0 4.7	14.9	0.7 2.0 0.7 0.7 6.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135 E 50.000 V 40.000 L 78.000	9 9 9 9 9 9 9 7 7 8 8 1 8 2 2 9 1 6 1 1 1 1 6 6 7 7
MEI ARG GLN THR ASP SER GLY SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU PRO ASP GLU VAL LEU VAL	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232	0.7 3.3 22.0 1.3 4.7 2.0 4.7 2.7 6.7 3.3 12.0 18.9 12.8 7.3 15.3 7.3 5.3	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1 22.7 2.0	16.0 0.7 17.3 29.3 0.7 8.7 24.0 12.8 12.2 50.0	1.3 1.3 74.0 2.7 2.0 0.7 0.7 0.7 4.7 4.0 1.3	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4 42.7	6.0 8.7 1.3 2.0 2.7 6.1 8.1 1.3 4.0	5.3 4.7 12.0 1.3 0.7 15.3 18.0 5.3 1.3	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7 1.3	6.0 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7 0.7 0.7 1.3 18.7 78.0 13.3 2.2	1.3	1.3 4.0 2.7 9.3 21.3 2.0 4.1 1.3	12.7 23.3 16.2 8.7	92.0 50.7 0.7 3.3 2.7 12.0 2.0 1.3 0.7 1.4 4.7 6.0	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4 6.0 1.3 2.0	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5 4.0 3.3	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4 4.7	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7 40.0 4.7 2.0	14.9	0.7 2.0 0.7 0.7 6.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135 E 50.000 V 40.000 L 78.000 G 42.667 P 42.67	9 9 9 9 9 9 7 8 2 9 1 6 1 1 6 6 7 3
MEI MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU PRO ASP GLU VAL LEU GLY ALA	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 226 227 228 229 230 231 232 233	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3 12.0 18.9 12.8 7.3 15.3 7.3 5.3 10.2	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1 22.7 2.0 2.0	16.0 0.7 17.3 29.3 0.7 8.7 24.0 12.8 12.2 50.0 0.7 6.1	1.3 1.3 74.0 2.7 2.0 0.7 0.7 0.7 4.7 4.0 1.3 6.8	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4 42.7 2.7	6.0 8.7 1.3 2.0 2.7 6.1 8.1 1.3 4.0 6.1	5.3 4.7 12.0 1.3 0.7 15.3 18.0 5.3 1.3	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7 1.3	6.0 37.3 0.7 2.0 10.7 2.0 10.7 8.0 13.3 2.7 0.7 0.7 1.3 18.7 78.0 13.3 2.0 0.5	1.3 0.7 0.7	1.3 4.0 2.7 9.3 21.3 2.0 4.1 1.3 6.8	12.7 23.3 16.2 8.7 9.5	92.0 50.7 0.7 3.3 2.7 12.0 2.0 1.3 0.7 1.4 4.7 6.0 2.7	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4 6.0 1.3 2.0 6.8	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5 4.0 3.3 8.2	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4 4.7 0.7	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7 40.0 4.7 2.0 4.1 8.2	14.9 1.3 8.2	0.7 2.0 0.7 0.7 6.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135 E 50.000 V 40.000 L 78.000 G 42.667 D 12.245 B 42.242	9 9 9 9 9 9 9 7 8 2 9 1 6 1 1 6 7 3 1
MEI MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU PRO ASP GLU VAL LEU GLY ALA	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 226 227 228 229 230 231 232 233 234 235	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3 12.0 18.9 12.8 7.3 15.3 7.3 5.3 10.2 4.1	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1 22.7 2.0 12.2 8.8	16.0 0.7 17.3 29.3 0.7 8.7 24.0 12.8 12.2 50.0 0.7 6.1 2.0 8.2	1.3 1.3 74.0 2.7 2.0 0.7 0.7 0.7 4.7 4.0 1.3 6.8 0.7	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4 42.7 2.7 3.4 32.7	6.0 8.7 1.3 2.0 2.7 6.1 8.1 1.3 4.0 6.1 8.8	5.3 4.7 12.0 1.3 0.7 15.3 18.0 5.3 1.3 0.7	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7 1.3	6.0 37.3 37.3 0.7 2.0 10.7 2.0 10.7 1.3 2.7 0.7 0.7 1.3 18.7 78.0 13.3 2.0 9.5 6.8	2.0 1.3 0.7	1.3 4.0 2.7 9.3 21.3 2.0 4.1 1.3 6.8 0.7 2.0	12.7 23.3 16.2 8.7 9.5 43.2 9.5	92.0 50.7 3.3 2.7 12.0 2.0 1.3 0.7 1.4 4.7 6.0 2.7 1.4 0.7	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4 6.0 1.3 2.0 6.8 1.4 1.4	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5 4.0 3.3 8.2 4.1 8.2	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4 3.4 4.7 0.7 1.4 3.4	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7 40.0 4.7 2.0 4.1 8.8 2.7	14.9 1.3 8.2	0.7 2.0 0.7 6.7 5.4 0.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135 E 50.000 V 40.000 L 78.000 G 42.667 D 12.245 P 43.243 G 32.652	9 9 9 9 9 9 9 7 8 2 9 1 6 1 1 6 7 3 1 4
MEI MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU PRO ASP GLU VAL LEU GLU VAL LEU GLY ALA PRO ASN	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 235 236	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3 12.0 18.9 12.8 7.3 15.3 7.3 5.3 10.2 4.1 8.8	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1 22.7 2.0 12.2 8.8 14.3 3.7	16.0 0.7 17.3 29.3 0.7 8.7 24.0 12.8 12.2 50.0 0.7 6.1 2.0 8.2 7.4	1.3 1.3 74.0 2.7 2.0 0.7 0.7 4.7 4.0 1.3 6.8 0.7	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4 42.7 2.7 3.4 32.7 0.7	6.0 8.7 1.3 2.0 2.7 6.1 8.1 1.3 4.0 6.1 8.8 1.4 2.9	5.3 4.7 12.0 1.3 0.7 15.3 18.0 5.3 1.3 0.7 1.5	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7 1.3 0.7 8.1	6.0 37.3 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7 0.7 0.7 1.3 18.7 78.0 13.3 2.0 9.5 6.8 2.2	2.0 1.3 0.7 0.7	1.3 4.0 2.7 9.3 21.3 2.0 4.1 1.3 6.8 0.7 2.0 1.5	12.7 23.3 16.2 8.7 9.5 43.2 9.5 24.3	92.0 50.7 3.3 2.7 12.0 2.0 1.3 0.7 1.4 4.7 6.0 2.7 1.4 0.7 8.1	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4 6.0 1.3 2.0 6.8 1.4 1.4 2.0	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5 4.0 3.3 8.2 4.1 8.2 6.6	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4 4.7 0.7 1.4 3.4 7 4	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7 40.0 4.7 2.0 4.1 8.8 2.7 4.4	14.9 1.3 8.2	0.7 2.0 0.7 6.7 5.4 0.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135 E 50.000 V 40.000 L 78.000 G 42.667 D 12.245 P 43.243 G 32.653 P 24.955	9 9 9 9 9 9 7 8 2 9 1 6 1 1 6 7 3 1 4 1
MEI MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL CLU PRO ASP GLU VAL LEU GLU VAL LEU GLU VAL ASP ALA PHF	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 231 232 233 234 235 236 237	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3 12.0 18.9 12.8 7.3 15.3 7.3 5.3 10.2 4.1 8.8 15.4 6.9	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1 22.7 2.0 12.2 8.8 14.3 3.7 6.2	16.0 0.7 17.3 29.3 0.7 24.0 12.8 12.2 50.0 0.7 6.1 2.0 8.2 7.4 6.9	1.3 1.3 74.0 2.7 2.0 0.7 0.7 4.7 4.0 1.3 6.8 0.7 2.9 1.5	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4 42.7 2.7 3.4 32.7 0.7 4.6	6.0 8.7 1.3 2.0 2.7 6.1 8.1 1.3 4.0 6.1 8.8 1.4 2.9	5.3 4.7 12.0 1.3 0.7 15.3 18.0 5.3 1.3 0.7 1.5 1.5	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7 1.3 0.7 8.1 3.8	6.0 37.3 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7 0.7 0.7 1.3 18.7 78.0 13.3 2.0 9.5 6.8 2.2 2.15	1.3 0.7 0.7	1.3 4.0 2.7 9.3 21.3 2.0 4.1 1.3 6.8 0.7 2.0 1.5 2.3	12.7 23.3 16.2 8.7 9.5 43.2 9.5 24.3 18.5	92.0 50.7 3.3 2.7 12.0 2.0 1.3 0.7 1.4 4.7 6.0 2.7 1.4 0.7 8.1 4.6	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4 6.0 1.3 2.0 6.8 1.4 1.4 2.9 1.5	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5 4.0 3.3 8.2 4.1 8.2 6.6 6 2	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4 7.4 7.4 7.4 7.4 7.4	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7 40.0 4.7 2.0 4.1 8.8 2.7 4.4 3.8	14.9 1.3 8.2	0.7 2.0 0.7 6.7 5.4 0.7	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135 E 50.000 V 40.000 L 78.000 G 42.667 D 12.245 P 43.243 G 32.653 P 24.265 L 21.538	9 9 9 9 9 9 7 8 2 9 1 6 1 1 6 7 3 1 4 1 1
MEI MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL GLU VAL GLU VAL LEU GLU VAL ASN ALA PRO ASN ALA PHE VAL	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 233 234 235 236 237 238	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 4.7 2.7 6.7 3.3 12.0 18.9 12.8 7.3 15.3 7.3 5.3 10.2 4.1 8.8 15.4 6.9 6.2	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1 22.7 2.0 12.2 8.8 14.3 3.7 6.2 8.5	16.0 0.7 17.3 29.3 0.7 24.0 12.8 12.2 50.0 0.7 6.1 2.0 8.2 7.4 6.9 6.2	1.3 1.3 74.0 2.7 2.0 0.7 0.7 4.7 4.0 1.3 6.8 0.7 2.9 1.5 8.5	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4 42.7 2.7 3.4 32.7 0.7 4.6 10.0	6.0 8.7 1.3 2.0 2.7 6.1 8.1 1.3 4.0 6.1 8.8 1.4 2.9	5.3 4.7 12.0 1.3 0.7 15.3 18.0 5.3 1.3 0.7 1.5 1.5 0.8	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7 1.3 0.7 8.1 3.8 9.2	6.0 37.3 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7 0.7 1.3 18.7 78.0 13.3 2.0 9.5 6.8 2.2 2.1.5 2.3	1.3 0.7 0.7	1.3 4.0 2.7 9.3 21.3 2.0 4.1 1.3 6.8 0.7 2.0 1.5 2.3 0.8	12.7 23.3 16.2 8.7 9.5 43.2 9.5 24.3 18.5 13.1	92.0 50.7 3.3 2.7 12.0 2.0 1.3 0.7 1.4 4.7 6.0 2.7 1.4 4.7 8.1 4.6 1.5	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4 6.0 1.3 2.0 6.8 1.4 1.4 2.9 1.5 0.8	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5 4.0 3.3 8.2 4.1 8.2 6.6 6.2 23.8	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4 4.7 0.7 1.4 3.4 7.4 7.4 7.3 8	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7 40.0 4.7 2.0 4.1 8.8 2.7 4.4 3.8 2.3	14.9 1.3 8.2 0.8 1.5	0.7 2.0 0.7 0.7 6.7 5.4 0.7 1.5 0.8	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135 E 50.000 V 40.000 L 78.000 G 42.667 D 12.245 P 43.243 G 32.653 P 24.265 L 21.538 S 23.846	9 9 9 9 9 9 7 8 2 9 1 6 7 3 1 4 1 1 2
MEI MEI ARG GLN THR ASP SER GLY SER THR ASP PHE HIS ASN VAL LYS VAL LEU GLU VAL LEU GLY ALA PRO ASN ALA PRO ASN ALA PHE VAL LEU	210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 233 234 235 236 237 238 239	0.7 3.3 22.0 1.3 4.7 2.0 4.7 4.7 2.7 6.7 3.3 12.0 18.9 12.8 7.3 15.3 7.3 5.3 10.2 4.1 8.8 15.4 6.9 6.2 15.4	0.7	54.0 1.3 4.0 28.0 24.7 6.0 10.1 35.1 22.7 2.0 12.2 8.8 14.3 3.7 6.2 8.5 13.5	16.0 0.7 17.3 29.3 0.7 24.0 12.8 12.2 50.0 0.7 6.1 2.0 8.2 7.4 6.9 6.2 3.8	1.3 1.3 74.0 2.7 2.0 0.7 0.7 4.7 4.0 1.3 6.8 0.7 2.9 1.5 8.5	6.0 2.7 97.3 10.0 0.7 14.0 2.7 1.4 3.4 42.7 2.7 3.4 32.7 0.7 4.6 10.0 11.5	6.0 8.7 1.3 2.0 2.7 6.1 8.1 1.3 4.0 6.1 8.8 1.4 2.9	5.3 4.7 12.0 1.3 0.7 15.3 1.8.0 5.3 1.3 0.7 1.5 1.5 0.8	2.0 5.3 4.0 4.7 6.7 3.3 5.4 2.7 1.3 0.7 8.1 3.8 9.2 17.3	6.0 37.3 37.3 0.7 2.0 10.7 2.7 8.0 13.3 2.7 0.7 0.7 1.3 18.7 78.0 13.3 2.0 9.5 6.8 2.2 21.5 6.8 2.2 2.1.5 2.3 1.9	2.0 1.3 0.7 0.7	1.3 4.0 2.7 9.3 21.3 21.3 2.0 4.1 1.3 6.8 0.7 2.0 1.5 2.3 0.8 1.9	12.7 23.3 16.2 8.7 9.5 43.2 9.5 24.3 18.5 13.1 3.8	92.0 50.7 0.7 3.3 2.7 12.0 2.0 2.0 1.3 0.7 1.4 4.7 6.0 2.7 1.4 0.7 8.1 4.6 1.5 17.3	96.7 2.7 1.3 15.3 4.7 12.7 37.3 6.0 6.1 1.4 6.0 6.1 1.4 6.0 1.3 2.0 6.8 1.4 1.4 2.9 1.5 0.8 7.7	12.0 0.7 96.7 52.7 2.7 10.7 1.3 4.0 2.7 4.0 2.0 13.5 4.0 3.3 8.2 4.1 8.2 6.6 6.2 23.8	1.3 7.3 84.7 30.0 2.7 18.0 4.0 2.7 4.7 2.0 3.3 1.4 3.4 7.4 7.4 7.4 7.4 7.4 7.3 8 3.8	0.7 1.3 82.0 6.7 1.3 3.3 86.0 4.7 66.0 0.7 0.7 40.0 4.7 2.0 4.1 8.8 2.7 4.4 3.8 2.3 1.9	14.9 1.3 8.2 0.8 1.5	0.7 2.0 0.7 0.7 6.7 5.4 0.7 1.5 0.8	Q 92.000 R 96.667 Q 50.667 T 84.667 D 54.000 S 96.667 G 97.333 S 52.667 V 82.000 T 18.000 F 74.000 E 29.333 D 24.667 V 86.000 R 37.333 V 66.000 E 24.000 A 18.919 D 35.135 E 50.000 V 40.000 L 78.000 G 42.667 D 12.245 P 43.243 G 32.653 P 24.265 L 21.538 S 23.846 KQ 17.308	9 9 9 9 9 9 7 8 2 9 1 6 1 1 6 6 7 3 1 1 1 1 1 1 1 2 1 1 1 1 2 1 1 1 1 1 1 1 2 1

PHE	241			50.0		16.7			16.7		8.3					8.3						D 50.000	3*
ILE	242								15.4		76.9			7.7								L 76.923	6
GLN	243	5.4				3.6	7.1			3.6	16.1	1.8		16.1	5.4	5.4	12.5	19.6	3.6			T 19.643	1
SER	244	1.3		3.3	4.7	6.7	0.7	2.0	4.7	2.0	2.7		2.7	4.0		7.3	22.0	34.7	1.3			T 34.667	4
GLU	245	8.0		1.3	3.3	0.7	0.7	0.7	1.3		1.3			59.3	2.7	4.7	0.7	2.0	12.7		0.7	P 59.333	4
ARG	246	2.0				34.7	6.0	0.7	0.7	0.7	4.7				4.0	26.0	1.3		0.7	2.0	16.7	F 34.667	4
GLY	247	40.0		4.0	2.7		3.3	1.3	2.0	0.7			8.0	9.3	5.3	0.7	17.3	4.0	1.3			A 40.000	4
SER	248	4.0	10.7				4.0	0.7			1.3				9.3		24.7	45.3				T 45.333	6
LEU	249		0.7			8.0			3.3		83.3	0.7						0.7	3.3			L 83.333	8
PHE	250	4.0	0.7	1.3		2.0	0.7	6.7	3.3		8.7		12.7			46.7	1.3	2.0	10.0			R 46.667	6
ALA	251	10.7				0.7	10.0		0.7		8.0		3.3	20.7			14.0	22.0	10.0			T 22.000	5
PRO	252	6.0	7.3					2.0	2.7		34.0	2.7		34.7	7.3			1.3	1.3		0.7	P 34.667	5
ILE	253	6.0				6.0	3.3	4.0	20.7		26.7	0.7			1.3		0.7	12.0	18.0		0.7	L 26.667	3
ALA	254	39.3				4.0	5.3	1.3	22.0		0.7	0.7			4.7		14.7	2.7	0.7	4.0		A 39.333	7
GLN	255							1.3							94.7	3.3					0.7	Q 94.667	9
LEU	256	4.7						• •	3.3		81.3	0.7	<u>-</u>		0.7		8.0	0.7	0.7			L 81.333	7
	257	6.0				40.7	0.7	2.0	26.7	0.0	10.7	1.3	2.7		4.0	0.7	0.7	3.3	46.0			V 46.000	6
PHE	258	04.0				40.7	4.0	6.7	2.0	2.0	40.0	3.3			1.3	0.7	3.3	00.7	00.0			F 40.667	8
	259	31.3	0.7		0.7	0.7	4.0	44.0	2.7		4.0		50.0		0.0	0.7	9.3	20.7	28.0		4.0	A 31.333	5
	200	ð. <i>1</i>	0.7		Z.1	0.7		14.0	07.0		0.7	2.2	59.3		8.0	0.7	Z.1	0.7	10.0		1.3	N 59.333	1
	201	0.7	0.7	0.0		27.3			21.5		30.0	3.3				1 2			12.0		62.2	L 30.000	0
	202	10.0	2.1	0.0		20.0			10.0		4.0				0.7	1.5		12	10.2		03.3	1 03.333	6
GLV	203	33					06.7		10.0		50.7				0.7			1.5	19.5			C 06 667	0
110	204	5.5					50.7		64.0		73	2.0	33				6.0	12.0	53			1.64.000	9
	266	92.0					53		04.0		1.5	2.0	5.5				13	0.7	0.7			Δ 92 000	q
HIS	267	3.3		07	53.3	07	27	27	07	07	60	07			18 7	6.0	1.3	0.7	0.7	13		F 53 333	5
GLY	268	27		0.7	00.0	•	96.0		0.1	•	0.0	•	07			0.0		•	•			G 96 000	8
ALA	269	92.0		•			1.3		1.3		0.7		•				1.3	0.7	2.7			A 92.000	9
LEU	270			0.7		23.3		0.7	0.7		72.0				1.3	0.7			0.7			L 72.000	7
ASP	271	28.0		16.0	24.7		0.7	0.7	0.7	4.0			2.7		11.3	4.0	2.7	4.0	0.7			A 28.000	1
ALA	272	22.0		5.3	44.0	4.7	0.7		0.7				0.7		7.3	1.3	0.7	8.7	3.3		0.7	E 44.000	4
ALA	273	91.3				0.7	6.7											0.7	0.7			A 91.333	9
ARG	274	14.7	1.3		0.7	0.7		1.3	2.0	12.7	13.3		1.3		0.7	36.0	7.3	1.3	6.0	0.7		R 36.000	4
GLU	275	10.7		22.0	27.3		4.0	4.0		6.0			2.7	1.3	6.0	11.3	2.0	2.7				E 27.333	1
TYR	276	1.3				12.0		2.7			2.0	1.3				1.3		2.0		4.7	72.7	Y 72.667	7
THR	277	2.0				1.3	0.7		2.7		4.0						2.7	62.0	24.7			T 62.000	7
ARG	278	2.7					0.7	2.7		6.0	17.3	0.7	1.3		4.7	50.0	2.0	6.0	6.0			R 50.000	4
THR	279	12.3		6.2	15.8		2.1	2.1		8.2	2.7		2.1		3.4	5.5	4.1	35.6				T 35.616	2
GLN	280	4.7		1.3	13.3		2.7	9.3		12.0			5.3		14.7	9.3	8.7	14.7	1.3	1.3	1.3	QT 14.667	1
ALA	281	20.1		0.7			11.4	2.0		0.7	0.7			1.3	2.7	3.4	23.5	31.5	2.0			T 31.544	5
ARG	282	0.7					1.4			8.1			0.7		2.7	79.7	6.1		0.7			R 79.730	8
PRO	283	23.0						0.7			0.7			73.0			2.0		0.7			P 72.973	6
TRP	284					2.0											0.7			97.3		W 97.279	9
THR	285	3.4			4.1	20.4	0.7	4.8	16.3	0.7	12.9	1.4	• •	17.7	2.0	1.4	2.7	2.0	8.8		0.7	F 20.408	2
PRO	286	16.8		2.7	10.1	5.4	2.0	9.4	0.7	3.4	8.1	1.3	2.0	4.0		3.4	4./	15.4	2.0		8.7	A 16.779	3
	287	14.7		1.3	0.7	0.7	13.3	0.0	0.7	0.7	2.2		4.0	0.7	10	0.7	66.7	2.0		0.0	0.7	S 66.66/	1
GLT	288	2.1		0.7	0.7	4.0	67.3	2.0	0.7	0.7	3.3		4.0	2.0	1.3	0.7	3.3	2.0	F0 7	2.0	0.7	G 67.333	2
	209	16.0		9.5	2.0	1.3	0.7	2.0	2.0		0.7		27	0.7	7 2	1.2	Z.1	4.0	12		0.7	V 02.007	5 1
GLN	290	53	0.7	10.7	42.1		2.0	17	0.7	67	0.7		0.7	0.7	8.7	34.7	4.7	4.0	1.5		0.7	E 42.007	1
	291	60.3	0.7	4./	5.5		2.0	5.3	1.3	0.7	0.7		0.7	17	0.7	54.7	53	27	47		13	A 60 333	7
	292	16.7		0.7	33		17	2.0	1.5	0.7	0.7		2.0	33	53	10	12.7	2.1	16.0		1.0	T 23 333	1
GLU	294	27		46.0	28.7		0.7	1.3	4.7	0.7	1.3		3.3	0.0	12 7	2.0	12.1	20.0	0.7			D 46 000	4
ASP	295	0.7		84.0	14.7								0.7			2.0						D 84.000	9
PRO	296	5.1		01.0	/	7.3	0.7	0.7			0.7		5.1	86.7		0.7			0.7	2.7		P 86.667	8
TYR	297					6.0	0.7	1.3			13.3				2.0					4.7	72.0	Y 72.000	7
THR	298	2.0				-		3.3	39.3		13.3	0.7	1.3		1.3			10.7	28.0		-	1 39.333	4
ILE	299	0.7						0.7	10.7	2.7	58.7				19.3	3.3			4.0			L 58.667	6
ARG	300	10.7		4.7	18.0		3.3	8.7		4.0	4.0		0.7		18.7	15.3	4.7	3.3	2.7		1.3	Q 18.667	4
SER	301	5.3		0.7	0.7		4.7	24.0	1.3	3.3	6.7		2.0		4.0	32.7	0.7	12.0	2.0			R 32.667	4
TYR	302	2.7				25.3		0.7	2.0		3.3	0.7						0.7	8.0		56.7	Y 56.667	5

GLY	303	4.7					95.3															G 95.333	9
GLU	304			19.3	54.0		2.0			0.7			10.0		4.7	7.3	0.7	1.3				E 54.000	5
PHE	305					33.3			1.3		52.7	11.3							0.7		0.7	L 52.667	7
THR	306	9.3		1.3	0.7	5.3	0.7	5.3	0.7	0.7	0.7	0.7			6.7	10.0	5.3	9.3	6.0	33.3	4.0	W 33.333	3
ILE	307	22.7					0.7		9.3		14.0						15.3	4.0	34.0			V 34.000	5
ALA	308	14.7		3.3	7.3		9.3	8.0		14.0	5.3		0.7	0.7	17.3	13.3	4.0	2.0				Q 17.333	2
LEU	309	6.7					0.7		8.0		58.0							9.3	16.7		0.7	L 58.000	5
GLN	310	6.7		1.3	14.0	0.7		0.7		7.3	3.3		1.3		14.0	34.0	2.7	1.3	4.7	8.0		R 34.000	6
GLY	311	66.7	0.7				12.7							4.0			16.0					A 66.667	7
ALA	312	66.0		2.0			3.3				1.3						10.0	4.7	12.7			A 66.000	7
ASP	313	13.3		7.3	26.7		2.7		8.0	1.3	0.7		0.7		3.3	19.3	5.3	8.0	3.3			E 26.667	3
ALA	314	62.7	0.7		2.7		0.7				23.3						2.0	0.7	7.3			A 62.667	7
ALA	315	2.0						1.3	0.7		94.7	0.7			0.7							L 94.667	9
ALA	316	60.0					0.7		1.3		11.3		0.7				2.7	12.0	10.7		0.7	A 60.000	6
ARG	317	1.3		64.0	14.0		0.7	0.7		1.3			5.3		2.7	7.3	0.7	1.3	0.7			D 64.000	5
GLU	318	10.0		2.0	10.7			4.0	2.0	8.0	5.3		2.0		10.7	34.0	6.0	2.0	2.7		0.7	R 34.000	1
ALA	319	86.0					1.3										2.0	2.0	8.7			A 86.000	8
ALA	320	51.3		0.7	0.7		26.0		1.3		4.7	0.7	3.3		1.3	1.3	1.3	3.3	4.0			A 51.333	4
HIS	321	19.3		10.0	16.0		3.3	6.0	1.3	1.3	6.7		1.3		7.3	18.7	4.7	0.7	2.7		0.7	A 19.333	1
LEU	322	37.3			14.0		0.7	0.7	1.3	4.7	9.3	1.3			10.7	6.7	6.0	4.0	3.3			A 37.333	2
LEU	323	2.7				12.7	2.0		11.3		48.7	2.0			0.7				18.7	0.7	0.7	L 48.667	4
GLN	324	1.3	0.7	38.7	9.3		0.7	0.7			2.0	0.7	0.7		32.0	2.7	6.0	2.7	1.3	0.7		D 38.667	4
THR	325	35.3	0.7	6.7	10.0		4.7	4.7	0.7	4.7	0.7		4.0		12.7	4.7	3.3	5.3	0.7	1.3		A 35.333	1
VAL	326	64.7	0.7		0.7		5.3	1.3	6.0		10.0						0.7	4.0	6.7			A 64.667	7
TRP	327	2.9	0.7	0.7		7.2		8.6	2.9		21.6		0.7			0.7	1.4	1.4	1.4	40.3	9.4	W 40.288	4
ASP	328	35.3		15.8	12.2	1.4	4.3	2.2	0.7		4.3		3.6	0.7	4.3	7.2	7.2		0.7			A 35.252	1
LYS	329	6.5	0.7	5.0	2.2	1.4		0.7	3.6	22.3	10.1		1.4	2.2	10.8	27.3	2.9	1.4	1.4			R 27.338	1
GLY	330	3.4		2.0	7.4		62.2	0.7		2.7				2.0	2.7	16.2	0.7					G 62.162	4
ASP	331	17.6		16.2	14.9	1.4	2.7	4.7		1.4	2.0		2.0	12.8	2.0	6.1	6.1	4.1	1.4	4.7		A 17.568	1
ALA	332	34.7		20.7	6.7		9.3	1.3		3.3	2.0		7.3		3.3	0.7	9.3	1.3				A 34.667	1
LEU	333					0.7			4.0		73.3			2.0				0.7	19.3			L 73.333	7
THR	334	1.3		3.3	1.3		3.3			0.7		0.7	1.3				12.0	76.0				T 76.000	7
PRO	335	49.3		9.3	18.7	4.0	0.7	1.3						7.3	0.7	1.3	2.0	0.7	1.3	2.0	1.3	A 49.333	4
GLU	336	16.0		22.7	29.3		2.0	1.3	<u> </u>				1.3	0.7	9.3	12.0	2.0	2.0	1.3			E 29.333	1
ASP	337	9.3	4.0	8.7	43.3	0.7	2.0	07	0.7	1.3	0.7	0.7	1.3		18.7	2.0	7.3	3.3	4.0	0.0	4.0	E 43.333	4
ARG	338	6.0	1.3			0.7	74.0	0.7					0.7			84.7	0.7		1.3	3.3	1.3	R 84.667	9
GLT	339	27.3		6.0	60.0		/1.3	0.7	0.7	2.2	1 2		0.7		0.7	0.2	2.0	0.7	2.0			G / 1.333	8
U EU	240	12.0	4.0	0.0	00.0	12		2.0	0.7	3.3	20.7				2.7	9.5	2.0	5.2	2.0			E 00.000	4
MET	242	74.0	4.0		33	1.0	0.7	2.0	1.5		20.7	13			0.7		18.7	1.3	0.7			A 74 000	4 0
	3/12	14.0	0.7		73		0.7		34.0		14.0	2.0					10.7	27	35.3			V 35 333	1
IYS	344	48.7	0.7	40	8.7			13	04.0	13	10.0	2.0				8.0	53	6.0	0.7	53		A 48 667	5
VAI	345	67	0.1	1.0	0.1		13	1.0	41.3	1.0	1.3					0.0	0.7	2.0	46.7	0.0		V 46 667	6
SER	346	68.0		33		27	27		11.0		1.0		07	07			14.0	2.0	10.1		8.0	A 68 000	7
GLY	347	38.7			20.7		1.3			0.7		2.0	••••	•	6.0		10.7	19.3	0.7			A 38.667	7
VAL	348	84.7					0.7		0.7		3.3						1.3	2.0	7.3			A 84.667	8
LYS	349	0.7			3.3					86.7			6.0			3.3						K 86.667	9
ALA	350	14.7	0.7						10.0		2.7				2.7		1.3	3.3	60.7		4.0	V 60.667	6
LEU	351	22.0				2.7		6.0	2.0		16.7	1.3	2.0		6.7	7.3	2.0	2.7	25.3	1.3	2.0	V 25.333	4
ALA	352	68.0	0.7						2.0								11.3	15.3	2.7			A 68.000	7
THR	353	12.7					6.7	12.7	2.0				2.0		3.3		13.3	43.3	4.0			T 43.333	7
ASN	354	0.7		17.3	12.7		0.7	2.7		13.3			6.7		4.7	40.0	1.3					R 40.000	4
ALA	355	31.3	0.7	2.7					6.0		3.3	0.7	2.0		1.3		0.7	21.3	30.0			A 31.333	5
ALA	356	46.0					32.0										18.7	1.3	2.0			A 46.000	6
LEU	357								2.7		80.0		2.7		3.3			1.3	10.0			L 80.000	8
ASN	358	3.3		33.3	40.7	2.0		2.7		1.3	1.3	0.7	2.7		2.0	8.7		0.7			0.7	E 40.667	4
ILE	359	10.7							27.3		7.3		1.3				2.7	3.3	47.3			V 47.333	4
SER	360	15.3	6.7				12.7						0.7	0.7			15.3	48.0	0.7			T 48.000	5
SER	361	9.3	0.7	0.7	8.0		1.3	3.3					10.0		6.7		49.3	10.0	0.7			S 49.333	5
GLY	362	12.0		2.0	8.0		11.3			11.3			3.3		9.3	40.7	0.7	1.3				R 40.667	5
VAL	363	3.3							30.0		32.0	10.0							24.7			L 32.000	5
PHE	364					88.7					6.0										5.3	F 88.667	8

0111	205			16.0	70.0										6.0							F 70 000	0
	300	10.7		16.0	78.0	2.0	0.7		67		20.7	0.7			1.0	0.7		0.7	52.2	0.7		E 78.000	8 6
	267	10.7	5.2			2.0	1.2		0.7		47	20.0			1.5	0.7	4.0	10.7	53.3	0.7		V 00.000	6
	307	10.0	5.5				1.0		Z.1		4.7	20.0			4.0		4.0	42.7	5.5			0 100 000	0
	300	00.0					100.0							0.7			67	11.0				G 100.000	9
	309	1.2		0.7			1.3	0.7		0.7	0.7			0.7	0.7	00.0	0.7	0.7				A 00.000	0
	370	1.3		0.7			0.7	0.7		2.1	0.7				0.7	00.0	4.0	1.2			0.7	K 00.000	0
	3/1	37.3					4.7				1.2						30.0	70.0	0.7		0.7	A 37.333	/
אר ופ	372	26.0		0.7			0.7	14.0		2.0	0.0		12	0.7	12	0.7	16.7	16.0	2.0			1 70.000	5
0	373	30.0		0.7	1.2		4.0	14.0	0.7	2.0	0.0		1.0	1.2	1.0	7.2	10.7	6.7	2.0			A 30.000	3
	275	10.2		4.7	2.0		4.0	2.2	0.7	22.0	2.0		0.7	0.0	1.3	12.0	10.0	0.7	0.7			A 37.333	4
10 /D	375	27		2.1	2.0	67	0.0	73		22.0	36.0		0.7	0.0	0.7	2.0	10.0	1.2	14.0		25.3	L 36 000	2
	370	4.7	0.7		1.5	0.7	673	0.7			30.0		10.7		0.7	16.0		1.5	14.0		20.0	C 67 333	7
	3/1	4.7	0.7			27.2	07.5	0.7			55.2	12	10.7			10.0			12		4.0	1 55 222	5
пс ер	270			02.2		31.3		6.0			55.5	1.5	0.7						1.5		4.0	L 00.000	0
	200			33.3				0.0	17		33		0.7			Q0 7			07			D 90.000	9
HE	300					60.7		20.0	4.1		0.0					30.7			0.7		10.2	F 60 667	e B
	301					00.7		20.0												00.3	13.3	1 00.007	0
	302					0.7										100.0				35.3		P 100 000	9
SN	303			16.0									8/1 0			100.0						N 84 000	9
ΔI	385	32.7		10.0					8.0		24.0		04.0		0.7				34.7			V 3/ 667	7
	286	52.1							0.0		24.0				0.7	100.0			J 4 .7			P 100 000	0
	297								2.0		0.7					100.0		82.7	14 7			T 82 667	9
	388					4.0		80.0	2.0		6.0				03			02.1	14.7		0.7	H 80.000	9
10 ED	280					4.0		00.0			0.0				9.0		15.3	847			0.7	T 8/ 667	9
	200										04.0						15.5	2.0	4.0			1 04.007	9
	390		0.7					96.7			54.0					07		2.0	4.0		2.0	H 96 667	9
SD	302		0.7	QN 7	27			50.7					6.0			0.7			0.7		2.0	D 90 667	9
	392			50.7	2.1								0.0	98.7	0.7		07		0.7			P 98 667	9
ΔΙ	394	10 1							12 1		20.1			0.7	0.1		0.1	13	55.7			V 55 705	6
FR	395	23.5		42.3	74	47		07			2011			27	20	8 1	47	0.7	3.4			D 42 282	7
YR	396	20.0		12.0				5.4						1.3	2.0	0.1	1.7	0.1	0.7	81	84.6	Y 84 564	, 8
YS	397							0.1		85.2				1.0		14.8			0.1	0.1	01.0	K 85 235	9
F	398	16 1			07	07		07	14.8	47	28.9		6.0		27	67	13	27	10 1		40	1 28 859	3
<u>ـــ</u>	399	27			0.1	0.1		5.4	0.7	87	27		0.7		15.4	61.1	0.7	0.7	0.7		0.7	R 61 074	6
SP	400	4.0		25.5	54 4		07	6.7	0.1	0.1	0.7		3.4		0.7	01.1	0.1	3.4	0.7		0.1	F 54 362	8
Δ1	401			20.0	•		0.1	•	19.5		37.6		0		•			•	43.0			V 42 953	7
i Y	402						100.0		10.0		01.0								10.0			G 100 000	9
YS	403	74		21.5	13 4					2.7	0.7		94		5.4	34 2	1.3	2.7	13			R 34,228	4
IS	404	0.7		20		15.4		18 1					v . 1		.	VE				40.3	25.5	W 40 268	4
HR	405	41.6			1.3	10.7			07		10 1	0.7			4.7	1.3		5.4	20.1	.0.0	34	A 41.611	5
EU	406					0.7			1.3		95.3							0,7	2.0		2.1	L 95.302	9
SN	407	0.7		3.4	1.3			1.3	1.3	2.0	12.8		43.0			3.4	7.4	23.5				N 42.953	5
LY	408	1.3		14.1	3.4		60.4	3.4		2.0			4.0		5,4	6.0	1.3	20.0			0.7	G 60,403	1
LN	409	9.4		2,7	25.5		- • • 1	1.3	3.4	5,4	0.7		1.3	0.7	12.8	12.1	2.7	16.1	6.0		2.1	E 25,503	1
YR	410	6.1			0.7	7.5		8.8	10.2	1.4	21.8			4.8		9.5	0.7		13.6	1.4	13.6	L 21,769	1
20	411	v . 1						0.0			20			100.0		0.0						P 100.000	9
E	412	10.8		5.9	36.3			2.9	5.9	8.8	2.0		2.0	2.0	1.0	2.0	2.9	13.7	3.9			E 36.275	1
20	413	2.2				1.1		1.1			-			94.6		-	1.1					P 94,565	8
LY	414	2.6		1.3			11.8						2.6			3.9	39.5	38.2				S 39.474	6
HE	415					70.2	2.1		4.3		4.3								2.1	17.0		F 70.213	6
HR	416																	6.5			93.5	Y 93.548	8
ER	417																100.0					S 100.000	6*

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